On the effect of the number of tests and their time of application in tracing policies against COVID-19. ⋆

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Abstract: In this paper we explore the effect of the number of daily tests on an epidemics control policy purely based on testing and selective quarantine, and the impact of these actions depending on the time their application starts. We introduce a general model incorporating a stochastic disease evolution, a particular weighted graph representing the population, and an optimal contact tracing strategy to allocate available tests. Simulations on a community of 50'000 individuals show that the evolution of the epidemic produces a clear non-linear response to the variation of the number of tests used and to the starting time of their application. These results suggest that not only a minimum number of tests is necessary to obtain a positive outcome from the tracing strategy but also that there exists a saturation on the contribution of additional tests. The results also show that the timing in the application of the measures is as important as the measures themselves and that an excessive delay can be hardly overcome.

Keywords: COVID-19, Modeling, Dynamics and control, Resource allocation, Monitoring.

1. INTRODUCTION

Since the start of the COVID-19 epidemic, many researchers and governments have studied the use of different strategies to ensure health safety while trying to lower the social costs associated to these measures (Viner et al., 2021). In this regard, the use of total lockdowns is currently seen as a last resort, backed by studies showing their harm not only to economy (Joshi et al., 2020) but also to mental health (Rossi et al., 2020). Generally, efficient strategies can be described as the ones that allow the containment (or total eradication if possible) of the epidemic while maximizing the social, economical, and psychological conditions of the citizens. These results can be achieved by applying focused measures, e.g. targeted quarantine. However, due to the relevant number of asymptomatic and pre-symptomatic transmissions of COVID-19, their effectiveness strongly depends on the testing (Matukas et al., 2020).

Accordingly, during the first stages of the COVID-19 epidemic, before the production of any vaccine, one of the main limiting factors to better handle the spread of the disease was precisely the limited number of available tests. This issue made the testing and tracking of the population an obvious problem of resource allocation concerning the use of available tests and associated quarantine policies.

Mostly sparked by the COVID crisis, the scientific community has produced a number of works tackling the problem of how to use efficiently a limited number of tests and how to design the associated control policies. Berger et al. (2020) propose a policy based on conditional quarantine and random testing. Kasy and Teytelboym (2020) present a trade-off strategy between quarantine and testing which is implemented by defining a threshold based on the infection probability and related to the cost of testing or quarantining an individual. Niazi et al. (2020) compute the number of tests that has to be used each day in order to minimize the peak of active cases. Ely et al. (2021) study how to allocate different kinds of tests with different accuracies in order to minimize a user-defined social-economical cost. Pezzutto et al. (2021) propose to test individuals based on an approximate estimation of the probability of being infected.

Following WHO indications, during the COVID19 pandemic most countries implemented similar contact tracing strategies. Contact tracing has been proved to be very effective in some countries (Kendall et al., 2020) but insufficient in others (Todd, 2020; Baker et al., 2020). Recent works have explored the limits and feasibility of contact tracing. For instance, Hellewell et al. (2020) show through mathematical modelling that for a basic reproduction number of 2.5, in the idealized situation where asymptomatic individuals do not transmit the infection, at least the 70% of contacts of a known positive have to be tested. Similar outcomes have been obtained by Bradshaw et al. (2021) where it is suggested that bidirectional tracing is essential to overcome the lack of perfect knowledge of the contacts. Moreover, Ferretti et al. (2020) show that without a quick and accurate contact tracing the control of the epidemic with no additional measurements is unfeasible.

The aforementioned works provide useful insights on the capabilities and weaknesses of contact tracing. However a number of important aspects have not been considered, yet. Firstly,

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existing works do not explore the relationship between number of tests carried out daily and the expected epidemic evolution. Secondly, the effects of the starting time of the testing campaign are usually not taken into account.

In order to evaluate these aspects, the first step is to select an adequate model to monitor the evolution of the epidemic. As shown by several new models tailored for the COVID-19 case (Giordano et al., 2020), compartmental models have been proved to provide accurate results on the evolution of the epidemic. However, compartmental models assume by nature a population homogeneously distributed in which individuals are randomly mixed. This assumption however does not inform about the granular distribution of the disease and might be a problem when evaluating aspects involving the spatial distribution of a population in an epidemic, which is a fundamental aspect of contact tracing strategies.

We believe that to model the granularity of the transmission of a disease, network diffusion models provide a better description of the distribution of the population and allow the identification of critical clusters of the spreading. Several works present in the literature apply this idea to complex network topologies (Keeling and Eames, 2005; Li et al., 2014). In these models, the population is represented by a graph where the individuals are the nodes and their interactions are modelled by the edges of that graph. This representation allows to model selective testing and quarantine policies, e.g. by removing the connections of certain individuals with the rest of the population (Nowzari et al., 2015), as well as time-varying interactions. However, these works usually consider unweighted graphs, so that the underlying assumption is that all the interactions have the same probability of transmitting the disease. This approach works well for certain applications but it is not able to capture the differences between interactions that are fundamental in order to implement contact tracing strategies. In fact, not all contacts of a known positive have the same probability of being infected and, when the number of tests is limited, it is important to distinguish between close and distant contacts.

In this paper, we introduce a general model based on a heterogeneous complex network of interactions to study contact tracing policies against COVID-19. More specifically, the infectious progression is represented through three logical states Susceptible, Infected, and Removed. The population is modelled by a weighted graph whose weights are set as the probability of transmission of the disease, and the contact tracing strategy is formulated as an optimal allocation problem. We study, through accurate simulations, the effects of contact tracing for a same population in function of the number of tests and of the timing at which the policy is initiated. The aim of this paper is to provide some insight on the use of contact tracing strategies in non-homogeneous structures similar to real population distributions. In particular we show how the evolution of the epidemic produces a clear non-linear response to the variation on the number of tests used and to the timing of the application of the measures. We believe that these results present important insights and guidelines concerning the management of epidemics.

The paper is structured as follows. In Section 2 we introduce our epidemic model together with the modelling of a contact tracing policy. Section 3 provides several simulations and discussions for different number of tests and for different dates of applications of the measures. Section 4 concludes the paper with a discussion of the results and on future works.

2. MATERIAL AND METHODS

2.1 Disease Model

Consider a population of N individuals where a disease is spreading. For each fixed day t, to each individual i it is associated a logical state $\xi_i(t) \in \{S, I, R\}$ defined as

- S - susceptible, the individual is healthy and was never infected before, so it is susceptible of being infected;
- I - infected, the individual is infected and can infect others;
- R - removed, the individual cannot be infected because it was infected in the past.

We introduce the transmission variable $T_{ji}(t) \in \{0,1\}$ which takes the value $T_{ji}(t) = 1$ if the infection is transmitted from j to i between day t and day $t+1$ *given that* the individual j was infected and the individual i was susceptible. Mathematically, $T_{ji}(t)$ is a Bernoulli random variable with mean $w_{ji}(t)$, where

$$w_{ji}(t) = \mathrm{P}\left(\xi_i(t+1) = I | \xi_i(t) = S, \xi_j(t) = I\right). \tag{1}$$

We assume that $T_{ji}(t)$ is independent of $T_{mn}(k)\ \forall m,n,k \neq i,j,t$ and of the initial state $\xi_n(0)\ \forall n$. The mean values are symmetric, i.e. $w_{ij}(t) = w_{ji}(t)$. For any pair i,j of individuals that have no contacts $w_{ij}(t) = 0$.

We denote with $u_i(t) \in \{0,1\}$ the binary stochastic input representing the stochastic contagion event at day t. This variable takes the value $u_i(t) = 1$ if the individual i has been infected between day t and day $t+1$, and $u_i(t) = 0$ otherwise. Based on the description of $T_{ji}(t)$, the variable $u_i(t)$ is defined as

$$u_i(t) = 1 - \prod_{j:\,\xi_j(t)=I} (1 - T_{ji}(t)). \tag{2}$$

Note that $u_i(t)$ can be equal to 1 even if $\xi_i(t) = I$ or $\xi_i(t) = R$. However, in that case, $u_i(t)$ has no effect on the state of individual i.

The recovery is also modelled as a random variable to capture the uncertainty of the recovery process. We denote as $r_i(t) \in \{0,1\}$ the binary stochastic variable representing the stochastic recovery event at day t. This variable takes value $r_i(t) = 1$ if the individual i becomes removed between day t and day $t+1$, and $r_i(t) = 0$ otherwise. We model $r_i(t)$ as a Bernoulli random variable with mean λ_i constant over time. Moreover, $r_i(t)$ is independent of $r_j(k)\ \forall j,k \neq i,t$, of $T_{mn}(k)\ \forall m,n,k$, and of the initial state $\xi_n(0)\ \forall n$.

The state of each individual evolves as follows

$$\xi_i(t+1) = \begin{cases} S & \text{if } \xi_i(t) = S \text{ and } u_i(t) = 0 \\ I & \text{if } \xi_i(t) = S \text{ and } u_i(t) = 1 \\ & \quad \text{or if } \xi_i(t) = I \text{ and } r_i(t) = 0 \\ R & \text{if } \xi_i(t) = I \text{ and } r_i(t) = 1 \\ & \quad \text{or if } \xi_i(t) = R. \end{cases} \tag{3}$$

The state evolution of each individual is depicted by Fig 1.

We assume the system to be partially observable as symptomatic individuals are only a small percentage of the infected population. The appearance of symptoms is modeled as a binary stochastic variable denoted by $e_i(t) \in \{0,1\}$. This variable takes the value $e_i(t) = 1$ if the individual i is infected and shows symptoms between day t and day $t+1$, and $e_i(t) = 0$ otherwise. We model $e_i(t)$ as a Bernoulli random variable with mean θ_i constant over time. We assume that $e_i(t)$ is independent of $e_j(k)$ and of $r_j(k)\ \forall j,k \neq i,t$, of $T_{mn}(k)\ \forall m,n,k$, and of $\xi_n(0)\ \forall n$.

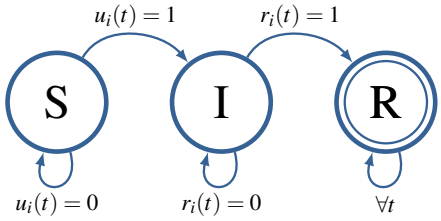

Fig. 1. Evolution of the state $\xi_i(t)$ of individual i.

This model can be easily extended to include other states of the infectious progression, e.g. Exposed, regarding individuals that are infected but are still not infectious nor detectable through tests, as well as other phenomena like the probability of rebecoming Susceptible after a Recovery. Please refer to Giordano et al. (2020) for a general set of possible states modelling the COVID-19 evolution.

2.2 Population model

Based on the proposed transmission model, the population can be represented through a weighted undirected time-varying graph $G(t) =< V, E(t) >$, where each node $v_i \in V$ represents an individual, an edge between two nodes $(i, j) \in E(t)$ represents an interaction between the individuals i and j at day t, and the weight is set equal to the probability of transmission $w_{ij}(t)$.

Contrary to usual models of epidemic spreading over complex networks, the presented population graph is weighted, which allows the distinction between close and distant contacts. In this regard, while network topologies that capture the presence of connections between individuals have been widely studied, to date, how to model the weight of these connections is still an open problem. In this work, we propose a multi-layer structure resembling the population structure. A layer $\mathscr{L}_n$ is defined as a set of disjoint, complete, weighted sub-graphs, i.e. $\mathscr{L}_n = \bigcup_k G_k^n$ where, for any k, G_k^n is a weighted graph $G_k^n =< V_k^n, E_k^n >$ with $V_k^n \subset V$, $\bigcup_k V_k^n = V$, $V_k^n \cap V_\ell^n = \emptyset$, and $w_{ij}^n > 0$ for any $i, j \in V_k^n$. Each graph in each layer is randomly generated. In this work, each set V_k^n is obtained by random extraction without replacement from V, the size is obtained from an integer uniform random variable, so $|V_k^n| \sim \mathscr{U}([N_{\min}^n, N_{\max}^n])$, and the weight is obtained from a real-valued uniform random variable $w_{ij}^n \sim \mathscr{U}([w_{\min}^n, w_{\max}^n])$ for $(i, j) \in E_k^n$. Layers are then combined as $G = \bigcup_n \mathscr{L}_n$ with weights $w_{ij} = 1 - \prod_n (1 - w_{ij}^n)$. Finally, the graph $G(t)$ has the same topology of G and weights $w_{ij}(t) = w_{ij}$ if neither i nor j are in quarantine at day t, and $w_{ij}(t) = \sigma w_{ij}$ otherwise, where $\sigma \in [0, 1)$ is a suitable scaling factor. In this way, quarantine is not an additional state of the individual but it is captured by the edge weight.

Note that, at each layer, sub-graphs can consist of only one node if $N_{\min}^n = 1$, i.e. some nodes may not have any connection on some layers. With this model, by opportunely setting the parameters $N_{\min}^n$, $N_{\max}^n$, $w_{\min}^n$, $w_{\max}^n$, it is possible to model different kinds of interaction: for instance, the layer of households can be modelled through a small $N_{\max}^n$ (e.g. around 6), and with a high (w.r.t. other layers) $w_{\max}^n$. Layers with $N_{\max}^n = 2$ can be used to model completely random connections. In line of principle, also other distributions of $|V_k^n|$ and w_{ij} can be chosen. Moreover, thanks to this layer structure, more complex time-varying combinations of sub-graphs can be considered. In particular, it is possible to model the fact that interactions between individuals (partially) change on a daily basis by appropriately activating only some of the sub-graphs.

2.3 Control action: contact tracing and quarantine

In this work, we consider the case where the control of the system is carried out through testing of individuals and targeted quarantine actions. In particular, we assume that a finite number T of tests is available each day. We consider tests for current infection, like PCR tests, namely tests whose outcome indicates if the individual is infected or not, while it is not possible to distinguish between susceptible and recovered. Based on the high accuracy of PCR tests for COVID-19, we assume that the tests are ideal, so neither false positives nor false negatives are present. Quarantine is based only on the test outcomes, i.e. only individuals that have been tested positive or close contacts of a known positive are quarantined, while generalized lockdowns are excluded. We assume that also quarantine is ideal, so infections from (and to) individuals that are in quarantine are excluded.

We introduce the binary selection variable $\alpha_i(t)$, that is equal to 1 if the individual i is tested at day t and 0 otherwise. In order to mathematically describe the control action, we introduce the following sets. Let $T_{t_1:t_2}$ be the set of individuals tested from day t_1 and day t_2

$$T_{t_1:t_2} = \{i : \exists \tau \text{ s.t. } \alpha_i(\tau) = 1, t_1 \le \tau \le t_2\}.$$

Let $D_{t_1:t_2}$ be the set of positive detected from day t_1 and day t_2

$$D_{t_1:t_2} = \{i : \exists \tau \text{ s.t. } \alpha_i(\tau) = 1 \text{ and } \xi_i(\tau) = I \text{ OR } e_i(\tau) = 1,\ t_1 \le \tau \le t_2\}.$$

For the sake of simplicity, we denote $T_{t:t} = T_t$ and $D_{t:t} = D_t$.

Test allocation is based on the tracing of relevant contacts of positive detected individuals. We now introduce a general model to describe this mechanism. We assign to each pair of individuals i and j a *correlation metric* at day t defined in general as

$$\omega_{ij}(t) = f(w_{ij}(t), \dots, w_{ij}(0)) \tag{4}$$

where $f : \mathbb{R}^t \to \mathbb{R}$ is a suitable function. Then, at day t, available tests are allocated to individuals with the highest correlation metric with the individuals detected the previous day. The resulting optimal allocation problem, referred to as optimal contact tracing, is mathematically formulated as

$$\begin{aligned} \alpha(t) = \arg\max_{\alpha} & \sum_{j \in D_t} \sum_{i=1}^{N} \alpha_i \omega_{ji}(t) \\ & \textstyle\sum_{i=1}^{N} \alpha_i \le T \\ & i \notin T_{t-\Delta_T:t} \\ & i \notin D_{0:t} \end{aligned} \tag{5}$$

where $\alpha = (\alpha_1, \dots, \alpha_N)$, $\alpha_i \in \{0, 1\}$ for any i, T is the number of tests available, and Δ_T is a suitable time window.

This model can capture the rudimentary contact tracing implemented in most countries. In particular, $f(\cdot)$ can be fixed as an indicator function that is equal to 1 if $\hat{w}_{ij}(\tau) > w$ for at least a τ in $t - \Delta < \tau < t$, where $\hat{w}_{ij}(\tau)$ is a rough estimate of $w_{ij}(\tau)$. Differently, in a ideal scenario, $w_{ij}(\tau)$ is known (possibly through advanced contact tracing apps) and more elaborated functions $f(\cdot)$ can be proposed. In particular, in this work, we consider

$$f(w_{ij}(t), \dots, w_{ij}(0)) = 1 - \prod_{\tau=t-\Delta}^{t} (1 - w_{ij}(\tau)). \tag{6}$$

where Δ is a suitable time window. Clearly, the detection capabilities of the test allocation policy strongly depend on the function $f(\cdot)$.

Quarantine is driven by the outcomes of the tests or known symptomatic individuals. In particular, for each $i \in D_t$, we consider to put into quarantine the L individuals for which the correlation metric $\omega_{ij}(t)$ is the highest and that have not been detected in the past, i.e. $j \notin D_{0:t}$, as they are either already in quarantine or known removed individuals. Mathematically, if individual j is in quarantine, $w_{ij} = w_{ji} = 0$ for any i. We assume that quarantine lasts for Δ_Q days without a test on exit.

Based on the policy above, the closest contacts of each detected individual are both quarantined and tested. However, when the number of new detected is high, less contacts can be tested: in particular, if $L > T/|D_t|$, some individuals are quarantined but not tested. In that case, quarantine is implicitly used to overcome missing tests. Note that, in this setup, also individuals that are negative but close contacts of a positive are quarantined. This is a common preventive measure in many countries. Note that, in the presented setting, also time-varying number of daily tests can be considered.

3. SIMULATIONS AND RESULTS

The simulations are carried out for a closed population of $N = 50'000$ individuals. We study two cases: the variation in the number of tests and the variation on the time of application of the measures.

The disease model parameters are set as $\lambda_i = \lambda = 1/14$ and $\theta_i = \theta = 0.0175$. They correspond to an average recovery time of 14 days and an average value of 20% of infected individuals that show symptoms during the course of the infection. This value estimates that a high percentage of infected is asymptomatic (Petersen and Phillips, 2020) and that not all symptomatic individuals communicate their state.

The graph representing the population is modeled using 5 main layers: $\mathscr{L}_1$ represents households, $\mathscr{L}_2$ represents coworkers, while $\mathscr{L}_3, \mathscr{L}_4, \mathscr{L}_5$ represent small groups of friends. We set

$$N^1_{\min} = 1,\ N^1_{\max} = 8,\quad w^1_{\min} = 0.75w,\ w^1_{\max} = 1.25w$$
$$N^2_{\min} = 1,\ N^2_{\max} = 40,\ w^2_{\min} = 0.25 \cdot 0.75w,\ w^2_{\max} = 0.25 \cdot 1.25w$$
$$N^n_{\min} = 2,\ N^n_{\max} = 8,\quad w^n_{\min} = 0.2 \cdot 0.75w,\ w^n_{\max} = 0.2 \cdot 1.25w$$

for $n = 3,4,5$ for a given parameter w. Other random interactions with average weight of $0.1w$ are added. We propose to set w such that the epidemic evolution with $T = 0$ fits the evolution of SIR model with basic reproduction ratio $R_0 = 2$. The value chosen aims at reproducing the spread of the COVID-19 when only very basic social distancing measures are adopted (D'Arienzo and Coniglio, 2020).

Test allocation is based on the contact tracing formalized in Sec. 2, with $\Delta = 15$. The quarantine policy is set to the quarantine of $L = 5$ individuals per positive test for $\Delta_Q = 14$ days.

Initial conditions $\xi(0)$, i.e. which individuals are initially infected, are stochastically generated in each simulation. Each simulation assumes that 0.05% of the population is initially infected. It is also assumed that not all connections between individuals are known in the search of closed contacts and that an average of 10% of contacts is completely unknown.

Simulations cover a time span of 300 days. The depicted data correspond to the averaged results of 100 simulations performed for each scenario. In each simulation, the initially infected individuals and the structure of the network are randomly generated.

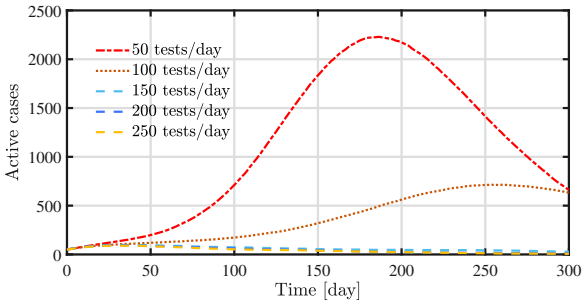

Fig. 2. Evolution of the number of active cases.

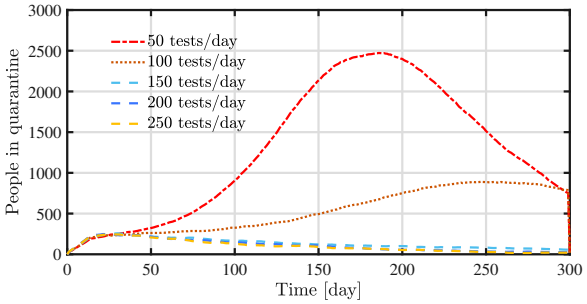

Fig. 3. Evolution of the number of people in quarantine.

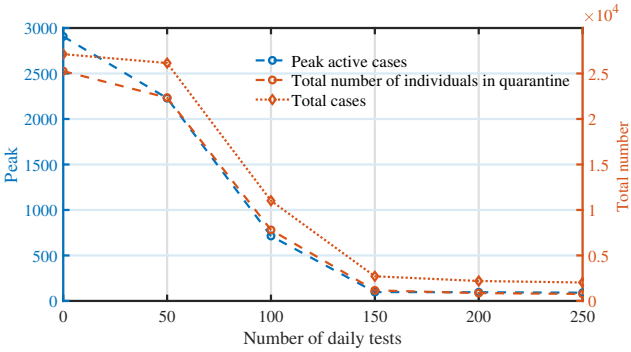

Fig. 4. Evolution of the performance of contact tracing with respect to the number of tests.

3.1 *Variation in the number of tests*

To study the variation with respect to the number of tests, we assume a testing capacity within the range of 0.1% up to 0.5% of the population daily tested. The upper limit is obtained based on the values reported by South Korea or USA in December 2020, `https://covidtracking.com/data`.

Figure 2 depicts the evolution of active cases. This plot shows the great difference in effectiveness when the number of daily tests decreases to 100 (0,2% of the population). In particular, the figure depicts the high non-linearity in the performance of a strategy like contact tracing. While the outcomes of the simulations between 150 and 250 tests (0.3% and 0.5% of the population, respectively) are almost identical, a reduction to 100 or 50 tests ($0.2\% - 0.1\%$) suddenly degenerates to a situation that is out of control.

The evolution of the number of people in quarantine is depicted in Fig 3. It is worth to note that the use of more tests, which provides a lower number of cases, does not require a higher number of quarantined individuals as the spread of the infection is never out of control.

The evolution of three important indicators, i.e., peak of active cases, total number of infected individuals, and total number of individuals in quarantine, with respect to the number of daily tests is depicted in Fig 4. It suggests that measures aiming at improving the test capacity are cost-effective only up to a "threshold level" (in this case 150 tests/day) after which extra investments in testing capabilities have a limited effect on the epidemic.

3.2 Delay on the application of measures

In this subsection we compare the evolution of the epidemic when the same measures (same strategy and testing capacity) are applied with different time delays. Simulations consider the same number of available tests, i.e. 250 per day (0.5% of the population), a number of tests that in the first subsection has been proved to be very effective. With respect to the timing of application, the scenarios go from *no delay* of action up to 50 days of delay w.r.t. to the appearance of the first infected individual.

In Fig. 5 we can observe the evolution in the number of active cases for the different scenarios. It can be seen that, in the case of 30 days of delay, the peak of active cases already surpasses the 500 infected individuals and it stays around that level for more than 100 days. This result shows that, even with a high number of daily tests, an excessive delay in the application of measures can dramatically affect the situation during various months. The previous subsection showed that 250 daily tests for the simulated conditions provided very good results and that a high efficiency in the control actions was already reached by 150 tests per day. However, even with this high margin in the testing capacity, Fig. 5 reveals that if the delay reaches 30 days, the peak of actives cases becomes very high.

Figure 6 shows the temporal evolution of the number of people in quarantine for the different cases. This plot shows the great number of people that needs to be quarantined after a late reaction despite the targeted approach of contact tracing.

To provide a better visualization of the effect of the delay, the evolution of the performance of the strategy with respect to postponement in the application of the measures is depicted in Fig. 7. From this figure it is clear that there exists a breakout point where all 3 indicators drastically increase, suggesting that the delay is too high to be compensated by the applied strategy.

3.3 Discussion of the results

A first important aspect that can be deduced from the simulations is that more testing does not necessarily imply more people in quarantine. In fact, the number of individuals in quarantine is much more influenced by the number of infected individuals than by the number of daily tests. Accordingly, testing more does not only imply to control better the epidemic, but also to limit the damage of the epidemic on the social and economical life of citizens.

Focusing on the response to the variation in the number of tests, it is very interesting to observe that this response is clearly non linear. It can be seen how a very small variation in the number of daily tests, with the same strategy and tracing knowledge, shows a rapid shift from situation under control to explosion in the number of cases. This high sensitivity to the number of tests and to the tracing capacity could explain

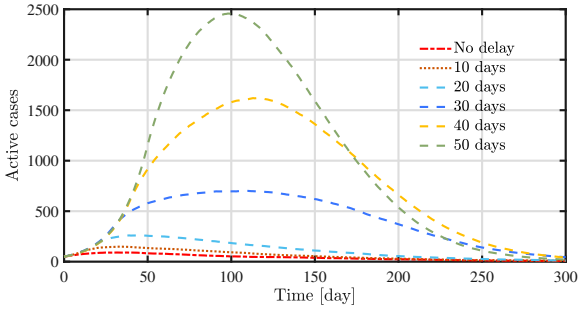

Fig. 5. Evolution of the number of active cases.

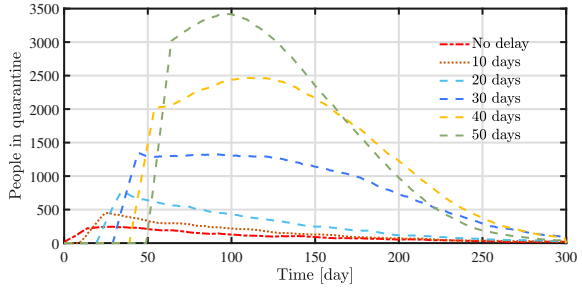

Fig. 6. Evolution of the number of people in quarantine.

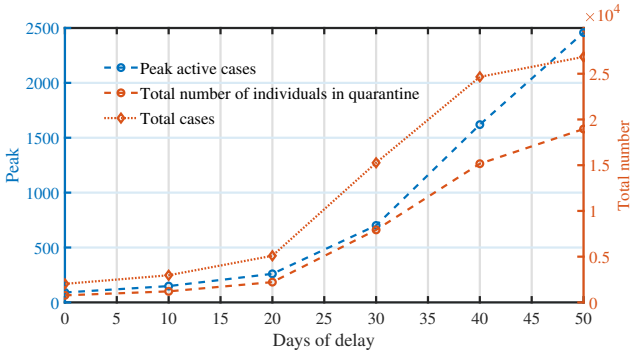

Fig. 7. Evolution of the performance of contact tracing with respect to the delay in the application of the measures.

the high variance observed in the outcome of similar strategies in different countries around the world. Additionally, the fact that there is a point where the contribution of additional tests becomes negligible suggests the existence of an optimal point regarding the number of tests and their efficiency in a contact tracing strategy.

For what concerns the effect of the delay in the application of measures, it must be noted that the delay is computed starting from the moment the first infected case appears in the population. Of course in several real-world scenarios it is unrealistic to have no delays, as decision makers must have the time to realize the situation, decide and communicate the policy to follow, and organize the logistics to implement it. However, this analysis gives a quantitative measure of the importance of making these operations as fast as possible and, whenever possible, to anticipate them before the actual outbreak, as every single day of delay counts. Along this line, these results encourage to maintain an aggressive contact tracing strategy also after a generalized lockdown, when promising indicators may entail less efforts in preemptive measures, or when vaccines start to

be less effective, due to new variants or because the immunity wanes.

Regarding the numerical simulations performed in this paper, it must be mentioned that the model used simplifies the period of incubation of the virus with respect to more complex models and considers a time-invariant use of the layers of the network. However, we believe that the graph-based network structure and the stochasticity of the model provide a realistic outcome and account for the high variability in the spreading and impact of the epidemic.

4. CONCLUSIONS

In this paper we provide a mathematical approach to model contact tracing and simulate its effect on a inhomogeneous population. We also analyze the efficiency of this kind of strategies with respect to the number of tests and the timing of application based on simulations on a realistic network. The results obtained in this paper suggest two very interesting facts: i) the evolution of the epidemic presents a clear non-linear response to the variation on the number of daily tests, and ii) the timing of application of the testing policy is as important as the policy itself.

We believe that these results can be helpful to understand the variation on the outcome of tracing strategies in different countries and at different moments of the pandemic.

Future works will focus on trying to mathematically define, if possible, the evolution of the epidemic based on the number of tests and the topology of the network. Additionally, a future line of research includes the improvement of the presented network model. The aim is to be able to adapt this model to more complex considerations regarding the transmission of a disease in order to obtain even more meaningful results.

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