

Project Report

Complex System and Network Science course

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Abstract. Viruses and epidemics have always been under the attention of scientists and never like nowadays has been highlighted the need and the importance of good measures to contrast these phenomena. The aim of this project is to study the evolution of the SARS-CoV-2 pandemic using a mathematical model and study possible actions to limit the epidemic spread like lockdown, social distancing, masks usage and contact tracing. Results show that prompt actions, cohesive behaviour and mixed strategies can lead to the reduction of the impact of the outbreak.

1 Introduction

Recorded history continuously documents the invasion of populations by infectious agents, some causing many deaths before disappearing, others reappearing in invasions some years later in populations that have acquired some degree of immunity, due to prior exposure to related infectious pathogens. As the movement of people, goods, and services across borders increases, the national health security is increasingly dependent on global health security. This statement highlights the link between emerging infectious disease threats that may not have available treatments or vaccines, and the security of the world's health since these diseases also know no boundaries and will easily cross borders. In this circumstances, adoption of countermeasures is critical for preventing, detecting and responding to disease outbreaks that may escalate into health emergencies. The purpose of this project is to study the evolution of the SARS-CoV-2 pandemic using a quarantine-isolation model and analyze possible actions to limit the epidemic spread like lockdown, social distancing, masks usage and contact tracing. The report is organized as follows: in **Preliminaries** there is a short introduction to the mathematical models used in epidemiology and to the method of contact tracing with graphs to trace contacts of possible infections; in the **Main Part** there is the explanation of the used model and how it has been implemented in NetLogo with all the parameters, this is followed by a first round of experiments with the variation of the model parameters only, then the countermeasures are introduced, explained and experiments are performed to see their effects.

2 Preliminaries

2.1 Epidemic models

Predictive mathematical models for epidemics are fundamental to understand the course of the epidemic and to plan effective control strategies. One commonly used model is the **SIR** model for human-to-human transmission, which describes the flow of individuals through three mutually exclusive stages of infection: susceptible (**S**), infected (**I**) and recovered (**R**). Let $S(t)$ denote the number of individuals who are susceptible to the disease, that is, who are not (yet) infected at time t . Let $I(t)$ denote the number of infected individuals, assumed to be infective and able to spread the disease by contact with susceptibles. Let $R(t)$ denote the number of individuals who have been infected and then removed from the possibility of being infected again or of spreading infection. Removal can be carried out either through isolation from the rest of the population, through immunization against the infection, through recovery from the disease with full immunity against reinfection, or through death caused by the disease. These characterizations of removed members are different from an epidemiological perspective but are often equivalent from a modeling point of view which takes into account only the state of an individual with respect to the disease. In many diseases, infectives return to the susceptible class on recovery because the disease confers no immunity against reinfection. We use **SIS** to denote this class of diseases with no immunity against reinfection, to indicate that the passage of individuals is from the susceptible class to the infective class and then back to the susceptible class. In addition to the basic distinction between diseases for which recovery confers immunity against reinfection and diseases for which recovered members are susceptible to reinfection, the **SIRS** class admits the possibility of temporary immunity. More complicated compartmental structures such as the **SEIR** and **SEIS** classes are also possible where an exposed (**E**) period is added between being infected and becoming infective.

2.2 Contact tracing using graphs

Graph theory has provided a lot of tools and mechanisms for describing networks, many of which have epidemiological applications. We can use an adjacency matrix, A , to describe the connections within a population, where $A_{ij} = 1$ if there is a connection such that infection could pass from individual i to individual j ; otherwise, $A_{ij} = 0$. The matrix A summarizes all connections within the network. Determining a complete network requires knowledge of every individual in a population and every relationship between individuals. For all but the smallest populations, this is an impractically time consuming task. Mainly, problems in building the graph concern data collection, but more fundamental is the question of how a network link is defined. If networks are to be used for epidemiological purposes, then connections should only be included if they describe relationships capable of permitting the transfer of infection.

One of the technique that can be employed to gather network information is **contact tracing** which aims to identify all potential transmission contacts from a source individual. This reveals a new set of individuals who might be infected and who can be the subject of further tracing effort. This method has been commonly applied not as a network evaluation device but as a control tool. In such case, the purpose of contact tracing is to identify asymptomatic infected individuals who can then be treated or quarantined. This means that the contacts of uninfected individuals are not sought, and thus only a subset of the full mixing network will be uncovered. Although a network uncovered via contact tracing is not complete and has biases, the network data obtained is of immediate epidemiological relevance.

3 Main part

3.1 A Quarantine Isolation Model

The model proposed is the SEQIJR, described in [1], for modelling an outbreak of a new disease, where no vaccine is available and the only control measures available are the isolation of diagnosed infectives and quarantine of people who are suspected of having been infected. The total population is partitioned into six states:

- **S**, susceptible (uninfected);
- **E**, exposed (asymptomatic infected, undetected);
- **Q**, quarantined (asymptomatic infected, detected);
- **I**, infected (symptomatic infected, undetected);
- **J**, hospitalized (symptomatic infected, detected);
- **R**, recovered (healed or dead).

The model used doesn't consider the difference between healed or deaths because the focus is more on the infection part of the outbreak. All the interactions among these states are ruled by the following assumptions which are also represented in Figure 1:

- Infected members may be infective with infectivity given by β ;
- Exposed members may be infective with infectivity reduced by a factor ϵ_E , $0 \leq \epsilon_E < 1$;
- Exposed members who are not quarantined become infective at rate κ_E ;
- Exposed members are quarantined at a proportional rate γ_Q in unit time;
- Infectives are diagnosed at a proportional rate γ_J per unit time and isolated;
- Quarantined members are monitored and when they develop symptoms at rate κ_Q they are isolated immediately;
- Quarantined and hospitalized members cannot transmit the infection anymore;
- Infectives leave the infective class at rate α_I ;
- Isolated members leave the isolated class at rate α_J .

The original SEQIJR model takes also into account that quarantine and hospitalization are not perfect but they only reduce the infectivity by a factor of ϵ_Q and ϵ_J respectively. While, in the model proposed, I assumed that the quarantine and hospitalization are perfect in a way that they don't allow further spreading of the infection and considering $\epsilon_Q = \epsilon_J = 0$. These assumptions lead to the

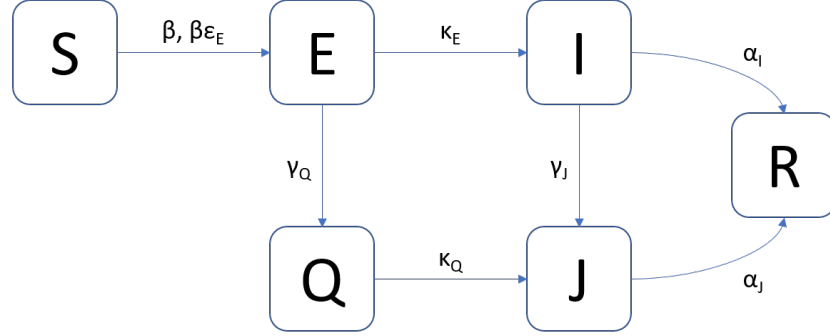


Fig. 1: Graphical scheme representing the interactions among different stages of infection in the proposed model

slightly simpler SEQIJR model

$$\begin{aligned}
S' &= -\beta S(\epsilon_E E + I) \\
E' &= \beta S(\epsilon_E E + I) - (\kappa_E + \gamma_Q)E \\
Q' &= \gamma_Q E - \kappa_Q Q \\
I' &= \kappa_E E - (\alpha_I + \gamma_J)I \\
J' &= \kappa_Q Q + \gamma_J I - \alpha_J J \\
R' &= \alpha_I I + \alpha_J J
\end{aligned}$$

3.2 NetLogo implementation

Individuals wander around the world in random motion. The whole world is adjustable in measure and is divided in regions by a number of yellow lines which is modifiable by the user. Upon coming into contact with an infected person, he or she has a chance of contracting the illness. An exposed individual shows symptoms and becomes infected after the given exposed time has elapsed. An infected individual recovers after the given recovery time has elapsed. The presence of the virus in the population is represented by the colors of individuals. Three colors are used: white individuals are uninfected, red individuals are infected and green individuals are recovered. Once recovered, the individual is permanently immune to the virus. A number of graphs are also plotted in this model: one showing the total percentage of individuals who have been infected or recovered

and the other the number of people that are susceptible, exposed, infected or recovered at any time step.

3.3 Using the model

The size of the world can be changed with the chooser **size-of-world** while the number of regions in the world can be modified with the choosers **rows** and **cols**. The **setup** button creates individuals according to the parameter values chosen by the user. Each individual has an **initial-infected** chance of being initialized as infected. Once the simulation has been setup, push the **go** button to run the model. It starts the simulation and runs it continuously until the button is pushed again or there are no more infected individuals. Each time-step can be considered to be in hours, although any suitable time unit will do. What follows is a summary of the sliders in the model:

- initial-people** (initialized to vary between 50 – 1000 people): the total number of individuals the simulation begins with;
- infection-chance** (0 – 100%): probability of disease transmission from one individual to another;
- exposed-reduction** (0 – 1): factor that reduce the probability of disease transmission from an exposed individual;
- average-exposed-time** (0 – 500 hours): time it takes for an individual to show symptoms, on average. The actual individual's exposed time is pulled from a normal distribution centered around this value, with a standard deviation of a quarter of it;
- average-exposed-detection-time** (0 – 200 hours): time it takes for an individual to be detected as an exposed, on average. The actual detection time is pulled, for any individual, from a normal distribution centered around this value, with a standard deviation of a quarter of it;
- average-infected-detection-time** (0 – 200 hours): time it takes for an individual to be detected as an infected, on average. The actual detection time is pulled, for any individual, from a normal distribution centered around this value, with a standard deviation of a quarter of it;
- average-recovery-time** (0 – 1000 hours): time it takes for an individual to recover, on average. The actual individual's recovery time is pulled from a normal distribution centered around this value, with a standard deviation of a quarter of it;
- average-hospitalized-recovery-time** (0 – 1000 hours): time it takes for an hospitalized individual to recover, on average. The actual time is pulled from a normal distribution centered around this value, with a standard deviation of a quarter of it;
- intra-mobility** (0 – 10 patches): this indicates how mobile an individual is. Usually, an individual at each time step moves by a distance 1. In this model, the person will move at a distance indicated by this value at each time-step. Thus, the lower the intra-mobility level, the less the movement in the individuals. Individuals move randomly by this assigned value.

To mimic a more realistic scenario a gathering mechanism is provided by simulating public events. This can be handled by the slider **events-probability** which indicates the probability of gathering in public places at each time steps and also **event-capacity** which indicates the number people involved in the gatherings.

The model, during the simulation, marks all the contacts that involve an exposed or an infected individual in order to build, at any time, the graph of the possible infection. This can be done with the button **write-matrix** which writes the adjacency matrix in a text file and afterwards this matrix can be read by another NetLogo model that is in charge to visualize the graph. This model called **visualize.nlogo** is a modified version of the *NW General Example* present in the model library and can be run by pushing the **setup** button, activating the graph visualization adaption with **layout** and loading the matrix file, from the current directory, with the button **load matrix**.

3.4 Experiments

For the experiments we used the **BehaviourSpace** tool from NetLogo which allows to run multiple simulations by changing the parameters, the file are then exported in csv format and analyzed with a python script to aggregate the results and show the plots. All the experiments done in this and in the countermeasure section have been done setting the probability of events to 0 because this lead to a more predictable and analyzable scenario to apply the different variations. Furthermore public gatherings only make the situation worse by giving a critical boost to the infection curve. All the experiments have been done with an initial percentage of the population infected equals to 5% and an intra-mobility of 2 patches, if not stated differently.

To resemble the COVID-19 pandemic, the parameters adopted are the taken from [2], except for the average-hospitalized-recovery-time which is higher but in our model, due to the fact that an hospitalized individual doesn't infect anyone, it only makes the simulation lasts longer.

```
infection-chance = 50%
exposed-reduction = 0.2
average-exposed-time = 190 hours
average-exposed-detection-time = 140 hours
average-infected-detection-time = 65 hours
average-recovery-time = 700 hours
average-hospitalized-recovery-time = 350 hours
```

The first experiment tried was asserting the working of the model and has been done with the above parameters without any countermeasure. It consists in the running of 10 simulations and averaging their outputs. Figure 2 reports the result of this experiment showing the known SEIR model curves and confirming the expectations.

Since we are interested in ways of contrasting the spreading of the epidemic, we started to vary the parameters of the model to see how the curves change in

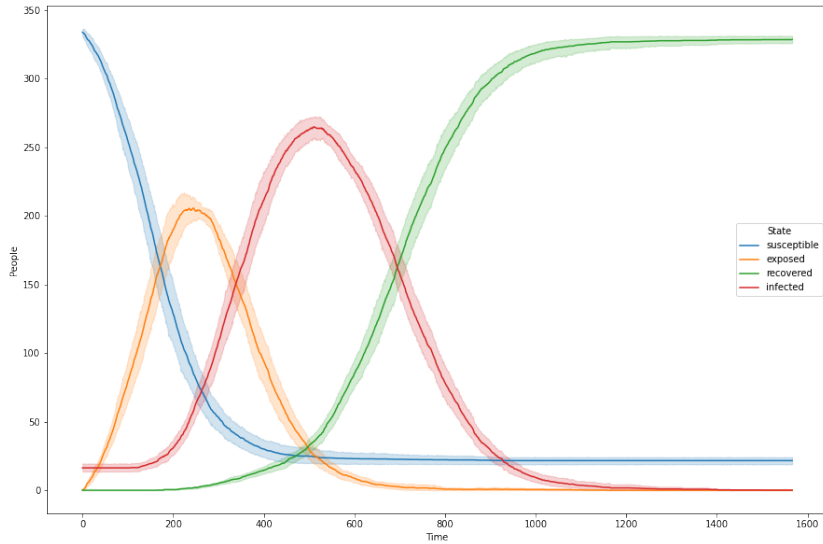


Fig. 2: Susceptible, exposed, infected and recovered average curves with their respective variations in the simulations.

order to find on which parameters act with the different countermeasures. We chose to vary the chance of infection and both the average detection time because they don't depend on the disease, like the incubation period which cannot be modified, and are more relevant than both the recovery times. The values for the parameters span from almost the half of the nominal value up to a single higher value linearly in five steps. We chose to monitor the infection curve and the cumulative number of infections because we think they are very important values to evaluate the danger of the epidemics with this modelling. The experiment was done by running each simulation 10 times and then aggregating the outputs with their average. Figure 3 shows the results of this second experiment: the most important parameter to flatten the infection curve is **infection-chance** which can be obtained by social distancing and using individual protection devices. Then the experiment shows also that it very important to discover exposed people, even though their infection chance is lower than an infected individual, in a shorter time by implementing some mechanism of contact tracing; while, for what concern the detection of infected individuals, it is important but not as much as the exposed one.

Moreover all this experiment with no movement restriction lead to highly connected and chaotic contact tracing graphs of possible infections. One of them is shown in Figure 4. Here we can see that the infection starting from an individual can reach any other individual through contact if no measures to limit the moving of people is adopted.

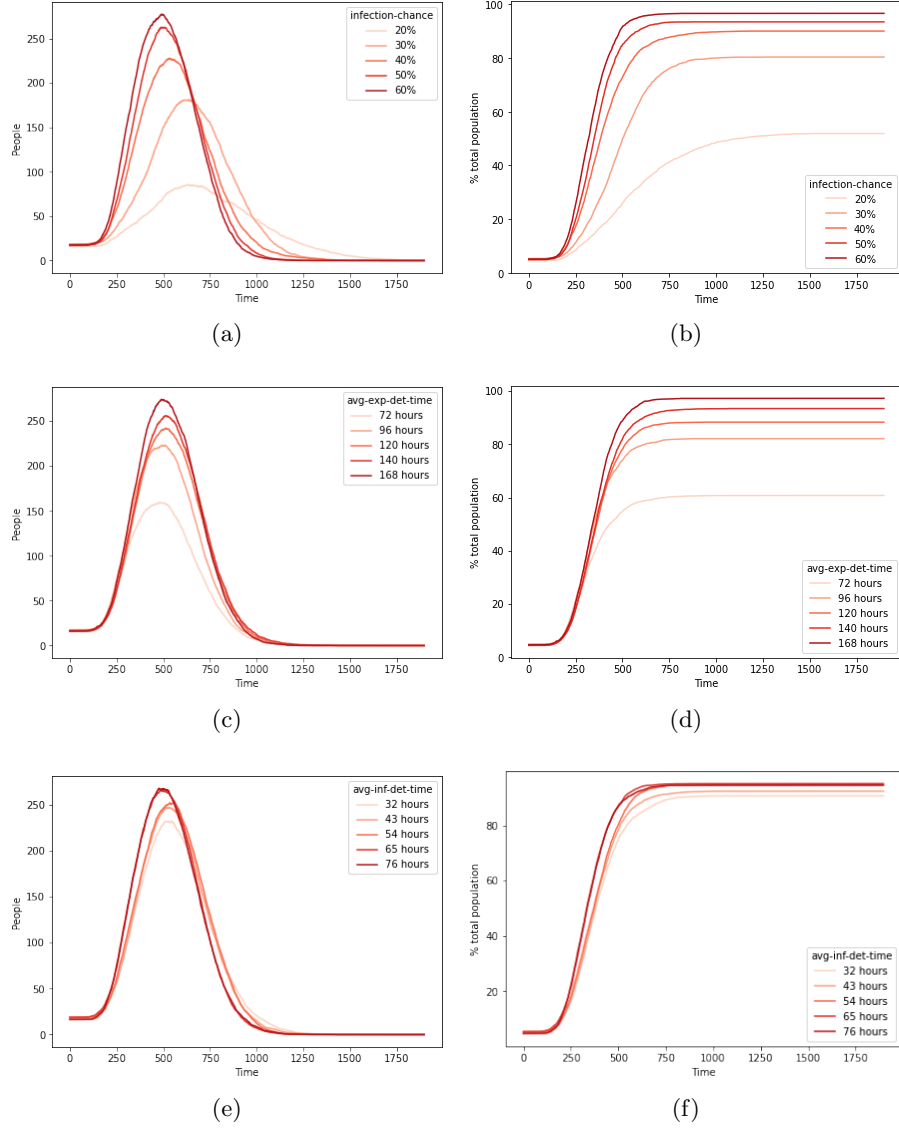


Fig. 3: Parameter analysis showing the effect of varying infection-chance, average-exposed-detection-time and average-infected-detection-time. Panels (a), (c) and (e) show the variation of the infection curve while panels (b), (d) and (f) show the variation in the total number of infected cases.

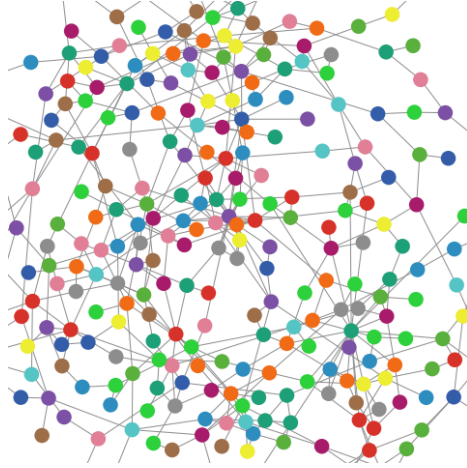


Fig. 4: Contact tracing graph of possible infections when no people movement restriction is adopted.

3.5 Countermeasures

There are many ways for contrasting the spreading of an epidemic, among them there are: avoiding movement and contact of people, using individual protection devices and adopting some mechanism of contact tracing. Each of these ways can be accounted with some measure like lockdown, social distancing, masks and some centralized method for tracing the contagion; all these countermeasures have been implemented in the model.

Lockdown mechanism The whole world has been divided into regions in order to avoid the movement between them in case of **region-lockdown**, in which case people continue to move normally but only in their limited area. While in more dangerous scenarios, a mechanism of **total-lockdown** has been provided in which only a small percentage of the population, namely **necessity-move**, can move at any time step for necessary reasons.

Mask usage and social distancing The usage of the masks is handled with the switch **masks-on** and is implemented by taking into account that not everybody is willing to wear it, this fact can be managed by the user with the slider **mask-tendency-percentage** which indicate the probability of a person to have an attitude to wear it. This attitude is set at creation time for each individual and never changed during the simulation. Masks reduce the infection chance by a factor which is given by **mask-reduction**. While, social distancing is implemented by setting the **maximum-contagion-distance** above which there is no possibility of transmission and the parameter **social-distance** which indicates

the mean of the distance of each interaction between individuals. The actual social distance is pulled, at each interaction, from a normal distribution centered around this value, with a standard deviation of a quarter of it to resemble the fact that people not always respect this restriction with everyone they meet.

Contact tracing The mechanism of tracing the spreading of the contagion from an infected source has been implemented by keeping a list of contacts (which are simply the persons met during the exposed or infected period) for each exposed and infected individual and at detection time isolate all the exposed and infected contacts, each one with a probability given by the **contact-tracing-efficiency** slider. This reflects the efficiency of the method used to trace the infection, which, for example, in case of contact tracing made with smartphone application (like *Immunis* [3]), can be the rate of adoption of the application by the overall population.

3.6 Experiments with countermeasures

The first experiment shows how these countermeasures mitigate the contagion regarding the types of lockdown. The experiment has been done by varying the moving condition of the total population from no lockdown, through region lockdown, to total lockdown with a necessity move of 5% but with different initial percentage of infection in the population (5% and 50%) to see how this measures act in different stages of the epidemics. The results are shown in Figure 5 and consist of the aggregation of the outputs of 10 simulations per curve. We can see that the region lockdown starts to decrease the contagion diffusion in case of 5% of initial infected but strictly depends on if there is an infected individual in that particular region. This can be confirmed by the graph of possible infections where the situation is better than in Figure 4 but there are clusters of contagion that resemble the restriction of the movement inside the region. In case of 50% of initial infected, region lockdown is equivalent to have no lockdown restriction. The scenario change drastically with the total lockdown where the curve is almost flat and decreasing in both cases and there is no infection spreading except for rare cases which are shown by the few connections in the contact tracing graph. These results confirm that acting on the overall movement of the population is important, that region lockdown is effective only when the epidemics is localized in few distinct regions and that the total lockdown is a very effective measure even when the outbreak is out of control.

The second experiment has been conducted to see the effects of the social interaction countermeasures like usage of masks and social distancing. This has been done by varying firstly only the reduction factor of the infection chance when everyone is wearing the mask; then, found a reasonable value for this factor, other simulations were run by varying the total amount of population wearing them. Then, other tests were made changing the value of the social distance with a maximum contagion distance set to 2 meters. The results are shown in Figure 6 and consist of the average of the outputs of 10 simulations per

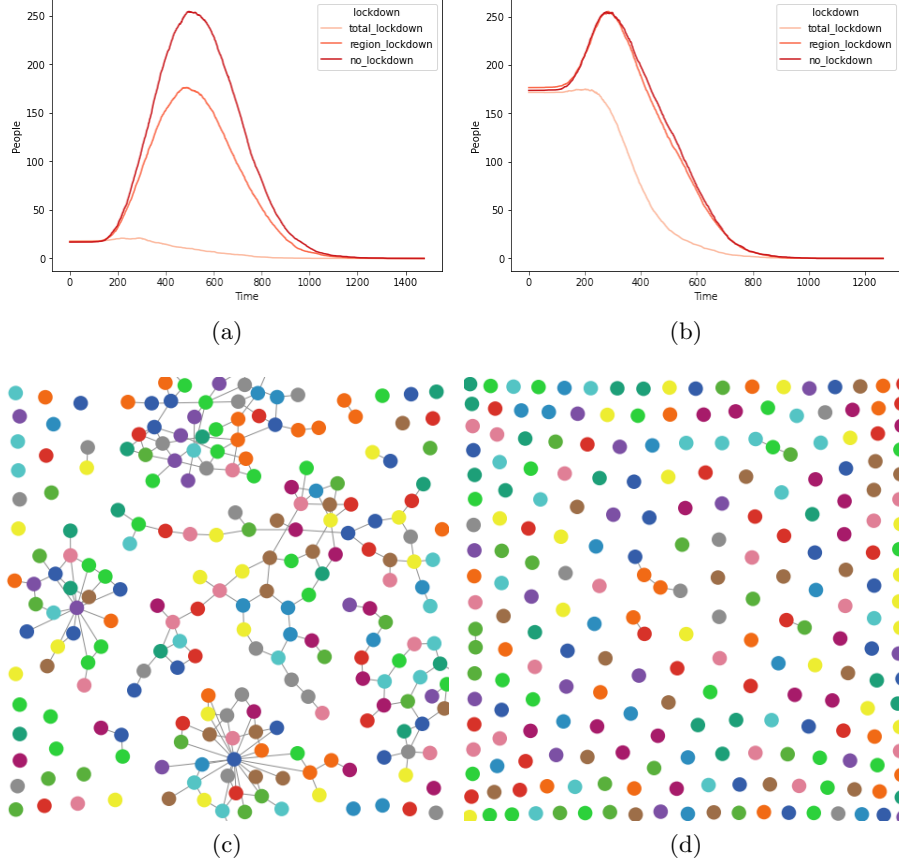


Fig. 5: The variation of the infection curve with different type of lockdown restrictions when the initial percentage of infected people is equal to 5% (a) and 50% (b). Then the contact tracing graph of possible infections is shown in case of region lockdown (c) and total lockdown (d) when the initial percentage of infected people is equal to 5%.

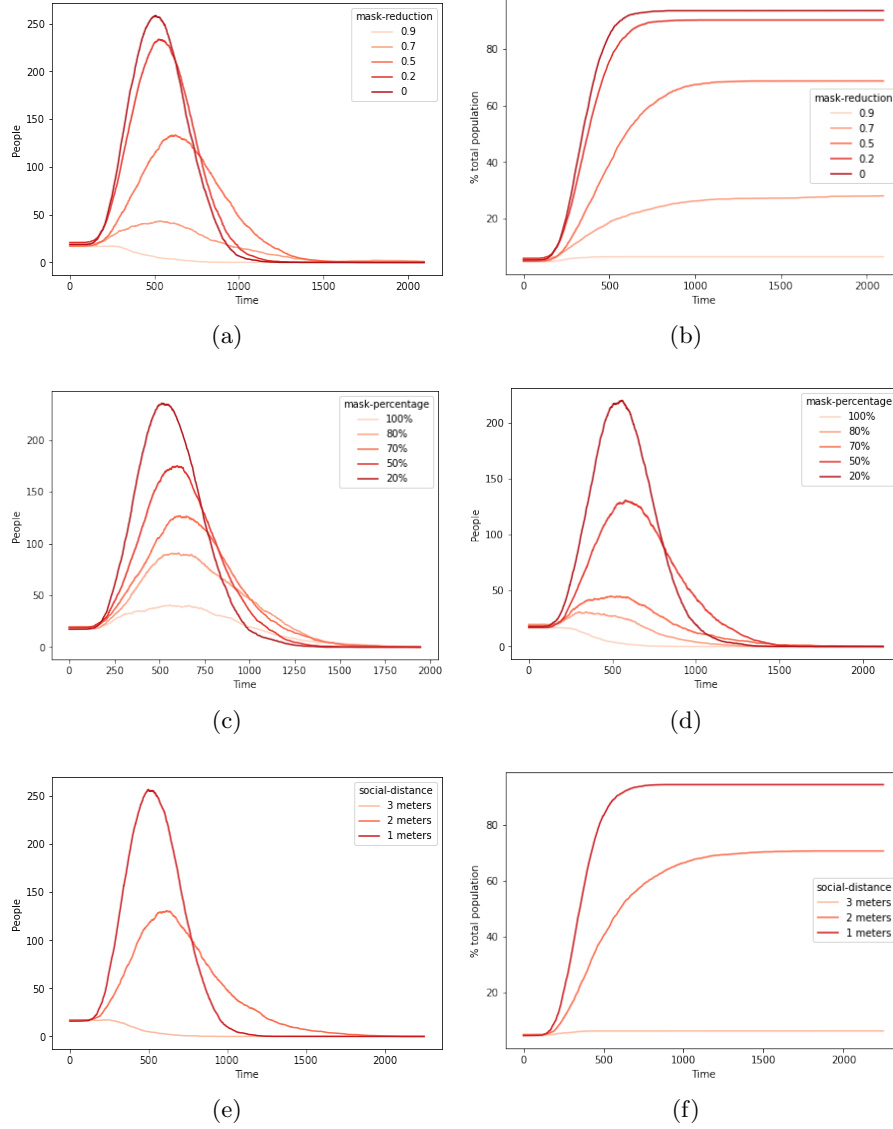


Fig. 6: Panels (a) and (b) show the variation of the infection curve and the total number of infected cases with different masks effectiveness when everyone is wearing them. Then the variation of the infection curve is shown with different percentage of adoption by the overall population when the mask infection reduction is equal to 0.7 (c) and 0.9 (d). Panels (e) and (f) show the variation of the infection curve and the total number of infected cases with different social distancing measures by assuming that the maximum contagion distance is 2 meters.

curve. The plots show that the masks start to become very effective when they reduce the infection chance by a factor of 0.7 if they are used by everyone. To have a significant improvement in containing the spreading, even if only the 70% of the population wears masks, we need to increase the masks reduction factor to 0.9. For what concerning the social distance the ideal case would be staying at an higher distance respect to the maximum distance for contagion which will lead to a curve similar to the one obtained with the total lockdown but keeping an high social distance with everyone and every time is not feasible in reality.

Another experiment regards the effect of contact tracing and has been done by varying its efficiency, that is to say varying the percentage of the contacts that are really traced. The experiment has been done by running each simulation 10 times and then aggregating the outputs with their average. As can be seen

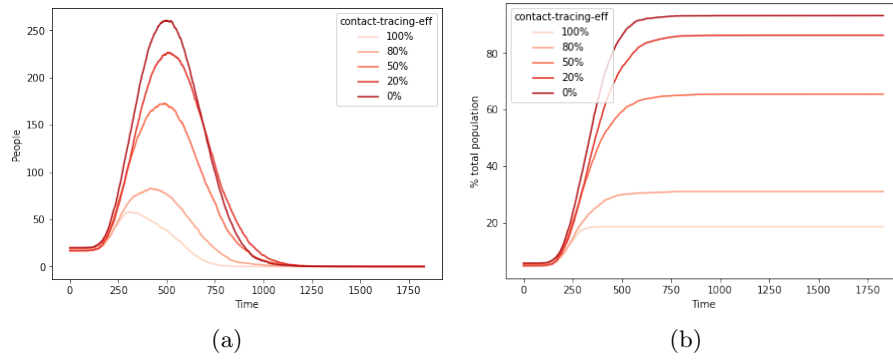


Fig. 7: Panels (a) and (b) show the variation of the infection curve and the total number of infected cases with different contact trace efficiency.

on the plots in Figure 7 and as expected, having a good and efficient mechanism of contact tracing can help in limiting the damage of the outbreak isolating as soon as possible infected individuals and preventing them from spreading the contagion.

All these three experiments have been done by applying only one of each countermeasure at time showing that only if they are highly functional they can improve the situation singularly. Masks have to be adopted by at least the 70% of the population and have to provide an infection reduction factor of 0.9, people should keep high social distance and the contact tracing method should trace at least the 80% of the contacts. This last measure, in practice, unlike the others which are of an individual nature, implies to determine an almost complete network of contacts and needs the implementation of a centralized structure to control the overall population involved and, in case of millions and millions of people, this is a very time consuming and resources demanding task. But if these measures limit the spreading of the contagion from different points we can try

to combine them to see if we could benefit from their cumulative effect. This is the purpose of the last experiment where the percentage of the population using masks, with an infection reduction factor of 0.5, is set to 50%, social distance to 2 meters and the contact tracing efficiency to 30%, which is more feasible in reality. The results are shown in Figure 8 and consist of the aggregation of the outputs of 10 simulations. As can be seen from the plots, the result is in

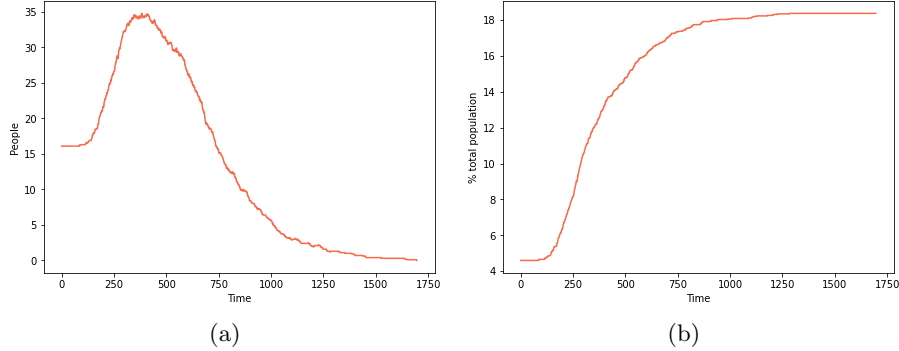


Fig. 8: Infection curve **(a)** and total number of infected cases **(b)** when the 50% of population is using masks with an infection reduction factor of 0.5, social distance of 2 meters and contact tracing efficiency of 30%.

line with the best results obtained with the highly functional countermeasures applied singularly. This is very reassuring because it shows that mixing different feasible actions is equivalent to apply a single fully working, but likely unfeasible, action.

4 Conclusions

The aim of the project was to study the possible actions to limit the epidemic spread like lockdown, social distancing, masks usage and contact tracing. From the experiments came out that these measure are very good for this purpose both applied individually and together. Moreover, their cumulative effect make up for the lackings due to an imperfect adoption of the single ones and make it suitable for a real scenario. These results show that prompt actions, cohesive behaviour and mixed strategies can lead to the reduction of the impact of the outbreak.

Concerning further improvements, the model proposed can be extended in any aspect as it represents only a simplified version of the reality. In fact, it is fully flexible and suited to include, for example, a distinction between age classes, which would require to put each individual into a specific category. Other possible extensions could be to consider also different levels of disease criticality and the

overloading of the healthcare systems, which will lead to an increased number of collateral problems not directly linked to the virus.

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