

The simulations behind the ‘*flatten the curve*’ figures

Daan H. Wielens¹

¹*University of Twente, The Netherlands*

The recent COVID-19 (corona) pandemic urges us to follow ‘social distancing’ in order to lower the maximum number of infected people at the same time. While the idea behind social distancing is clear - reduce the spreading rate of the virus - news articles often do not present clear numbers or figures that show the results of taken measures. Here, we use a simple SIR (Susceptible, Infectious, Recovered) compartmental model to simulate the effects of social distancing. Rather than using rate equations we use a physical model of persons walking around in a confined area, infecting each other by scattering events. We find that social distancing indeed flattens the curve, and we furthermore find that stopping with social distancing while the virus is still spreading may lead to a secondary increase in the maximum number of infected people.

I: INTRODUCTION

The ongoing corona (or, more correctly, COVID-19) pandemic puts a huge pressure on society. Governments either put their countries in full lockdown, or, like the Netherlands, ask people to follow the rules of ‘social distancing’. With social distancing, healthy people are allowed to meet small groups of people, but people feeling ill are urged to stay at home [1, 2]. In places where people gather and could easily spread the virus, such as supermarkets, the advice is to pass each other at a distance > 1.5 m to prevent transfer of virus particles. Although the social distancing measures are taken seriously by most of the people, some doubt the effects of such measures or reason that as long as they feel healthy, they do not pose a threat to society. Unfortunately, this is not true, as people can spread the virus before symptoms of illness arise [3].

In this article, we follow up on a simulation study that was presented in the news recently [4]. The model is explained, after which several parameters are changed

to see the effects of certain measures. Here, we present results in more detail and use extensive averaging of different runs of the simulations to get coherent results.

II: THE MODEL

The model consist of a number of people N which are confined in a square area. Every person is a circle with radius r , moving around the box with a velocity v , which has a fixed magnitude but a random direction. When a person collides with a wall, he simply reflects from it; when a person meets another person they will both scatter elastically. During the latter collision type, a virus transfer is guaranteed to take place when one of the two persons is infected or ill - the model does not take incubation time into account and assumes that a person can infect others immediately after being infected.

Every person p has a set of parameters, $p(x, y, v_x, v_y, r, \text{status}, t_{\text{inf}})$. The first four parameters specify the location and velocity of the person within the (x, y) grid. The radius r is kept constant for every person, although it could be changed. The ‘status’ parameters keeps track of the person’s state, with integers 0, 1, 2 meaning susceptible (healthy), infectious (or ill) and recovered (immune), respectively. This classification system makes our model of the SIR type (susceptible, infections, recovered), which is well known to the epidemiology community [5]. The final parameter, t_{inf} , stores the timestamp of the moment when the person becomes infected (ill) by the virus.

Without social distancing, every person in the area is moving around, potentially infecting others. When social distancing measures are taken, some people ‘stay home’ or minimise interactions, which is accomplished by giving them a velocity that is zero. Hence, the persons do not actively spread the virus. However, they can still be infected by someone colliding with them, or pass the illness along if a healthy person collides into them. We argue that this is a realistic way of simulating

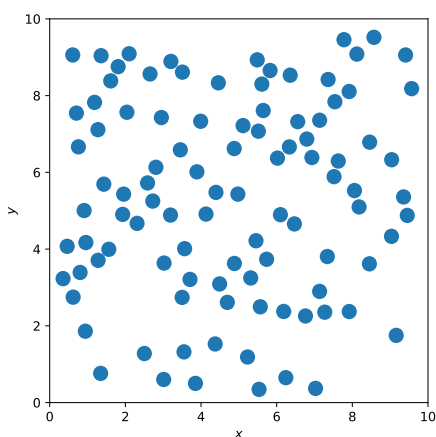


FIG. 1: Square area of 10×10 with 100 people in it after the initialisation process is finished.

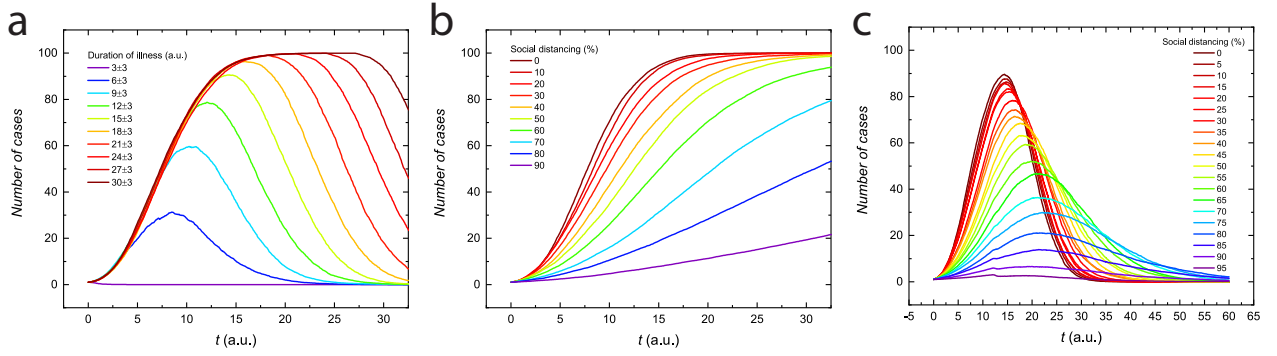


FIG. 2: Simulation results for different parameters. We plot the number of people that are currently ill versus time. This would reflect the number of hospital beds required for patients rather than the total number of people that have been ill. The curves shown are the average results of 200 simulations. (a) Without any social distancing, the duration of the infectious state (illness) is varied. (b) With an infinite illness duration, the amount of social distancing is varied. (c) We vary the amount of social distancing, with an illness duration of $t = 15 \pm 3$.

social distancing, as there is a smaller but finite chance of infecting others; this is different from a complete quarantine.

Initialisation

At first, N people are generated one-by-one. Their position and initial velocity are determined randomly, with the only constraint on the position that the person may not have overlap with any person that was already generated. To determine the overlap between two persons we simply determine whether their distance vector is smaller or larger than twice their radius (since all persons have the same r . Hence, we say that two persons have overlap (or, equivalently, are colliding) when

$$\|\mathbf{r}_i - \mathbf{r}_j\| < 2r \quad (1)$$

where $\mathbf{r}_i = (x, y)$ is the position vector of the i -th person. In our simulations, we chose a square area of 10×10 a.u., with a persons radius being $r = 0.2$ a.u., and we simulated for $N = 100$ people. At this stage, a typical area with people is depicted in Fig. 1.

Main loop

After initialisation the simulation's main code is executed. Here, for every time step dt we run the following sequence: (1) move people, (2) check for collisions, (3) check if people need status updates and the count number of ill people. We will now discuss each

part of the sequence individually.

(1) Move people

To move people, we simply take their current position and use their velocity vector to compute the new position. In vector notation,

$$\mathbf{r}_{t+dt} = \mathbf{r}_t + \mathbf{v}t \quad (2)$$

(2) Check for collisions

To check whether two people are colliding, two equations should be satisfied. Firstly, the distance between the two people should be less than twice their radius, which is the same criterion for overlap as shown in Eqn. 1. However, if two persons do have finite overlap (because of time discretisation) but are not moving towards each other, they might falsely been triggered to collide and would hence bounce back and forth into each other, always maintaining finite overlap. Therefore, to truly distinguish whether they moved towards each other and hence are colliding, we must also satisfy [\[Ref here\]](#)

$$(\mathbf{r}_2 - \mathbf{r}_1) \cdot (\mathbf{v}_1 - \mathbf{v}_2) > 0 \quad (3)$$

where we check if the vectors are partly aligned (i.e. moving towards each other) or not. If two persons fulfill both criteria (that is, they satisfy both Eqns. 1 and 3), they are colliding.

Since we loop over all persons, we only consider the collision from the perspective of one person and update his parameters only; the other person's parameters will be updated once we iterate over him. We perform the following tasks. Firstly, we check whether the person that is collided upon is ill. If so, we pass on the illness

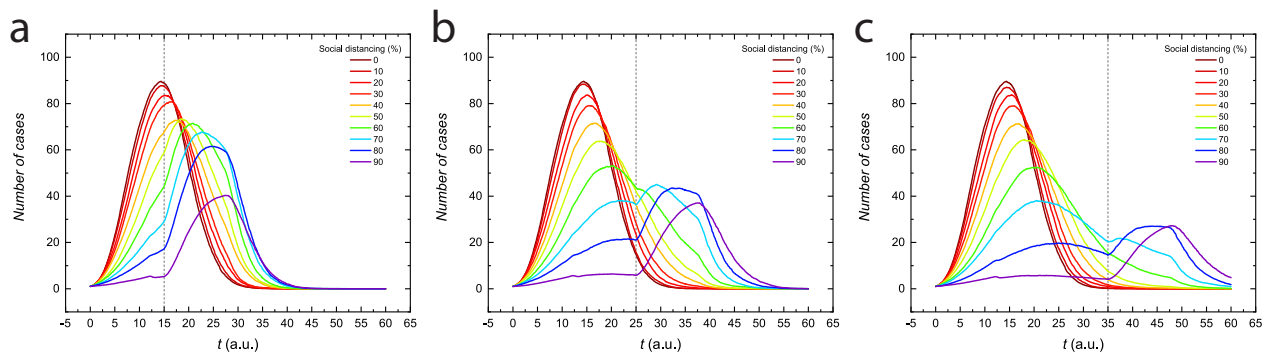


FIG. 3: Simulation results where the social distancing measures were only temporary. The duration of the illness is, as before, $t = 15 \pm 3$. The dashed vertical line indicates the time at which the social distancing ‘stops’ (i.e. every person gets a non-zero velocity), which is 15, 25 and 35 seconds for panels (a) through (c), respectively.

to our person. We also store the current timestamp to the parameter t_{inf} . Secondly, our person should scatter elastically. Since the magnitude of an elastic scattering event does not change, we simply can rotate the velocity vector. To do so, we note the following. The difference vector $\mathbf{r}_2 - \mathbf{r}_1$ acts as a mirror plane for the velocity vector: the new velocity vector is a mirrored version (across this plane) of the original one. To calculate the vectors, we first compute the angle (within the (x, y) grid) of the difference vector, which we call θ . Then, we calculate the angle of the original (initial) velocity vector, ω_i . To reflect the velocity vector with respect to the mirror plane, we simply compute the final velocity vector to be

$$\omega_f = \omega_i - 2(\omega_i - \theta) \quad (4)$$

Of course, a person can also collide with a wall. Here, the situation is easier: we only check if the person’s coordinate (including his radius) would go out of the grid. So, if a person would collide with a vertical wall (0 or 10 in our simulation) we check for

$$x < r \text{ or } x > 10 - r \quad (5)$$

If this is the case, we simply flip the x -part of the velocity vector to reflect from the wall,

$$v_x = -v_x \quad (6)$$

Bouncing of a horizontal wall is programmed similarly by interchanging x and y .

(3) Check if people need status updates

After we finished the collisions, we loop over each person once more and monitor the duration of their illness, which is the difference between the current time t and the infection timestamp t_{inf} . If this exceeds the preset duration of the illness, the person’s status is changed from ill (2) to recovered (3). Then, we count the number

of ill people and store this to an array.

Data storage

Since the initialisation stage is completely random, we run the entire simulation 200 times for every set of parameters. From every run, we store the number of ill persons at every time step, $N_{\text{ill}}(t)$. Before writing all data to a `.csv` file, we also compute the average of all 200 simulations and save this too. In what follows, we always plot the averaged results over the 200 simulations.

III: RESULTS

In our simple model we choose to vary two parameters: the duration of the illness and the amount of people that engage in social distancing. After varying them separately, we combine them and discuss the results.

In Fig. 2 we show the results of the initial simulations, along with the ‘flatten the curve’ simulation. Here, we plot the number of cases versus time. Note that the number of cases does not say how many people got ill in the end, but rather says how many people could end up in the hospital at the same time. We will now discuss every panel in detail.

In panel (a), we ignored social distancing and let all people move around the grid. We varied the duration of the infectious state. The variation of ± 3 that was added to the duration is calculated randomly for every time step in the simulation. Hence, different people cure after different durations. The figure shows that the rate of spreading (slope of the curve) is the same for all simulations, until people recover and the curve flattens. Although varying the duration of the infectious state is not

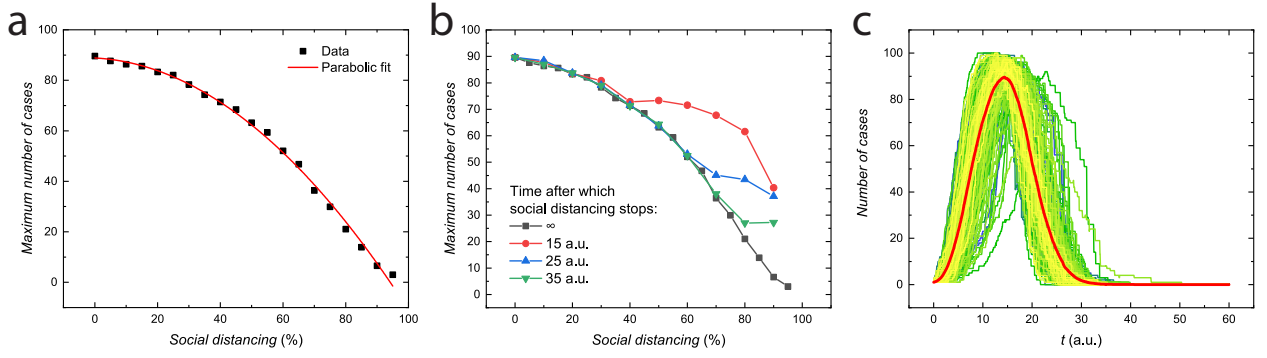


FIG. 4: Panels (a) and (b) show the extracted maxima of the curves presented in Fig. 2(c) and all panels in Fig. 3, respectively. Panel (c) shows a simulation for one specific set of parameters, where we do not only show the average result (red curve), but also the 200 individual results (blue-yellow curves).

something we can physically control, it is useful to see the influence of it.

In panel (b) we set the duration of the infectious state to infinity, meaning that no one will recover. Then, we vary the amount of social distancing to see how the infection rate is affected by the taken measures. As expected, we observe a decreasing infection rate when the amount of social distancing is increased.

Panel (c) shows the results of a simulation where we combined a finite duration of the illness (chosen to be $t = 15 \pm 3$) with the social distancing. Combining the two leads to the ‘flatten the curve’ figure, where we see that increasing the amount of social distancing reduces the peak height. Furthermore, it increases the width of the peak. Since the number of people that are being hospitalised because of the virus scales directly with the total number of people that get ill, the figure clearly shows that social distancing helps us to prevent hospitals from having too few beds to treat all patients.

Now that we have established the ‘flatten the curve’ figure, we adapt our simulations to compute the effects of people taken only temporary measures regarding the social distancing. Some people, or even governments, think that once the peak in the number of cases has passed, we can stop social distancing and continue our daily lives. To prove them wrong, we adapt our simulations as follows. After a preset time, the people that were social distancing at first, gain a random velocity (same magnitude as the others) and start moving as well. We varied this preset time for the case where the illness duration is again $t = 15 \pm 3$, and show the results in Fig. 3. We will not discuss the panels individually, but we note that especially for a high percentage of the initial social distancing, the peak in the number of cases occurs after people stop with social distancing. Especially for these high percentages of social distancing

- the most realistic numbers that most countries during the corona pandemic will be in - the peak *after* stopping the social distancing will be even higher than it was during the social distancing. Hence it is very important not to stop too early.

Finally, in Fig. 4 we present two different types of figures. First, we present the extracted maximum for each curve in panels 2(c) in Fig. 4(a). We note a trend that looks parabolic (with exception of the tail near 100% social distancing) and show the result of the parabolic fit as well. From this, it becomes evident that the more people engage in social distancing, the more effective it will be.

In panel (b) we copied panel (a), but now also include the extracted maxima from the data presented in all three panels of Fig. 3. While at low percentages they follow the same trend - meaning that stopping social distancing has no influence on the peak height - they start to deviate at different percentages of social distancing. The longer people remain socially distant, the closer the curve remains to the black one where we keep our distances until the virus is ‘gone’.

To conclude, panel (c) shows the reproducibility of a single simulation. As discussed earlier, every curve shown so far is the average of 200 simulations with persons starting at random locations, having random directions for their velocities. Here we show that most of the simulations give very similar results and that the average represents a good measure for the simulation, although the spread in the data of panel (c) also means that the error margin within every presented curve in the other figures is significantly. After all, we live in one single world which can be any of the simulated curves of panel (c). We just don’t know which one it is.

IV: CONCLUSION

We have shown that a simple SIR simulation can reproduce the ‘flatten the curve’ figure that has been all over the news recently. We furthermore show the influence of social distancing on the spreading rate of viruses in general. We also show the effects of stopping social distancing in a preliminary stage of a virus that is still spreading, showing that the effect of social distancing is destroyed in these cases.

We are aware of rate equations that can accomplish similar results and allow for one to calculate results faster. While our results qualitatively agree with the mathematical models, we did not compare them any further.

-
- [1] RIVM, *Aanvullende maatregelen 23 maart*, <https://www.rijksoverheid.nl/actueel/nieuws/2020/03/24/>

- aanvullende-maatregelen-23-maart*, (2020). Accessed online: 2020-03-29.
- [2] Johns Hopkins Medicine, *Coronavirus, social distancing and self-quarantine*, <https://www.hopkinsmedicine.org/health/conditions-and-diseases/coronavirus/coronavirus-social-distancing-and-self-quarantine>, (2020). Accessed online: 2020-03-29.
- [3] Centers for Disease Control and Prevention, *Coronavirus Disease 2019 (COVID-19) - How it spreads*, <https://www.cdc.gov/coronavirus/2019-ncov/prevent-getting-sick/how-covid-spreads.html>, (2020). Accessed online: 2020-03-29.
- [4] The Washington Post, *Why outbreaks like coronavirus spread exponentially, and how to “flatten the curve”*, <https://www.washingtonpost.com/graphics/2020/world/corona-simulator/>, (2020). Accessed online: 2020-03-22
- [5] H.W. Hethcote, *The Mathematics of Infectious Diseases*, SIAM Rev., **42** (2), 599-653, (2000).