Particle modeling of the spreading of Coronavirus Disease (COVID-19)

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By the middle of May 2020, the COVID-19 pandemic had infected nearly five million people and had spread to almost all countries worldwide. In response, many countries all over the world have used different methods to reduce the infection rate, such as including case isolation, the closure of schools and universities, banning public events, and mostly forcing social distancing, including local and national lockdowns. In our work, we use a Monte-Carlo (MC) based algorithm to predict the virus infection rate for different population densities using the most recent epidemic data. We test the spread of the Coronavirus using three different lockdown models, and eight various combinations of constraints, which allow us to examine the efficiency of each model and constraint. The main prediction of this model is that a cyclic schedule of one week without restrictions and two weeks of lockdown can help to control the virus infection. In particular, this model reduces the infection rate when accompanied by social distancing and complete isolation of symptomatic patients.

\section{Introduction}

Statistical mechanics provides a set of very powerful tools to model a number of biological and medical problems (see, for example, Refs. \cite{1,2} and many more). One of the most studied these days is the diffusion of pandemics, prompted by the current COVID-19 emergency (see, for example, Ref. \cite{3}). Many techniques currently employed are based on the solution of differential equations (see, for example, Refs. \cite{4,5} and many more) or fitting formulae (see, for example, Refs. \cite{6,7}) based upon parameters that are varied to obtain several scenarios that are then treated as parts of a statistical ensemble to analyze. For example, in many countries (e.g., Germany, Italy), there is an ample discussion about the role of the so-called $R_0$ parameter, i.e., the average number of individuals that a single actively infectious person can pass the virus to. The procedures to estimate $R_0$ are all based on a-posteriori analyses, but are usually part of the parameters that governments use to decide on measures to be taken.

In this paper, we propose a method that is essentially based on modeling a population as a set of interacting classical particles, each one with three states relative to the health status (susceptible of infection, infected and contagious, and recovered/died), in which standard thermodynamical parameters (temperature, density) are used to describe the characteristics of the population, allowing to apply the model to very different situations, ranging from the population of a city suburb to a single university classroom. The algorithm is based on standard Monte-Carlo procedures or sampling the transition among subsequent states, which are essentially sampled from a statistical distribution, in the spirit of transport MC algorithms.

In our model, a healthy person (i) can become sick with a daily probability, $P_i = \sum_j P_{ij}$, where $P_{ij}$ is a function of the distance between each infected person (j) in the area and the healthy person (i). We are treating the Coronavirus spread as a “one-way” Ising-model: A healthy person become sick as a result of an interaction with a sick person (or people), but a sick person stops being sick (i.e., recovered or died) within an average time of $\approx$ 14 up to 40 days for the sever cases (see Ref.\cite{10} for the epidemiology data). After that time, the recovered person cannot infect another person anymore.

In contrast to other infection models, such as SEIR \cite{5,6,7} in this approach, the parameter $R_0$, is a direct outcome of the simulation and not pre-assumed. This is achieved by the relation between $R_0$ and the doubling time $T_d$, which is a direct result of the infection probability chosen, which is, in turn, a function of observable epidemiological data and features of the studied population (e.g., average density on a given area or mobility). In the following, we will present the results of several simulations, meant to reproduce the spread of the Coronavirus in the presence of different lockdown constraints. The high flexibility of the model enables us to control many parameters such as social distancing, infection from an unknown source, etc. In Section II, we will describe some details of the model. In Section III, the different models of lockdown considered will be discussed. Section IV is devoted to the presentation and discussion of the results, and Sec. V to the Conclusions.

\section{The Parameters and Preliminary Assumptions}

Given the scarce information available, we had to make some assumptions based on current data, which may be more stringent than it might be required by the real nature of the virus. In particular, we based on Ref. \cite{10} for
the Coronavirus epidemiology data.

All simulations are performed, assuming a surface area unit of 1 km$^2$. Periodic boundary conditions are used, allowing to get rid of broad confinement effects (e.g., the lockdown of an entire province or city) and look at the local dynamics of the infections within that area. The population density is a function of the number of households in a certain area since it is crucial to distinguish between the infection among household and non-household contacts[11].

A. Parameterization of the model

We have identified a list of parameters, and corresponding values, that describe the population and the kinetics of the infection. This list is obviously partial, but it could be quite easily extended.

1. The probability of developing symptoms over time $t$. This is described by a Gaussian peaked at $t = 5$ days and with standard deviation $\sigma_t = 1$ day.

2. The number of effective households, denoted by $N$.

3. The fraction of "silent carriers," which have no symptoms (AKA asymptomatic) but who can infect other people. Their fraction in the population is denoted by: $a_{silent}$, and the probability of transmitting the infection has been set to 0.5.

4. Each sick person is considered contagious between the 3rd and the 7th day.

Simulations are started with a single infected person (the zero patient). In some runs, infections from an unknown source (a healthy person that becomes sick without interacting with a known sick person) are allowed. There is a period, estimated to be of 14 days, in which the infection has not been detected, and the population walks freely without any restrictions. In some of the simulations, we "force" sick people with symptoms to keep 8 meters (i.e., stay at home) after day 14. This restriction reduces the probability of the non-household infection.

B. Population dynamics

Our model is based on the principles of Brownian motion, such that for each day the population displacement is given by:

$$ R \rightarrow R + \Delta R , $$

where $\Delta R = \sqrt{\Delta x^2 + \Delta y^2}$ is distributed normally:

$$ P[\Delta R] = \frac{1}{2\pi \sigma_R^2} \exp \left( -\frac{x^2 + y^2}{2\sigma_R^2} \right) , $$

where $\sigma_R^2$, the variance, is a function of the diffusion constant, $D$:

$$ \sigma_R^2 = 2Dt , $$

where $t = 1$ day. For a Brownian motion the diffusion coefficient, $D$, would be related to the temperature, $T$, using the Einstein relation:

$$ D = \mu k_B T , $$

where $\mu$ is the mobility, $k_B$ is Boltzmann’s constant and $T$ is the absolute temperature. By fixing $T = 1$, Diffusion coefficient would be directly related to the mobility, but it is interesting to notice that the mobility could be in principle be directly interpreted as a sort of thermal parameter. In our model, the time period when the population is allowed to move without restrictions is characterized by a large value of $\sigma_R$, (namely $\sigma_{high} = 500$ meter), i.e. high temperature, while a lockdown is characterized by a lower $\sigma_R$, (here $\sigma_{low} = .5 \times 10^{0.5}$ meter, i.e. low temperature. Thus, one can consider the infection rate problem in terms of heating/cooling of the system.

C. The infection probability

The core of the model, that contains most of the epidemiological data, is the probability for the $i^{th}$ healthy person to become sick. We assume that for each contact with another sick person this process can be described by a Gaussian function of the distance, weighted with a factor that parametrizes the conditions and social interaction of the sick person:

$$ P_i = int \left\{ \sum_{j=1}^{n_{sick}} P_{ij} + \xi \right\} = int \left\{ \sum_{j=1}^{n_{sick}} \exp \left[ \frac{(r_i - r_j)^2}{2\sigma_f^2} \right] \times f(a_{silent}, n_{out}) + \xi \right\} $$

where:

- $r_i (x_i, y_i)$ is the location of the $i^{th}$ healthy person and $r_j (x_j, y_j)$ is the location of the $j^{th}$ sick person, so $|r_i - r_j|$ is the distance between them.
- $n_{sick}$ is the total number of sick people in the area.
- $\sigma_f$ is the standard deviation (here $\sigma_f = 2.4$ meters) since recent studies show that even a slight breeze can drive droplets arising from a human cough over more than 6 meters [12].
- $f(a_{silent}, n_{out})$ is a function that considers the social activity of the sick person and whether he has symptoms, which affects the spread of the virus.
outside the house. In our model, we take into account that infection by asymptomatic people is approximately 50% lower than patients with symptoms.

- $\xi$ is a random number between 0 and 1, which allows us to consider some violation of the lockdown and the fact that even during a full lockdown, people continue going out of their homes to buy groceries, take a walk, etc.

In addition, we considered that each sick person will infect some of his household members. Since the latest estimates of the household infection are $\sim 15\%$ from the known cases (without lockdown, [13]), we estimated that the number of household infections is are of uniformly distributed between 0 and 3. This number is constant for all the simulations and does not depend on the population density or the lockdown constrain.

III. LOCKDOWN STRATEGIES

To date, lockdown is still being imposed in many countries to reduce $R_0$ and, as a result, to increase $T_d$, the doubling contagion time. It still remains an option in case the disease starts spreading again without control, or if new local outbreaks should appear. In our work, we tested three different types of lockdown strategies. This choice is just representative of a potentially much wider set of options that could be analyzed by means of this method simply varying the corresponding parameters, and with a very limited computational cost. For all the models presented in this paper we assumed the following conditions:

- Days 1-14: no restrictions.
- Days 15-50: full lockdown with moderate social distancing (SD), i.e., people are forced to keep 3 meters from each other.
- Days 51-200: people must wear face-masks so that the daily infection probability (for the non-household members) is reduced to:

$$\text{int} \sum_{j=1}^{n_{silch}} 0.7 \times \exp \left[ \frac{(r_i - r_j)^2}{2\sigma_i^2} \right] \times f(n_{silent}, n_{out}) + \xi$$

A very recent HKU hamster research shows that by wearing a proper mask the infection probability can be reduce by a factor of 3 [14]. Therefore, given that not all the population wears a mask properly, we estimated the probability of infection when wearing masks 1.4 times lower than without masks.

Days 1-14 are the heating phase of the system. Thus, we expect the fastest increase in the number of patients these days. For days 15-50, we are predicting a phase transition from a hot system to a colder system (almost solid-like), which will reduce the infection rate. The system phase on days 51-200 is a result of the different models such that:

1. Model 1: Days 51-200: no restrictions.
2. Model 2: Days 51-200: cycles of one week with no restrictions and one week of full lockdown.
3. Model 3: Days 51-200: cycles of one week with no restrictions and two weeks of full lockdown.

Each model was tested with the following constraints:

- with and without moderate social distancing (SD) on days 51-200;
- with and without infection from unknown sources (infected people not traceable to any known infection chain);
- with and without strict SD for symptomatic patients after the 14th day (sick people with symptoms are forced to keep 8 meters from healthy people, equivalent to strict home isolation).

Hence, for each population density, $N$, we have 24 different simulations that will use later to assess the effect of both SD and lockdown on the number of cases as a function of time.

IV. RESULTS

For COVID-19 epidemics, the observed values of $R_0$, suggest that each infection directly generates $2 - 4$ more infections in the absence of countermeasures like social distancing [3 15]. The doubling time, $T_d$, is a function of $R_0$ [16], such that the higher $R_0$, the lower $T_d$. In particular, $T_d = 2.5$ days corresponds to $R_0=4$. 
For recovery is 14 day (though up 40 days for very severe cases) and the typical infection period ranges from the 3rd day until the 7th day, the decreasing rate of the number of active cases during the lockdown is much slower than the increasing rate of the number of active cases without restrictions (as seen in various countries around the world[17]). Hence, we find that for an initial heating period of 14 days, the necessary lockdown period (i.e., the cooling time) required to control the number of active cases is much longer than 14 days.

As of today, many countries examine different exit strategies due to the decreased number of active cases. In our simulations, we have tested several a few such exit strategies using different constraints. All of our numerical results indicate that the isolation of symptomatic patients (strict social distancing, panels (b) and (d)) of Figure 2 is effective and can reduce the peak number of active cases by about a factor two without further restrictions, and up to a factor of 10 for model 4. Also, from Figure 2 we find that moderate social distancing can reduce the number of active cases, but never as effectively as home isolation of symptomatic patients.
FIG. 2. Numerical results for the percentage of active cases from the total population for the case of infection. For all panels, the solid (dotted) line is model 1 with (without) moderate social distancing (SD). The long (short) dashed line is model 2 with (without) moderate SD, while the long (short) dotted-dashed line is model 3 with (without) moderate SD. The dashed vertical line is located at day 15, the first day of the lockdown. Errorbars in panel (a) originate from the simulation’s rmse, computed from the 100 different samples generated to compute each curve. Uncertainties on the other curves are similar and are omitted for improving the readability of the figures.

FIG. 3. Inset of Figure 2 (b) for the case of infection with additional unknown sources. The solid (dotted) line is model 1 with (without) social distancing (SD). The long (short) dashed line is model 2 with (without) SD, while the long (short) dotted-dashed line is model 3 with (without) SD.

Fig. 4 shows that, as predicted, for instance, in Ref. [5], impose lockdown in models 2 and 3, which is reflected in a more moderate increase in the number of active cases in comparison to that of days 51 until 57. The increased effectiveness of model 4 in reducing the number of active cases originates from the fact that, since it takes more than a week to cool the system, a week-week strategy model 3 cannot cause significant cooling of the system. An effective exit strategy might be based on cycles, including at least ten days of lockdown (see, for example, Ref. [5]). In Figure 2 we present our numerical results for a 4-10 days cyclic exit strategy for different $\sigma_{low}$. Similar to Figure 2 also here, the upper (lower) panels of Fig. 2 are the numerical result without (with) unknown sources. For both cases, in panels (b) and (d), the numerical results are for the case that sick people with symptoms must keep 8 meters from healthy people (strict SD).
FIG. 4. Numerical results for the percentage of active cases from the total population for the case of infection. The upper (lower) panels are the numerical result without (with) unknown sources for all panels. The solid (dotted) line is for $\sigma_{\text{low}} = 0.5 \times 10^{-1}$ meters with (without) moderate social distancing (SD). The long (short) dashed line is for $\sigma_{\text{low}} = 0.5 \times 10^{-3}$ meters with (without) moderate SD, while the long (short) dotted-dashed line is for $\sigma_{\text{low}} = 0.5 \times 10^{-4}$ with (without) moderate SD.

might be used for controlling the infection rate when accompanied by home isolation of symptomatic patients.

V. CONCLUSIONS

In this paper, we presented a kinetic Monte-Carlo algorithm for modeling different scenarios of the infection rate of the novel Coronavirus disease. The main feature of this model lies in its extreme flexibility and in the fact that the parameter $R_0$ is obtained from the simulation and not pre-assumed. It can rather be used, in principle, as a way to better tune up the other parameters based on the post-processing of clinical and epidemiological data. Although it is challenging to model the specific characters of each Coronavirus infected area, our results show that strict social distancing and a cyclic pattern might help to keep the infection rate under control over a long time span, even for an intrinsic doubling time of 2.5 days and in the presence of infection from unknown sources. From the physical point of view, effective strategies for controlling the infection rate of a specific area should lower its effective temperature as much as possible by keeping social distancing but also avoiding creating hot spots such as those related to high concentrations of people on a daily basis.

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