Two-level modeling of quarantine

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Continuum models of epidemics do not take into account the underlying microscopic network structure of social connections. This drawback becomes extreme during quarantine when most people dramatically decrease their number of social interactions, while others (like cashiers in grocery stores) continue maintaining hundreds of contacts per day. We formulate a two-level model of quarantine. On a microscopic level, we model a single neighborhood assuming a star-network structure. On a mesoscopic level, the neighborhoods are placed on a two-dimensional lattice with nearest neighbors interactions. The modeling results are compared with the COVID-19 data for several counties in Michigan (USA) and the phase diagram of parameters is identified.

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I. INTRODUCTION

There are two drawbacks \[1\] in the standard SIR and SEIR models \[2\] of the spread of an epidemic. The first drawback is related to the rate of recovery of an infected individual. The modeling implies a Poisson process, which means an exponential distribution of individual disease duration. This is in contrast to observations showing that the distribution is peaked around an average disease length. The second drawback is the assumption of an equal number of contacts for each individual, i.e., ignoring the underlying microscopic structure of the social network \[1\]. Different individuals have a different average number of contacts, depending not only on their social behaviour, but on their profession. The inhomogeneity in the number of contacts becomes especially well-pronounced during the time of quarantine, when the majority of people work from home, but some individuals (like cashiers in a grocery store) still maintain hundreds of contacts per day. The present work addresses both issues and presents a basic model of disease dynamics during a quarantine.

II. THE MODEL

The model consists of two levels. The microscopic modeling describes a single neighborhood assuming a star network \[3\], a structure, where every node (a household) is connected to the central hub (a grocery store). The neighborhood consists of a large number of households (denoted by \( N \)) not connected to each other and not interacting with each other (mimicking the quarantine). A representative from each household visits the grocery store twice a week and interacts with a cashier. If the store visitor is ill, the cashier can be infected with probability \( \beta \) or vice-versa, - if the cashier is ill, the store visitor can be infected with probability \( \beta \) (this is the first important parameter of the model). Different stages of the disease are considered. Apart from susceptible (healthy individuals who can catch the disease), there are exposed individuals who are infected but cannot infect others (this period lasts approximately 5 days \[4\]). The next step in the disease progression is infected without symptoms; it is assumed that this period lasts 3 days and during this time the infected individual can infect others. Then a person might develop symptoms, in which case they stay at home (this period lasts about 15 days). Finally, an infected individual can recover or die. The overall considered duration of the disease for a single individual is in agreement with the literature \[5\].

The main idea of the star network is the importance of the central node: the cashier. Once a cashier gets the infection and shows symptoms, they are replaced by a new cashier. During the time the cashier is already infected and still working, they can infect many customers, leading to an outbreak of the disease in the neighborhood. Monte-Carlo simulations show that in many cases, the infected customers eventually infect the new cashier, continuing the outbreak. Prescribing a certain mortality rate (the second important parameter of the model), one can compute the average number of deaths in a single neighborhood as a function of time since the start of the epidemic.

The duration of the outbreak in a single neighborhood increases with \( \beta \), but it is substantially shorter than the duration of the epidemic in a large county, containing hundreds of neighborhoods. To compute this time, we performed 10000 simulations of a single neighborhood, in which we produced an outbreak in a neighborhood by starting with an infected cashier. Then we measured the time dependence of the average number of exposed individuals and performed an exponential fit in the form \( A \exp(-t/\tau) \). Figure 1 shows these measurements and the resulting characteristic duration of the outbreak \( \tau \) as a function of \( \beta \) for two values of \( N \) (1000 households and 700 households in a neighborhood).

As expected, the outbreak in a single neighborhood lasts longer for higher values of \( \beta \) and for larger number of households \( N \). This duration time \( \tau \) (or the rate of recovery of a neighborhood, \( 1/\tau \)) is used in the next level of modeling: many neighborhoods on a lattice, see Figure 2 for the schematic representation of a system.

When on a lattice, each neighborhood can be in one of three states: susceptible, infected or recovered. Ini-
FIG. 1: The number of exposed in a single neighborhood as a function of time for $\beta = 0.05$. The exponential fit (red dashed curve) provides the characteristic duration of the outbreak $\tau$. The inset shows this $\tau$ as a function of $\beta$ for two values of the number of households in a neighborhood: $N = 1000$ (the dashed line with circles) and $N = 700$ (the dotted line with x symbols).

FIG. 2: Schematic representation of the system: weakly coupled SIR-like neighborhoods on a lattice. Each neighborhood has a star-network structure.

Initially, all of the neighborhoods are susceptible, but since some households are already infected, there is a certain initial rate of “self-infection” of a susceptible neighborhood. The lattice sites are weakly interacting since a person from one neighborhood can visit the grocery store in the neighboring neighborhood, but these visits are significantly less frequent than the visits to their own grocery store. Still, a susceptible neighborhood can catch the infection from a neighboring infected neighborhood. All of the relevant rates are computed in “microscopic” single neighborhood simulations. Then we performed extensive Monte-Carlo simulations of neighborhoods on a lattice and, measuring the times at which various neighborhoods got infected, we computed the death toll and the number of infected cases as a function of time. The consensus in the community is that the official total number of cases is substantially underestimated, since only a fraction of infected people is tested, so we compared our results with the Michigan death toll data. Figure 3 shows this comparison for Oakland County, the second largest county in Michigan with a population of over 1.2 million people. One can see that a perfect agreement is achieved for two different sets of parameters: low $\beta$ (less infectious) with high mortality and high $\beta$ (more infectious) with low mortality.

FIG. 3: Death toll as a function of time in Oakland county, Michigan (USA). The initial time is March 1, 2020. In each panel, circles represent the official data [6], and solid curves show the results of simulations of neighborhoods on a lattice (10 such simulations are shown in each panel to demonstrate the effect of stochasticity). The upper panel corresponds to $\beta = 0.04$ and mortality of 1.15 percent, while the lower panel corresponds to $\beta = 0.07$ and mortality of 0.3 percent. Both panels show an excellent agreement with the data. Assuming $N = 1000$ households in a neighborhood with an average of 3 persons in a household, Oakland county was simulated on a 20x20 lattice, a total of 400 neighborhoods.

This implies that there is a curve on the phase plane of parameters ($\beta$–mortality), each point of which describes the current death toll data well. We computed this curve not only for Oakland county but also for two other counties in Michigan: Macomb county (with total population of above 850 thousand) and Genesee county (with total population above of 400 thousand), see Figure 4. How can one constrain the parameter space? First, one would...
FIG. 4: Phase diagram of parameters for three counties in Michigan (USA). Each point of the curve corresponds to a set of parameters that perfectly describes the current death toll data for the respective county. Assuming \( N = 1000 \), Oakland county (dashed line, circles) was simulated on a 20x20 lattice, Macomb county (dotted line, squares) was simulated on a 17x17 lattice, and Genesee county (dotted line, diamonds) was simulated on a 12x12 lattice. For comparison, we also show simulations of Oakland county for \( N = 700 \) and 24x24 lattice (solid line, pluses).

FIG. 5: Fraction of susceptible households (blue solid curve) and fraction of susceptible cashiers (red dashed curve) as a function of time. The inset shows the fraction of infected households. Simulations of Oakland county, Michigan on a 20x20 lattice for \( N = 1000 \), \( \beta = 0.05 \) and mortality of 0.62 percent.

III. SUMMARY AND DISCUSSION

This work focuses on modeling disease dynamics during the quarantine, when most people dramatically decrease their number of contacts, but some individuals still maintain hundreds of contacts per day. This pattern is modeled by a star network, where the central node (say, a cashier in a neighborhood) is connected to all other nodes, but all other connections are prohibited. A big county is modeled as many such neighborhoods on a lattice, Figure 2. Simulations show that the results do not strongly depend on the number of households \( N \) in a single neighborhood if changing \( N \) is compensated by adjusting the number of neighborhoods on a lattice to keep the county population constant. But the results strongly depend on the two main parameters: the transmission coefficient \( \beta \) and the mortality. Stochastic simulations of this two-level model show a sloppy behavior [8]: different sets of these parameters can describe the same death toll data in the county. We were able to identify the region in the phase plane of parameters that reproduces the observations in different counties and estimate the mortality rate to be 0.5 − 0.8 percent, which also suggests that the real number of coronavirus cases in these counties is 20 times larger than the number of reported cases. This number is 3 − 4 times lower than in a recent controversial study in Santa Clara County [9], but still very high.
In some places, where the outbreak is (was) particularly severe (for example, certain parts of Italy), the official death toll might be underreported [10]. The situation in Michigan hospitals is substantially better, so it was assumed that the Michigan death toll data is accurate.

The presented model is phenomenological and aims at capturing basic features of a quarantine and avoiding the drawbacks of continuum modeling. It can be easily modified to include more details: other essential workers with a large number of connections (for example, health care workers and more cashiers in the same grocery store) and population structure in a county. Yet, phenomenological models are useful for our basic understanding of the underlying physical mechanisms and can produce good predictions. Figure 5 shows that the fraction of infected cashiers is very large, justifying the assumption that a recovered neighborhood during the quarantine can not be infected again. However, when the quarantine is lifted, more high-degree nodes (people with many contacts per day, for example, university teachers of general physics classes) will return to work, a substantial fraction of whom are still susceptible. This is likely to lead to the second wave of the disease outbreak.

In order to perform simulations of neighborhoods on a lattice, one needs to use a microscopic model of a neighborhood to compute the recovery rate. This idea of two-level modeling, measuring the rates in a microscopic model and using them in a more macroscopic model, has recently been employed in a completely different problem of rare cell clustering on a substrate [11].

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