A percolation model for epidemics

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In this paper, we propose a percolation model to describe the spread of epidemics. Contrary to the standard SIR model, our model takes into account the spatial dependence of disease transmission. We first derive the probability of direct transmission as a function of distance in our framework. Then we look at the probability of a chain of infections. Finally, we use these results to analyze the critical phenomena of our model.

I. INTRODUCTION

In light of the recent COVID-19 pandemic, understanding disease spread is more important than ever. Such understanding is crucial for controlling a pandemic by providing guidance on the most effective ways to curb its spread.

Often, epidemic dynamics is described in terms of the SIR model [1]. In this model, the population is classified as either susceptible (S), infected (I), or recovered (R) and are related by a system of ODEs as

$$\begin{aligned}\frac{\mathrm{d}S}{\mathrm{d}t} =& -\beta SI\\ \frac{\mathrm{d}I}{\mathrm{d}t} =& \beta SI - \nu I\\ \frac{\mathrm{d}R}{\mathrm{d}t} =& \nu I\end{aligned}$$

Here, β represents the disease transmission rate and ν represents the recovery rate. Solutions to these equations can then allow us to predict the epidemic curve. However, such methods assume uniform mixing of the population and are unable to describe how a disease spreads realistically through a population.

Percolation theory is a natural way to describe disease spread. For example, at the start of an epidemic, we can assume each person infects a constant new number of people, which naturally leads to percolation on the Bethe lattice as described in [2]. However, this model still fails to consider spatial dependence of disease transmission.

In this paper, we present a percolation model which explicitly accounts for the roles of spatial dependence and recovery in disease transmission. We first investigate dependence of the probability of direct infection on the distance between two people. We then analyze the probability of infection from a chain of infections. Finally, we find the critical point of this model and analyze the scaling of infection clusters as we approach the critical density.

II. MODEL

Suppose people live in random locations with density ρ. We want to capture the fact that people interact more with their neighbors than with people further away. Thus, we assume the rate of infection to be gaussian distributed as

$$\lambda N_g e^{-x^2/\xi^2} \tag{1}$$

where N_g is the normalization for a 2 dimensional Gaussian and λ is a constant. Further, let us suppose recovery time is given by a constant τ_0. For simplicity, we model recovery as a decay process where in each small time interval there is a $\frac{\Delta t}{\tau_0}$ chance an infected person recovers.

A. Transmission probability

Denote by $p_i(x,t)$ the probability an infected person infects a person at position x after a time t. In any small time interval, the probability of infection increases proportional to the probability of still being infections, the transmission rate, and the probability of being susceptible. Since recovery rate is $1/\tau_0$, the probability the person is still infectious is e^{-t/τ_0}. The transmission rate is just (1) while the probability of susceptibility is $1 - p_i(x,t)$. Thus, we have

$$\frac{\partial p_i(x,t)}{\partial t} = \lambda N_g e^{-x^2/\xi^2}(1 - p_i(x,t))e^{-t/\tau_0}. \tag{2}$$

We can solve this using separation of variables to find

$$p_i(x,t) = 1 - \exp\left(\lambda\tau_0 N_g e^{-\frac{x^2}{\xi^2}}(e^{-t/\tau_0} - 1)\right). \tag{3}$$

For large times, this probability which we denote by $p_i(x)$ just becomes

$$p_i(x) = p_i(x,\infty) = 1 - \exp\left(-\lambda\tau_0 N_g e^{-\frac{x^2}{\xi^2}}\right). \tag{4}$$

We can clearly see that transmission probability decreases as we increase distance, decrease recovery time, or decrease λ.

B. Infection chains

Now, let us randomly distribute a collection of people in $\mathbb{R}^2$ with density ρ. The probability of transmission ever occurring between any pair of people is given by

(4). We seek to find the critical behavior where there is an infinite cluster of infected people.

Suppose a person located at the origin is infected. We want to find the probability a person located at x gets infected. This can happen directly or through chains of infections through intermediate people. Consider a chain of n people. The probability $p_n(x)$ of an n person infection chain is given by

$$p_n(x) = \int \mathrm{d}^2x_1 \dots \mathrm{d}^2x_{n-1} \rho^{n-1} p_i(x_1) p_i(x_2 - x_1) \dots p_i(x - x_{n-1}). \tag{5}$$

To evaluate this, we first expand (4) to get

$$p_i(x) \approx \lambda\tau_0 N_g e^{-\frac{x^2}{\xi^2}}.$$

Then (5) becomes

$$\begin{aligned} p_n(x) =& \rho^{n-1}(\lambda\tau_0 N_g)^n \int \mathrm{d}^2x_1 \dots \mathrm{d}^2x_{n-1} \\ & \exp\left(-\frac{x_1^2}{\xi^2} - \frac{(x_2 - x_1)^2}{\xi^2} - \dots - \frac{(x - x_{n-1})^2}{\xi^2}\right) \end{aligned} \tag{6}$$

$$\begin{aligned} =& \rho^{n-1}(\lambda\tau_0)^n N_g \exp\left(-\frac{x^2}{n\xi^2}\right) \\ =& \frac{N_g}{\rho} \exp\left(n \ln(\rho\lambda\tau_0) - \frac{x^2}{n\xi^2}\right) \end{aligned} \tag{7}$$

where we noted we can complete the square for each x_i and integrate them out to simplify.

III. CRITICAL BEHAVIOR

A. Percolation threshold

We can approximate the probability that the person at 0 infects the person at x by summing all the chain probabilities $p_n(x)$ given in (7). First, we note that for $\rho\lambda\tau_0 > 1$, then the $n \ln(\rho\lambda\tau_0)$ term grows as we increase the chain length. This means that as long as $\rho\lambda\tau_0 > 1$, the infection will spread to everyone through a long enough chain.

Next, for $\rho\lambda\tau_0 < 1$, we note that $\ln(\rho\lambda\tau_0)$ is negative. In particular, we can find that $n \ln(\rho\lambda\tau_0) - \frac{x^2}{n\xi^2}$ is maximized for

$$n^* = \frac{x/\xi}{\sqrt{-\ln(\rho\lambda\tau_0)}}.$$

In particular, we can bound the sum of the probabilities as

$$\begin{aligned} \sum_n p_n(x) =& \sum_n \frac{N_g}{\rho} \exp\left(n \ln(\rho\lambda\tau_0) - \frac{x^2}{n\xi^2}\right) \\ <& \frac{N_g}{\rho} \sum_{n=1}^{n^*} \exp\left(-\frac{2x/\xi}{\sqrt{-\ln(\rho\lambda\tau_0)}}\right) \\ & + \frac{N_g}{\rho} \sum_{n=n^*}^{\infty} \exp\left(-\frac{2x/\xi}{\sqrt{-\ln(\rho\lambda\tau_0)}}\right) (\rho\lambda\tau_0)^{n-n^*} \\ <& \frac{N_g}{\rho} \left(\frac{x/\xi}{\sqrt{-\ln(\rho\lambda\tau_0)}} + \frac{1}{1 - \rho\lambda\tau_0}\right) \\ & \times \exp\left(-\frac{2x/\xi}{\sqrt{-\ln(\rho\lambda\tau_0)}}\right). \end{aligned} \tag{8}$$

Now, it is easy to see that the bound goes to 0 for large values of x. Thus, for $\rho\lambda\tau_0 < 1$ the largest cluster is finite. This shows that the critical point is given by the condition

$$(\rho\lambda\tau_0)_c = 1. \tag{9}$$

Note that this implies the density of people plays a crucial role in determining the spread of a pandemic. Intuitively this makes sense, reduced density has the same effect as a reduced transmission rate.

B. Scaling of clusters

Now we turn our attention to how the size of infection clusters grow as we approach the critical density. This tells us how effectively decreasing population density by quarantining is. First, we note that (7) can be written as

$$p_n(x) = \frac{N_g}{\rho} \exp\left(-\frac{x}{\xi}\sqrt{-\ln(\rho\lambda\tau_0)}\left(\frac{n}{n^*} + \frac{n^*}{n}\right)\right). \tag{10}$$

For large x, we can use a saddlepoint approximation to write

$$p(x) = \sum_n p_n(x) \sim \exp\left(-\frac{x}{\xi}\sqrt{-\ln(\rho\lambda\tau_0)}\right). \tag{11}$$

We can now read off the effective size of a cluster as

$$\langle x \rangle \propto \frac{1}{\sqrt{-\ln(\rho\lambda\tau_0)}} \approx \Delta(\rho\lambda\tau_0)^{-\frac{1}{2}} \tag{12}$$

where $\Delta(\rho\lambda\tau_0) = 1 - \rho\lambda\tau_0$.

IV. CONCLUSION

We introduced a percolation model for epidemics that takes spatial relations into account. In particular, we assumed transmission rate is Gaussian in the separation between two people. By assuming a constant recovery,

we were able to derive the probability of a direct infection between any two people in terms of the separation. We also used this result to calculate the probability of a chain of infections.

Next, we analyzed the critical behavior of our model. We found that there is a critical density above which the disease spreads through the whole population. We also looked at the size of the infection clusters as we approached the critical density and found it scaled to the power of $-\frac{1}{2}$.

In the future, we hope to provide a more in depth analysis of this model. We hope to connect it to existing models such as the SIR model. We also hope to compare apply it to data from real epidemics.

[1] H. H. Weiss, "The SIR model and the foundations of public health," *Materials matematics*, pp. 0001–17, 2013.

[2] I. F. Mello, L. Squillante, G. O. Gomes, A. C. Seridonio, and M. de Souza, "Epidemics, the ising-model and percolation theory: a comprehensive review focussed on covid-19," *Physica A: Statistical Mechanics and its Applications*, p. 125963, 2021.