Stochastic Epidemiological Modeling with the help of Random Walks in the SIR and SIS Models

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1 Introduction

Closed regions of high population density such as residential university campuses, apartment complexes and communities, etc. are very susceptible to epidemics. Without proper precautions, an infection can go out of control. It's thus very important to be able to act preemptively and accordingly.

Tackling such a problem requires an extensive study in the domain of epidemiology where the dynamics of infectious disease and stochasticity of epidemics are taken into consideration.

This paper aims to provide reliable predictions to identify critical points at which infections end up in a complete exponential growth i.e. an uncontrolled spread. These results could be used to effectively control the spread of disease in small, closed populations. It will also identify optimal points for the declaration of emergencies.

2 Historical Discourse

There have been many publications discrediting the use of computational or mathematical models to predict the progression of epidemics. Seprianus et al. have suggested that the standard epidemiology model or the susceptible - infectious - recovered (SIR) model is inaccurate since it assumes a homogeneous population where every individual is equally likely to infect another. In practice, every person has only a finite number of connections to spread infection.[1]

Other publications have suggested that without proper data regarding the transmissibility and efficacy of preventive measures, models are generally not useful in making accurate predictions[2]. This was made even more evident by studies carried out during and post the 2020 SARS-CoV-2 pandemic, during the initial

stages of which there was a lack of useful data[2][3]. Data collected during epidemics is generally very noisy, and as a result work has been done in favour of *practical identifiability*[4].

Although the SIR model was largely unhelpful during the pandemic, its use has been prevalent in the epidemiology of diseases such as Ebola, cholera, H1N1, etc.[5][6][7][8].

3 Paradigms

Determining the threshold for an emergency during an epidemic is an optimization problem. However, first, it is important to identify an appropriate epidemiological model. The SIR model mentioned previously is described by categorizing a closed sum of individuals into fractions $s(t), i(t), r(t)$ where each function represents the fraction of people susceptible, infected or recovered at any given time t.

$$s(t_0) + i(t_0) + r(t_0) = 1, \ \forall \ t_0 \geq 0$$

The deterministic model is given by the following ordinary differential equations

$$\frac{d}{dt}s(t) = \lambda s(t)i(t)$$

$$\frac{d}{dt}i(t) = \lambda s(t)i(t) - \gamma i(t)$$

$$\frac{d}{dt}r(t) = \gamma i(t)$$

where λ represents the *infection rate* constant and γ represents the *recovery rate* constant.

The *basic reproduction number* R_0 is defined as

$$R_0 = \frac{\lambda}{\gamma}$$

The SIR model is generally preferred for viral infections, whereas the alternative SIS model: susceptible - infected - susceptible model is largely used for bacterial diseases where recovered individuals are still likely to be infected once again.

The SIS model is given by the differential equations

$$\frac{d}{dt}s(t) = \gamma I - \lambda s(t)i(t)$$

$$\frac{d}{dt}i(t) = \lambda s(t)i(t) - \gamma i(t)$$

Solving the system of ODEs for either model results in a deterministic solution that describes the behavior of the population over time. It is important to note, however, that deterministic models are accurate only for larger populations as the inherent stochastic natures of epidemics are averaged out[9]. It is thus more appropriate to use a stochastic model for SIR or SIS to determine how a smaller population may behave.

No.	Paradigms	Scope	Limitations
1	Deterministic SIR Model	Predicts the behavior of large populations reliably for typically viral epidemics. Useful in any epidemic where an individual gains immunity after recovery.	Does not work well with smaller populations with pronounced stochastic behavior or for infections with risk of infection after recovery.
2	Deterministic SIS Model	Predicts the behavior of large populations reliably for typically bacterial epidemics or any disease where the individual need not gain immunity after recovery.	Does not work well with smaller populations with pronounced stochastic behavior. This model completely breaks down when used for diseases with post-recovery immunity.
3	Stochastic SIR / SIS Model	Predicts the behavior of a population while taking into account the stochastic nature of an epidemic where individuals develop/ do not develop post-recovery immunity.	This model is far more computationally heavy than deterministic models.

Table 1: Comparing Paradigms

4 Argumentation

This paper aims to model epidemics in smaller populations. It would thus be more appropriate to use a stochastic epidemiological model that takes into account the stochastic nature of epidemics[9]. Stochastic models take into account

off - chance events. For example, an actual epidemic with a *basic reproduction number* greater than one may stop spreading due to the possible isolation of certain infected individuals. While this is completely possible in a small population, a deterministic model would miss these nuances.

The different approaches to building a stochastic model are discussed below. Random walk simulations that take into account the stochasticity of both con-

No.	Model	Pros	Cons
1	Random Walk Simulation Models - Stochasticity of contact is handled by a random walk.	Takes into account probabilistic contact and probabilistic transmissions discretely.	Computationally heavy simulation - The run time increases exponentially with population size.
2	Network Based Models - Individuals are treated as nodes in a network.	Captures heterogeneous contact patterns which is crucial for high density populations.	Require mapping of individual interactions. Data collection in this regard is tedious.
3	Branching Process Models - The spread of infection is modeled by treating each infected individual as a branch has a probability $P = P(R_0)$ of infecting another individual.	Effective in capturing the probability of an outbreak in the early stages of an epidemic, where small fluctuations may be magnified.	This model does not simulate realistic contact patterns.

Table 2: Comparing Models

tact and transmission, paired with Monte Carlo Simulations will yield results with different initial parameters. This offers great insight into the range of possible outcomes if certain parameters are uncertain due to the lack of data or if they are inherently complex to ascertain. Monte Carlo Simulations also allow sensitivity analyses to be performed, which is essential for an understanding how certain parameters may be magnified or diminished in a highly stochastic system.

This flowchart of the Random Walk Simulation model demonstrates the logic to be followed.

Simulations of the same parameters may be repeated several times and results averaged over to determine the mean expected outcomes.

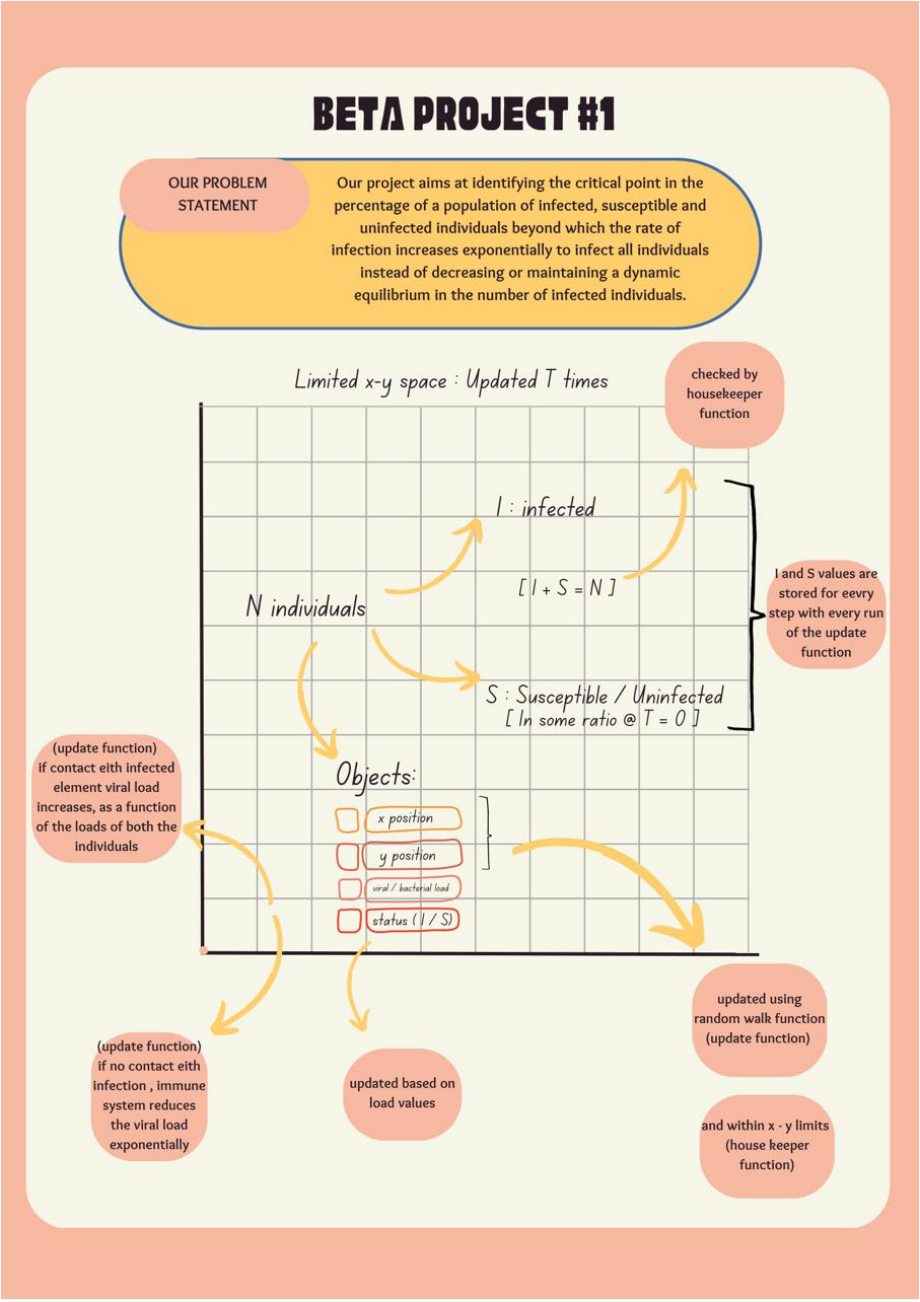

Figure 1: Logic Flowchart

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