The Infection of Epidemics

0.1 Summary

This study investigates the the infection of epidemics on the total population. Given the current situation of the ongoing COVID-19 around the world, scientists are eager to find out to what degree it would effect the total population. By using the stochastic SIR model to simulate the susceptible population, we can conclude that the epidemics will only infect at most 10% of the total population, and the public health sector can take corresponding precautions.

0.2 Introduction

The COVID-19 disease has thrown people's lives into chaos since the end of 2019. While it's hypothesized that the epidemics will only infect 10% of the total population due to the heterogeneous susceptibility. We implemented the stochastic SIR model to simulate the infection twice and investigated infected population of each simulation to help public health sector better understand the situation of COVID-19.

0.3 Method

As we are doing the analysis on the infectious disease COVID-19, it's reasonable to implement the susceptible-infected-removed (SIR) model of each variant:

$$S_t + I_t + R_t = 1 \quad \text{for all } t$$

$$\frac{dS_t}{dt} = -\beta S_t I_t \qquad \frac{dI_t}{dt} = \beta S_t I_t - \gamma I_t \qquad \frac{dR_t}{dt} = \gamma I_t$$

where S_t, I_t and R_t are the proportion of susceptible, infectious, removed individuals respectively in the population at time t. β is the transmission rate and γ is the removal rate.

We plan to do the simulation, so we use the likelihood-based inference approach in addition to the stochastic model. The likelihood function is:

$$\ell(\beta, \gamma) = \prod_{i=1}^{n-1} \mathbf{P}\left(\begin{array}{c} S(t_{i+1}) = S_{i+1} \\ I(t_{i+1}) = I_{i+1} \end{array} \middle| \begin{array}{c} S(t_i) = S_i \\ I(t_i) = I_i \end{array} \right)$$

with the maximum likelihood estimator:

$$(\hat{\beta}, \hat{\gamma}) = \arg\max_{\beta, \gamma} \ell(\beta, \gamma)$$

Then we can start the simulation based on the maximum likelihood with the purpose of investigating heterogeneity in susceptibility and set up the following models:

$$P_i(t) = 1 - \{\exp -[S_i(\sum_{j \in I(t)} \tau) + \epsilon]\}$$

where S_i is the susceptibility for person i, and assume the constant transmissibility $T_j = \tau$

$$S_i \sim \text{Gamma}(\frac{1}{5}, \frac{1}{5})$$

Then we simulate $S_i = X_i\beta$ with the matrix $X_{i1} \sim \text{Gamma}$ and $\beta = 1$.

0.4   Result

From Figure 1 we could see that the peak of the COVID-19 is at the beginning of the pandemic for both simulation 1 and 2 where the density is within the range of 0.010 to 0.015. There isn't much difference between the two simulations, and the cases disperse after the peak. Therefore, our hypothesis is correct that the infection within the population is at most around 10%
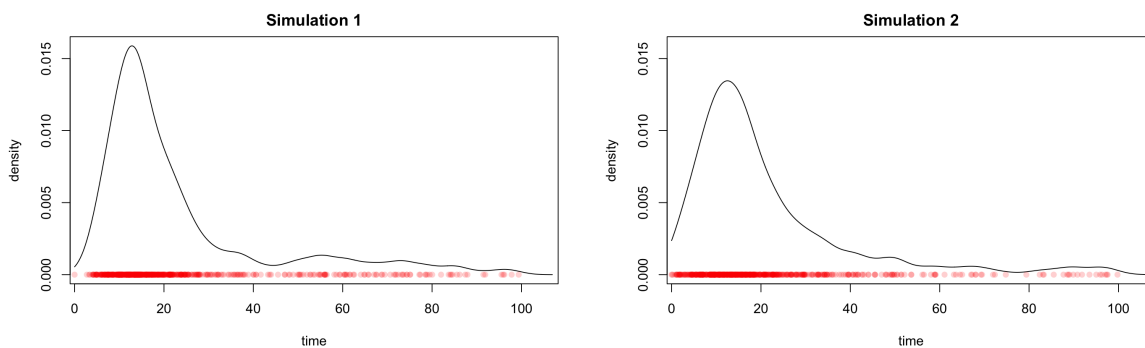

Figure 1: Infectious Times

Based on Figure 2, the cumulative infectious of both simulations become smoother and smoother over time. It proves that the overall trend of pandemic is declining or stabilizing eventually.
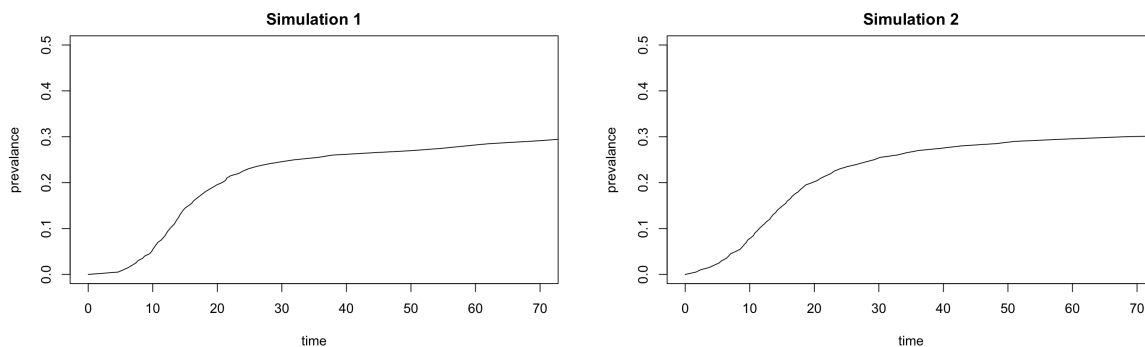

Figure 2: Cumulative Infections Over Time

0.5 Conclusion and Discussion

According to the data analysis, we could see that COVID-19 has a high infectious rate at the beginning and reached to around 10% at the peak point. Then the pandemic has become smoother and smoother even for emerging infectious disease. Therefore, we can conclude our hypothesis is correct and report to the public health sector to avoid panic.