Modeling Approaches for COVID-19 with Differential Efficacy of Vaccines in two Socio-Economically Contrasting Cities

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Research Objectives

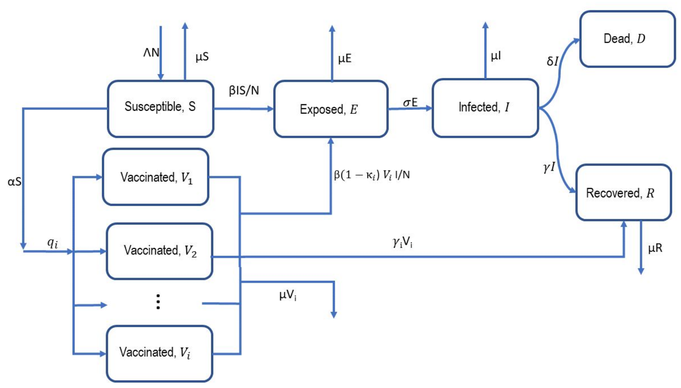
In an attempt to control the spread of COVID-19, various types of vaccines, including the mRNA, viral vector, and traditional vaccines, have been approved for implementation globally. This research work develops deterministic and stochastic models with multiple vaccines in a community to simulate population dynamics. The incidence data from Bogota D.C. and New York City were used to estimate the vaccines-related parameters using maximum likelihood estimation and simulations. Finally, we conclude the efficacy of vaccination for controlling the spread of viruses, and a comparison of two cities has been analyzed.

Introduction

Coronaviruses belong to a family of viruses that can cause mild to moderate respiratory illnesses and severe acute respiratory infections (SARI). The outbreak of SARS-CoV-2, known as COVID-19, started in December 2019 in Hubei Province, China and quickly spread globally.

- We focus on overall impact of available vaccines (mRNA, viral vector, and traditional vaccines)
- We formulate a deterministic and a stochastic model to address research objectives
- We estimate vaccine-related parameters for both models using incidence data from Bogota D.C. and New York City, and conduct numerical simulation to examine the fit of these two models to the data

Model Flow Diagram



Methods

- Stochastic perturbations are introduced to the model via the infection rate, β :
  - β = β + ϵB(t), where β is the constant deterministic infection rate and B(t) is Brownian Motion (*Gray, et. al.*)
- Model with Stochastic Perturbations:

$$
\begin{aligned}
dS(t) &= \left(\Lambda N - \alpha S(t) - \beta\frac{S(t)I(t)}{N} - \mu S(t)\right)dt - \epsilon\frac{S(t)I(t)}{N}dB(t),\\
dE(t) &= \left(\beta\frac{S(t)I(t)}{N} + (1-\kappa)\beta\frac{I(t)V_1(t)}{N} - \sigma E(t) - \mu E(t)\right)dt + \epsilon\frac{(S(t)+(1-\kappa)V_1(t))\,I(t)}{N}dB(t),\\
dV_1(t) &= \left(\alpha q_1 S(t) - (1-\kappa)\beta\frac{I(t)V_1(t)}{N} - \gamma_1 V_1(t) - \mu V_1(t)\right)dt - (1-\kappa)\epsilon\frac{V_1(t)I(t)}{N}dB(t)\\
dI(t) &= \left(\sigma E(t) - (\gamma+\delta)I(t) - \mu I(t)\right)dt,\\
dR(t) &= \left(\gamma I(t) + \gamma_1 V_1(t) - \mu R(t)\right)dt,\\
dD(t) &= \delta I(t)dt.
\end{aligned}
$$

- In general, we use i vaccine compartments, but for our work we use i=1, to represent aggregate compartment of all vaccine types
- S, V, and I compartments contain both a deterministic part and a stochastic part
- Stochastic element is used to address the randomness of the spread of infection

Deterministic Model Analysis

- Disease-Free Equilibrium:

$$E_0 = \left(\frac{\Lambda N^*}{\mu+\alpha}, \frac{\alpha q_1 \Lambda N^*}{(\gamma_1+\mu)(\mu+\alpha)}, \frac{\alpha q_2 \Lambda N^*}{(\gamma_2+\mu)(\mu+\alpha)}, \ldots, \frac{\alpha q_n \Lambda N^*}{(\gamma_n+\mu)(\mu+\alpha)}, 0, 0, 0\right)$$

- Reproductive Number(R_0):

$$R_{0v} = \left(\frac{\sigma\beta}{(\sigma+\mu)(\gamma+\delta+\mu)}\right)\left(\frac{\Lambda}{\mu+\alpha}\right)\left(1+\sum_{i=1}^{n}(1-\kappa_i)\frac{\alpha q_i}{\gamma_i+\mu}\right)$$

Stochastic Model Analysis

- We use the Euler-Maruyama method to discretize and solve our stochastic equations
- The algorithm for the Euler-Maruyama method is as follows:

Algorithm 1: Euler - Maruyama method:
Result: Numerical solutions of the SDEs system
define $f(X_t), g(X_t)$
input $t_0, X_{t_0}, \Delta t, n$
for $i := 0$ *to* $(n-1)$ **do**
  $B_i \sim N(0,1)$
  $X_{t_{i+1}} = X_{t_i} + f(X_{t_i})\Delta t + g(X_{t_i})\sqrt{\Delta t}B_i$
  $t_{i+1} = t_i + \Delta t$
  print t_{i+1} and $X_{t_{i+1}}$

Table of Parameters

- The parameters in bold are the ones whose values are estimated, and the rest of the parameter values are found online (ex. CDC, WHO).
- Deterministic model: maximum likelihood estimation
- Stochastic model: least squares estimation

Table 1. Parameter Values for Deterministic Model

Parameter	Parameter Description	Parameter Value for Bogota Dataset	Parameter Value for NYC Dataset	Percent Difference
Λ	Natural birth rate	0.01651	0.0572	246%
β	Transmission rate of COVID-19	0.8	0.91	13%
σ	Fraction of exposed individuals moving to infected	0.167	0.069	59%
γ	Recovery rate	0.969	0.76	22%
δ	Death rate due to COVID-19	0.0255	0.0308	21%
μ	Natural death rate	0.00553	0.0572	934%
κ	**Efficacy of vaccines in preventing COVID-19 infection**	**0.99**	**0.72112**	**27%**
α	**Overall rate of vaccination**	**0.01183**	**0.66195**	**5496%**
q	**Proportion vaccinated**	**0.0016**	**0.6899**	**43019%**
γ_1	**Recovery rate of individuals vaccinated**	**0.0007**	**0.05247**	**7396%**

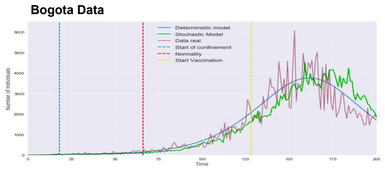
Table 2. Parameter Values for Stochastic Model

Parameter	Parameter Description	Parameter Value for Bogota Dataset	Parameter Value for NYC Dataset	Percent Difference
σ	Fraction of exposed individuals moving to infected	0.167	0.069	59%
δ	Death rate due to COVID-19	0.0255	0.0308	21%
μ	Natural death rate	0.00553	0.0572	934%
Λ	**Natural birth rate**	**0.07143**	**0.0682**	**5%**
β	**Transmission rate of COVID-19**	**0.8**	**0.988**	**23%**
κ	**Efficacy of vaccines in preventing COVID-19 infection of vaccines**	**0.21739**	**0.3424**	**57%**
α	**Overall rate of vaccination**	**0.10526**	**0.8154**	**675%**
γ	**Recovery rate**	**0.2**	**0.0543**	**73%**
γ_1	**Recovery rate of individuals vaccinated**	**0.09901**	**0.0452**	**54%**

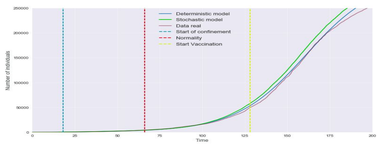
Results

In order to test the performance of our deterministic and stochastic models, we use the estimated parameters to carry out numerical simulations or the deterministic and stochastic models. On each of the figures below, we graph the real data, the result of the deterministic model, and the result of the stochastic model. We then compare the results of the two models and their accuracy to the data.

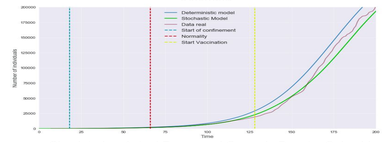
Bogota Data



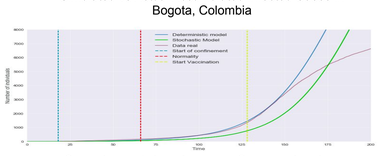
Simulated vs Actual Active Infected Cases in Bogota, Colombia



Simulated vs Actual Accumulated Infected Cases in Bogota, Colombia

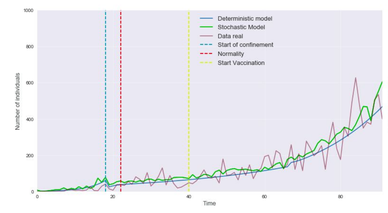


Simulated vs Actual Recovered Cases in Bogota, Colombia

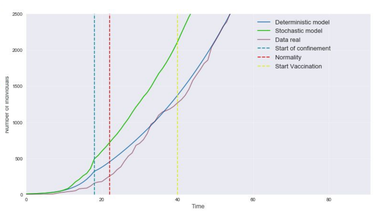


Simulated vs Actual Deceased Cases in Bogota, Colombia

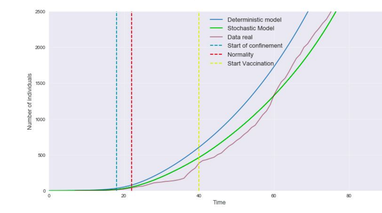
NYC Data



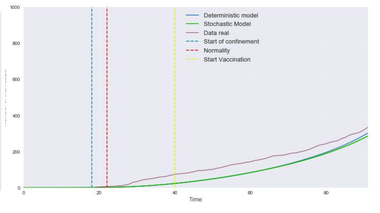
Simulated vs Actual Active Infected Cases in New York City, NY, USA



Simulated vs Actual Accumulated Infected Cases in New York City, NY, USA



Simulated vs Actual Recovered Cases in New York City, NY, USA



Simulated vs Actual Deceased Cases in New York City, NY, USA

Conclusion and Discussion

In this work, we studied the effectiveness of vaccines and infection in an effort to control the COVID-19 pandemic, and analyzed using real data from two socio-economically contrasting cities of Bogotá D.C. and New York City. While rate of transmission, **β**, is 23.5% greater for New York City, the city has a 57% higher vaccine efficacy and much higher overall rates of vaccination, based on the estimates for the stochastic model, compared to Bogotá D.C. Due to socioeconomic differences, vaccines are much more available in New York City. Higher vaccine efficacy could be attributed to the type of vaccines available in New York City (more mRNA-type vaccines) vs Bogotá D.C.

Future Work

Moving forward, we plan to incorporate multiple vaccines into our parameter estimation and numerical simulations. We want to compare the results of our model with different types of vaccines and in different countries.

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