Title: Epidemiologic Study of Prince George’s County COVID-19 Data over the period February 1, 2020 – September 30, 2020

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1. **Introduction**

Our project focuses on the Prince George’s County infection and death rates during the COVID-19 pandemic. A predominantly democratic county, it faced relatively typical infection rates for the virus, but also was predicted to have an interestingly high mortality rate.

We implemented the SIR and SEIR models described in class; we optimized these models to more effectively model and subsequently predict the infection rates and fatalities of COVID within the county.

1. **Background/Methods**

The SIR (Susceptible, Infected, Recovered) Model is a deterministic model that is intended to simulate states of an individual who has or has not been exposed to the disease we wish to model. It uses the three states listed above and presents the transitions as differential equations that we solved using the Euler method for initial value problems.

(Talk about SEIR here)

We used these models primarily because they are particularly inclined to model this exact situation: they are relatively simplistic and allow for the information gained from them to be optimized easily. By using the Euler method on the equations, we can quickly redo simulations when we need to change coefficients to better fit the measured data.

We parameterized the data using four general parameters: alpha (a), beta (b), gamma (c), and rho (p). Alpha is used to represent the infection period of the disease, or how long it stays transmissible after a patient becomes contagious. Beta we used to represent the number of daily contacts an infected individual has with susceptible people. In our data, we used R0 to represent b/a, or the number of individuals one infected person interacts with over their infectious period. Gamma was used to represent the fatality rate after infection. That is, what percentage of people died after being infected instead of recovering after their infectious period. Finally, we used rho to determine the undercounting factor of infections. Often, people would become infected with COVID and not report the illness to authorities or counting officials. Thus, they would be data points we would not know about, and we would have to scale the modelled infections down to represent that. We parameterized this model by creating an overall accuracy function, J, which includes differences between our predictions and measured data points.

(Presents Models and Algorithms designed for this problem.

Explanation of why the models/algorithms are the way they are.

Explain how these models are parametrized. What do these parameters mean.)

1. **Results**

For the SIR Model, much of what we obtained was relatively consistent with expectations.

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Above are the results for p = 1. The herd immunity for [0, 1] = 0.462 (about 46%), [1, 1] = 0.526.

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Above are the results for p = 2. The herd immunity for [0, 1] = 0.462, [1, 1] = 0.526.

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Above are the results for p = infinity. The herd immunity for [0, 1] = 0.406, [1, 1] = 0.462.

Here are what the prediction parameters for our program were estimated to be.

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Notice that the rho and gamma values are all relatively consistent except for the case where: [cI, cY] = [0, 1] and p = infinity. We see that the rho value is 1 and the gamma is 0.085.

Below are graphs for each of the models.

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1. **Discussion**

The results we obtained from this modelling were interesting. What remained constant was the relatively small death rate between each of them, and the fact that alpha almost consistently pushed the upper bounds of its range. We also discovered that the herd immunity numbers were much larger than expected. Around 40% of the population being completely uninfected does not seem to mirror the real-world virus very well.

**References**

Cite any source you used for your report.

PG Demographics: <https://elections.maryland.gov/pdf/vrar/2022_10.pdf>