A Feedback SIRD Model for the Spread of Infectious Disease with Application to COVID-19 Pandemic

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***Abstract*— The COVID-19 global pandemic has highlighted the importance of identifying effective ways to control the spread of an infectious disease in a population. A solid understanding of the dynamics and the underlying mechanisms that govern this spread is an important step toward such a goal. Susceptible-Infected-Recovered (SIR) models and their variants have played an important role in providing such insight. However, these models have limited explanatory and predictive power due to policy and behavior changes over time. Here we present a modified version of the standard SIR models by introducing feedback in the disease transmission rate. We apply this model to publicly available COVID-19 US and international infection data. We show this model is more robust to parameter variations due to public health interventions and has much better explanatory and predictive power**

I. INTRODUCTION

II. A FEEDBACK MODEL FOR THE EARLY SPREAD OF INFECTIOUS DISEASE

A. Modeling

B. Feedback Model

III. FITTING THE MODEL TO COVID-19 INFECTION DATA

A. COVID-19 Infection Data and Non-Pharmaceutical Interventions (NPIs)

The data to evaluate our model is from OWID (Our World in Data), a publically available database, from which we extract data about COVID-19 for different countries (i.e. total infections, daily tests, population). In order to fit our model to the data we must interpolate the current infections of a given region. We can model the current infections as

$$I(t) = I_{total}(t) - R_{total}(t) - D_{total}(t)$$

Which is to say the current infected is any of the total infected who have not yet recovered or died. Total deaths and total tested positive individuals are reported but we must estimate the recovered population. To do this we assume R_{total} is a shifted version of I_{total}. To determine the shift we consider that for most infections are resolved within 10 days of becoming symptomatic and for 3 days prior to syptoms the individual is infectious. Therefore, we use a shift of 13 to dertermine the recovered individuals which returns us with a realistic infection curve.

$$R_{total}(t+s) = I_{total}(t) - D_{total}(t+s)$$

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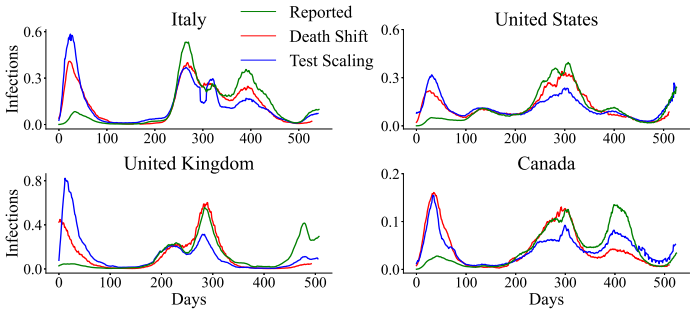

Fig. 1. Comparing methods of estimating current infections. Our method (blue) corrects the reported number based on the number of tests performed. This compensates for the under reporting of infections during the beginning of the pandemic. Another method using death scaling (red), yields different but comparable results. For all methods, scaling is arbitrary and purely serve as comparisons.

Next, we must consider that the given infection data for a region is highly dependent on the number of tests. Since relatively low testing was performed during the beginning of the pandemic, we expect the reported infections during this time to be an underestimation of the true numbers. There are multiple methods to estimate the true number of infections. We advocate for using the number of tests to scale each day accordingly. This is done by

$$I_{estimated}(t) = \alpha I_{reported}(t)/Tests(t)$$

A similar approach using test data has previously been applied successfully [1]. The scaling, α of $I_{estimated}$ is arbitrary and does not affect our model or it's predictive power. To normalize the data we let the scaler be such that the total infections over the period = .25. The results yielded by this method are similar in effect to other methods such as REMEDID [2], which uses death data and are compared in Figure 1.

B. Data Fitting Procedure

In order to fit the data, we must find the optimal parameters and simulate our model. Our parameters we need to fit are $A(0)$, $I(0)$, κ_1, κ_2, κ_3, β_1, β_2, and β_3. To do this we begin with reasonable random starting values of parameters and optimize using the Nelder-Mead method from scipy.optimize. This method is used since it is effective at escaping local minima, which our model is prone to having. This is done several times to explore a wide range of the space and to ensure a good fit. We are optimizing for a least squared error function.

Simulate using:

$$\dot{A}(t) = \frac{\beta_1}{1 + (\beta_2 I)^{\beta_3}} A(t) - \kappa_1 A(t)$$
$$\dot{I}(t) = \kappa_2 A(t) - \kappa_2 I(t)$$

Minimize:

$$\frac{1}{T} \sum_{t=0}^{T} (I_{actual}(t) - I(t))^2$$

IV. Analysis

A. Performance of the Model

Running our model on data from various countries yields promising results and can be seen in FIGURE TO BE ADDED. Typically the position and height of the major waves is captured well. This implies there is feedback on the number of infections, meaning the populus reacts to the recent infection numbers and tightens or loosens their behavior accordingly, changing the transmission rate. Across periods of high government intervention we expect our model to perform worse, since these interventions are immediate and non-gradual, but overall fit for most of the applied countries are still overall accurate.

1) Intervals of No NPI Activity: While data for NPI's (non-pharmaceutical interventions) typically aren't compiled under a single dataset, for some countries we have manually gathered data on when large government policies have taken place (i.e. Stay at home orders, business closures, mask mandates). For these countries even during periods of no NPI's we still observe oscillatory behavior in the infection curve. This supports our position for their being a degree of feedback within the populus beyond governmental measures.

2) Overall Performance:

3) Incorporating NPI Data:

4) Model Predictive Power:

B. Analysis of Feedback Model

V. CONCLUSIONS

THIS IS FOR TESTING THE BIBLIOGRAPHy. [3]

APPENDIX

Appendixes should appear before the acknowledgment.

ACKNOWLEDGMENT

The preferred spelling of the word acknowledgment in America is without an e after the g.

References

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