

A Novel SEIRV Compartmental Model for COVID-19

CoronaVIRES

Shinjini Ghosh, Lay Jain, Pawan Goyal

OVERVIEW



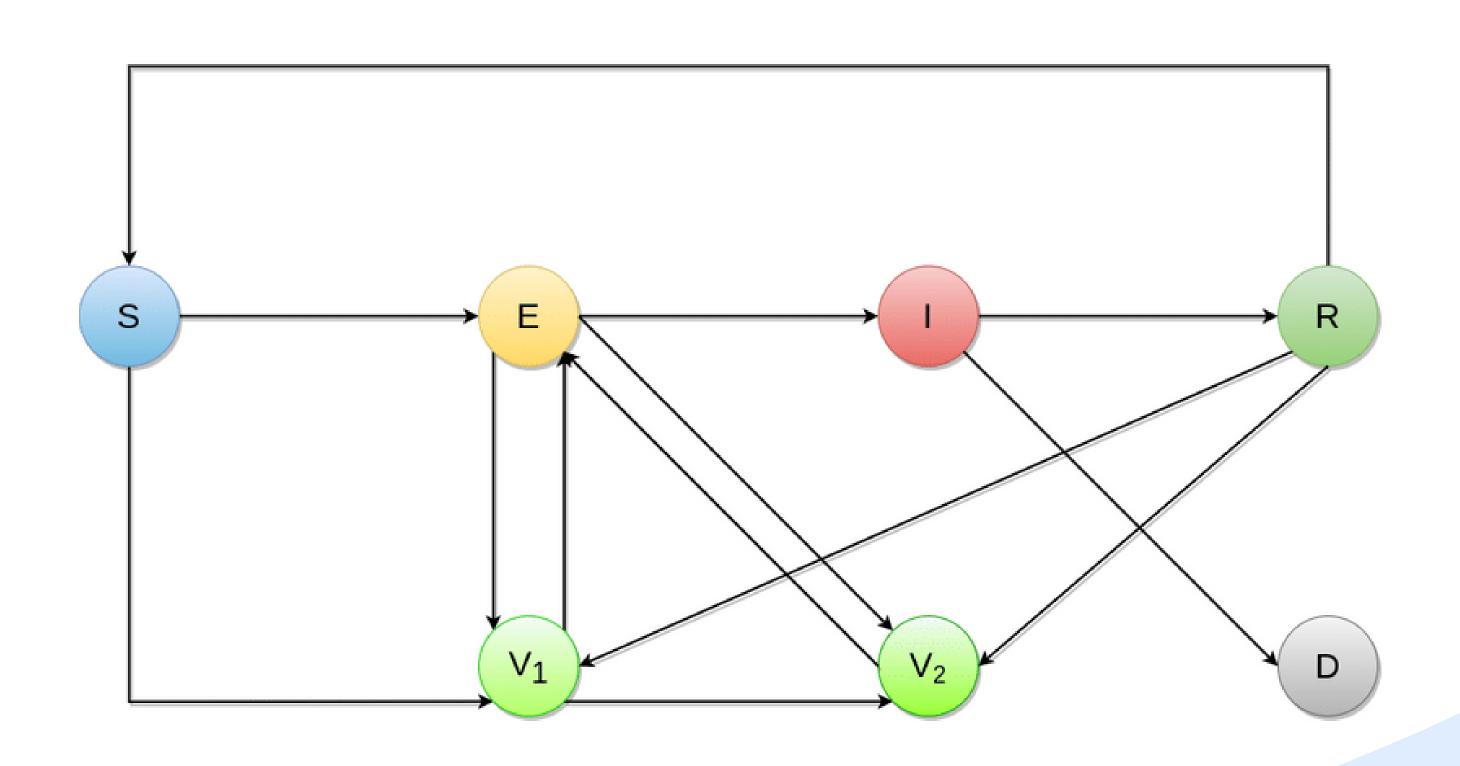


CoronaVIRES

- We developed an extension of the widely used SEIR model called SEIRV, introducing an additional Vaccination Compartment
- Using the model, we tried to fit the curves for deaths and infected people and tried to unravel the underlying dynamics
- We also tested our model for future predictions and compared it to the baseline SEIR model

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CoronaVIRES Model Structure



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MODEL DYNAMICS

$$\dot{S} = \alpha R_S - \frac{S}{N}\beta I - \frac{S}{N}\chi E - \rho S$$

$$\dot{V}_1 = \rho S + \rho R_S - \frac{V_1}{N}\beta I - \frac{V_1}{N}\chi E - \phi V_1$$

$$\dot{V}_2 = \phi V_1 + \phi' R_1 + (1 - \delta_2)I_2 - \frac{V_2}{N}\beta I - \frac{V_2}{N}\chi E$$

$$\dot{E}_1 = \frac{V_1}{N}\beta I + \frac{V_1}{N}\chi E - \theta E_1$$

$$\dot{E}_2 = \frac{V_2}{N}\beta I + \frac{S}{N}\chi E - \theta E_2$$

$$\dot{E}_S = \frac{S}{N}\beta I + \frac{S}{N}\chi E - \theta E_S$$

$$\dot{I}_1 = \theta E_1 - \delta_1 I_1 - (1 - \delta_1)I_1$$

$$\dot{I}_2 = \theta E_2 - \delta_2 I_2 - (1 - \delta_2)I_2$$

$$\dot{I}_S = \theta E_S - \delta_S I_S - (1 - \delta_S)I_S$$

$$\dot{R}_1 = (1 - \delta_1)I_1 - \phi' R_1$$

$$\dot{R}_S = (1 - \delta_S)I_S - \rho R_S - \alpha R_S$$

$$\dot{D} = \delta_1 I_1 + \delta_2 I_2 + \delta_S I_S$$

where $I = I_1 + I_2 + I_3$ $E = E_1 + E_2 + E_3$ $N = S + V_1 + V_2 + E_1 + E_2 + E_S + I_1 + I_2 + I_S + R_1 + R_2 + R_S + D$

Susceptible Exposed Infectious Recovered Vaccinated

Model Parameters

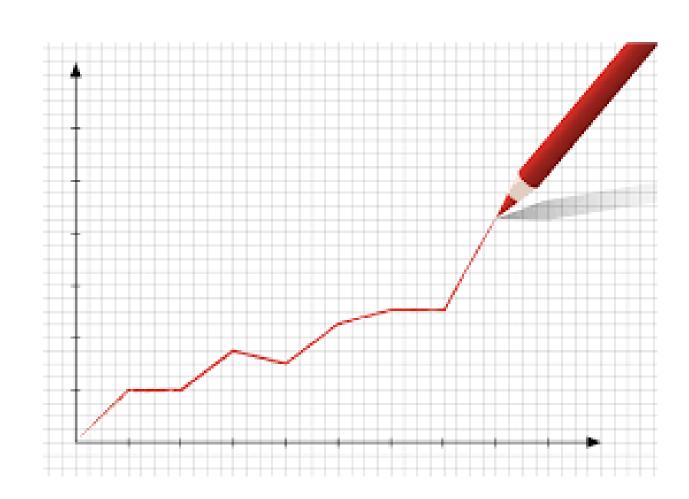


Parameter	Description		
α	Temporary Immunity rate		
β	Contact and infection rate of transmission per contact from infected class		
θ	Transition rate of of exposed individuals to the infected class		
δ_i	The death rate of the Infected classes		
ρ	The vaccination rate		

Comparing these parameters lets us delve into how different countries dealt with the pandemic and investigate underlying dynamics (e.g., how much are people mingling, how long does natural immunity typically last, etc.)

ESTIMATION OF MODEL PARAMETES





- The parameters of the model may be considered as proxies to various interactions in society.
- We used scipy.curvefit in order to fit the model curve
- We considered all the hyperparameters of the models as unknown and tried to estimate them through data

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Cleaning and Preprocessing the data

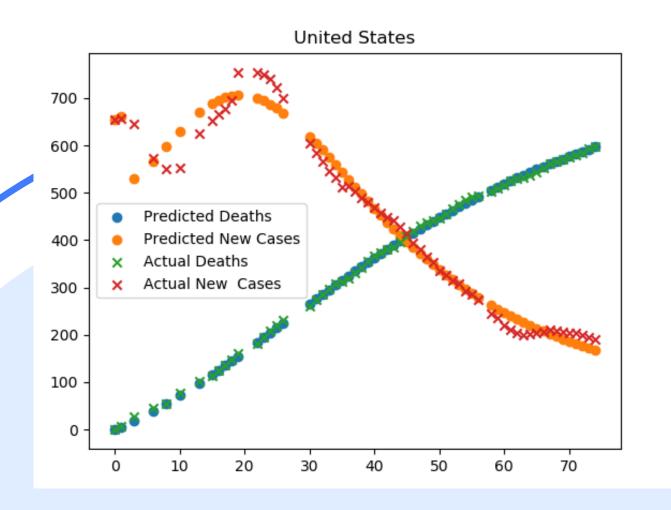
- We mainly focused on owid-covid-data and restricted our timeframe to the vaccination phase, namely from Jan 1, 2021, till present
- We then looked for the top ten countries in terms of the number of days since the country started its vaccination.
- We removed all the entries for which either vaccination or new_cases or new_deaths data were unavailable and then used this final processed data to fit the curve

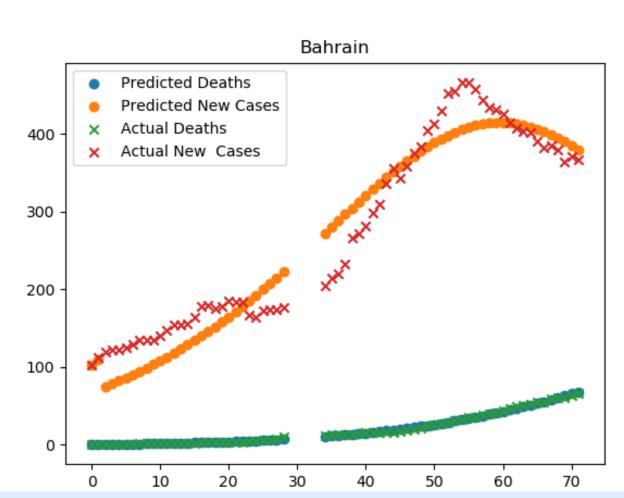


Standardization of Y Labels

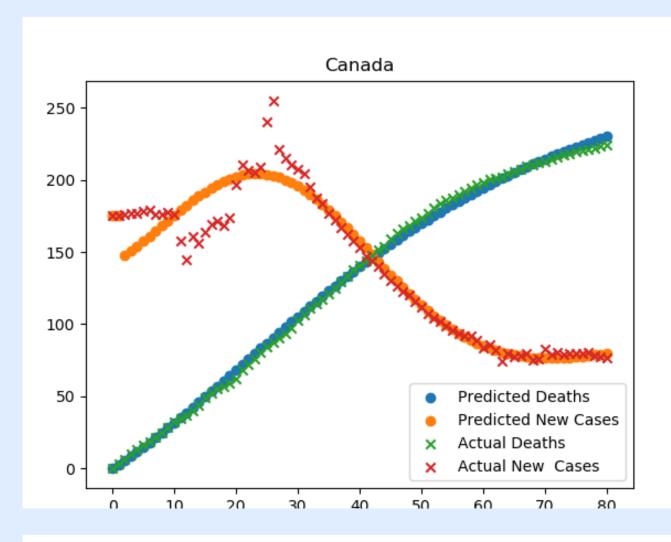


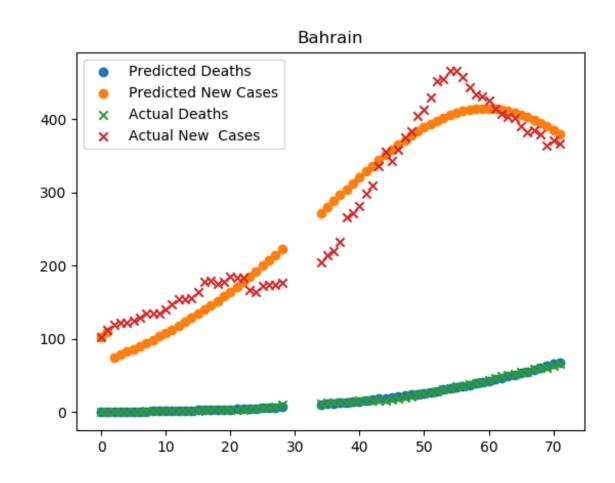
- We used new_death_smoothed_per_million, new_cases_smoothed_per_million and total_deaths_per_million to fit our model
- The primary motivation to choose the first two was the stability of derivatives over absolute value (thus preferring new_cases over total_cases) while the thought process behind total_deaths_per_million was to give more weightage to predicting correct deaths over correct infected cases.
- We further standardized our model for a unit population (thus dividing all the above relevant statistics by 10^6 and setting N = 1 in the above SEIRV model equations)
- This was a crucial step in fitting as it made all hyperparameters in the range (0,1), thus making it much easier for scipy.curve_fit to find the right fit.





Results







COVID-19 | 2021

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Understanding the parameters

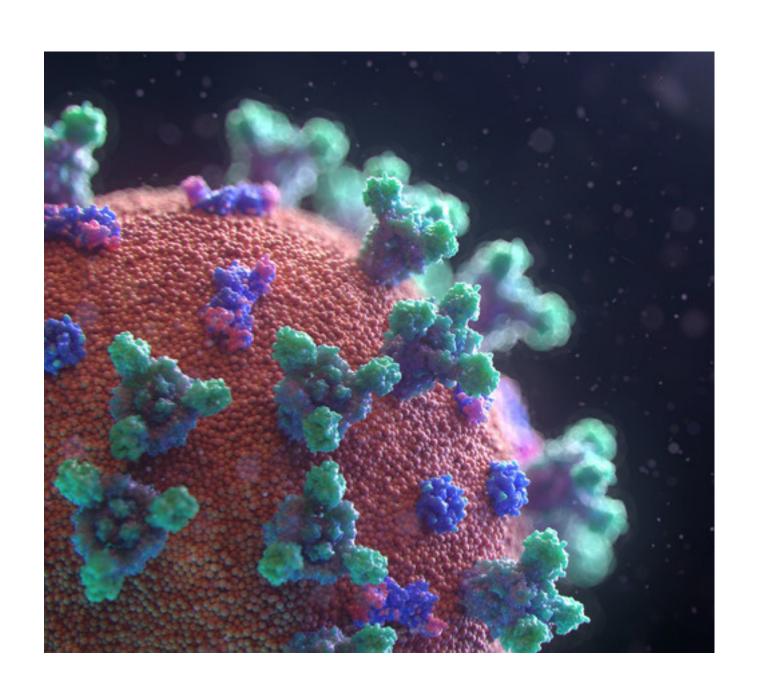
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Our model performs as expected on changing these parameters. For example, increasing interaction, or decreasing immunity results in more new positive cases in a day. Increasing vaccinations, reduces the death count. Similarly, increasing the disease fatality or reducing vaccine effectiveness increases the death rate.

Citizens

PREDICTING THE FUTURE

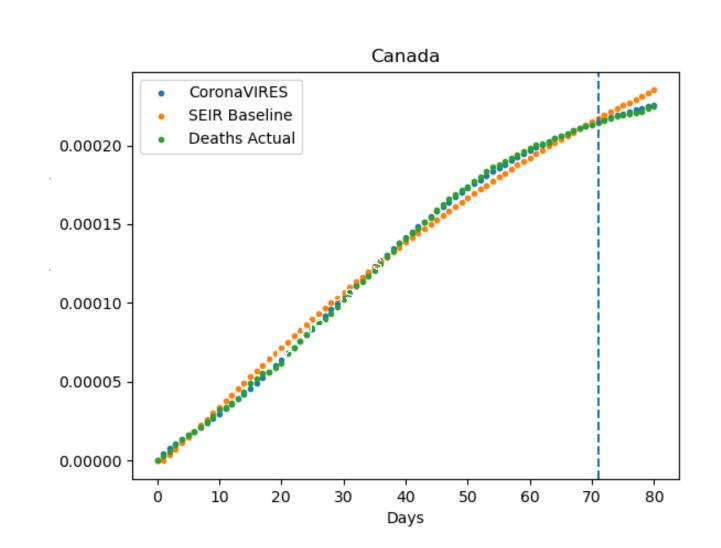


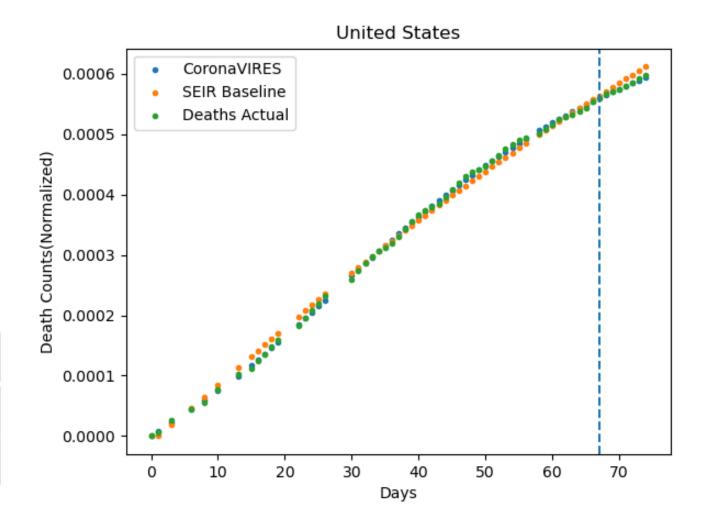


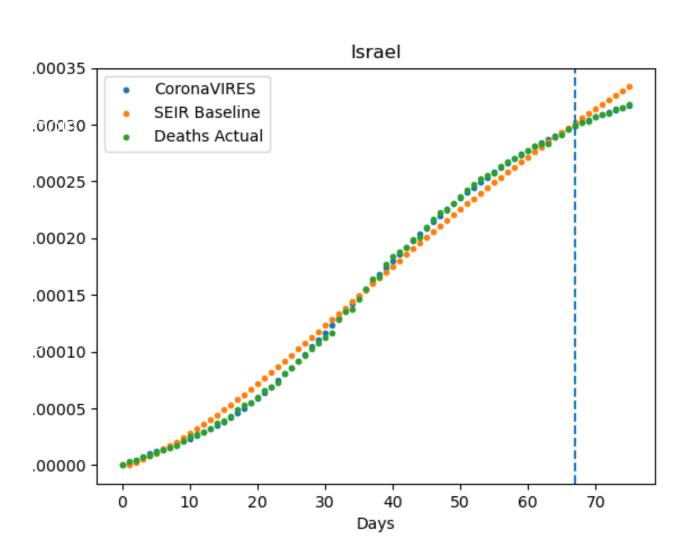
- We also used our model to predict future statistics.
- To this end, we train our model with a fraction of past data-points and compare the predictions with the remaining data-points.
- We used the SEIR model (without Vaccinations) as a baseline.
- We also calculated the root mean squared error for both the models and then results are tabulated on the table below

Testing our future predictions

Model Error×10 ⁶ /Country	Chile	United States	Canada	Israel
CoronaVIRES	2.07	2.19	1.23	5.91
SEIR Baseline	9.98	11.22	7.51	10.62





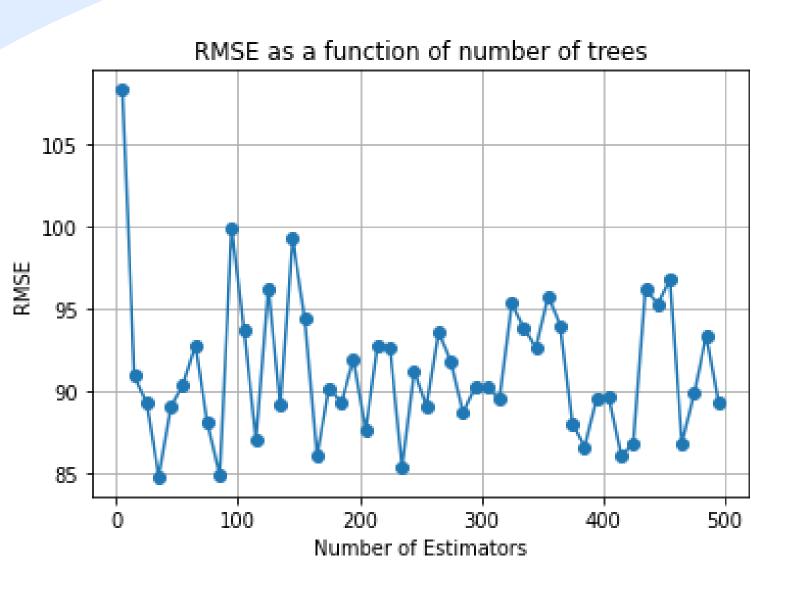






RANDOM FOREST MODEL





- Mean Absolute Error: 6.860685082449395 Mean Squared Error: 313.43947320621186
- Root Mean Squared Error: 17.704221903439073

- We also developed and tested a Random Forest Regression model.
- Train features are date, median age, stringency index of government policies, smoking, population density, hospital bed density and human development index.
- We attempt to predict the smoothed number of new cases per million people.
- Best model (least RMSE) uses 35 estimators and has accuracy 95.01% (MAPE value to the left).

CONTRIBUTIONS

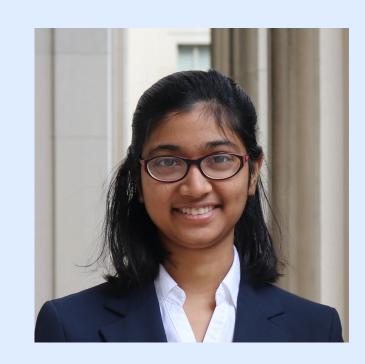
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- Introduced a novel SEIRV model named CoronaVIRES
- Built the model and used it to fit the curves for infections and deaths
- Investigated the parameters to investigate underlying dynamics
- Used our model to predict the future cases and deaths, especially in the face of vaccinations
- Can simulate any public policy measure to visualize its effects before they are implemented
- Also implemented a random forest regressor model



WHO WE ARE

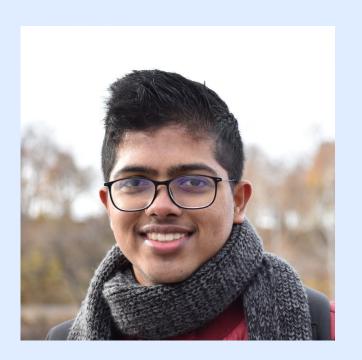
MIT Undergraduates



Shinjini Ghosh
Junior



Lay Jain
Junior



Pawan Goyal

Junior



THANK YOU!

We would love to hear from you

Phone Number

(857) 253-9545

Email Address

shinghos@mit.edu / layjain@mit.edu / pawan14@mit.edu

Respository

https://github.com/layjain/BRD-21