Geographical SEVIRD COVID-19 Model With Travel Restrictions

Nirmal Patel
Department of Systems and Computer Engineering
Carleton University
Ottawa, Ontario
nirmalpatel3@cmail.carleton.ca

***Abstract*—An existing SEVIRD (Susceptible-Vaccinated-Exposed-Recovered-Deceased) model is used to include effect of travelling population from one country to another country and how it affects the spread of the virus. The model for SEVIRD with travel restriction is designed using Cell-DEVS formalism. To define irregular cells (each country is one cell in cellular automata model) the Cadmium JSON library is used. This paper describes geographical modeling of pandemic model with movement of the population from one cell to another using Cell-DEVS and Cadmium JSON library. The input parameters to the model are not accurate according to actual data, but the results and effects of imposing travel ban or restriction can be studied using this model and best possible strategy can be employed.**

***Index Terms*—SEVIRD, Cell-DEVS, Cadmium JSON, Geographical modeling**

I. Introduction

The new coronavirus spread started from late 2019 and is still in existence with more than 3 variants in almost all the countries around the globe. The countries in which the population density is higher the severity of the virus is experienced more due to high fraction of population being infected and resulting in higher number of deaths. Now, the countries in which the virus spread is not as bad as these countries with dense population would likely impose some restrictions or even ban an individual from these countries to enter their country.

In this paper, we will look into existing SEVIRD model which includes two doses of vaccination for the susceptible population and here it is assumed that once an individual is recovered from the infection of the virus, they will not become susceptible again.

After that, the travel rules are applied to this model, which allows us to observe the effectiveness of travel restriction. To compare different strategy, three kind of travel rules are studied. The first one being, no travel restriction at all, that is any individual can travel to any neighbouring cell(country) without any condition. The second scenario is in which there is total travel ban from one country to all/some of it's neighbouring countries, this simulates the effect of country-wide lockdown, in which individuals can interact internally and hence spreading the virus within the country. The last one which, most of the countries are using currently, as they cannot afford lockdown any more. In this strategy there are some conditions an individual should satisfy to travel, that is his original country's 75% of population is fully vaccinated (have received at least 2 doses of vaccine or 75% of population is fully recovered from infection (in the case where re-susceptibility is not considered) and less than 10% of population is infected. All the results from these three strategy is analyzed and presented in this paper. In next section, the present SEVIRD model is described.

II. Existing Cell-DEVS SEVIRD Model

The existing Cell-DEVS model implemented using Cadmium JSON library includes geograohical cells which shares boundary with some other cells. In this model the neighbourhood of a geographical region (cell) is defined by the geographical regions which share a physical boundary with it. The length of the boundary shared between two regions is also used for calculating correlation factor of these two neighbouring regions. In order to study the pandemic in geographical sense with spatial and temporal evolution of the virus we need to use cellular automata based model.

Regular cellular automata(CA) is a mathematical formalism that describes an N dimensional space of adjacent "cells" that contain values that can change over time. Any number of dimensions may be represented in CA, but the most practical models are in either two or three dimensions. Many pandemic based CA models have been studied in the past [1]. But these models does not necessarily model the geographical aspect of the scenario. Therefore, it overlooks the complex nature of geography and the movement of the population from one location to another and consequently spreading the virus. So, by simplifying the pandemic models using regular cellular model we neglect a very important aspect which plays major role in spreading the pandemic.

Now if we decide to use irregular cellular model with geographical regions as cells, the question is how is these areas related to each other. A simple heuristic principle of geographical relation is: Every geographical area is related to every other geographical area, but near areas are more related than distant areas [2]. The simple correlation factor can be assumed to be binary 0 or 1, if the two geographical areas are connected with each other than correlation factor is 1 else it is 0. But these correlation factor relation doesn't account for how strongly or weakly two geographical areas are connected.

To calculate the population flow from one geographical region to another, we could use the length of shared boundary by the two regions and the total circumference of a region. To calculate the shared boundary and total length of a region we have to use a "gpkg" file which contains geographical data in terms of latitude and longitude which corresponds to a polygon of a geographical region. And using this ".gpkg" file and geopandas library from python we can calculate the desired geographical parameters to calculate correlation factor between two regions *i* and *j*,

$$c_{ij} = \frac{\frac{z_{ij}}{l_i} + \frac{z_{ji}}{l_j}}{2} \tag{1}$$

In eq.(1), z_{ij} and z_{ji} denotes the length of shared boundary between two regions, intuitively we can say that $z_{ij} = z_{ji}$. And the lengths of the regions are denoted by l_i and l_j. Here the correlation factor between two regions i and j, is same both ways, meaning $c_{ij} = cji$, the movement of population between two regions is dependent of same correlation factor. However, in reality it is not true, for instance the flow of population from India to USA is way higher than the flow of population from USA to India. But for the simplicity we can assume the flows from and to for two countries is same.

Here we have only considered correlation factor between two geographical regions if they share a common boundary, but realistically it is not true as the population can flow from one region to another via air travel even if they don't share physical boundary. We need to define correlation factor for this case as well, which is described in next section. But first, we will look into geographical SEVIRD specification for Cell-DEVS formalism.

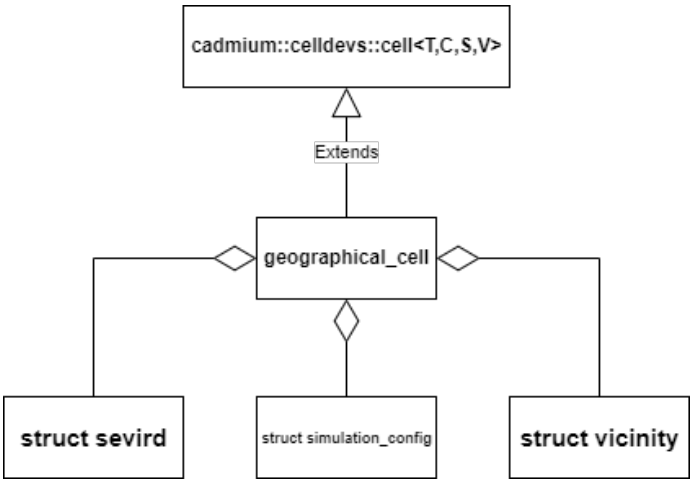

Fig. 1. Class diagram for geographical cell

III. Geographical SEVIRD Specification

The geographical SEVIRD model using Cell-DEVS formalism can be described as coupled Cell-DEVS model, where each cell is a geographical region and it has a unique cell-id(it will be country name in our case). Each geographical cell is consist of SEVIRD state variables, neighborhood and

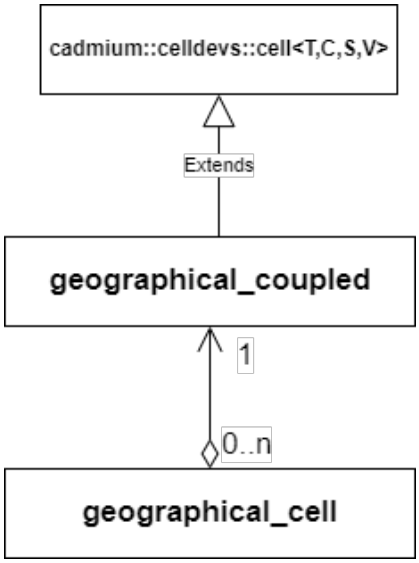

Fig. 2. Example of a figure caption.

simulation configuration data. All geographical cells are placed in a top level coupled cell model called geographical_coupled. All the state variables, configuration data and neighbourhood data about each cell is placed in a single JSON file, which is used by the top model class. The detailed information about how this model is implemented can be found here [3]. The population of each geographical region is divided into five age groups to better understand effect of virus on different age group. The differential equations to calculate population in different phase of the pandemic SVERID model is given by following equations. But first we need to discretized the state variables,

$$DS^t_{i,a} = \frac{[AS^t_{i,a}]}{A} \tag{2}$$

$$DE^t_{i,a}(q) = \frac{[AE^t_{i,a}(q)]}{A} \tag{3}$$

$$DI^t_{i,a}(q) = \frac{[AI^t_{i,a}(q)]}{A} \tag{4}$$

$$DR^t_{i,a}(q) = \frac{[AT^t_{i,a}(q)]}{A} \tag{5}$$

$$DF^t_{i,a} = \frac{[AF^t_{i,a}]}{A} \tag{6}$$

Here q denotes number of phases for respective state. 'A' is the precision divider which is multiplied with the state variable and then the resultant value is rounded (denoted by the square brackets) and divided again by 'A' to get discretized value.

Now we can run the model with two configuration, with re-susceptibility enabled, i.e., the recovered population becomes susceptible again after the recovery phase and with re-susceptibility disabled, which assumes that an individual is immune to the virus after getting infected and recovered once as his body has developed antigen for the virus.

TABLE I
TRANSITION RULE SYMBOLS

Symbol	Definition
$f_a(q)$	Fatality rate of Infected stage q for age group a, after correcting for hospital capacity effects
$\lambda_a(q)$	Virulence rate for Infected stage q of age group a
$\mu_a(q)$	Mobility rate during Infected stage q for age group a
c_{ij}	Geographical Correlation factor between cell i and j
k_{ij}	Correction factor applied to both cell i and j
$\epsilon_a(q)$	Incubation rate of exposed stage q for age group a
$\gamma_a(q)$	Recovery rate of Infected stage q for age group a

The transition rules to determine state variables for next time stamp is given as follow,

$$F_{i,a}^{t+1} = F_{i,a}^{t} + \sum_{q\epsilon\{T_e+1,\ldots,T_e+T_i\}} f_a(q) I_{i,a}^{t}(q) \tag{7}$$

$$E_{i,a}^{t+1}(1) = \sum_{j\epsilon\{1,2,\ldots,k\}q\epsilon\{T_e+1,\ldots,T_e+T_i\}} c_{ij}k_{ij}\lambda_a(q)\mu_a(q)S_{i,a}^{t}I_j^{t} \tag{8}$$

$$E_{i,a}^{t+1}(q) = (1-\varepsilon_a(q-1))\cdot E_{i,a}^{t}(q-1) \tag{9}$$

$$I_{i,a}^{t+1}(T_e+1) = E_{i,a}^{t}(T_e) + \sum_{q\epsilon\{1,\ldots,T_e-1\}} \varepsilon_a(q) E_{i,a}^{t}(q) \tag{10}$$

$$I_{i,a}^{t+1}(q) = I_{i,a}^{t}(q-1)(1-\gamma_a(q-1)-f_a(q-1)) \tag{11}$$

$$R_{i,a}^{t+1}(T_e+T_i+1) = I_{i,a}^{t}(T_e+T_i) + \sum_{q\epsilon\{T_e+1,\ldots,T_e+T_i-1\}} \gamma_a(q) I_{i,a}^{t}(q) \tag{12}$$

$$R_{i,a}^{t+1}(q) = R_{i,a}^{t}(q-1) \tag{13}$$

$$S_{i,a}^{t+1} = 1 - \sum_{q=1}^{T_e} E_{i,a}^{t+1}(q) - \sum_{q=T_e+1}^{T_e+T_i} I_{i,a}^{t+1}(q) - \sum_{q=T_e+T_i+1}^{T_e+T_i+T_r} R_{i,a}^{t+1}(q) - F_{i,a}^{t+1} \tag{14}$$

All the equations (7) to (14) are from [3], and is not explained in detail here. These equations are used as base model and extended for vaccinations for the population with two doses and further include travel rules which allows the population to migrate from one geographical regions which is explained in next section. The configuration variables used in the equations above is given in table I.

Existing model also considers the hospitality capacity to determine the fatality rate, if the total infected population cannot be served by hospitals then naturally the fatality rate should go up,

$$f_a(q) = \begin{cases} f_a(q), & \text{if } \sum I < HospitalCapacity \\ f_a(q)F, & \text{if } \sum I < HospitalCapacity \end{cases} \tag{15}$$

Here $f_a(q)$ is initial fatality rate for population in age group a and F is constant fatality rate multiplier. The calculation for correlation factor different than the existing model. The calculation for correlation factor and travel rules is explained in the next section.

IV. EXTENSION OF THE EXISTING MODEL

A. Correlation Factor

In the existing model the correlation factor depends only on the length of shared boundary and the length of the region itself. But this gives correlation factor of 0 if the two geographical regions are not connected with each other by land. To study the effect of travelling population we need to consider air-travel as well. To include the effect of air travel as well, we can use the distance between two countries as the parameters to calculate the correlation. Intuitively, the more the distance between two countries the less correlation they will have. For example, travelling from France to Canada is faster and easier compared to travelling from Japan to Canada. Also we will only consider direct flights as the indirect flights will be automatically accounted for in our direct flights.

```
def distance_correlation(gdf, id1, id2):
    g1 = gdf[gdf[area_id] == id1].geometry.iloc[0]
    g2 = gdf[gdf[area_id] == id2].geometry.iloc[0]
    dist = g1.boundary.distance(g2.boundary)
    if(dist==0):
        return shared_boundaries(gdf, id1, id2)
    return A/dist
#distance_correlation
```

Fig. 3. Function for calculation correlation factor.

In Figure 5, the python function for calculating correlation for two regions which are not connected by the land is given. Here the first parameter gdf is the gpkg file for our geographical regions. And the other two parameters, ids, are the cell-id for the regions for which we need to calculate correlation. First we get the polygon defined by those id from the gdf object and then we use geopandas distance function for calculating distance between the boundaries of two polygons. If the distance is 0, that means these two regions are connected by land, then we go back to our original function from equation 1. If distance is not 0 then we inverse the distance and multiply by a large constant (100,000) to get reasonable value for the correlation. After we have calculated the correlation factors, we can generate out scenario JSON file and run the existing model without any changes and it will give us the simulation data. But we need to add some rules to enable the population flow from one region to another.

B. Travel Rules

We can include three variants for travel rules. Which are described individually as follows,

1) No Travel Restriction: Applying travel restriction is dependent on each country, different countries may use different restriction strategy. This strategy is defined in the configuration JSON property called "travel_restriction". If the "travel_restriction": "none" meaning there is no travel restriction to enter this country. Anyone from another region can enter this region without any conditions. As we can suspect this should lead to more exposed and consequently more infected population.

2) Total Travel Restriction: Total travel restriction is opposite of no travel restriction, in which a country may impose complete ban on the incoming passengers and closing the borders for individuals from another countries. This strategy will impose a country wide lockdown, in which individuals are free to move within the country but are not allowed to travel international. Since these limits number of susceptible and exposed population to its own population, we can expect to lead far less infection compared to no travel restriction strategy.

3) Partial Travel Restriction: As we know no travel restriction will lead to far more fatalities and total travel restriction may effect the economy of the country. Therefore, most country has applied partial travel restriction for international travel. In this strategy a country can impose different rules for individuals entering the country. But since we are considering a country as a cell and the population is divided in different states (susceptible, infected, exposed, vaccinated), we can only apply restriction based on these states. For example in the model the JSON parameter "travel_restriction": "partial" means that the travelling individual's origin country's 75% of population should be vaccinated or 75% of the population should be recovered and less than 10% of the population is infected and then also only vaccinated individual can enter the country. As we can see it restricts a lot of exposed travellers which gives the results comparable with total travel restrictions and also allows travel. It is an ideal strategy which does not effect economy as much and also restricts the spread of the virus to an extent.

In the next section, we will analyze results using different travel restrictions and also by changing the re-susceptibility variable.

V. Results

For simulating the described model with cadmium Cell-DEVS, we have used 13 countries and used QGIS to get the gpkg file and geojson file for generating the scenario and visualizing the results. The countries used are given in the figure (4), In other csv file the list of countries are given which denotes the relation from which we can determine if it is possible to travel from one country to another in one day or not. For instance, the adjacency csv file will have an entry 2,12 as it is possible to travel from Canada to USA in one day, there will be an entry 12,2 in this file as well. Please note that, the entries filled in the adjacency csv is not necessarily mimic the actual air travel scenario. Also, if there is no entry from one country to another it is still possible to travel, it is just that the passenger will have to go to another country first and then they can go to the destination. However, it will take as many days as there are hops in between. In the upcoming subsections we will try to study effect of different travel restriction strategy.

COUNTRY_ID	population	Name
1	25928876	Australia
2	38222087	Canada
3	83953870	Germany
4	5822172	Denmark
5	46739249	Spain
6	119093189	Ethiopia
7	65492887	France
8	1399018324	India
9	125874548	Japan
10	2953172	Qatar
11	145903457	Russia
12	333726738	United States of America
13	60349065	South Africa

Fig. 4. Countries used for running the model

A. No Travel Restriction

As we can expect with no travel restriction there will be steep rise in the infections initially and as the population is vaccinated around the world, the total number of infections will come down, as we have considered that re-susceptibility is not possible. The configuration regarding vaccination, re-susceptibility and travel restriction is given below,

```
"Re-Susceptibility": false,
"Vaccinations": true,
"travel_restriction": "none"
```

Fig. 5. Default configuration

As we can see from figure 6, there is a steep rise in exposed and infections in a very few days. This figure shows the aggregate population data, so by allowing travel in the pandemic we can see there are high number of infections across the countries. In this case we have considered that the re-susceptibility is false, that means once an individual is recovered they cannot get infection again.

The second case we can consider with no travel restriction is by enabling re-susceptible. We should get more exposed and infected population due to re-susceptibility and consequently the death across the countries should also rise up. Figure 7 shows the data for this scenario. Also it is worth comparing newly exposed, infected and recovered population fraction on

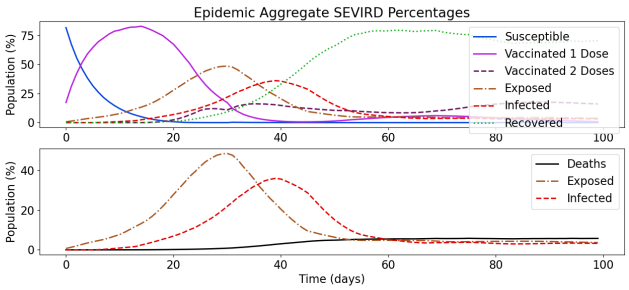

Fig. 6. Aggregate SEVIRD for re-susceptible disabled, vaccination enabled and no travel restriction

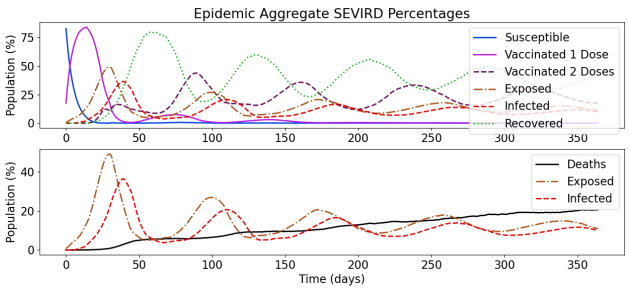

Fig. 7. Aggregate SEVIRD for re-susceptible enabled, vaccination enabled and no travel restriction

each day. Figure 8 and 9 shows newly exposed, infected and recovered population for re-susceptibility disabled and enabled respectively. We can see that the new exposed and infected

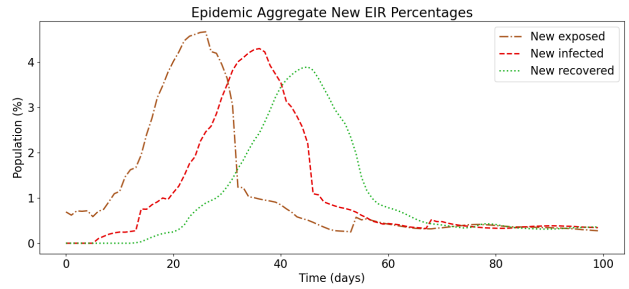

Fig. 8. New Exposed, Infected and Recovered population for re-susceptibility disabled

population is higher compared to figure 8, we can see only slight increase in percentage for the first spike but since it is for aggregate population, even small increase in percentage means millions of exposed and infected cases in this 13 countries combined. Moreover, in the re-susceptibility disabled case, the exposed and infected population comes down and saturates at 0 eventually, but in the re-susceptible enabled case it oscillates between 1 and 2%, which will lead to a high number of fatality.

B. Total Travel Restriction

The total travel restriction strategy, is completely opposite of the no travel restriction. In this case no individual is allowed to travel internationally. As we can expect total number of

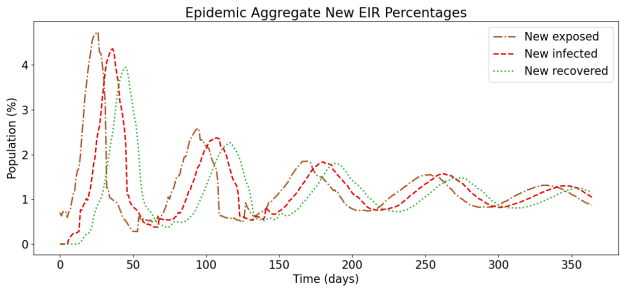

Fig. 9. New Exposed, Infected and Recovered population for re-susceptibility enabled

exposed and infected population should be lower compared to no travel restriction in both re-susceptible disabled and enabled cases. If we compare figure 6 and 10 then by only

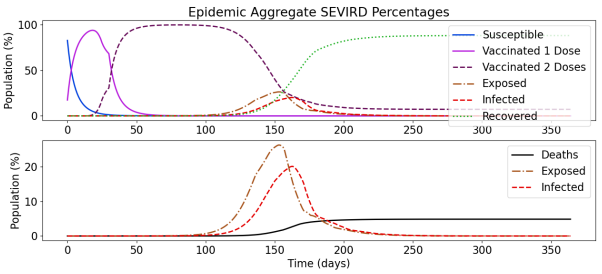

Fig. 10. Aggregate SEVIRD for re-susceptible disabled, vaccination enabled and total travel restriction

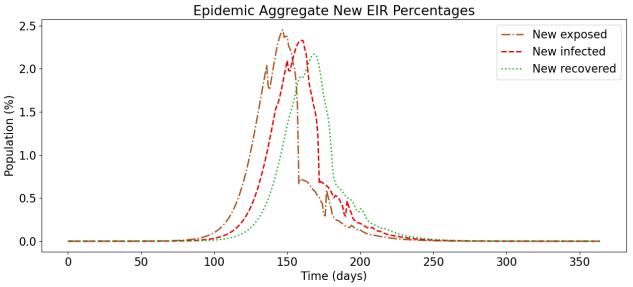

Fig. 11. New Exposed, Infected and Recovered population for re-susceptibility disabled

changing travel restriction from none to total leads to almost half exposed population and that too very late in simulation time, in no travel restriction case the exposed cases rises to 40% in 20-30 days, while in total travel restriction total exposed cases rises to 20% after 100 days. Which means the governments and the medical facilities have more time to better handle the pandemic. Same goes for new exposed and infected population it peeks up to only 2.5% whereas it was more than 4% new cases with no travel restriction. Here also it takes 150 days to peek number of new cases each day compared to 40 days with no travel restrictions. Now, it is also worth analyzing how total travel restriction strategy behaves when re-susceptibility is enabled.

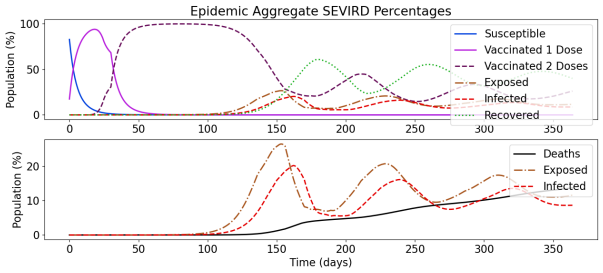

Fig. 12. Aggregate SEVIRD for re-susceptible enabled, vaccination enabled and total travel restriction

As expected the epidemic has spread more compared to figure 10 and 11, but it is still less severe and delayed compared to figure 7 and 9. Also from the results from no travel restriction and total travel restriction we can notice that the graphs for total travel restriction are smoother compared to no travel restriction, it is because in no travel restriction at each day a small but random fraction of population travels from one country to another, and introducing randomness in the total population of that country.

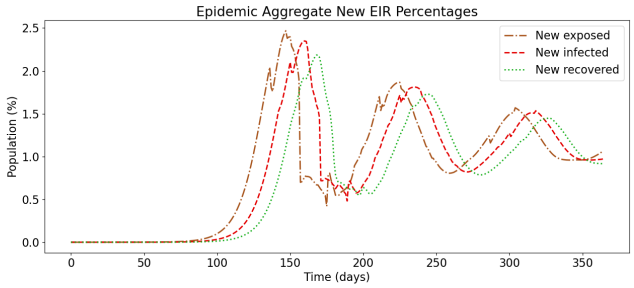

Fig. 13. New Exposed, Infected and Recovered population for re-susceptibility enabled

C. Partial Travel Restriction

Now let us look into a strategy that falls in between the two discussed before. With partial restriction there will be some conditions to travel, which must be satisfied to be eligible to travel. We should get the results close to total travel restrictions even after allowing some travel. From the figure 14 we

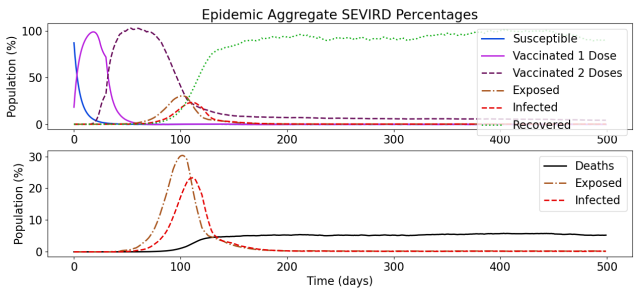

Fig. 14. Aggregate SEVIRD for re-susceptible disabled, vaccination enabled and partial travel restriction

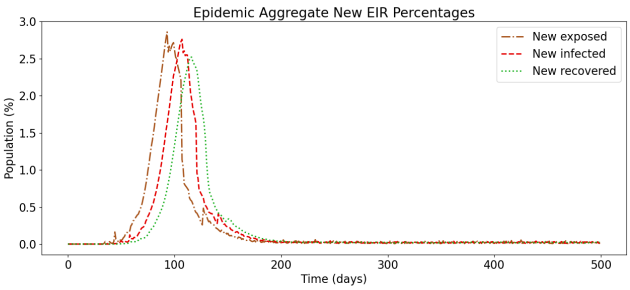

Fig. 15. New Exposed, Infected and Recovered population for re-susceptibility disabled

can say that total exposed cases are lower compared to no travel restriction (30 compared to 40), but they are higher compared to total travel restriction. Also new exposed cases are higher compared to total travel restriction but again is lower compared to no travel restriction. In terms of number of days it takes to peek the new exposed cases it peeks after around 100 days, where as it has peeked after 150 days in total travel restriction case. But it is still very late compared to no travel restriction (20 days). Again it is worth observing the re-susceptible enabled scenario. As expected, it behaved

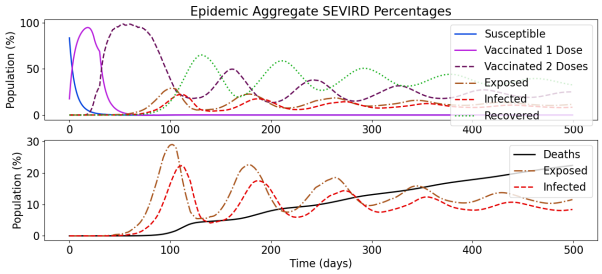

Fig. 16. Aggregate SEVIRD for re-susceptible enabled, vaccination enabled and partial travel restriction

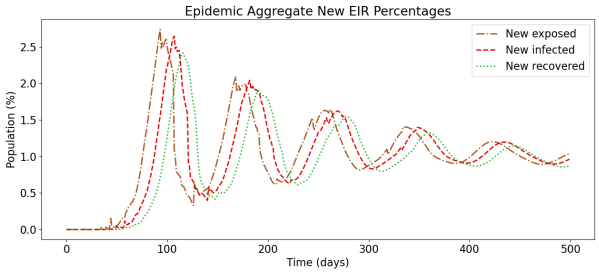

Fig. 17. New Exposed, Infected and Recovered population for re-susceptibility enabled

similar to previous two scenarios with just the change in the peek new exposed cases in a day and total exposed cases peek, lower compared to no travel restriction and higher compared to total travel restriction.

VI. Conclusion and Future Work

In conclusion, it is worth noting that no travel restriction policy will lead to severe pandemic outbreak around the glob and also will lead to more deaths. Ideally, we would like to employ total travel restriction policy but it is not feasible for the world economy. So, the idea strategy would be to employ partial travel restrictions and do a trade-off for total cases with allowing essential travel.

This model can be extended to cover the asymptotic active cases, introduction of new variants and booster shots for the population and also dynamic travel restriction policies, like if the pandemic outbreak peeks in other countries beyond certain threshold then impose total travel restriction otherwise impose partial travel restriction with variable parameters.

References

[1] S. Zhong, Q. Huang, and D. Song, "Simulation of the spread of infectious diseases in a geographical environment," Sci. China Ser. Earth Sci., vol. 52, no. 4, pp. 550–561, 2009, doi: 10.1007/s11430-009-0044-9.

[2] N. Waters, "Tobler's First Law of Geography," Dec. 2017, doi: 10.1002/9781118786352.wbieg1011.

[3] G. Davidson, "Geographical SEIRDS COVID-19 Model", https://github.com/SimulationEverywhere-Models/Geography-Based-SEIRDS-Vaccinated/blob/master/Geographical%20SEIRDS%20COVID-19%20Model.pdf