# Integrating COVID-19 compartmental models and DL models

jabir and nelson October 2021

## 1 The Idea

Its is well known that the prediction accuracy of neural networks is higher than that of traditional prediction methods. This is primarily related to the neural network's features. Neural networks are good at capturing the properties of complicated systems with high non-linearity that are difficult to represent using a precise mathematical model, and they are also very adaptable. In-fact COVID-19 dynamics within populations is a complex system with random mutation of the virus and due to the complexity of social mobility. LSTM layer is a type of Recurrent Neural Network (RNN) that utilizes learning from concurrent data.

Initially, we had this exciting idea of forecasting COVID-19 trends by predicting parameters of deterministic compartment based model for COVID-19 in each time step from trends in previous time steps using some deep learning models. And then we the solve the compartmental model ODE's to predict the trends in the particular time step, and so on with the succeeding time steps. But unfortunately, from a recent google search, we found that, people had already thought of it, and they had already done fantastic works based on this idea, especially using LSTM, as in [1, 4]. And they have got very good results. Therefore, we will try to give a short combined review of [1, 2, 3, 4] in this report and propose to use the idea in our project.

## 2 Compartmental modeling for infectious diseases

Regardless of the nature of transmissibility of human infectious diseases, the individual life-course of infection can be conveniently represented by a sequence of transitions between a few epidemiological classes, or compartments, triggered by specific processes and parameters. For new pathogens, such as a pandemic flu virus, all individuals are initially susceptible to the infection (class S), which they acquire at a rate  $\lambda$  entering the exposed class (E), a latency or incubation phase where individuals are infected, i.e. the virus is replicating in their body, but not yet infective, which they become at some rate  $\alpha$ . Individuals belonging

to the infective class (I) will usually recover, at a rate  $\gamma$ , acquiring immunity and entering the removed class (R). Such modelling can be illustrated as shown in Fig. 1

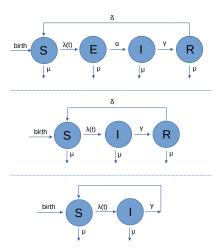


Figure 1: The compartmental representation SEIRS, SIRS and SIS models for some important classes of infections of individual course. The circles are identified epidemiological classes and arrows are marked as the process of class change, entry and exit due to demographics.

Based on this illustration of the individual course, we can model the spread of an infectious disease by describing the dynamics of infections at the population level, by assigning a dynamic variable to each compartment denoting the number (or the proportion) of individuals in that class at each instant of time. So, lets denote the total population size and N, and X (S = X /N), H (E = H /N), Y (I = Y /N), Z (R = Z /N) as the numbers (proportions) of individuals who respectively occupy the various classes at time t, with N = X + H + Y + Z , and S + E + I + R = 1.

The population as a whole can be related to concept of homogeneous (or random) mixing, which in this context, refers to an infection spreading by direct person-to-person contacts in a closed homogeneous social medium, the population, whose agents have an approximately identical social activity. So, if C is the number of contacts made by a susceptible individual per unit time, then the probability that the contact made is with an infected individual is obviously I = Y/N. And if  $\beta_I$  is the probability that the disease will be transmitted to the susceptible individual from the infected individual, then the rate  $\lambda$  at which individuals leave from the succeptible class S in Fig. 1 can be written as  $\lambda =$ 

 $\beta_I CI$ . Setting  $\beta = \beta_I C$ ,  $\lambda = \beta I$ .

Now, assuming that a population N has an unique and globally stable equilibrium  $N_e$  such that birth rate  $b(N_e)$  and mortality  $m(N_e)$  rate of the population are the same, i.e.,  $b(N_e) = m(N_e) = \alpha$ , and that the population is at this steady state, then we can translate the SEIRS diagram in Fig. 1 into the following mean-field system of ODEs,

$$S' = \mu(1 - S) + \delta R - \beta SI \tag{1}$$

$$E' = \beta SI - (\alpha + \mu)E \tag{2}$$

$$I' = \alpha E - (\gamma + \mu)I \tag{3}$$

complemented by R = 1 - S - E - I. Thus, the Model of Eqs. 1-3 is the so-called deterministic SEIRS model.

#### 2.1 SEIR modifications for COVID1-19

People had considered different modifications of SEIR model, such as adding extra compartments as done in [4], or combining multiple SEIR models with different parameters in-order to model spread between networks (eg. cites, house holds, workplaces etc) as used in [1], specifically for modeling COVID-19 spread with better accuracy.

## 3 Methodologies of incorporating DL models to compartmental models

Ref.[3] where the first to propose a deep learning based solution for Covid-19 spread prediction solely based on the known reported cases of Covid-19. They designed a deep neural network, which consist of LSTM (Long Short Term Memory) layer, dropout layer, and fully connected layers, to analyze the reported Covid-19 cases and predict the possible future scenarios for the spread in China, Europe, Middle East and worldwide. Their approach predicts the cumulative number of cases, cumulative number of deaths and daily new cases worldwide. All their predictions are done for the next 10 days given the actual time series data of Covid-19. They evaluate their approach on the last 3 days of actual data using Root Mean Square Error (RMSE) metric. They present results from the networks that give the minimum RMSE values. Thus, the network with minimum RMSE is used to predict the future scenarios. As new data arise daily, the network can be re-train in order to adjust the real-time predictions. Further, they present the deep neural network used for forecasting and evaluate their approach with RMSE, and finally illustrate and discuss the possible scenarios for Covid-19 spread regionally and worldwide. [2] also uses the similar and improved approach.

Now coming to the idea we propose, [4] considers SIRJD model for COVID-19 (a modified version of SIR model). They construct the in-sample SIRJD time series to come up with an in-sample time series for  $\beta$  and  $\gamma$  (the most critical daily transmission parameters). Further they constructed a confirmed/dead-case time series from the starting date of their data set. Then they apply two deep learning algorithms; the standard deep neural networks (DNN) and the LSTM to fit the confirmed/dead in-sample time series and predict the out-of-sample time series, that is further development of confirmed/dead cases for 35 and 42 days in their work. This confirmed/dead in-sample time series is then used as training data and the in-sample  $\beta$  and  $\gamma$  time series from Step 2 as training label. And then DNN and LSTM is applied again to predict  $\beta$  and  $\gamma$  for 35 and 42 days (out-of-sample time series). And finally, the predicted (out-of-sample) transmission parameters ( $\beta$  and  $\gamma$ ) from the starting date is used to simulate 35- and 42-day progressions (out-of-sample time series) of the SIRJD model (particularly the SIR portion) in a recursive manner, starting with the data point of the last time step from the in-sample SIRJD time series.

Fig. (2) shows the flow chart that [4] used to demonstrate their methodology.

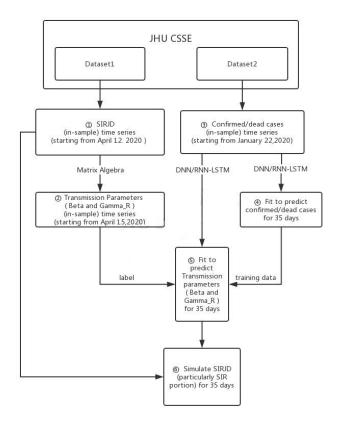


Figure 2: Flow chart from [4]

Ref.[1] is also has the same approach as [4]. But they use a better epidemiological model (SEIR) for heterogeneous population, which is called the meta-population model and they incorporate it with DNN and LSTM. The framework of methodology in [1] is illustrated in Fig.(3)

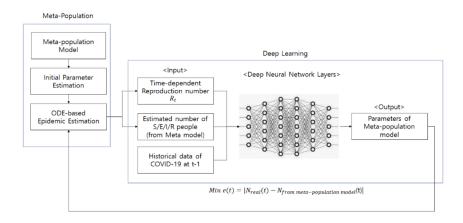


Figure 3: Framework from [1]

### 4 The scope of the idea to our project

We had tried many regression based model, but we failed to get more consistent and more realistic result. We are excited to explore more on this idea to incorporate and test it in our project. But its quite challenging. Interestingly, the meta-population model incorporated with DNN and LSTM in [1] seems to be a very consistent approach with the objective of our project for state wise prediction.

#### References

- [1] Hybrid Deep Learning-Based Epidemic Prediction Framework of COVID-19: South Korea Case, Firda Rahmadani and Hyunsoo Lee.
- [2] Peipei Wang, Xinqi Zheng, Gang Ai, Dongya Liu, Bangren Zhu. Time series prediction for the epidemic trends of COVID-19 using the improved LSTM deep learning method: Case studies in Russia, Peru and Iran, Chaos, Solitons & Fractals, Volume 140, 2020, 110214, ISSN 0960-0779, https://doi.org/10.1016/j.chaos.2020.110214.
- [3] Worldwide and Regional Forecasting of Coronavirus (Covid-19) Spread using a Deep Learning Model. Cem Direkoglu and Melike Sah.

[4] Dynamics and Development of the COVID-19 Epidemic in the United States: A Compartmental Model Enhanced With Deep Learning Techniques, Qi Deng.