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HIGHLIGHTS

- Deep learning data-driven analytical model of Covid-19 pandemic to study disease transmission and prevention mechanism.
- Artificial Neural Network (ANN) based adaptive incremental learning technique used for model parameter learning and model updating with evolving training data.
- Simulation and forecasting of different epidemic scenarios.
- An effective strategy to minimize the number of deaths through controlled natural immunization in absence of availability of vaccination at mass level.
A Novel Adaptive Deep Learning Model of Covid-19 with focus on mortality reduction strategies

Junaid Farooqa,∗, Muhammad Abid Bazazab

∗Department of Electrical Engineering, National Institute of Technology Srinagar, India

Abstract
We employ deep learning to propose an Artificial Neural Network (ANN) based and data stream guided real-time incremental learning algorithm for parameter estimation of a non-intrusive, intelligent, adaptive and online analytical model of Covid-19 disease. Modeling and simulation of such problems poses an additional challenge of continuously evolving training data in which the model parameters change over time depending upon external factors. Our main contribution is that in a scenario of continuously evolving training data, unlike typical deep learning techniques, this non-intrusive model eliminates the need to retrain or rebuild the model from scratch every time a new training data set is received. After validating the model, we use it to study the impact of different strategies for epidemic control. Finally, we propose and simulate a strategy of controlled natural immunization through risk based population compartmentalization (PC) wherein the population is divided in Low Risk (LR) and High Risk (HR) compartments based on risk factors (like comorbidities and age) and subjected to different disease transmission dynamics by isolating the HR compartment while allowing the LR compartment to develop natural immunity. Upon release from the preventive isolation, the HR compartment finds itself surrounded by enough number of immunized individuals to prevent spread of infection and thus most of the deaths occurring in this group are avoided.

Keywords: Covid-19, Deep Learning, Incremental Learning, Policy Making, Immunisation

1. Introduction

Covid-19 is a highly contagious epidemic disease caused by novel coronavirus (SARS-CoV-2) that originated in Wuhan, Hubei Province of China in late December 2019. World Health Organization (WHO) declared Covid-19 as a pandemic on 12th March 2020 [1]. Researchers are policy makers are working round the clock to find solutions and design strategies to control the pandemic and minimize its impact on human health and economy.

The transmission of SARS-CoV-2 in humans is mostly through respiratory droplets (sneezing, coughing and while talking) and through contaminated surfaces [2]. The most significant property of SARS-CoV-2 is that it can persist on a variety of surfaces from hours to 9 days at room temperature which makes its transmission more rapid [3]. This virus can cause Acute Respiratory Distress Syndrome (ARDS) or multiple organ dysfunction, which may lead to physiological deterioration and death of an infected individual [4].

Mathematical modeling of infectious diseases and epidemics has been employed as an important tool for analysis of disease characteristics and investigation of disease spread ever since the ground breaking work of Kermack and McKendrick in 1972 [5]. It plays a useful role in efficient decision making and optimal policy framing. Different models have been developed to analyse the transmission dynamics of many infectious diseases like malaria (Ronald Ross model) [6], cholera (Capasso and Pareri-Fontana model, 1979) [7], gonorrhea (Hethcote and Yorke model, 1984) [7], Ebola [8], H1N1 [9] etc.

In this work, we employ deep learning to propose an Artificial Neural Network (ANN) based real-time online incremental learning technique to estimate parameters of a data stream guided analytical model of Covid-19 to study the transmission dynamics and prevention mechanism for SARS-Cov-2 novel coronavirus in order to aid in optimal policy formulation, efficient decision making, forecasting and simulation. Modeling and simulation of such problems poses an additional challenge of continuously evolving training data in which the model parameters change over time depending upon external factors. Our main contribution is that in a scenario of continuously evolving training data, unlike typical deep learning techniques, this model eliminates the need to retrain or rebuild the model from scratch every time a new training data set is received. Using a data science approach, model parameters are intelligently adapted to the new ground realities. To the best of our knowledge, this paper develops for the first time a deep learning model of epidemic diseases with data science approach in which parameters are intelligently adapted to the new ground realities with fast evolving infection dynamics.
The Covid-19 data from India has been taken as the case study. The first case of COVID-19 in India was reported on 30th January 2020 originating from Wuhan, China [10]. As on 13 June 2020, the total number of cases reported in India is 308,993 with 154,330 recoveries and 8,884 deaths [11]. Hence the number of active cases is 145,779. The government of India imposed a country wide complete lockdown on 24th March 2020 with strict restrictions on the movement of people while allowing only the essential services to operate under the supervision of administration and health officials. The lockdown was renewed thrice on 14 April, 3 May and 18 May 2020 and has been relaxed since 8 June 2020 [12].

India is the second largest populated country in the world with a total population of around 1.35 billion. The health care facilities in India are considered poor with 0.55 hospital beds per thousand people of the population [13]. Therefore, the Covid-19 pandemic has emerged as a major challenge for the people, health workers and policy makers of the country.

Using a control theory approach, we analyze the stability of different disease prevention strategies. Finally, we propose a strategy of controlled natural immunization of the population by dividing it in Low Risk and High Risk compartments based on various risk factors like age and comorbidities. The two groups are treated separately and subjected to different disease mechanics with the aim to minimize the total number of deaths given the fact that the probability of death is very high in the High Risk group as compared to the Low Risk group. The two compartments are isolated from each other for a certain period of time. The low risk compartment is allowed to fully brace the infection with maximum speed and develop immunity owing to its very low death rate while as the high risk compartment is put under preventive isolation till the infection growth curves flattened for the Low Risk group. Upon release from the preventive isolation, the high risk group finds itself surrounded by enough number of immunized individuals to prevent spread of infection and thus most of the deaths occurring in this group are avoided. We simulate this strategy in Matlab environment to establish its effectiveness in significant reduction in the number of deaths while demonstrating the usefulness of the deep learning based mathematical model. To the best of our knowledge, such an approach to reduce mortality has not been modeled and simulated earlier by the scientific community.

2. SIRVD Epidemiological Model

SIRVD refers to Susceptible, Infected, Recovered, Vaccinated and Deceased states of individuals in a population going through an epidemic.

2.1. Basic and Modified SIR Models

The pioneer work in development of mathematical models for infectious diseases was carried out by by [5] known as the susceptible-infectious-recovered (SIR) model. As one of the most classical models, it has been used by many researchers to study and analyse many infectious diseases like seasonal flu [14, 15], pandemic flu [16, 17], HIV/AIDS [18], SARS [19, 20] etc. These studies have shown that SIR models are reliable for analysis of the infectious disease spread and evaluation of the impact of prevention schemes in different scenarios.

The basic SIR model is described by the following differential equations:

\[
\frac{dS}{dt} = -\beta \frac{SI}{N} \tag{1}
\]

\[
\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I \tag{2}
\]

\[
\frac{dR}{dt} = \gamma I \tag{3}
\]

where \(S\), \(I\) and \(R\) are functions of time representing the number of susceptible, infected and recovered individuals in a population of size \(N\) at time \(t\). \(\beta\) is the rate of transmission and \(\gamma\) is the rate of recovery of infected individuals. It is assumed that those recovered develop immunity and do not catch the infection again in the time span of interest.

The basic SIR model can be modified in various ways to accommodate different scenarios. A modified SIR model known as SIRD (Susceptible-Infected-Recovered-Deceased) model is of our interest here and is based on the following assumptions:

(i) This model is fatal unlike a typical non-lethal SIR model which means that there is a positive probability of an infected person dying, \(P(\text{Death}) = \delta\) and \(\delta > 0\).

(ii) A typical SIR model assumes that the Recovered group gains full immunity from reinfection. However, this model accommodates the possibility of a recovered person being reinfected with probability of reinfection, \(P(\text{Reinfection}) = \sigma\) and \(\sigma > 0\).

(iii) The impact of new births and unrelated deaths in ignored and the total population remains constant, \(N = \text{constant}\) \(\forall t\).

(iv) The population is distributed randomly over the area.

Therefore, there are four classes of individuals: Susceptible (S), Infected (I), Recovered (R) and Deceased (D) as described by the following equation:

\[
\frac{dS}{dt} = -\beta \frac{SI}{N} + \sigma R \tag{4}
\]

\[
\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I - \delta I \tag{5}
\]

\[
\frac{dR}{dt} = \gamma I - \sigma I \tag{6}
\]

\[
\frac{dD}{dt} = \delta I \tag{7}
\]

where \(\beta = \text{rate of infection}\), \(\sigma = \text{rate of susceptibility}\), \(\gamma = \text{rate of recovery}\) and \(\delta = \text{rate of death}\).
2.2. Model with Vaccination - SIRVD

Since the final cure for Covid-19 pandemic is the successful discovery and optimal administration of the vaccine in the population, therefore we introduce the effect of vaccination with a given rate of vaccination under resource limited settings. This is achieved by adding a new class of individuals called Vaccinated (V) in the population. It can be fairly assumed that there is no limit on the total number of vaccines produced as all the available resources for vaccine production are employed to eliminate the epidemic. However, the vaccine production capacity will have some limit based on availability of resources and facilities. Therefore, there will be a limited number of vaccines available at a particular point of time. Thus, it is assumed that the per capita rate of vaccination, \( \alpha < \epsilon \) where \( \epsilon \) is a constant. It is assumed that the vaccination imparts long term immunity against the disease in the vaccination individuals. Based on these assumptions, we propose a final model as described by the following first order Ordinary Differential Equations (ODE’s) and it illustrated by Figure 1:

\[
\begin{align*}
\frac{dS}{dt} &= -\frac{\beta S I}{N} + \sigma R - \alpha S \\
\frac{dI}{dt} &= \frac{\beta S I}{N} - \gamma I - \delta I \\
\frac{dR}{dt} &= \gamma I - \sigma I \\
\frac{dV}{dt} &= \alpha S \\
\frac{dD}{dt} &= \delta I
\end{align*}
\]

where:

- \( \alpha \) : Rate of Vaccination
  \( \alpha < \epsilon \) and \( \epsilon \) = constant (limited resources)
- \( \beta \) : Rate of Infection
  (Transmission of susceptible to infected)
- \( \gamma \) : Rate of Recovery
  (Transmission of infected to recovered)
- \( \delta \) : Rate of Death
  (Transmission of infected to deceased)
- \( \sigma \) : Rate of Susceptibility
  (Transmission of recovered to susceptible)

It must be noted here that the process of mass action transmission is described by the non-linear term \( \beta S I / N \) where \( \beta = \) number of contacts per unit time by a person in group I required to transmit the disease to a person in group S, \( N - 1 \approx N = \) total number of possible contacts of a person, \( S / N = \) the fraction of possible contacts of a person that are from group S, \( I = \) the number of infected persons at time \( t \), therefore \( \beta S I / N = \) Number of people transmitted from group S to group I per unit of time.

3. ANN based Adaptive Incremental Learning (ANNAIL) of Model Parameters

The next task is to learn the model parameters which can be quite challenging in an epidemic scenario like Covid-19 as the model parameters are supposed to change with time. This section proposes an Artificial Neural Network (ANN) based Adaptive Incremental Learning technique (ANNAIL) for online learning of the SIRVD Model parameters with the following assumptions:

(i) The rate of vaccination \( \alpha \) as a function of time \( t \) is set by the vaccine production capacity decided by availability of skilled labour, resources and facilities and by vaccination policy as well. Maximum vaccine production capacity \( \alpha_{max} \) has been assumed to be constant indicating that there is no change in vaccine production infrastructure, technology or facilities.

(ii) The rate of infection \( \beta \) as a function of time \( t \) is the major challenge for parameter learning. It is affected by external factors like degree of social distancing, lockdown etc. In case of a lockdown \( \beta \) decreases exponentially. Therefore, in order to take into account both the lockdown and no lockdown scenarios, \( \beta \) has been modelled as:

\[
\beta = \begin{cases} 
\beta_0, & \text{Outside Lockdown} \\
\beta_0 e^{-\frac{t}{\tau_l}} + \beta_1, & \text{During Lockdown}
\end{cases}
\]

\[
(13)
\]

where \( t_l \) is the time when the lockdown begins. Therefore, the learning algorithm has to learn 3 parameters \( (\beta_0, \beta_1, \tau_l) \) to find \( \beta \).

(iii) The rate of reinfection \( \sigma \) has been assumed to be zero for Covid-19 Disease as the human body develops antibodies to prevent re-infections in future against such a virus [21].

(iv) Rate of Recovery \( \gamma \) and Rate of Death \( \delta \) are affected by factors like change in health care facilities, possible overcrowding of hospitals, development of new drugs to manage or treat the disease etc. Both of these have been assumed to be constant in this paper.
For a typical neural network or any other technique of model parameter estimation, the training data is required first to train the model before applying it on future scenarios. However, in case of an epidemic like Covid-19, the training data is continuously evolving with time and the model needs to be trained and executed at the same time as the model parameters may change over time based on different external factors like government policies, social distancing etc which can be known only from newly arriving data sets. Therefore, we propose a technique for the model to learn these parameters from new data sets in an adaptive manner while continuously updating the old models without the need to build the model from scratch every time a new training data set is received.

### 3.1. Adaptive Incremental Learning

Deep learning and other machine learning techniques stand out in solving problems of data based model parameter estimation due to their state-of-the-art results. However, they face the problem of catastrophic forgetting which reduces their performance as new training data becomes available with time. This is because the typical neural networks require the entire dataset to update the model each time a new training data set becomes available as in case of an epidemic modelling problem where the training data becomes available incrementally with time. To address such issues, different incremental learning algorithms have been suggested in the literature [22, 23, 24].

Incremental Learning refers to an online learning technique of continuous model adaptation under a scenarios of continuously evolving training data. Therefore, storage or access to the previously observed data is not required at each time a new data set is received, as in case of an epidemic like Covid-19. In order to adapt the model parameters in light of new data, it is not needed to use all the previously accumulated data for developing the model from scratch. Rather, the Learning Network modifies the previous hypothesis to adapt to the new data chunk.

#### 3.2. Problem Formulation

In this paper, we propose hypothesis generation via an Artificial Neural Network (ANN). Let $D_{t-1}$ be the data set received between time $t_{j-1}$ and $t_j$, and $h_{j-1}$ be the hypothesis generated on this data set. The hypothesis $h_j$ for a new data set $D_j$ received between time $t_j$ and $t_{j+1}$ is a function of $D_j$ and $h_{j-1}$ only as under:

$$h_j = f(h_{j-1}, D_j)$$

The experience gained from this step is stored and integrated to support in future adaptation process. Thus the objective here is to integrate the previously learned knowledge into the new raw data set to adapt the model parameters accordingly; and to accumulate this experience over time to increase the model efficiency, accuracy and flexibility.

### 3.3. Proposed Framework

The proposed framework for the above problem is shown in Figure 2. The ANN is based on a non-linear activation function for successful regression analysis. The hidden layers are represented by the function $f_{NN}$. With the continuous data stream, the weight distribution functions are generated to describe the learning capability of the ANN where the decision boundary is adjusted to focus especially on the hard to learn data examples. The algorithm for this framework is given in Algorithm 1.

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**Algorithm 1: The ANN-AIL framework**

1. **Inputs:**
   - **Previous Knowledge at time** $(t-1):$
     - $D_{t-1}$ with $m$ instances: $(x_i, y_i), (i=1,2,...,m)$, where $x_i$ represents the input vector and $y_i$ represents the output.
     - Associated mapping function output: $\Phi_{t-1}$.
     - Associated hypothesis $h_{t-1}$.
   - **New Data set at time** $t$
     - $D_t$ with $m$ instances: $(x_i, y_i), (i=1,2,...,m)$.

2. **Learning Procedure**
   (i) Find initial distribution function for $D_t$,
   $$\phi_{t-1} = f_{NN}(D_{t-1}, D_T, \Phi_{t-1})$$
   where $f_{NN}$ is the ANN defined mapping function.
   (ii) Apply hypothesis $h_{t-1}$ to $D_t$, and find the pseudo-error $e_{t-1}$
   $$e_{t-1} = \sum_{j=1}^{m} \phi_{t-1}(j)$$
   (iii) Define
   $$\Upsilon_{t-1} = \frac{e_{t-1}}{1 - e_{t-1}}$$
   (iv) Update the ANN’s mapping function for $D_t$:
   $$\Phi_{j}(j) = \frac{\phi_{t-1}(j)}{\Upsilon_{t-1}} \times \begin{cases} \Upsilon_{t-1} & \text{if } h_{t-1}(x_j) = y_j \\ 1 & \text{otherwise} \end{cases}$$
   where $N_i$ is a normalization constant.
   (v) Develop new hypothesis $h_t$ from $D_t$ and $\Phi_t$ using
   $$h_t = f_{NN}(h_{t-1}, D_t)$$
   (vi) Repeat the above procedure for $D_{t+1}$.

3. **Output**
   The final hypothesis is:
   $$h_{fin}(x) = \arg \max_{y \in Y} \sum_{j=1}^{m} \log \left( \frac{1}{\Upsilon_{t}} \right)$$
   where $T$ is the set of incrementally developed hypotheses in the learning life.

This algorithm is run in a top-down and horizontal signal flow, as shown in Figure 2. The adaptive nature of this algorithm is due to the mapping function based on ANN which estimates the initial distribution function $\Phi_{t-1}$ for $D_t$ while providing a quantitative approach to indicate the learning power of the
new data set based on previously trained model. \( \Phi_{t-1} \) is applied to the new data set to find pseudo-error, \( \Upsilon \). Thus a hard to learn example will have higher \( \Upsilon \) in step (iii) of the Learning procedure, and will in turn receive higher weight in step (iv). This ensures the adaptive nature of the algorithm.

3.4. Mapping Function Design

Mapping function connects the past experiences to the new data in an adaptive fashion. There can be many ways to design the mapping function. However, we implemented the non-linear regression by an ANN based approximation of mapping function owing to its flexibility. Any such Neural Network based function approximation technique can be used. As in illustration we take the Multilayer Perceptron (MLP) in this paper. This is shown in Figure 3.

The input is an \( n \)-dimensional vector (for example, Number of infections, deaths, recoveries in an epidemic) of example \( i \). The distribution function is currently estimated as \( J_{t-1} \). \( W \) represents the weights of a layer. Backpropagation is used to tune the weights \( W \) of different layers, where error function is defined as:

\[
e(k) = J_{t-1}(k - 1) - \Phi_{t-1}(k - 1)
\]

\[
E(k) = \frac{1}{2} e^2(k)
\]

where \( k \) is the training epoch of the backpropagation. The neural network gives the following output:

\[
J(k) = \frac{1 - e^{-\nu}}{1 + e^{-\nu}}
\]

\[
\nu(k) = \sum_{f=1}^{N_h} w^{(2)}_{f}(k)g_f(k)
\]

\[
g_f(k) = \frac{1 - e^{-h_f(k)}}{1 + e^{-h_f(k)}}, \quad f = 1, ..., N_h
\]

\[
h_f(k) = \sum_{q=1}^{n} w^{(1)}_{fq}(k)x_q(k), \quad f = 1, ..., N_h
\]

where \( h_f \) represents the input to \( f \)-th hidden node while as \( g_f \) represents its output, \( \nu \) is the input to the final node, \( N_h \) is number of hidden neurons, and \( n \) is the total number of inputs. Weights on the ANN are updated by applying the above defined backpropagation strategy as explained below.

**Backpropagation:** Weight adjustment for the hidden to out-
put layer is described as:
\[
\Delta w^{(2)} = \alpha(k) \left[ - \frac{\partial E(k)}{\partial w^{(2)}(k)} \right]
\]
(21)
\[
\frac{\partial E(k)}{\partial w^{(1)}(k)} = \frac{\partial E(k)}{\partial J(k)} \cdot \frac{\partial J(k)}{\partial \sigma(k)} \cdot \frac{\partial \sigma(k)}{\partial w^{(1)}(k)} = e(k), \frac{1}{2} (1 - (J(k))^2) \cdot g_f(k)
\]
(22)
Similarly, weight adjustments for the input to hidden layer is described as:
\[
\Delta w^{(1)} = \alpha(k) \left[ - \frac{\partial E(k)}{\partial w^{(1)}(k)} \right]
\]
(23)
\[
\frac{\partial E(k)}{\partial w^{(1)}(k)} = \frac{\partial E(k)}{\partial J(k)} \cdot \frac{\partial J(k)}{\partial \sigma(k)} \cdot \frac{\partial \sigma(k)}{\partial w^{(1)}(k)} = e(k), \frac{1}{2} (1 - (J(k))^2) \cdot g_f(k)
\]
(24)

where \(\alpha(k)\) describes the learning rate. Estimation of initial distribution function \(\hat{\phi}_0\) for \(D\) required only the feedforward path of the MLP.

3.5. Model Validation
This model was validated for Covid-19 in India where the first 80% of data was used for training and the remaining 20% was used for testing as shown in Figure 4.

It is clearly evident from the plots shown in the figure that the results given by the model during testing are very close to the actual data. The inputs and outputs in this algorithm were:

**Inputs**: Number of New infections, deaths and recoveries; rate of vaccination \(\alpha\).

**Outputs**: \(\beta_0, \beta_1, \tau_0, \delta, \gamma\)

These outputs are fed to the analytical SIRVD model at every time instant when a new set of input data is received to simulate and forecast different scenarios.

4. Control Strategies and Solutions
In this section, we analyse three possible strategies to combat an epidemic like Covid-19: (i) Herd Immunity, (ii) Complete Vaccination, (iii) Complete Lockdown and finally our proposed (iv) Controlled Natural Immunization through risk based Population Compartmentalization is discussed in the next section. However, following definitions are needed beforehand:

**Definition 1.** (Stability) If the Jacobian Matrix \(J\) for a system of \(n\) differential equations has eigenvalues \(\lambda_1, \lambda_2, \ldots, \lambda_n\), for a trivial steady state equilibrium at \((0,0,\ldots,0)\), then the stability of the solution is determined as following:

(i) If \(\Re(\lambda_i) < 0 \ \forall \ i = 1, 2, \ldots, n\) then the system has Uniform and Asymptotic Stability (UAS).

(ii) If \(\Re(\lambda_i) \leq 0 \ \forall \ i = 1, 2, \ldots, n\) and the algebraic multiplicity equals the geometric multiplicity whenever \(\lambda_i = 0\) for any \(i\), then the system has Uniform Stability (US).

(iii) If \(\Re(\lambda_i) > 0\) for any \(i\) and the algebraic multiplicity is greater than the geometric multiplicity whenever \(\lambda_i = 0\) for any \(i\), then the system has instability.

Since the impact of new births and unrelated deaths has been fairly ignored for the purpose of this study and it has been assumed that the total population \(N\) stays constant throughout the epidemic, therefore the system of ODEs (8 - 12) describing the model satisfies the following two conditions:

\[
\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} + \frac{dV}{dt} + \frac{dD}{dt} = 0
\]  
(25)

\[
S + I + R + V + D = N
\]
(26)

This shows that a state of equilibrium always exists in the system.

**Definition 2.** (DFE) A Disease Free Equilibrium (DFE) is defined as a state of equilibrium according to (25, 26) in which the number of infected and recovered individuals equal to zero such that there are no further deaths \((I \rightarrow D)\), infections \((S \rightarrow I)\) or reinfections \((R \rightarrow I)\):

\[
I = R = 0
\]
\[
\frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = \frac{dV}{dt} = \frac{dD}{dt} = 0
\]
which gives us the following from the system of ODEs (8 - 12):

\[
-\beta \frac{S I}{N} + \sigma R - a S = 0
\]  
(27)

\[
\beta \frac{S I}{N} - \gamma I - \delta I = 0
\]  
(28)

\[
\gamma I - \sigma R = 0
\]  
(29)

\[
aS = 0
\]  
(30)

\[
\delta I = 0
\]  
(31)

We take the Jacobian Matrix of the above system to evaluate its stability. However, the fifth differential equation (representing \(D\)) is uncoupled from the first four differential equations and it can be derived from the first four equations using (25, 26),
therefore we consider the Jacobian for the first four equations only which is given as:

$$J(S, I, R, V) = \begin{bmatrix} -\beta \frac{I}{N} - \alpha -\beta \frac{S}{N} & 0 & \sigma & 0 \\ \beta \frac{I}{N} & \beta \frac{S}{N} - \gamma - \delta & 0 & 0 \\ 0 & \gamma & -\sigma & 0 \\ \alpha & 0 & 0 & 0 \end{bmatrix} \tag{32}$$

Given below is the investigation of DFE stability for different epidemic control strategies.

4.1. Herd Immunity

Herd immunity is the idea that a virus cannot spread easily after enough people develop immunity against it. This reduces the chances of the virus transmitting from person to person and infecting those who haven’t been infected yet [25]. Such an immunity can be induced artificially by a vaccine, however it can also be developed naturally by the infection itself as the immune system of the body develops antibodies against the virus which prevent reinfection in future.

This is based on the fact that the human body produces a non-specific innate response to a viral infection initially using neutrophils, macrophages, and dendritic cells. However, this is followed by a more specific adaptive response in the form of development of proteins called immunoglobulins which act as antibodies specifically binding to the virus. This is coupled with the formation of T-cells which generate cellular immunity by identifying and eliminating the cells that are infected with the virus. Generally, sufficient presence of such antibodies in collaboration with cellular immunity prevents reinfection after recovery. Although every recovered patient may not develop complete immunity, but that is the case for the most of them [21].

In case of Covid-19, although research is till going on to reach a conclusive opinion, promising studies suggest that nearly all the recovered patients develop such antiviral immunoglobulin-G (IgG) antibodies and are immune to reinfection [26]. This lays the basis for mass Serological testing for Covid-19 being practised by many governments across the world in which the blood samples of people are tested for the presence of these antibodies indicating present or past Covid-19 infection. Further, the data on reinfection, even if rare, is not available.

Therefore, the idea of Herd Immunity is to let the infectious disease take its natural course of action and let the population naturally develop immunity against the disease after most of the population gets infected. The DFE after Herd Immunity has the following form:

$$(S, I, R, V, D) = (0, 0, N - D_0, 0, D_0)$$

where $D_0$ is the total number of Deaths at the time of DFE and thus $R = N - D_0$. Since there is no vaccination, therefore $\alpha = 0$ and $V = 0$. Further, the rate of reinfection $\sigma$ is zero as well, meaning Recovered people cannot catch the infection again. Using these values in (32), the Jacobian at the DFE after Herd Immunity is given as:

$$J(0, 0, N - D_0, 0) = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & -\gamma - \delta & 0 & 0 \\ 0 & \gamma & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

Equating characteristic equation for this Jacobian to zero gives:

$$\det(J - \lambda I) = 0$$

$$(-\lambda)(-\lambda)(-\gamma - \delta - \lambda)(\lambda) = 0$$

Therefore, the eigenvalues of this system are:

$$\lambda_1 = \lambda_2 = \lambda_3 = 0$$

$$\lambda_4 = -\gamma - \delta < 0$$

Thus, all the eigenvalues have real parts less or equal to zero: $Re(\lambda_i) \leq 0 \quad i = 1, 2, \ldots, n$ and $D_0 \in R \cap [0, N]$. Hence, according to Definition 1, the DFE for Herd Immunity possesses Uniform Stability (US). In this case, there are no chances of retriggering of the disease after the DFE has been reached.

However, this approach has been criticised as dangerous as it will result in a large number of deaths [27]. To develop herd immunity for COVID-19 in the population, roughly 70 % or more of the population needs to have gone through the infection [28]. The current death rate in India due Covid-19 is around 3 % which means that if this death rate is maintained, nearly 2.1 % of the population will die till 70 % gets infected. This leads to nearly 28 million deaths. The actual number of deaths would be more than this, because with rapid growth of the infectious disease, hospitals would be over-flooded and health care infrastructure will not be able to cater to the demands of high number of patients leading to increase in the death rate. The growth of disease in India is shown in Figure 5 if the disease is allowed to take its natural course without any intervention and control.

Figure 5: Herd Immunity

4.2. Complete Lockdown

The strategy of complete lockdown focuses on minimization of mobility and contact among the population with maxi-
maximum possible social distancing. Therefore, it minimizes $\beta$ (the rate of infection). The DFE under complete lockdown has the following form:

$$(S, I, R, V, D) = (N - D_0, 0, 0, 0, D_0)$$

where $D_0$ is the total number of Deaths at the time of DFE and thus $S = N - D_0$. Since there is no vaccination, therefore $\alpha = 0$ and $V = 0$. Using these values in (32), the Jacobian at the DFE under complete lockdown is given as:

$$J(N - D_0, 0, 0, 0) = \begin{bmatrix}
0 & -\beta \frac{N - D_0}{N} & \sigma & 0 \\
0 & \frac{\beta}{N} - \gamma - \delta & 0 & 0 \\
0 & \gamma & -\sigma & 0 \\
0 & 0 & 0 & 0
\end{bmatrix}$$

Furthermore, equating characteristic equation for this Jacobian to zero gives:

$$det(J - \lambda I) = 0$$

$$(-\lambda)(-\lambda)(\frac{\beta}{N} - \gamma - \delta)(-\sigma - \lambda) = 0$$

Therefore, the eigenvalues of this system are:

$$\lambda_1 = \lambda_2 = 0$$

$$\lambda_3 = \beta \frac{N - D_0}{N} - \gamma - \delta > 0$$

$$\lambda_4 = -\sigma < 0$$

Thus, real part of one of the eigenvalues is always greater than zero: $Re(\lambda_3) > 0 \ \forall \ D_0 \in R \cap [0, N]$. Hence, according to Definition 1, the DFE under complete lockdown is always unstable. Thus, whenever a DFE is reached in this case, the tendency for the disease to be triggered again is always there. Even a single case of infection can restart the disease. Apart from the chances of reemergence of the disease, the time taken by the system to reduce the number of active infections to zero may be large enough to make the total lockdown unsustainable and practically impossible. The impact of lockdown on the disease growth in India is shown in Figure 6. It has been assumed that the lockdown ends on day 250 of the disease after it starts on day 55. It can be compared with Figure 5 which shows the disease growth in case no preventive measures are taken. These results confirm that the infection plots shoot up as soon as the lockdown is lifted and there is no significant difference in terms of total number of infections or deaths. The only benefit of lockdown, as can be seen from these plots, is that the peak of infection is delayed which can be useful for the administration to buy some time to prepare the healthcare infrastructure of the country to brace for the full blown impact of the disease.

4.3. Complete Vaccination

Researchers and health industries worldwide are working around the clock to discover a vaccine against SARS-CoV-2. Moderna, a pharmaco-logical company had started clinical testing of its mRNA- based vaccine (mRNA-1273) just 2 months after the complete sequencing of COVID 19 was done and published by different research groups [30]. The most potential candidate for the vaccine development would be to induce our immune system to synthesize neutralizing antibodies against the viral spike protein which block its entry via ACE2 receptors [31].

The DFE with Vaccination of all living members of the population $N$ has the following form:

$$(S, I, R, V, D) = (0, 0, 0, N - D_0, D_0)$$

where $D_0$ is the total number of Deaths at the time of DFE and thus $V = N - D_0$ as the rest of population has been vaccinated and is now immune to the disease. Using these values in (32), the Jacobian at the DFE with full Vaccination is given as:

$$J(0, 0, 0, N - D_0) = \begin{bmatrix}
-\alpha & 0 & \sigma & 0 \\
0 & -\gamma - \delta & 0 & 0 \\
0 & \gamma & -\sigma & 0 \\
\alpha & 0 & 0 & 0
\end{bmatrix}$$

Furthermore, equating characteristic equation for this Jacobian to zero gives:

$$det(J - \lambda I) = 0$$

$$(-\lambda)(-\alpha - \lambda)(-\gamma - \delta - \lambda)(-\sigma - \lambda) = 0$$

Therefore, the eigenvalues of this system are:

$$\lambda_1 = 0$$

$$\lambda_2 = -\alpha < 0$$

$$\lambda_3 = -\gamma - \delta < 0$$

$$\lambda_4 = -\sigma < 0$$

Thus, all the eigenvalues have real parts less or equal to zero: $Re(\lambda_i) \leq 0 \ \forall \ i = 1, 2, ..., n$ and $D_0 \in R \cap [0, N]$. Hence,
according to Definition 1, the DFE with full Vaccination possesses Uniform Stability (US). In this case, there are no chances of re-triggering of the disease after the DFE has been reached. The impact of Vaccination on the growth of disease is shown in Figure 7. Here we simulate a hypothetical scenario where lockdown is imposed on Day 55 and lifted on day 200 while as vaccination starts from Day 100 with 10 million vaccinations per day in the country. The results are shown in Figure 7 with comparison to a scenario where lockdown is started indefinitely from Day 55 (These plots are shown with legends followed by numeric 1, for example Infected Vs Infected 1). These results suggest that the only significant difference vaccination would make in such a hypothetical situation would be in the number of deaths. For better results, the lockdown should have been more strict or the vaccination should have begun much earlier. These results show that successful vaccination of all the living members of the population is the way to completely eliminate the disease and its chances of re-triggering as well. However, successful development of a vaccine for SARS-CoV-2 has still a long way to go. Further, a vaccination rate of 10 million per day is highly ambitious for a country like India. Therefore, elimination of the current wave of Covid-19 epidemic and minimization of number of deaths by vaccination is practically impossible as the successful development and mass administration of a vaccine is expected to take more than a year, at least. However, vaccination may still be necessary to prevent new waves of the disease in future.

5. Controlled Natural Immunization

The strategy of Herd Immunity discussed in the previous section aims at minimizing the number of S (Susceptible) and maximizing the number of R (Recovered) people who are supposed to have developed the immunity. This will minimize the factor $\frac{SI}{N}$ in the SIRVD Model ODE’s discussed in Section 2. However, this strategy results in the maximum number of deaths.

$$\begin{align*}
\text{Min } D &= \int_0^t \delta I \, dt \\
\text{s.t } \frac{dS}{dt} &= -\beta \frac{SI}{N}, \\
\frac{dI}{dt} &= \beta \frac{SI}{N} - (\delta + \gamma)I, \\
\alpha &= \sigma = 0
\end{align*}$$

The death rate ($\delta$) is very high in the High Risk group while as it is very low in the Low Risk group. The most prevalent comorbidity for Covid-19 is hypertension, followed by diabetes with mean age of around 48.9 years [32]. In India, the percentage of population above 50 years of age is 19.28% while as the percentage above 60 is nearly 8% [33]. Most of the people having comorbidities are expected to fall in above 50 age group. In this study, the High Risk group has been assumed to be 20% of the population.

$$N = N_L + N_H$$

$$N_H = 0.2N$$

where L represents the Low Risk compartment while as H represents the High Risk compartment.
It is proposed that these two population groups be subjected to different disease mechanics. The High Risk group is subjected to a preventive quarantine or isolation wherein they are isolated from the Low Risk group by placing them in separate rooms or sections in homes with minimum contact with the low risk group. Whatever necessary contact is required, it should be done with maximum preventive measures like wearing of face masks, sanitization etc. Very high risk individuals may be placed in designated care centers where their health needs are met by medical professionals. Therefore, for the High Risk compartment, \( \beta \) is reduced to minimum as in the case of a lockdown. Meanwhile, the Low Risk group is subjected to maximum mobility and contact among its members effectively increasing \( \beta \) to the maximum possible value. There should be no social distancing and other preventive measures for this group. As a result, the infection will spread very quickly in the low risk group and its members shall develop the immunity and transfer from \( S \) to \( R \) having gained the immunity naturally with a very low death rate. Once this is achieved or in other words once the disease curves are flattened for the Low Risk group, the High Risk group is released from the preventive isolation and allowed to mix with the low risk group. Since most of the population (70 - 80 %) is already immune and the value of \( S \) and \( I \) is low, the chances of the high risk group receiving infection from the low risk is very low because the factor \( \frac{SI}{N} \) has already been reduced to minimum. During PC, \( \beta \) is minimum for High Risk group while as after PC, \( SI \) is minimum. After PC, the mobility and the contact in the population, represented by \( \beta \), should be kept moderate. Since, \( \alpha \) and \( \sigma \) are zero, therefore:

**During PC:**

\[ (a) \beta = 2x \]

\[ (b) \beta = 3x \]

\[ (c) \beta = 4x \]

\[ (d) \beta = 5x \]
and:

\[
\begin{align*}
\frac{dS_H}{dt} &= -\beta_H S_H I_H N_H^{-}\gamma_H I_H - \delta_H I_H \\
\frac{dI_H}{dt} &= \beta_H S_H I_H N_H - \gamma_H I_H - \delta_H I_H \\
\frac{dR_H}{dt} &= \gamma_H I_H \\
\frac{dD_H}{dt} &= \delta_H I_H \\
\frac{dS_L}{dt} &= -\beta_L S_L I_L N_L^{-}\gamma_L I_L - \delta_L I_L \\
\frac{dI_L}{dt} &= \beta_L S_L I_L N_L - \gamma_L I_L - \delta_L I_L \\
\frac{dR_L}{dt} &= \gamma_L I_L \\
\frac{dD_L}{dt} &= \delta_L I_L
\end{align*}
\]

Our incremental learning model estimates the following mean values for the period of lockdown in India (24 March to 8 June, 2020):

\[
\beta = 0.0811, \delta = 0.0024, \gamma = 0.0429
\]

Here, \(\beta\) represents the rate of infection which depends upon the mobility and contact among the population. Due to the lockdown, this can be considered the lowest possible \(\beta\) in India.
Table 1: Impact of Population Compartmentalization (PC) on the number of deaths in India.

| Compartmentalization Duration in Days ($T_{PC}$) | 130-200 | 130-250 | 130-300 |
|-------------------------------------------------|---------|---------|---------|
| $\beta = 2x$                                     | 50      | 15      | 4       |
| $\beta = 3x$                                     | 25      | 7       | 3       |
| $\beta = 4x$                                     | 18      | 8       | 6       |
| $\beta = 5x$ (During PC), $\beta = 2x$ (After PC) | 15      | 9       | 8.5     |
| $\beta = 5x$ (During PC), $\beta = 2x$ (After PC) | 10      | 2       | 1.3     |

We have simulated the PC Strategy with different values of $\beta_{L}$ ranging from 2 to 5 times of $\beta$ given above to account for high mobility and contact during PC. $\beta_{H} = 0.2\beta$ to assume that the isolation of High Risk individual is at least 5 times stronger than the social distancing practised by the whole population during the nation wide lockdown.

$\delta$ and $\gamma$ are complementary in the sense that an individual either recovers or dies from the infection. To distribute the current death and recovery rate in low and high risk groups:

$$\gamma = \gamma_{H}\gamma_{L} \quad \delta = \delta_{L}\delta_{H}$$

Based on available statistical data [34] [35], it has been assumed that the death rate in High Risk group (having comorbidities and aged above 50 years) is 10 times to that of the Low Risk group.

$$\delta_{H} = 10\delta_{L}$$

Using this in $\delta = \delta_{L}\delta_{H}$;

$$10\delta_{L}^{2} = 0.0024$$

Therefore, $\delta_{L} = 0.0155; \delta_{H} = 0.1548$

Similarly,

$$\gamma_{L} = 10\gamma_{H}$$

Using this in $\gamma = \gamma_{H}\gamma_{L}$;

$$10\gamma_{H}^{2} = 0.0429$$

Figure 11: Disease growth for $\beta = 5x$ during PC and $\beta = 2x$ after PC.

We have simulated the PC Strategy with different values of $\beta_{L}$ ranging from 2 to 5 times of $\beta$ given above to account for high mobility and contact during PC. $\beta_{H} = 0.2\beta$ to assume that the isolation of High Risk individual is at least 5 times stronger than the social distancing practised by the whole population during the nation wide lockdown.

Therefore,

$$\gamma_{H} = 0.0655; \gamma_{L} = 0.655$$

Integrating the equations of SIRVD Model for this case:

$$S(t) = S(t_{0})e^{-\int_{t_{0}}^{t} \gamma_{L}dt} > 0, \quad \forall t \in [t_{0}, t_{f}] \quad (34)$$

$$I(t) = I(t_{0})e^{-\int_{t_{0}}^{t} (\gamma_{L}+\delta_{L})dt} > 0, \quad \forall t \in [t_{0}, t_{f}] \quad (35)$$

where $S(t_{0})$ and $I(t_{0})$ are initial states. This is true for both Low and High Risk groups. However, for High Risk group,

$$S_{H}(t_{0}) = I_{H}(t_{0}) = 0$$

while as for Low risk group;

$$S_{L}(t_{f}) = I_{L}(t_{f}) = 0$$

where $t_{f}$ is the time when PC ends and the two groups are allowed to remix.

After PC:
\[ \frac{dS}{dt} = -2\beta \frac{SI}{N_H + H_L} \]
\[ \frac{dI}{dt} = \beta H \frac{SI}{N_H + N_L} - \gamma I - \delta I \]
\[ \frac{dR}{dt} = \gamma I \]
\[ \frac{dD}{dt} = \delta I \]

where

\[ S(t_0) = S_H(t_f) + S_L(t_f) \]
\[ I(t_0) = I_H(t_f) + I_L(t_f) \]
\[ R(t_0) = R_H(t_f) + R_L(t_f) \]
\[ D(t_0) = D_H(t_f) + D_L(t_f) \]

\( \delta \) and \( \gamma \) have been restored to original values while as \( \beta \) has been multiplied by a factor of 2 to signify higher level of mobility and contact than lockdown albeit with social distancing.

The stability analysis and eigenvalues for this case are same as that of Herd Immunity i.e, it posses Uniform Stability.

This strategy was simulated using the model proposed in Section 1 and 2. The results of the simulation are shown in Figure (9 - 10). In all these figures, black line represents the number of deaths, blue is the total number of cases, red is the active number of infections while as green line represents the number of recovered people. In Figure 9, the preventive quarantine or compartmentalization of the population is done from day 130 after the start of the population till Day 200 while as in in Figure 10 the same is continued till day 300. The rate of infection \( \beta \) is shown as a multiple of the average rate of infection during the nation wide lockdown from 24 March to 08 June, 2020 which was the minimum possible. Increase of \( \beta \) is achieved by increase of mobility and contact among the population, for example \( \beta = 5 \times \) means five times mobility and contact as compared to the days of nation wide lockdown. If no preventive measures are taken, then as per the current trend in the disease growth we may expect more than 55 million deaths in the country if all the population gets infected. This is shown in Figure 8. 55 Million Deaths is not surprising even if linear growth of the disease is assumed with 2.8% death rate for a population of 1.35 billion.

Different hypothetical experiments were simulated and their results are given in Table 1. As discussed earlier, \( \beta \) is supposed to be kept on lower side after the end of PC and social distancing is advised. These results show that the total number of deaths can be reduced to 1.3 million from 55 million, if mobility and contact is made 5 times to that of the lockdown period and PC is ended on day 300 of the pandemic while as after the end of PC, the mobility is reduced to two times. The growth of disease in such a scenario is shown in Figure 11.

6. Conclusion

In this work, we developed an analytical epidemiological model for Covid-19 pandemic where model parameters are continuously updated to intelligently adapt to new data sets using an ANN based Adaptive online Incremental Learning technique. In a scenario of continuously evolving training data, unlike typical Deep Learning techniques, the model eliminates the need to retrain or rebuild the model from scratch every time a new training data set is received. The model was validated and different scenarios were simulated to demonstrate its usefulness and significance. India was taken as a case study. However, this model can be applied to any population in the world and would be a useful tool for policy makers, health officials and researchers in improving decision making efficiency, policy formulation and forecasting. The simulation work was carried out in Matlab environment.

Using this model, we simulated preventive measures like lockdown, vaccination and herd immunity to study their impact on the evolution of Covid-19 disease. Finally we proposed an effective method to significantly reduce the number of deaths caused by the pandemic in case a vaccine is not available at the mass level. This technique aims to develop natural immunity in the low risk group of the population by subjecting them to the full blown impact of SARS-COV-2 virus while as subjecting the high risk group to preventive isolation during this time period. Once the low risk group develops natural immunity and its disease curves are flattened, the high risk group is released from the preventive isolation. Upon release, the high risk group doesn’t find enough infected or susceptible people in the environment to catch the infection at a high rate and in this way the maximum number of deaths are avoided in the high risk group. The impact of this strategy has been simulated and it has been shown the the number of deaths can be reduced from 55 million to 1.3 million if the Population Compartmentalization starts tomorrow and ends on Day 300 of the pandemic in India. During this period, the mobility and contact in low risk group has to be made five times as compared to the lockdown period and upon remixing of the two groups the mobility and contact should be reduced to 2 times from 5.

The novelty of this paper lies in the use of real-time online incremental learning technique in epidemic disease modeling. Many machine learning techniques have been used in epidemic disease modeling [36], however this paper is the first instance of development of an incremental learning algorithm as a real-time adaptive deep learning technique for parameter estimation of an epidemiological model thus providing the model with the capability to work online i.e, unlike typical machine learning techniques, it doesn’t require to rebuild or retrain the model from scratch every time a new data set is received but intelligently adapts the model to ever changing infection dynamics. Since the model is non-intrusive, adaptive, intelligent, real-time and online in nature, therefore it can be employed to monitor, forecast and simulate the growth of any infectious disease over a large sized population without losing accuracy, fidelity or com-
Computational performance due to limitations like run-time duration, size of training data, computational complexity, change in transmission dynamics due to mutations in virus or bacteria, change in prevention mechanisms or government policies. Even if the epidemic continues for decades in the whole world, the model will keep working efficiently on daily basis without any decay in performance or RRT (run-time environment). Further, to the best of our knowledge, population compartmentalization to achieve natural immunity against an infectious disease while significantly reducing the mortality has been modeled and simulated for the first time in this paper.

These findings could be highly useful to policy makers around the world to reduce the number of deaths in any country in case a vaccine is not readily available and lockdown is not sustainable economically. Further, this is a demonstration of the usefulness and efficiency of deep learning based incremental learning algorithm in model parameter estimation and simulation of different epidemic scenarios.

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Junaid Farooq received Bachelors in Electrical Engineering from National Institute of Technology (NIT) Srinagar, India in 2015. After working as Automation Engineer in the industry at Dubai, UAE for two years, he completed Masters in Electrical Engineering from NIT Srinagar in 2019. Currently he is pursuing PhD in Artificial Intelligence at the same university. His research interests include epidemiological modeling, model order reduction, machine learning, application of artificial intelligence in power systems and control systems.

Muhammad Abid Bazaz received Bachelors in Electrical Engineering from NIT Srinagar in 2000. He completed Masters and PhD in Control and Automation from Indian Institute of Technology Delhi, India in 2008 and 2013 respectively. Currently he is working as Associate Professor at the Department of Electrical Engineering, NIT Srinagar. His research interests include control and automation, model order reduction, deep learning, epidemiological modeling and artificial neural networks.
Declaration of interests

☒ The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

☒ The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:

Junaid Farooq
(Corresponding Author)
Electrical Engineering Department
National Institute of Technology Srinagar, India - 190006
Email: junaid_phd017@nitsri.net

Muhammad Abid Bazaz
(Co-author)
Electrical Engineering Department
National Institute of Technology Srinagar, India - 190006
Email: abid@nitsri.net