# DISCRETE EPIDEMIC MODELS: NEURAL NETWORK APPROACH

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ABSTRACT. In this paper we consider a discrete epidemic SIR/COVID model. Since models can be used for early warning and to forecast the behavior of an epidemic and develop intervention strategies it is critical to be able to effectively predict transmission and recovery rates. Based on available daily infection and death data from South Carolina for the period December 1, 2020, to June 1, 2021 we develop a discrete model and analyze evolution of the model using optimization, artificial neural network, machine learning and Grey model inferring the daily, transmission, and reproduction rates, and recovery for each day of the period.

The models and results are consistent with the observations. The models developed using data help us understand the recovery and transmission rates, hence the evolution of the epidemic. The infection and recovery increasing in South Carolina do not show improvement in the period covered. The number of dead people tends to increase although by small amount. Forecasting data for a short time in the future can be used to judge the possible evolution of the epidemic and intervention.

Models were developed based on the available data. For the period December to June there were no available data on recovered populations and we have to determine them as well as transmission and recovery rates based on data of infected populations and dead population using artificial neural networks and optimization methodologies where transmission, recovery, relapsation immunity and death rates from infection are considered as decision variables.

From the data from CDC we see that the number of infected population is increasing. We have also data for the number of dead population due to the virus. Our models are consistent with the data we have available for the infected and dead population. However, there were no data for recovered population in South Carolina for the entire period December 1 to June 1. We have to use our model to come up with recovered population number. One thing we observe is that the number of infected population was increasing. One of the control measures that are believed to be reliable methods of curbing the spread of the virus is quarantine. We include a model that includes quarantine in our work. In our quarantine we see that if 100,000 susceptible people in the whole state were quarantined there would have been a considerable decrease in the number of infected population.

AMS (MOS)Subject Classification. 34H05, 34D20, 68T07, 92B20. Key Words and Phrases. Optimal control, Reproduction number.

## 1. INTRODUCTION

The rapid spread of a disease in regions (epidemic) or the global outbreak of a disease (pandemic), can have a detrimental effect on health systems and economical activities locally and globally. Measures to reduce the pandemic spread include curtailing close interactions

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Received September 27, 2024 ISSN 1056-2176(Print); ISSN 2693-5295 (online) www.dynamicpublishers.org https://doi.org/10.46719/dsa2024.33.07 between using social distancing and face masks and vaccinations. Social distancing has negative economic effects. It is useful to understand the significance of these interventions,  $([4], [22], [15], [24]).$ 

Mathematical models have been used in epidemiology in describing the dynamical evolution of infectious diseases for many years, going back to the eighteenth century. Most of the models are compartmental models, with the population divided into classes and with assumptions being made about the rate of transfer from one class to another. Here we begin by considering a Susceptible-Infectious-Recovered (SIR) model to describe the spread of the virus and compute the number of infected and dead individuals. SIR model is one of the classical epidemic models. There are models that include exposed and migration. The goal is to compute the number of infected, recovered, and dead individuals on the basis of the number of contacts, probability of disease transmission, incubation period, recovery rate, and fatality rate. The epidemic disease model predicts a peak of infected and dead individuals as a function of time and assumes that births and natural deaths are balanced, since we are dealing with a very short period of time. The population members solely decrease due to the disease as dictated by the fatality rate of the disease. The differential equations are solved with a forward Euler scheme, ([12]).

## 2. MATHEMATICAL MODELS

Mathematical and statistical methods provide essential input for governmental decision making that aims at controlling the outbreak. Statistical methods frequently aim at early detection of disease outbreaks ([22]). Another approach is to develop models that indicate the outbreak dynamics using compartmental models ([22]). In compartmental models we consider a fraction of the population to be susceptible, a fraction to be infected, a fraction that has recovered. In some models exposed group is part of the model. Compartmental models have been used to model HIV epidemic, malaria, and corona virus outbreak,  $([11], [18], [13], [22], [24])$ . In this paper we consider SIR model. SIR model can be modified in several ways, for example, by including demographics, deceased populations, hidden population, i.e., exposed populations (SEIR). In an accelerating epidemic outbreak contact tracing , the SEIR model needs to be modified to account for it. In the current paper we have two main objectives: (i) to report some new analytical results about SIR model and (ii) to introduce an optimization/neural network approach for the estimation of the parameters of the SIR model from real time series data. The SIR model is formulated in terms of three populations of individuals. The susceptible population,  $z_1$ , consists of all individuals susceptible to the infection of concern. The infected population population,  $z_2$ , comprises the infected individuals. These persons have the disease and can transmit it to the susceptible individuals. The recovered population,  $z<sub>3</sub>$ , represents the immune individuals, who cannot become infected and cannot transmit the disease to others.

Mathematical models give insight in analyzing the spread and control of infectious diseases. Appropriate assumptions, and variables parameters are required to model epidemics. Mathematical models have been critical in the study of infectious diseases  $([12]$ ,  $[22]$ ,  $[23]$ ). They have been used in studying tuberculosis([21], HIV ([13]), and dengue fever ([1]) models, etc. We start with appropriate model and relevant parameters to be determined. In epidemic models parameters of importance to be determined are contact rates, recovery rates, relapse rates,

infection reproduction rates  $R_0$ , death rates, immunity rates, etc. Vaccination, quarantine, lockdown are also relevant. Although vaccinated people are unlikely to be infected contributing to immunity, there is still a possibility of relapse.

Again, we use the CDC data of infected population and dead people day by day from December 1, 2020, to June 1, 2021. We use our model to estimate the number of recovered people.

We consider discrete models with neural network and optimization, Grey model are presented later  $([2], [3], [6], [7], [23]$ ).

We first present an SIR epidemic disease model. The total (initial) population, N, is categorized into four classes, namely, susceptible,  $S(t)$ , infected-infectious,  $I(t)$ , and recovered,  $R(t)$ , where t is the time variable. We consider discrete and continuous models.

The initial value problem we consider is

$$
\frac{dz_1}{dt} = \lambda_{SC} \cdot z_1 - (\mu_{SC})z_1 - u \cdot z_1 z_2 (1/N), \n\frac{dz_2}{dt} = u \cdot z_1 z_2 (1/N) - (v + w) z_2 - (\mu_{SC}) z_2 + u \cdot z_2 z_3 (1/N), \n\frac{dz_3}{dt} = v \cdot z_2 - (\mu_{SC}) z_3 - u \cdot z_2 z_3 (1/N),
$$

where  $\lambda_{SC} = birth\ rate, \mu_{SC} = natural\ death\ rate, \text{u=transmission rate}, \text{v=recovery rate},$ w= death rate of infected, N=5149000, susceptible population in SC.

We solve the above system of differential Equations by using MATLAB Euler-scheme. The results are shown below. To determine the necessary parameters, we used data obtained from CDC and optimal control methodology as well as neural network and machine learning tools.

## 3. DISCRETE MODEL

We use data covering the period December 1, 2020, to June 1, 2021. In this period vaccination has been available although not taken advantage of by a lot of people. In addition, social distancing and face making have been less and less adhered to.

We consider the following discrete model covering the period December 1, 2020, to June 1, 2021. We have data for infected population and dead population for this model. We are going to rely on our model to estimate the recovered populations day by day covering this period. The recovered population for Dec. 1, 2020, is known to be 115152.

In the models below,  $\lambda_{SC} = .058$  birth rate;  $\mu_{SC} = .0095$ , natural death rate  $vc = .40, vc \cdot N$  represents proportion of vaccinated people, N=the susceptible population, 5149000,

$$
S(n + 1) = S(n) + \lambda(n) \cdot S(n) - \mu \cdot S(n) - \beta(n)S(n)I(n)(1/N) + e(n) \cdot R(n),
$$
  
\n
$$
I(n + 1) = I(n) + \beta(n)S(n)I(n)(1/N) - \gamma(n) \cdot I(n) \cdot R(n) - (\mu + w)I(n),
$$
  
\n
$$
R(n + 1) = R(n) + \gamma(n) \cdot I(n) \cdot R(n) - \mu R(n) - e(n) \cdot R(n).
$$

We use neural networks to deal with the epidemic model. We have input signals, in this case the states. We apply weight factors to the input signals to generate the next output layer. In this process we need the transmissions rates between the states from one neuron layer to the next. Transformation factors are determined using sigmoids. The sigmoid that we use should create output values between 0 and 1 and the discrete model then gives us the next layer of states. Thus we use the sigmoid function  $\sigma(z) = a \cdot 1/(1 + exp(-z))$  and we apply the following formulas to approximate the parameters  $\beta(n)$ ,  $\gamma(n)$ , and  $e(n)$ .

$$
\beta(n) = \sigma(\theta_{11}S(n) + \theta_{12}I(n) + \theta_{13}R(n)), \n\gamma(n) = \sigma(\theta_{21}S(n) + \theta_{22}I(n) + \theta_{23}R(n)), \n e(n) = \sigma(\theta_{31}S(n) + \theta_{32}I(n) + \theta_3R(n)).
$$

(3.1)

Now, given the data  $I(n)$  and  $D(n)$  we solve the above discrete equations to determine the state variables  $S(n)$ ,  $R(n)$  and the parameters  $\beta(n)$ ,  $\gamma(n, e(n))$  using optimization and proceed to the next layer of states. This process is repeated. We note discrete model is suitable for neural network application.



Figure 1. Infected and Dead.

In the absence of additional data we may predict additional transmission parameters using the ones we have. For example we use the values of  $\gamma(n)$ ,  $\beta(n)$ ,  $e(n)$  n=130 to n=150, to determine  $w_{11}, w_{12}, w_{13}, w_{21}, w_{22}, w_{23}, d1, d2$ . in the following optimization problem, which comes from the machine learning algorithm (SVM) support vector machine, to decide the



Figure 2. Recovered and Recovery Rate.



Figure 3. Transmission Rate.

acceptability of predicted values of gamma(.), beta(.),  $e(.)$  for  $n=151$  to 180 using Grey

System. Relevant details of Grey System are presented in the next section ([16]).

$$
\min\{(1/2)(w_{11}^2 + w_{12}^2 + w_{13}^2 + w_{21}^2 + w_{22}^2 + w_{23}^2) + (S(i) - x(7))^2 + (I(i) - x(8))^2\}
$$
\nsubject to\n
$$
w_{11}\gamma(i) + w_{12}\beta(i) + w_{13}e(i) + d1 = S(i),
$$
\n
$$
w_{21}\gamma(i) + w_{22}\beta(i) + w_{23}e(i) + d2 = I(i).
$$

We use Karush-Kuhn-Tucker Theorem(KKT). We set

$$
x(1) = w_{11}, x(2) = w_{12}, x(3) = w_{13}, x(4) = w_{21}, x(5) = w_{22}, x(6) = w_{23}, x(7) = d1, x(8) = d2.
$$

We use  $x(9)$  as the Lagrange multiplier for the first constraint and  $x(10)$  as the Lagrange multiplier for the second constraint. The KKT conditions require that the gradient of

$$
f(x(1),...,x(8)) = (1/2)(x(1)^{2} + x(2)^{2} + x(3)^{2} + x(4)^{2} + x(5)^{2}
$$
  
+x(6)<sup>2</sup>) + (S(i) – x(7))<sup>2</sup> + (I(i) – x(8))<sup>2</sup>  
+x(9)(x(1)\gamma(i) + x(2)\beta(i) + x(3)e(i) + x(7) – S(i))  
+x(10)(x(4)\gamma(i) + x(5)\beta(i) + x(6)e(i) + x(8) – I(i))

(3.2)

with respect to  $x(1), x(2), x(3), x(4), x(5), x(6), x(7), x(8)$  should be zero. That is, we need

$$
x(1) + x(9)\gamma(i) = 0,
$$
  
\n
$$
x(2) + x(9)\beta(i) = 0,
$$
  
\n
$$
x(3) + x(9)e(i) = 0,
$$
  
\n
$$
x(4) + x(9)\gamma(i) = 0,
$$
  
\n
$$
x(5) + x(10)\gamma(i) = 0,
$$
  
\n
$$
x(6) + x(10)e(i) = 0,
$$
  
\n
$$
2(x(7) - S(i)) + x(9) = 0,
$$
  
\n
$$
2(x(8) - I(i)) + x(10) = 0.
$$

Once we determine  $w_{11}, w_{12}, w_{13}, w_{21}, w_{22}, w_{23}, d1, d2$  we can decide the acceptability of the transmission, recovery, and the transfer parameter from recovered to susceptible predicted by the Grey model below. We can also use the relative percentage error (RPE) below.

3.1. Forecasting Using Grey System. We use the parameters  $\beta(n)$ ,  $\gamma(n)$ ,  $e(n)$  for  $n =$ 111, ..., 160 to predict 50  $\beta(.)$ ,  $\gamma(.)$ ,  $e(.)$  parameters so that we have now 210 parameters. We verify the newly generated 50 parameters good forecasts testing them using the SVM machine learning algorithm above. The traditional forecasting model  $GM(1, 1)$  is as follows. We start with a nonnegative sequence

$$
X^{0} = \{x^{0}(1), x^{0}(2), x^{0}(3), \dots, x^{0}(n)\}
$$

of raw data and its accumlating generation (AGO) sequence

$$
X^{1} = \{x^{1}(1), x^{1}(2), x^{1}(3), \ldots, x^{1}(n)\}
$$

where  $x^1(1) = x^0(1)$ , and

$$
x^{1}(k) = \sum_{1}^{k} x^{(0)}(i), \ k = 1, 2, ..., n
$$

and the mean sequence generated consecutive neighbours of  $X<sup>1</sup>$  is

$$
Z^{1} = \{z^{1}(1), z^{1}(2), z^{1}(3), \ldots, z^{1}(n)\}
$$

where

$$
z^{1}(k) = (x^{1}(k) + x^{1}(k-1))/2, k = 2, ..., n.
$$

The equation

$$
x^0(k) + az^1(k) = b
$$

is called basic form of the  $GM(1,1)$  model and the whitenization equation is established

$$
dx^{(1)}/dt + ax^{(1)} = b.
$$

The whitenization equation is solved and the prediction values of  $X(1)$  can be calculated as follows.

$$
x^{(1)}(k) = (x^{(0)}(1) - b/a)e^{(-a(k-1))} + b/a, k = 2, 3, ...
$$

Therefore the predicted values can be generated by

$$
x^{(0)}(1) = x^{(0)}(1),
$$

$$
x^{(0)}(k) = x^{(1)}(k) - x^{(1)}(k-1), k = 2, 3, ..., n.
$$

Relative percentage error (RPE) and mean absolute percentage error (MAPE) are used to evaluate the overall forecast performance accuracy of the prediction models. They are defined as follows:

$$
RPE(k) = |\frac{x^{(0)}(k) - x^{(0)}}{x^{(0)}(k)}| \times 100 \text{ } 0/0
$$

$$
MAPE = 1/n \sum_{k=1}^{n} RPE(k).
$$

. The REP (Relative error percentage) between the predicted 50 cases of infected and the actual 110th day to the 160th day of infected people is

$$
|((IP(k) - I(k+110))/I(k+110)| \cdot 100 \text{ } 0/0
$$

where  $IP(k)$ ,  $I(k + 110)$ ,  $k = 1, 2, ..., 50$  represent the forecasted infection, and the actual infection numbers. A sketch of the REP is shown in figure 5. The REP numbers are less than 0.5 per cent show a good accuracy.



Figure 4. Predicted Infected and Predicted Recovered.



FIGURE 5. Forecasting Accuracy and Death Prediction.

3.2. Discrete SEIR Model. We will consider the SEIR Model given below and calculate the reproduction number.

(3.3)  
\n
$$
\begin{aligned}\n\frac{dS}{dt} &= \lambda S - \mu S - \beta SI/N + eR, \\
\frac{dE}{dt} &= \beta SI/N - (\mu + K)E, \\
\frac{dI}{dt} &= KE - (\mu + \gamma + \delta)I, \\
\frac{dR}{dt} &= \gamma I - \mu R - eR.\n\end{aligned}
$$

(3.4) 
$$
\begin{aligned}\n\frac{dE}{dt} &= \beta SI/N - (\mu + K)E, \\
\frac{dI}{dt} &= KE - (\mu + \gamma + \delta)I.\n\end{aligned}
$$

We rewrite (3.4) as

(3.5) 
$$
\frac{dz}{dt} = (F + V)z,
$$

where  $z^T = (E, I)$ , and

(3.6) 
$$
F = \begin{bmatrix} 0 & \beta S/N \\ K & 0 \end{bmatrix},
$$

and

(3.7) 
$$
V = \begin{bmatrix} \mu + K & 0 \\ 0 & \mu + \gamma + \delta \end{bmatrix}.
$$

Now,

(3.8) 
$$
FV^{-1} = \begin{bmatrix} 0 & \beta \frac{S}{N} \frac{1}{\mu + \gamma + \delta} \\ \frac{K}{\mu + K} & 0 \end{bmatrix}.
$$

The reproduction number  $R_0$  is the dominant eigenvalue of  $-FV^{-1}$ , and is given by

$$
R_0 = \sqrt{(\beta S/N)K/((\mu + K)(mu + \gamma + \delta)}.
$$

We consider the discrete SEIR model.

(3.9) 
$$
S(n + 1) = S(n) + \lambda S - \mu S - \beta SI/N + eR,
$$

$$
E(n + 1) = E(n) + \beta SI/N - (\mu + K)E,
$$

$$
I(n + 1) = I(n) + K \cdot E - (\mu + \gamma + \delta)I,
$$

$$
R(n + 1) = R(n) + \gamma I - \mu R - eR.
$$

The reproduction number  $R_0$  is bigger than 1 as seen in figure 7.



Figure 6. TransmissioRate and RecoveryRate.



Figure 7. Reproduction Number(SEIR) and Exposed.

3.3. Effect of Quarantine. In Figure 1 above we see that the number of infected people is increasing. The figure of infected people shown is in complete agreement to the data gotten



Figure 8. Predicted Dead.

from CDC. It is not acceptable to see the number is increasing. It is known that the disease of COVID-19 is transmitted through different mechanisms, such as hand contamination followed by mucosal inoculation, and droplets or aerosols disseminated by coughing and sneezing. Some measures that control the transmission of COVID-19 involve simple habits such as washing one's hands continuously, sneezing into one's hand or elbow, use of face mask low mobility, quarantine. Quarantine includes all of these measures. What we want to show is what could be the outcome if quarantine had been implemented from the very beginning. We will see a model where an initial quarantine of 110,000 susceptible people, which decreases very fast, leads to a significant decrease in the infected population and corresponding increase in the recovered population. The system (3.10) is the discrete model of infected when there is no quarantine and infected during quarantine.

(3.10) 
$$
S(n + 1) = S(n) + \lambda S - \mu S - \beta SI/N + eR + cQ,
$$

$$
I(n + 1) = I(n) + \beta SI/N - (\mu + \gamma + \delta)I,
$$

$$
R(n + 1) = R(n) + \gamma I - \mu R - eR,
$$

$$
Q(n + 1) = Q(n) + bS(n) - (\mu)Q(n) - cQ(n).
$$

In our quarantine model we use the same contact, recovery, relapse and immunity rates that were obtained in the optimal control method. Thus, we proceed to solve the system (3.10). The graphs of the infected before and after quarantine are shown in Figure 9.

#### 4. CONCLUSION

Epidemic models give insight into the dynamics of diseases and designing intervention strategies. Epidemics exert pressure on healthcare systems, societies, and governments. The motivation of the current work was to use limited information regarding the epidemic for





Figure 9. TransmissionRatio:(BeforeQuarantine/afterQuarantine) and Quarantine People.

getting insight into other aspects of the epidemic dynamic.

For certain diseases, such as malaria, spatial heterogeneity due to time varying disease onset times, regionally different contact rates, and the time dependence of the contact rates are important in the implementation of containment strategies for long time. For some models a quick intervention is important and one has to rely on limited data to design intervention strategies. Mathematical models using control theory, optimization, and neural network methodologies can help in approximating missing and necessary data. In this work we use data from December 1, 2020, to June 1, 2021, of infected and dead populations to have some ideas on the transmission, recovery, and effect of quarantine strategy. We also considered forecasting strategy that could be used in having insight into the epidemic dynamics.

The pictures presented give insight in the dynamics of the disease around the period when the data was collected.

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## REFERENCES

- [1] D. Aldila, T. Gotz, E. Soewono, An optimal Control problem arising from a dengue disease transmission model, Math. Biosci. 242 (1)(2013), 9-16.
- [2] Allen, L: Some discrete time SI, SIR, and SIS epidemic models. Math.Biosci.124,83-105(1994)
- [3] Allen, L, Burgin, A: Comparison of deterministic and stochastic SIS and SIR models in discrete time. Math.Biosci.163, 1-33 (2000)
- [4] Anastassopoulou C, et.al, Anastassopoulou C, Russo L, Tsakris A, Siettos C. Data-based analysis, modelling and forecasting of the COVID-19 outbreak. PLoS ONE 15(3): e0230405. https://doi.org/10.1371/journal.pone.0230405
- [5] F. G. Ball, E. S. Knock, P.D. O'Neil Control of emerging infectious diseases using responsive imperfect vaccination and isolation , Math. Biosci. 216 (1) (2008), 100-113.
- [6] Halis Bilgil, New grey forecasting model with its application and computer code, AIMS Mathematics, 6(2): 1497–1514, 20 November 2020.
- [7] MARCUS DE BARROS BRAGA, ET AL, Artificial neural networks for short-term forecasting of cases, deaths, and hospital beds occupancy in the COVID-19 pandemic at the the Brazilian Amazon, PLOS https://doi.org/10.1371/journal.pone.0248161 March 2021.
- [8] C. Castilho , Optimal Control of an epidemic through educational campaigns , Electron. J. Differ. Equ. 2006 (2006), 1-11.
- [9] Jie Cui , Si-feng Liu a, Bo Zeng , Nai-ming Xie, A novel grey forecasting model and its optimization, Applied Mathematical Modelling 37 (2013) 4399–4406.
- [10] H. GAFF, E.SCHAEFER, Optimal control applied to vaccination and treatment strategies for various epidemiological models, Math. Biosci. Eng. 6 (3) (2009), 469-492.
- [11] K. HATTAF, N. YOUSFI, Optimal Control of a delayed HIV infection model with immune response using an efficient numerical method , Int. Sch. Res. Netw. (2012) (2012), 1-7.
- [12] HETHCOTE, The mathematics of infectious diseases. SIAM Rev. Vol. 42, 2006, 599-653.
- [13] HAIL-FUNG HUO ET. AL., Modeling and stability of HIV/AIDS epidemic model with treatment, Hail-Feng Huo, Rui Chen, Xun-Yang Wang, Applied Mathematical Modelling 40(2016) 6550-6559.
- [14] H. LAARABI, A. ABTA, K. HATTAF, Optimal Control of a delayed SIRS epidemic model with vaccination and treatment , Acta Biotheor. 63 (15) (2015), 87-97
- [15] Lin Q, et.al, Lin Q, Zhao S, Gao D, Lou Y, Yang S, Musa SS, Wang MH, Cai Y, Wang W, Yang L, He D. A conceptual model for the coronavirus disease 2019 (COVID-19) outbreak in Wuhan, China with individual reaction and governmental action. Int J Infect Dis. Vol. 93, 2020; pp. 211-216.
- [16] Jian Luo, Tao Hong , and Shu-Cherng Fang,Robust Regression Models for Load Forecasting, IEEE TRANSACTIONS ON SMART GRID, VOL. 10, NO. 5, SEPTEMBER 2019, pp. 5397-5404.
- [17] Xia Ma, Yicang Zhou, Hui Cao,Global stability of the endemic equilibrium of a discrete SIR epidemic model, Advances in Difference Equations 2013, 2013:42 http://www.advancesindifferenceequations.com/content/2013/1/42
- [18] MACDONALD, G. The epidemiology and control of malaria. Oxford University, 1957, Mandal, S. et al.
- [19] Mathematical Models of Malaria A Review, Malaria Journal (2011).
- [20] P. Ogren, C. F. Martin, Vaccination strategies for epidemics in highly mobile populations. Appl. Math. Comput. 127 (2002), 261-276.
- [21] C. J. SILVA, D. F. TORRES, Optimal Control strategies for tuberculosis treatment: a case study in angola , Numer. Algebra Control Optim. 2 (3) (2012), 601-617
- [22] UNKEL S, ET.AL, Statistical methods for the prospective detection of infectious disease outbreaks: a review. J R Stat Soc, Ser A, Stat Soc. 2012;175(1):49-82.
- [23] Valeri M. Mladenov, Nicholas G. Maratos, Neural Networks for Solving Constrained Optimization Problems, Proc. of CSCC'00, Athens, Greece.
- [24] WU JT ET.AL, Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan, China. Nature Medicine Vol. 26, 2020, pp. 506-510.
- [25] Xia, Y. S., Further Results on Global Convergence and Stability of Globally Projected Dynamical Systems, journal of optimization theory and applications: Vol. 122, No. 3, pp. 627–649, 2004.
- [26] G. Zaman, Y.H. Kang, J.H. Jung, Optimal treatment of an SIR epidemic model with time delay , Biosystems 98 (1) (2009), 43-50.