AN SEIR MODEL FOR ISOLATED COVID-19 PATIENTS AND THE EPIDEMIC IS CONSTRUCTED – USING THE DELAY DIFFERENTIAL EQUATION

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ABSTRACT:

The novel Corona virus (Covid) started to spread across the globe in 2019, Still the researches was not able to find whether surviving a COVID-19 infection is possible. In this situation the mathematical models are used to find the Suspected, Isolated, Recovered and deceased coronavirus patients. In future the mathematical model will helps to find the virus and its dynamical behavior to point out. This research paper explore SEIR compartmental model for the COVID-19 pandemic (SEIR COVID). This SEIR models will state that helps to control the pandemic. This study, examined the isolated people who are affected by covid, and also this helps to predict in particular time period, how many people affect. Here we using Routh Hurwitz criterion we find the stable of the virus and also time decay equation.

INTRODUCTION

According to theory of probability Analysis, and interpretation of numerical data are devoted by using this theory COVID-19 epidemiological statistics, the epicenters of the epidemic of India is identified.Our country faces challenges in order to control COVID-19 virus.This model (SEIR) helps to control the virus and isolate the patients who are affected by COVID-19. To find the solution approximately a compartmental SEIR (Susceptible, Exposed, Infectious and Recovered). The SEIR COVID helps to sort out who are affected by COVID-19 which makes them isolate. The testing Result gives the individual who have developed symtoms, When it is asymptomatic infection then it is referred to as positive cases. This determines whether it is Positive or Negative by the system of stabililty.

The Differential equation and algebraic equations are used for SEIR COVID in order to estimate epidemic based on the rate of transmission. Taking SEIR model we have proved positive and negative cases by using SIR model (feature are Susceptible(S), Infected(I), and Recovered(R)). This model helps to track the incubation period of virus. This model was published by the authors to anticipate the occurrence time for peak numbers cases in china. The model SEIR COVID is used for calculating the number of confirmed cases. Based on this cases, the local Government try to avoid infectious disease in various methods. The goal of this model is to find infected person and made them to isolate. In 2020, Zhou Tang.X founded Prediction of New Coronavirus Infection Based on a Modified SEIR Model.

According to SEIR for COVID-19 the treatment such as Quarantine can minimize the contact rate of latent persons. As a solution for tracking COVID-19 infection an SEIR COVID model is used in misdiagnosed patients and those in isolated. This paper helps to estimate COVID-19 spread by using delay differential equation.

2. MODEL DESCRIPTION

A fundamental epidemic model, the SIR model, predicts a theoretical number of disease infectious cases in a confined community over time. Assume that the population for the SIR model is fixed and that the communicable agent's development period is short. The compartment model is made up of three boxes that divide the population into several unique groups.

S - People who are at risk of contracting the epidemic.

I - People who have already been affected and can spread the disease to the S.

R- Recovered or deceased individuals.

Most infectious diseases have different incubation periods depending on their nature. The incubation or growth phase (immunity period delay, infection period delay, and incubation period delay) can be added to the basic model to affect the system's behavior.

One of the most popular and commonly used techniques for capturing biological backgrounds is SIR models with time delay. We develop a new group called the Revealed Group to take the fundamental model to a more realistic level (C).
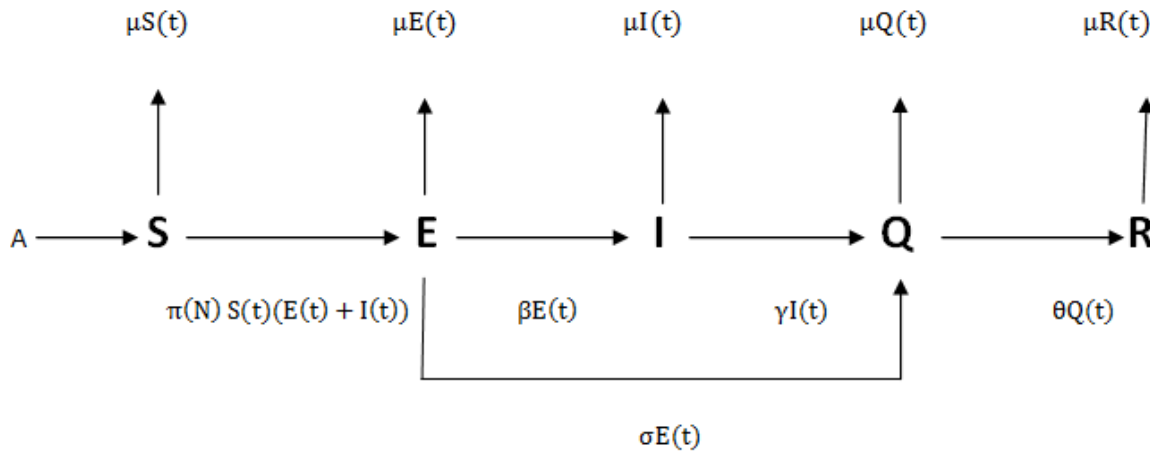
S – Susceptible Population

E – Exposed Population

I – Infected Population

Q – Isolated Population

R – Recovered Population

π–The Rate at which the Susceptible Population moves to Infected and Exposed   Population.

$\beta \rightarrow$ The rate at which an exposed population becomes infected.

σ —Presents the rate at which exposed people take onside as isolated.

γ—The at which infected people were added to an individual is displayed.

θ — The rate at which an isolated persons recovered.

μ — The rate at natural death plus the rate of death caused by disease.

The proposed SEIR_COVID model is

$$\frac{dS(t)}{dt} = A-\mu S(t) - \pi(N)S(t)\big(E(t) + I(t)\big)$$

$$\frac{dE(t)}{dt} = \pi(N)S(t)\big(E(t) + I(t)\big) - \beta E(t) - (\mu + \sigma)E(t)$$

$$\frac{dI(t)}{dt} = \beta E(t) - \gamma I(t) - \mu I(t)$$

$$\frac{dQ(t)}{dt} = \sigma E(t) + \gamma I(t) - \theta Q(t) - \mu Q(t)$$

$$\frac{dR(t)}{dt} = \theta Q(t) - \mu R(t) \qquad (1)$$

For System (1) , Let $N=A/\mu$, $S=S/N$, $e=E/N$, $i=I/N$, and $q=Q/N$ and rescale the system (1) to get the normalized form.

$$\frac{dS(t)}{dt} = A - \mu s - \pi N s(e + i) \qquad (2)$$

$$\frac{dE(t)}{dt} = \pi Ns(e + i) - \beta e - (\mu + \sigma)e \qquad (3)$$

$$\frac{dI(t)}{dt} = \beta e - \gamma i - \mu i \qquad (4)$$

$$\frac{dQ(t)}{dt} = \sigma e + \gamma i - \theta q - \mu q \qquad (5)$$

$$\frac{dR(t)}{dt} = \theta q - \mu r \qquad (6)$$

Model outputs: The outputs of the mathematical model used to asses the simulation results are presented here.

The number of cases Susceptible on day t is

$$S(t) = s_0 + \int_0^t \left[A - \mu S(t) - \pi(N)S(t)\big(E(t) + I(t)\big) \right] dt$$

The number of cases Exposed on day t is

$$E(t) = e_0 + \int_0^t \left[\pi(N)S(t)\big(E(t) + I(t)\big) - \beta E(t) - (\mu + \sigma)E(t) \right] dt$$

The number of cases Infected on day t is

$$I(t) = i_0 + \int_0^t \left[\beta E(t) - \gamma I(t) - \mu I(t) \right] dt$$

The number of cases Isolated on day t is

$$Q(t) = q_0 + \int_0^t \left[\sigma E(t) + \gamma I(t) - \theta Q(t) - \mu Q(t) \right] dt$$

The number of cases Recovered on day t is

$$R(t) = r_0 + \int_0^t \left[\theta Q(t) - \mu R(t) \right] dt$$

Where h_0, h_{n0}, r_0, d_0 are the initial values in their respective states.

2.1.Analysis of Stability

The steady states and characteristic equations from the set of delay differential equations will be required to analyze the stability of delay differential equations.

We can find E(t) after we know S(t) and I(t) because the term E(t) appears only in the differential equation, $\frac{dE(t)}{d(t)}$ derivative of itself.

The steady states can then be found by solving the differential equation above for zero, i.e.

$$\frac{dS}{dt} = \frac{dI}{dt} = \frac{dQ}{dt} = \frac{dR}{dt} = 0$$

It's simple to prove that the system has two positive equilibrium states, namely

1) Zero Disease equilibrium $E_0 = (S_0, I_0, Q_0, R_0)$

2) Pandemic Equilibrium $E^* = (S^*, I^*, Q^*, R^*)$

The Zero disease, Pandemic Equilibrium and stability of system (2) depends on the basic reproductive number R_0, which is determined with the help of the next generation matrix method[15].

Therefore, The first steady state Equilibrium $E_0 = (1,0,0,0)$

Consider the following matrices for finding the basic reproductive number R_0.

$$F = \begin{pmatrix} \pi NS(e + i) \\ 0 \end{pmatrix}$$

$$V = \begin{pmatrix} \beta e + (\mu + \sigma)e \\ -\beta e + \gamma i + \mu i \end{pmatrix}$$

Now Jacobian of F and V at C are,

$$F=\begin{pmatrix} \pi N & \pi N \\ 0 & 0 \end{pmatrix}$$

$$V=\begin{pmatrix} \beta+\mu+\gamma & 0 \\ -\beta & \gamma+\mu \end{pmatrix}$$

The dominant eigen value of FV^{-1} represents R_0 which is

As the reproduction number $R_0 = \dfrac{\pi N}{(\beta+\mu+\sigma)}$

Implies $S^* = \dfrac{1}{R_0}$

From equ (3)

$$\Rightarrow e^* = \dfrac{(\gamma+\mu)i}{\beta}$$

From equ (1)

$$\Rightarrow i^* = \dfrac{\beta\mu(R_0-1)}{\pi N(\gamma+\mu+\beta)}$$

From equ (4)

$$\Rightarrow q^* = \dfrac{\sigma(\gamma+\mu)+\gamma\beta}{\beta(\theta+\mu)}i^*$$

From equ (5)

$$\Rightarrow r^* = \dfrac{\mu(R_0-1)(\theta\sigma(\gamma+\mu)+\gamma\beta\theta)}{\pi N\mu(\gamma+\mu+\beta)(\theta+\mu)}$$

Therefore, The second state pandemic equilibrium is

$$E^* = \left(\dfrac{1}{R_0}, \dfrac{\beta\mu(R_0-1)}{\pi N(\gamma+\mu+\beta)}, \dfrac{\sigma(\gamma+\mu)+\gamma\beta}{\beta(\theta+\mu)}i^*, \dfrac{\mu(R_0-1)(\theta\sigma(\gamma+\mu)+\gamma\beta\theta)}{\pi N\mu(\gamma+\mu+\beta)(\theta+\mu)} \right)$$

2.1.1. Theorem 1:

The SEIR_COVID system's Zero Disease equilibriumis asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof:

Consider the Jacobian Matrix equations below

$$\dfrac{dS}{dt} = \mu - \mu S - \beta NS(e+i)$$

$$\dfrac{dI}{dt} = \beta e - \gamma i - \mu I$$

$$\dfrac{dR}{dt} = \theta q - \mu R$$

Jacobian Matrix for the above equation

$$J=\begin{bmatrix} -\mu S & -\pi NS & 0 \\ 0 & -(\gamma+\mu) & 0 \\ 0 & \sigma & -(\theta+\mu) \end{bmatrix}$$

At the deceased equilibrium point, the Jacobian Matrix is written as

$$J_{E0}=\begin{bmatrix} -\mu & -\pi N & 0 \\ 0 & -(\gamma+\mu) & 0 \\ 0 & \sigma & -(\theta+\mu) \end{bmatrix}$$

The characteristic equation for the Jacobian matrix JE_0 is $\det(JE_0 - \lambda I) = 0$ where I is the 3x3 unit matrix. Therefore,

$$\begin{vmatrix} -\mu - \lambda & -\pi N & 0 \\ 0 & -(\gamma + \mu) - \lambda & 0 \\ 0 & \gamma & -(\theta + \mu) - \lambda \end{vmatrix} = 0$$

$(-\mu-\lambda)\,(-\gamma - \mu - \lambda)(-\theta - \mu - \lambda) = 0$

$-\mu - \lambda = 0, \quad -\gamma - \mu - \lambda = 0, \quad -\theta - \mu - \lambda = 0,$

$\lambda_1 = -\mu$

$\lambda_2 = -(\gamma + \mu)$

$\lambda_3 = -(\theta + \mu)$

Therefore, all the Eigenvalues of the characteristic equation are negative if $R_0 < 1$. Hence the equilibrium point E_0 is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

2.1.2. Theorem 2 :

As a result, if $R_0 > 1$, everyone of the eigen value of the characteristic equation are positive, indicating that the pandemic equilibrium E* is asymptotically stable locally.

Proof:

The Jacobian matrix is

$$J = \begin{bmatrix} -\mu S & -\pi N S & 0 \\ 0 & -(\gamma + \mu) & 0 \\ 0 & \sigma & -(\theta + \mu) \end{bmatrix}$$

Pandemic equilibrium point E^*, then the Jacobian matrix is

$$J_{E^*} = \begin{bmatrix} -\mu\left(\frac{1}{R_0}\right) & -\pi N\left(\frac{1}{R_0}\right) & 0 \\ 0 & -(\gamma + \mu) & 0 \\ 0 & \gamma & -(\theta + \mu) \end{bmatrix}$$

The characteristic equation for the Jacobian matrix is $\det(JE^* - \lambda I) = 0$

$$\begin{vmatrix} \frac{-\mu}{R_0} - \lambda & \frac{-\pi N}{R_0} & 0 \\ 0 & -(\gamma + \mu) - \lambda & 0 \\ 0 & \gamma & -(\theta + \mu) - \lambda \end{vmatrix} = 0$$

$\Rightarrow \left(\frac{-\mu}{R_0} - \lambda\right)\left[(-(\gamma + \mu) - \lambda)(-(\theta + \mu) - \lambda) - 0\right] = 0$

$\Rightarrow \lambda^3 + \lambda^2[\mu R_0 + 2\mu + \gamma + 1] + \lambda[2\mu^2 R_0 + R_0(\mu\theta + \mu\sigma) + \theta(\mu + 1) + \mu(\gamma + \mu)]$

$+[\mu^3 + \mu^2(\gamma + \theta) + \mu\gamma\theta] = 0$

$\Rightarrow \lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$

Where $R_0 > 0$, that is

$a_1 = \mu R_0 + 2\mu + \gamma + 1 = 0$

$a_2 = 2\mu^2 R_0 + R_0(\mu\theta + \mu\gamma) + \theta(\mu + 1) + \mu(\gamma + \mu)$

$a_3 = \mu^3 + \mu^2(\gamma + \theta) + \mu\gamma\theta$

If $R_0 > 1$. i.e.) a_1, a_2 and a_3 are positive if $R_0 > 1$.

If $a_1, a_3 > 0$ and $a_1, a_2 > a_3$ according to the Routh-Hurwitz criterion, the system is asymptotically stable.

Then $E^* = \left(\dfrac{1}{R_0}, \dfrac{\beta\mu(R_0-1)}{\pi N(\gamma+\mu+\beta)}, \dfrac{\mu(R_0-1)[\sigma\theta(\gamma+\mu)+\gamma\beta\theta]}{\pi N\mu(\gamma+\mu+\beta)(\theta+\mu)} \right)$

Is asymptotically stable.

3. Data Analysis, Model fitting, and results

COVID-19 epidemic in India with an R_0 value of November to May are represented in table 1. In India, the pandemic is certainly not spreading at that rate. In figure 1 represents as the day wise COVID-19 cases (confirmed, active, isolated and recovered) in India and day wise COVID-19 Isolated cases of India are shown in figure 2.

Table 1. R_0 value of India

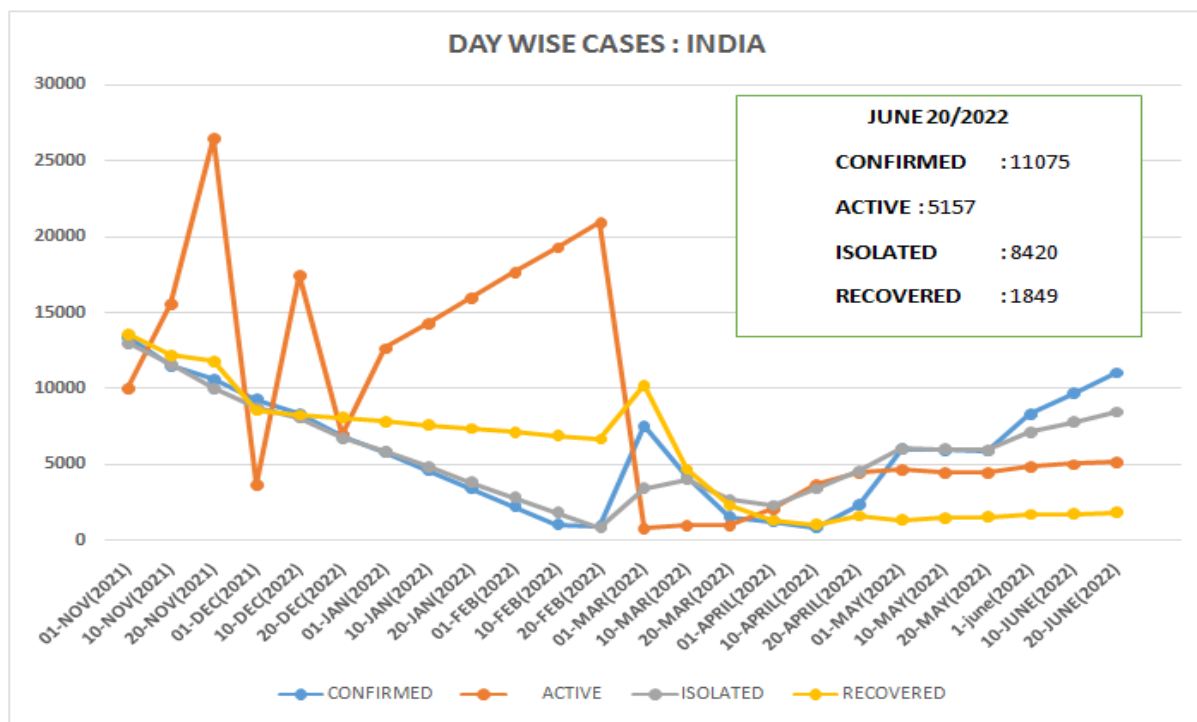| Month	R_0
November	1.01
December	1.22
January	2.2
February	2.9
March	0.93
April	1.07
May	1.36

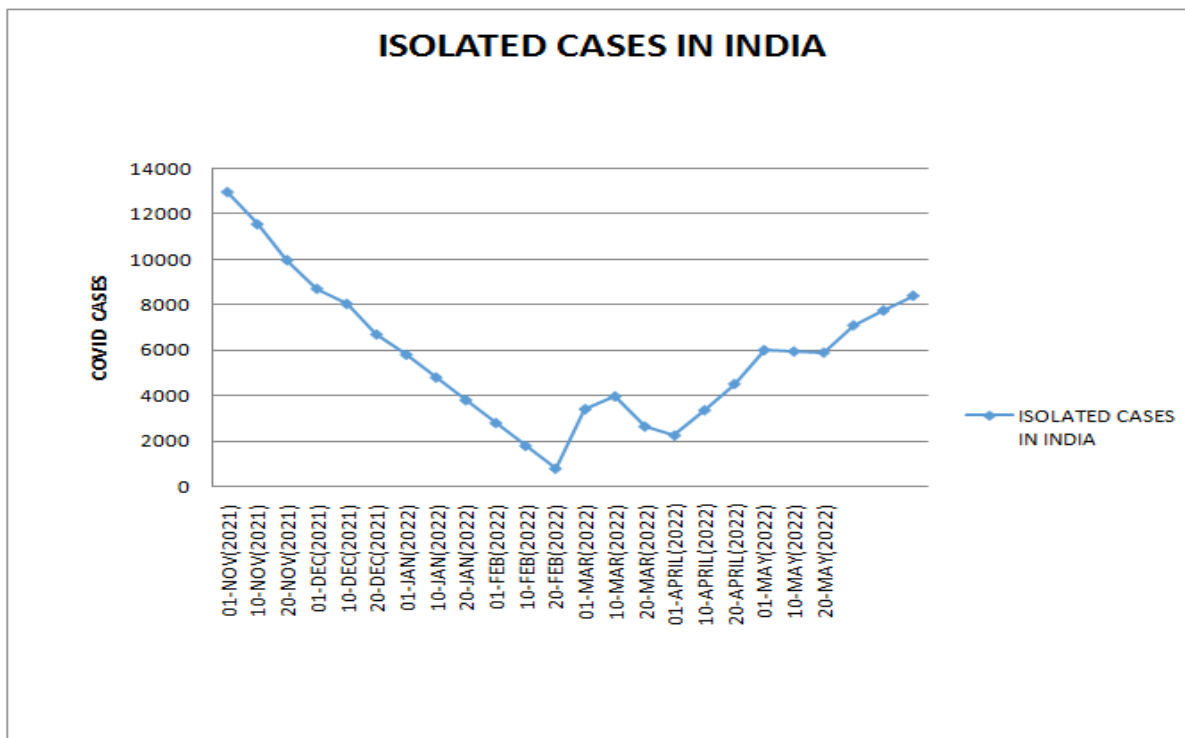Figure 1: Day Wise Cases India

Figure 2: Isolated Cases in India

4. Conclusion

The SEIR Compartmental model is used to diagnosed COVID-19 for Isolation and analysed. Routh-Hurwitz criteria were used to investigate the steady-state of this model. In this SEIR COVID model, zero disease equilibrium and pandemic equilibrium variables were employed to improve infection prognosis. The COVID-19 epidemic will be predicted effectively using our suggested SEIR COVID model.

References

[1] Al-Sheikh,S.A.(2012).Modeling and Analysis of an SEIR Epidemic Model with   LimitedResource for Treatment. Global Journal of Science FrontierResearch Mathematics and DecisionSciences .

[2] Batista, M. Estimation of the final size of the coronavirus epidemic by SIR model,ResearchGtae, 2020.

[3] Can Hou, J. C. (2020, April). "The effectiveness of quarantine of Wuhan city against the Corona Virus Disease 2019 (COVID-19): A well- mixed SEIR model analysis. Journal of Medical Virology .

[4] David W. Berger, K. F. (2020, March). An SEIR Infectious Disease Model with Testing and Conditional Quarantine. NBER Working Papers and Publications .

[5] Dhamodharavadhani, R. Rathipriya, and J. M. Chatterjee, "COVID-19 Mortality Prediction for India Using Statistical Neural Network Models," Frontiers in PublicHealth,vol. 8,   2020.

6] S. Dhamodharavadhani and R. Rathipriya, "Forecasting Dengue Incidence Rate in TamilNadu Using ARIMA Time Series Model," Machine Learning for Healthcare, pp. 187202, 2020

[7] Fairoza Amira Binti Hamzah, C. H.-w. (2020, March). CoronaTracker:COVID-19 Outbreak Data Analysis and Prediction. World Health Organization, Bull World Health Organ .

[8] Gui-Hua Li, Y.-X. Z. (2017, April). Dynamic behaviors of a modified SIR model in epidemic diseases using nonlinear incidence and recovery rates. /doi.org/1 0.1371/ journal.pone. 0175789,PLOS one .

[9] Haider Ali Biswas, Md L. T. (2014). A SEIR Model for Control of Infectious Diseases with Constraints. Mathematical biosciences and engineering:MBE .

[10] Ming, W. Huang, V. and Zhang, C.J.P.Zhang, "Breaking down of the healthcare system:Mathematical Modelling for controlling the novel coronavirus (2019-nCoV) outbreak in Wuhan, China," medRxiv and biorxiv,2020

[11] NaYi, Q. K. (2009, November). Analysis and control of an SEIR epidemic system with nonlinear transmission rate. Mathematical and Computer Modelling .

[12] Nesteruk, I. "Statistics-based predictions of coronavirus epidemic spreading in Mainland China," Innovative Biosystems and Bioengineeering, Vol.4, no.1,pp.13-18,2020

[13] Shi Pengpeng, C. S. (2020, February). SEIR Transmission dynamics model of 2019 nCoV coronavirus with considering the weak infectious ability and changes in latency duration. medRxivpreprint .

[14] Trawicki, M. B. (2016, November). "Deterministic Seirs Epidemic Model for Modeling Vital Dynamics, Vaccinations, and Temporary Immunity. Academic Editor: Brigitte Servatius .

[15] Van den Driessche, P. and Watmough, J. "Further notes on the basic reproduction number ," in Mathematical Epidemiology, Lecture Notes in Mathematicis, F.Brauer, P.Driessche, J.Wu, Eds.,pp.159-178,2008

[16] Zhou Tang, X. (2020). Prediction of New Coronavirus Infection Based on a Modified SEIR Model. doi: https://doi.org/10.1101/2020.03.03.20030858, medRxiv .