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AN INTRODUCTION: A SIMPLE MATHEMATICAL MODELING FOR COVID-19.

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ABSTRACT

A numerical model is proposed for quantitative depiction of the flare-up of the novel Covid pandemic. In this paper, we plan to gauge and foresee the circumstance of the new Covid pandemic (COVID-19) in nations under isolate measures. To start with, we present another discrete-time numerical model portraying the development of the COVID-19 out of a populace under isolate. The examination with the public information shows that careful arrangements of the model lead to the outcomes, which are in acceptable concurrence with the deliberate information in China and the quantity of new dynamic Covid cases is expanding steadily across the globe. India is presently in the second phase of COVID-19 spreading, it will be a pestilence rapidly if appropriate assurance isn't under-taken dependent on the data set of the transmission of the illness. This paper is utilizing the current information of COVID-19 for the numerical demonstrating and its dynamical examination. We acquire another portrayal to evaluate and deal with the episode of irresistible illness COVID-19 through SEQIR pandemic model, which depends on the notion that the contaminated yet undetected by testing people are ship off isolate during the brooding time frame. During the brooding time frame assuming any individual be contaminated by COVID-19, that concerned contaminated people are confined and the fundamental medicines are orchestrated so they can't spoil different inhabitants locally. Elements of the SEQIR model is introduced by fundamental generation number Ro and the far reaching dependability examination.

Keywords:

NONLINEAR MATHEMATICAL MODEL, Novel Corona VIRUS, Seqir MODEL.

1. INTRODUCTION

Covids (CoV) are a huge group of zoonotic infections, that is, they are communicated from creatures to people, and that cause side effects going from the normal virus to more genuine sicknesses like Middle East Respiratory Syndrome (MERS) which is sent from dromedary to people and serious intense respiratory condition (SARS) which is sent from civet to people. A few known Covids that have not yet tainted people are circling in certain creatures. The Covid sickness 2019 (COVID-19) has prompted high bleakness and mortality in China, Europe, and the United States, setting off uncommon general wellbeing emergencies all through the world. On March 11, 2020, the World Health Organization (WHO) pronounced COVID-19 as a worldwide pandemic.

Coronavirus is brought about by a novel Covid which is currently named serious intense respiratory disorder Covid 2 (SARS-CoV-2). SARS-CoV-2 is viewed as the third zoonotic human Covid arising in the current century, after SARS-CoV in 2002 and the Middle East respiratory condition Covid (MERS-CoV) in 2012.Mathematical models have for some time been producing quantitative data in the study of disease transmission and giving helpful rules to episode the executives and strategy improvement. Specifically, various displaying reads have been performed for COVID-19. The new Covid SARS-CoV-2 is another strain of Covid that have not yet been distinguished in people, where respiratory side effects, fever, hack, windedness, and dyspnea, are basic indications of the disease with the new Covid pandemic, COVID-19. In more extreme cases, this infection can cause pneumonia, serious intense respiratory disorder, kidney disappointment, and even demise. The WHO standard suggestions to the overall population for diminishing openness to, and transmission of, a scope of illnesses are the accompanying and incorporate hand cleanliness, respiratory cleanliness, and great sanitation rehearses.

(I) Wash your hands frequently with a hydro alcoholic solution or with soap and water

(II) Cover your mouth and nose with the crease of your elbow or with a handkerchief if you cough or sneeze; throw the handkerchief immediately after and wash your hands.

(III) Avoid close contact with people who have a fever and cough.

(IV) In case of fever, cough, and difficulty in breathing, consult a doctor without delay and tell him the trips made.

(V) In markets located in areas where there are currently cases of the new corona virus, avoid unprotected direct contact with live animals and with surfaces in contact with animals

(VI) Consumption of raw or undercooked animal products should be avoided. In accordance with good food safety practice, raw meat, milk, or organ meats should be handled with care to avoid cross contamination with raw food.

2. MATHEMATICAL MODEL

The first nontrivial biological model used for calculation and the time evolution of the total world population of people was created in 1838 by Verhulst. His model is usually called the logistic model and has the form (in dimensionless variables)

$$dU/dt = U (1 - U), U(0) = N0 > 0, \qquad (1)$$

And is the classical example in any textbook on Mathematical Biology. Its exact solution is well known

$$U (t) = N_0e^t/1 + N0 (et - 1) \qquad (2)$$

And depending on the value N0 suggests three different scenarios for the population evolution. In particular, the useful curve, the so-called sigmoid, is obtained if N0< ½.

We have noted that the data [9] for the total number of the COVID-19 cases in China and some other countries can be approximated by a sigmoid with the correctly specified parameters. Having this in mind, we introduce a smooth function u(t), which presents the total number of the COVID-19 cases identified up to day t (for any integer number t). We assume that the first case (cases) u0 was (were) identified at t = 0. Obviously, the function u(t) is non decreasing. Therefore, we obtain

$$du/dt= u(a - bu), u(0) = u_0 \geq 0, \qquad (3)$$

Where a and b are positive constants. One may define a as a0S, where a0< 1 is the infection rate and S is an average number of healthy persons, who was contacted by a fixed infected person (the so-called mechanism of the virus transmission). Obviously, each infected person can be in contact only with a limited number of people (usually it is relatives and close friends). The term bu has an opposite meaning to a, because one reflects the efforts B, in order to avoid contacts with infected persons and to make other restrictions introduced by the government. The coefficient B should increase with growing u(t). In other words, the government and ordinary people should apply stronger measures in order to stop growing u(t), otherwise the control on the epidemic process will be lost. Therefore, we assume that $B \approx bu^{1+\gamma}$ with $\gamma > 0$,, therefore the term $bu^{1+\gamma}$ (here b > 0) leading to the equation(correction)

$$du/dt=u(a-bu^{\gamma}),u(0)=u0\geq 0 \qquad (4)$$

is derived.

In the case γ=1, Equation (**2**) coincides with (**1**). We note that the nonlinearity in (**2**) was introduced by Ayala, for describing competition between species, while the logistic equation in epidemiology occurs naturally and it is shown under some general assumptions.

During the epidemic process there are two possibilities for the infected persons. A majority, say *w*, among them will recover, while some people, *v*, will die. Obviously, the equality

$$u=v+w$$

takes place at any time *t*. A typical equation for the time evolution of *v* (see the last equation in the SIR model) is

$$dv/dt=k(t)u, v(0)= v_0\geq 0 \qquad (3)$$

(A similar equation can be written for *w* but there is no need to use more equations), where v0 is the number of deaths at t=0. Here the coefficient k(t)>0 reflects the effectiveness of the health care system of the country (or a region) in question. From mathematical point of view, this coefficient should have the asymptotic behaviour k(t)→0, if t→∞, otherwise all infected people will die. In particular, the useful form is

$$k(t)=k_0\exp(-\alpha t), \alpha>0.$$

- u(t) the total number of the COVID-19 cases at the time t
- v(t) the total number of deaths at the time t
- w(t) the total number of recovered patients and those under treatment at the time t
- a the coefficient for the virus transmission mechanism
- b the coefficient for the effectiveness of the government restrictions (quarantine rules)
- *g* the exponent, which guarantees that the total number of the COVID-19 cases is bounded in time
- k(t) the coefficient for effectiveness of the health care system during the epidemic process

On the other hand, it is well known that the COVID-19 outbreak in several countries is so severe that the mortality rate is rather high, i.e., the assumption u≫v is not true. For example, v≈0.14u in Italy (up to date as of 5 May 2020). In such cases, the model (**2**)–(**3**) should be generalized as follows

$$du/dt=(u-v)(a- b(u-v)^{\gamma}), u(0)= u_0\geq 0, \qquad (5)$$

$$dv/dt=k(t)(u-v), v(0)= v_0\geq 0. \qquad (6)$$

In fact, the time evolution of the function *u* cannot depend on the infected persons who already died. Similarly, the number of new deaths cannot depend on the people who already died. Taking into account the equality u−v=w, the model (**4**)–(**5**) is reducible to the form

$$dw/dt=w(a-k(t)-bw\gamma), w(0)= w_0= u_0- v_0\geq 0, \qquad (7)$$

$$dv/dt=k(t)w, v(0)= v_0\geq 0. \qquad (8)$$

Now we realize that the nonlinear equation in (**6**) is the known Bernoulli equation. Thus, solving the initial problem (**6**) and substituting *w* into (**7**), we arrive at the exact solution in the explicit form

$$w(t) = \exp(at - \int_0^t K(\tau)d\tau)(w_0^{-\gamma} + b\gamma \int_0^t exp\ (\gamma a\tau - \gamma \int_0^t K\ (z)dz)d\tau)^{-\frac{1}{\gamma}}(8)$$

$v(t)= v_0+\int_0^t K(\tau)w(\tau)d\tau$,(9)

$u(t)= v_0+w(t)+\int_0^t K(\tau)w(\tau)d\tau$.(10)

Obviously the further calculations depend essentially on the form of the coefficient k(t). In particular, setting $k(t)=k0\exp(-\alpha t),\alpha>0$ we obtain

$w(t)=\exp(at+\frac{k_0}{\alpha}e^{-\alpha t})(e^{\frac{\gamma k_0}{\alpha}}w_0^{-\gamma}+b\gamma\int_0^t exp(\gamma a\tau+\gamma\alpha e-\alpha\tau)d\tau)-1\gamma$,

$v(t)= v_0+ k_0\int_0^t e^{-\alpha t}w(\tau)d\tau$,

$u(t)= v_0+w(t)+ k_0\int_0^t e^{-\alpha t}w(\tau)d\tau$.

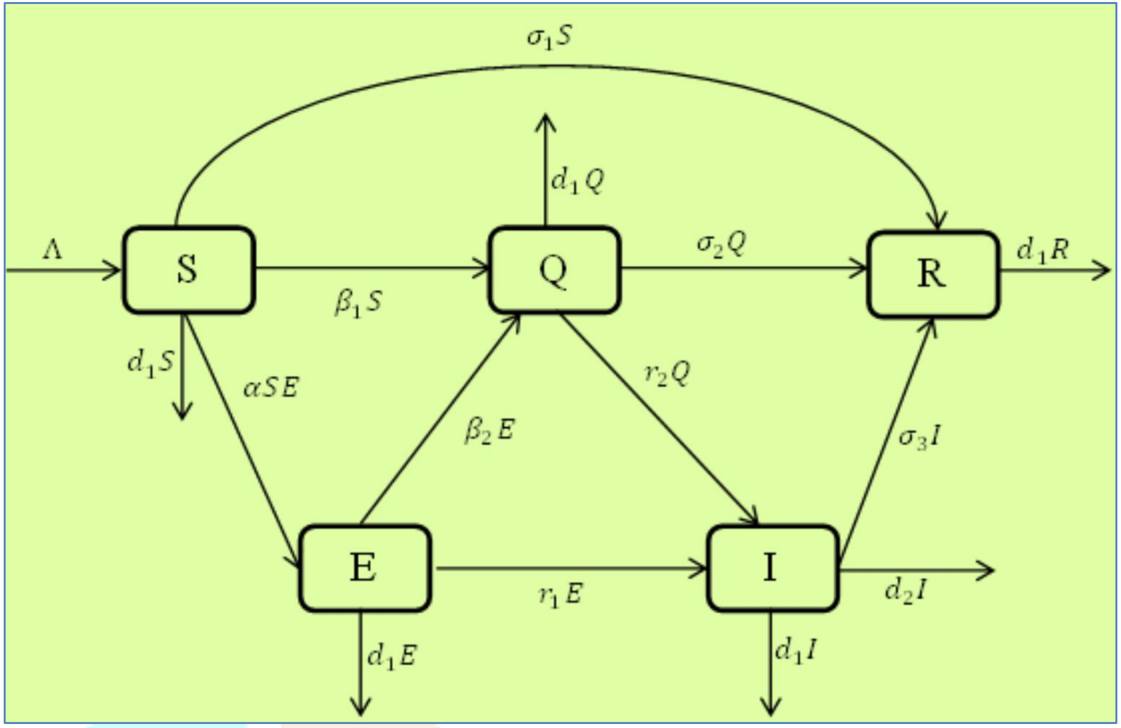
In the subsequent sections we concentrate ourselves on the countries, in which $u\gg v$ so that the simplified model (**2**)–(**3**) can be used.

3. MODEL DERIVATION OF NOVEL CORONA VIRUS DISEASE:

In this section we will discuss about the MODEL derivations of Novel Corona Virus Disease. They are as follows:

A few specialists have recently conceived numerical model for spread of irresistible sicknesses. India is additionally influenced by this imported illness and the quantity of dynamic COVID-19 patients builds step by step at the present time. Contingent upon the new circumstance, India Government has taken a few systems to quit spreading COVID-19 infection. This segment presents a SEQIR model of COVID-19 dependent on the momentum circumstance of the sickness in Indian climate. We embrace a substitute that recreates a few key epidemiological properties of COVID-19 infection. The current model construction of COVID-19 portrays the elements of five sub-populaces of Indians like helpless (S(t)),

Infected yet not identified by testing populace (E(t)), isolated (Q(t)), Conformed contaminated populace who are in under treatment in segregation word (I(t)) just as populace who are lived in got zone not influenced by COVID-19 infection (R(t)). We accept all out populace size of India is N(t) and N(t) = S(t) + E(t) + Q(t) + I(t) + R(t). In this model, isolate alludes to the partition of contaminated people from the normal Indian populace when the general population is tainted yet not irresistible. By Infected Indian populace, we surmise that the Indian person who have adjusted tainted by the COVID-19 infection. Again by populace in got zone, we assume those Indian people who have not influenced by Covid infection. To make our proposed SEQIR model more sensible, we incorporate a few segment impacts by assuming a corresponding regular passing rate d1 > 0 in every one of the five Indian sub-populaces. Besides, we join a net inflow of helpless Indian people into the district (India) at a rate (> 0) per unit time. contains new birth of Indian kid, migration and resettlement from and in India. The stream graph of the COVID-19 contamination model in current circumstance of India is portrayed through Figure 1



Modeling of susceptible population (S(t)): By recruiting individuals into the region (India) at a rate Λ the susceptible population is augmented and condensed by natural death d_1. Also the susceptible population decreases through interaction between a susceptible individual and infected but not detected by testing individual. This population is also decreased by constant rates β_1 and σ_1 respectively to be converted into quarantined individual, as well as recovered individual.

It is a real fact in India especially in the districts (Purulia, Murshidabad, Birbhum (West Bengal), Gaya, Bhagalpur (Bihar), etc.) that the susceptible population is directly sent to secured zone population due to fear effect among the inhabitants. This situation arises due to lack of proper or adequate treatment or testing facility for the large number of population in India. Therefore, the rate of change of susceptible population are governed by the following differential equation:

$$\frac{ds}{dt} = \Lambda - \alpha SE - \beta_1 S - \sigma_1 S - d_1 S \quad (1)$$

Modeling of Infected but not detected by testing population (E(t)): The infected but not detected by testing population indicates those individuals who are infected but their infection is not detected due to inadequate testing facility. This population increases at a rate _ by the interaction between a susceptible individual and infected but not detected by testing individual. This population decreases due to quarantine at a rate β_2 and due to natural death rate d_1. Due to very high population density, it is very difficult for the Indian Government to isolate some infected but not detected by testing individual, and send them for quarantine period. Keeping this fact in mind, let this population also directly decrease by infected population at a rate r_1.

Therefore, the rate of change of infected but not detected by testing population is governed by the following differential equation:

$$\frac{dE}{d} = \alpha SE - r_1E - \beta_2E - d_1E \qquad (2)$$

Modeling of quarantine population (Q(t)): Incubation period for COVID-19 is 2 days to 14 days. This period is very crucial for disease transformation from one individual to another individual. Therefore, we have to isolate those individual from susceptible and infected but not detected by testing individual for 14 days to control spread of COVID-19 in India. This mentioned population is known as quarantined population. Quarantined population is increased at a rate β_1 and β_2 from susceptible as well as infected but not detected by testing population respectively. This population is decreased at a rate r_2 and σ_2 due to infected population and population in secured zone correspondingly. Let the natural death rate be d1 of this population, hence the rate of change of quarantine population is as follows:

$$\frac{dQ}{d} = \beta_1S + \beta_2E - r_2Q - \sigma_2Q - d_1Q \qquad (3)$$

Modeling of confirmed infected population (I(t)): The infected population who have confirmed positive report by the COVID-19 test, is increased by infected but not detected by testing at a rate r_1 (infected but not detected by testing, such all population are not possible for quarantined due to lack of space or other reasons. Infected but not detected by testing individual may become illness for COVID-19, and subsequently their test report becomes positive. So they enter directly to the infected population, this particular case is very harmful to protect spreading COVID-19 in India), and also increased at rate r_2 from quarantined population as usual. Infected population is decreased at rate σ_3; and d_1 due to recovered population respectively. Let the natural death rate be d1 and to make it more realistic d_2 is the rate of death for infection, and hence the rate of change of infected population is governed by the following differential equation:

$$\frac{dI}{dt} = r_1E + r_2Q - \sigma_3I - d_1I - d_2I \qquad (4)$$

Modeling of secured zone population not affected by COVID-19 (R(t)): We assume that susceptible, quarantine as well as infected individuals recover from the disease at rates σ_1; σ_2 and σ_3 respectively and enter in secured zone population. This population is reduced by a natural death rate d1. Thus, rate of change of secured zone population is not affected by COVID-19 virus is governed by the following differential equation:

$$\frac{dR}{dt}=\sigma_1 S+\sigma_2 Q+\sigma_3 I-d_1 R \tag{5}$$

Combining equations ((1)-(5)) our wished-for model structure takes the following:

$$\frac{dS}{dt}=\Lambda-\alpha SE-\beta_1 S-\sigma_1 S-d_1 S$$

$$\frac{dE}{dt}=\alpha SE-r_1 E-\beta_2 E-d_1 E$$

$$\frac{dQ}{dt}=\beta_1 S+\beta_2 E-r_2 Q-\sigma_2 Q-d_1 Q$$

$$\frac{dI}{dt}=r_1 E+r_2 Q-\sigma_3 I-d_1 I-d_2 I$$

$$\frac{dR}{dt}=\sigma_1 S+\sigma_2 Q+\sigma_3 I-d_1 R$$

With initial densities: $S(0)>0, E(0)\geq 0, I(0)\geq 0, Q(0)\geq 0, R>0$

4. PARAMETERS MEANING

In this section we try to discuss about the meaning of each and every parameters. They are as follows:

Λ - The recruitment rate at which new individuals enter in the Indian population

α - The transmission rate from susceptible population to infected but not detected by testing population

β_1 The transmission coefficient from susceptible population to quarantine population

β_2 - The transmission coefficient from infected but not detected by testing population to quarantine population

σ_1 - The transmission rate from susceptible population to secured zone population

σ_2 - The transmission coefficient from infected but not detected by testing population to secured zone population

σ_3 -The transmission rate from quarantine population to secured zone population

r_1 - The transmission rate from infected but not detected by testing population to infected population for treatment

r_2 - The transmission rate from quarantine population to infected population for treatment

d_2 - Death rate of infected population due to Covid-19 infection

d_1 - Natural death rate of all five sub-populations

The above SEQIR model formulation

$$\frac{ds}{dt} = \Lambda - \alpha SE - AS$$

$$\frac{dE}{dt} = \alpha SE - BE$$

$$\frac{dQ}{dt} = \beta_1 S + \beta_2 E - CQ$$

$$\frac{dI}{dt} = r_1 E + r_2 Q - DI$$

$$\frac{dR}{dt} = \sigma_1 S + \sigma_2 Q - \sigma_3 I - d_1 R$$

Where

$$A = (\beta_1 + \sigma_1 + d_1)$$

$$B = (r_1 + \beta_2 + d_1)$$

$$C = (r_2 + \sigma_2 + d_1)$$

$$D = (\sigma_3 + d_2 + d_1)$$

5. CONCLUSION

In this current paper we have detailed and considered a pandemic model of COVID-19 infection which is moved from one human to another. So far the everyday affirmed COVID-19 cases are expanding step by step around the world. Along these lines, forecast about contaminated individual is a lot of significant for wellbeing concern plan of the residents. It is likewise critical to control spread pace of the COVID-19 infection with confined stock. Our numerical investigation depends on COVID-19 infection spread in India. For starters 170 areas of India are areas of interest zones, where quick testing office is accessible for general society. As the time progress more techniques are applied by the Government of India just as all state Governments to stop the spread of COVID-19 infection in India.

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