Review

An Insight into the Simplified RP Transmission Network, Concise Baseline and SIR Models for Simulating the Transmissibility of the Novel Coronavirus Disease 2019 (COVID-19) Outbreak

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Abstract: The World Health Organization has reported about a Severe Acute Respiratory Syndrome, Coronavirus 2 (SARS-CoV2) (a virus of Wuhan, China pneumonia). The present investigation explores the transmissibility of the novel Coronavirus Disease (COVID-19) using some suitable mathematical models such as (a) a simplified Bats-Hosts-Reservoir (Wuhan Seafood Market)-People (BHRP) transmission network model useful in mapping the spread of the novel COVID-19 from its source (may be bats) to humans, (b) a concise baseline model based on individual behavioral response and control measures taken to control the transmission of the novel COVID-19 and (c) an exponential and the Susceptible-Infected-Recovered (SIR) models to predict the transmission of the pandemic on day-to-day basis. The basic Reproduction number (R_0) (for the next generation matrix) was derived to estimate the transmission of the novel COVID-19 using the simplified BHRP transmission network model. The logic estimates that around *2.30* persons could be affected by the reservoir and around *3.58* persons could be affected by the community (individual person to community population). On the other hand, the concise model based on real-time time-dependent data, such as day-to-day number of tests, appreciates the initiatives (control measures) of the Chinese government to break the transmission chain of the pandemic in the capital city of Hubei province. Furthermore, the basic Reproduction number (R_0) for India is reviewed to be in the range between *1.4* and *3.9* using the classical SIR model and thus, the transmission rate is the same as that of California and Washington. The review also outlines the epidemiological SIR model (based on real-time time-dependent data) which estimates about the equilibrium stage of the pandemic by the last week of May, 2020. The predictions of the age-structured epidemiological SIR model could be more accurate if data such as day-to-day number of tests are correctly fed during evaluation of the results. The present investigation emphasizes over the need of effective implementation of mitigatory strategies such as social distancing to prevent the transmission of the SARS-CoV2 outbreak in India.

Keywords: Novel Coronavirus, COVID-19, SARS-CoV2, Pandemic, Model, Transmission

Introduction

The novel Coronavirus (COVID-19) pandemic found its way from Wuhan Seafood Market, China (WHO, 2020a)

and the outbreak of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV2) has spread across the globe. The report indicates that SARS-CoV2 is identical to a bat coronavirus (reservoirs) (Zhou *et al.*, 2020; Li *et al.*, 2020a;

Huang *et al*., 2020; Fraser *et al*., 2004; Jung *et al*., 2020). The parameter such as basic Reproduction number (R_0) (for the next generation matrix) was evaluated using the inputs of time between different intervals of the novel COVID-19 pandemic and differences between birth and death rates (intrinsic evaluation rate) (Li *et al*., 2020a; Zhao *et al*., 2020a; 2020b). The next generation matrix (R_0) was modeled using ordinary differential equations and solved using the Markov Chain Monte Carlo methods (Chen *et al*., 2020; Wu *et al*., 2020a; Rao and Diamond, 2020).

The worldwide death toll from the novel COVID-19 pandemic has surged to over 486,128, as of 25th June 2020 (20:48 GMT+8), according to the source (NHCPRC, 2020). The concise baseline model was based on individual behavioral responses and control measures taken to control the transmission of the novel COVID-19 (TAC, 2020; CDC, 2019). Lin *et al*. (2020) mapped community transmission (individual person to community population) of the novel COVID-19 using a concise baseline model. Their model was based on key inputs such as individual behavioral responses and control measures taken by the government to control the transmission of the novel COVID-19. The authors did not forget to consider the efforts of the government such as initiatives to implement lockdown regulations, run quarantine centers, hospital conversion trends, etc., in their model to meet its objective. It is observed that during the initial few days, the symptoms of the novel COVID-19 are similar to the flu (Zhao *et al*., 2020c).

The novel COVID-19 spreads from an infected patient to a healthy person who comes in contact with him (patient) through tiny droplets from the nose, mouth and eyes, if the patient coughs, sneezes and speaks (Singhal, 2020; Ma *et al*., 2020; Araujo and Naimi, 2020; Salman and Salem, 2020; Luo *et al*., 2020). The incubation period of SARS-CoV2 is up to 14 days (Singhal, 2020; Linton *et al*., 2020; Lipsitch *et al*., 2020; Reich *et al*., 2009). India is having a large population density and thus the risk of transmission of the pandemic is quite high unless the Indian government implements mitigatory measures such as lockdown across the nation and social distancing to prevent the pandemic (Ma *et al*., 2013; Hethcote, 2000; Singh and Adhikari, 2020; Sahasranaman and Kumar, 2020; Bukhari and Jameel, 2020; Dey, 2020). The present review aims to explore the efficient mathematical modeling such as (a) the simplified Bats-Hosts-Reservoir (Wuhan Seafood Market)-People (BHRP) transmission network model, (b) a concise baseline model based on individual behavioral response and control measures and (c) an exponential and

Susceptible-Infected-Recovered (SIR) models for in-depth understanding of the transmission of outbreak of the novel Coronavirus Disease (COVID-19). The modified age-structured epidemiological SIR model (based on real-time time-dependent data), which estimates about the equilibrium stage of the pandemic due to the sustained lockdown with some relaxation for effective implementation of social distancing measures, is also reviewed in-depth to emphasize over the need of mitigatory measures to prevent the transmission of the novel COVID-19 outbreak in India.

The Simplified Bats-Hosts-Reservoir (Wuhan Seafood Market)-People (BHRP) Transmission Network Model

Li *et al*. (2020a) mapped the initial outbreak of the virus of Wuhan pneumonia to the first few confirmed SARS-CoV2 infected patients and concluded with the evidence of community transmission. The data used in modeling were taken from the report published by these authors. The first case was reported on 07th December, 2019 in Wuhan, China (CAN, 2020; FT, 2020; BI, 2020; WHO, 2020b; MSN, 2020). Chen *et al*. (2020) performed analysis on the data of infected persons published until 01st January, 2020 as the Chinese central government took the step to shutdown the Wuhan Seafood Market from 01st January, 2020 after the outbreak of the novel Coronavirus (COVID-19) pandemic (WHO, 2020a).

The pandemic curve used in the modeling was plotted in the time interval between 07th December, 2019 and 01st January, 2020 with a simulation time step of 1 *day*. In a nutshell, the relationship between the variables on the x and y axes was established through a curve plotted using the Runge-Kutta method of fourth-order (tolerance level was set to 0.001). The fitting of the curve was best observed with the coefficient of determination (R^2). The transmission network model was based on the fact that SARS-CoV2 was carried from infected bats (I_B) Fig. 1a to some wild animals, or infected hosts (I_H), who were killed and sold in Wuhan Seafood Market, China (reservoir of the novel COVID-19) and shortly thereafter, people got infected from the SARS-CoV2 (Chen *et al*., 2019).

There were four categories of bats (B) such as Susceptible (S_B), Exposed (E_B), Infected (I_B) and Removed bats (R_B). The parameters such as birth rate (n_B) and population of bats (N_B) were used to calculate the population of infants bats (Λ_B). The parameters of infection of bats such as Incubation period ($1/\omega_B$) and

Infectious period $(1/\gamma_B)$ were used in the modeling to understand the transmissibility of the novel COVID-19. Like bat, there were also four categories of hosts (H) such as Susceptible (S_H), Exposed (E_H), Infected (I_H) and Removed hosts (R_H). The parameters such as birth rate (n_H) and population of hosts (N_H) were used to calculate the population of infants hosts (Λ_H). The parameters of infection of hosts such as Incubation period $(1/\omega_H)$ and Infectious period $(1/\gamma_H)$ were used in the modeling to understand the transmissibility of the novel COVID-19. The S_B was supposed to get the novel COVID-19 from the I_B with the transmission rate of β_B and S_H was supposed to get the novel COVID-19 from the I_B and I_H with the transmission rates of β_{BH} and β_H, respectively. The other terms such as SARS-CoV2, buy rate and pervasiveness of SARS-CoV2 in sell activities were expressed as W (at Wuhan Seafood Market, the reservoir in our case), a and I_H/N_H respectively. Therefore, the rate at which the transmission of the novel COVID-19 (in Wuhan Seafood Market) from hosts took place was aWI_H/N_H (where N_H was used to express the population of hosts).

The model fills the gaps as much as possible as it also assumed the possibility of those persons with and without symptoms of SARS-CoV2 who might export SARS-CoV2 into the reservoir (W) with the transmission rates of μ_P and μ'_P, respectively. Such virus could result in W space in the reservoir at a rate of εW (where $1/\varepsilon$ was used to express the lifespan of the SARS-CoV2). It was assumed that there were five categories of persons (P), such as Susceptible (S_P) Exposed (E_P), Infected (I_P), Removed persons (R_P) and persons without symptoms (A_P) of the novel COVID-19. The parameters such as birth rate (n_P) and population of persons (N_P) were used to calculate the population of infants (Λ_P). The parameters of infection of persons such as incubation period $(1/\omega_P)$ and latent period $(1/\omega'_P)$ were used in the modeling of understand the transmissibility of the novel COVID-19. The other terms such as infectious periods of A_P and I_P were expressed as $1/\gamma_P$ and $1/\gamma'_P$, respectively, as well as the number of persons without symptoms was expressed as δ_P. The S_P was supposed to get the novel COVID-19 from the I_P and W with the transmission rates of β_P and β_W, respectively. The model was driven with some constant κ as it was expressed as a transmission coefficient of I_P and further assumed as the export potential of A_P was κI_P (where, $0 \le \kappa \le 1.$) (Chen et al., 2019).

The BHRP transmission network model was further simplified to a Reservoir (Wuhan Seafood Market)-People (RP) transmission network model due

to the export of SARS-CoV2 from reservoir (Wuhan Seafood Market) in quick time. Therefore, bats and hosts were removed from the study and the overall ordinary differential equations were quite simplified. Chen et al. (2019) further modified the value of W using an impulse function (Chen et al., 2014a; Yi et al., 2019) for the simulation of transmission of the novel COVID-19, Equation (1):

$$Transmission = impulse\left(n, t_0, t_i\right) \tag{1}$$

where, the terms such as n, t_0 and t_i were used to express the transmission of SARS-CoV2 to Wuhan Seafood Market, beginning of the transmission study in simplified modeling and the time interval of transmission of the virus, respectively.

Chinese were celebrating the New Year during the outbreak of the novel COVID-19. The death rate and birth rate were negligible during the period. Chinese were travelling into and out from the capital city of Hubei province (People's Republic of China), so n_P was used to express the rate at which people were travelling into the city and m_P was used to express the rate at which people were travelling out from the city. Chen et al. (2014b) normalized the simplified RP transmission network model because both reservoir viruses and humans had different dimensions, Equation (2):

$$s_P = \frac{S_P}{N_P}, e_P = \frac{E_P}{N_P}, i_P = \frac{I_P}{N_P}, a_P = \frac{A_P}{N_P}, r_P = \frac{R_P}{N_P},$$
$$w = \frac{\varepsilon W}{\mu_P N_P}, \mu'_P = c\mu_P, b_P = \beta_P N_P, b_w = \frac{\mu_P \beta_W N_P}{\varepsilon} \tag{2}$$

where, the term c was used as the coefficient of relative shedding of A_P with respect to I_P.

The simplified RP transmission network model was expressed in its general form using the set of Equations (3):

$$\frac{ds_P}{dt} = n_P - m_P s_P - b_P s_P \left(i_P + \kappa a_P\right) - b_W s_P w$$
$$\frac{de_P}{dt} = b_P s_P \left(i_P + \kappa a_P\right) + b_W s_P w - \left(1 - \delta_P\right)\omega_P e_P - \delta_P \omega'_P e_P - m_P e_P$$
$$\frac{di_P}{dt} = \left(1 - \delta_P\right)\omega_P e_P - \left(\gamma_P + m_P\right)i_P$$
$$\frac{da_P}{dt} = \delta_P \omega'_P e_P - \left(\gamma'_P + m_P\right)a_P \tag{3}$$
$$\frac{dr_P}{dt} = \gamma_P i_P + \gamma'_P a_P - m_P r_P$$
$$\frac{dw}{dt} = \varepsilon \left(i_P + ca_P - w\right)$$

The basic Reproduction number (R_0) (for the next generation matrix) was derived in the simplified RP transmission network model to describe the different stages of the novel COVID-19, such as its outbreak ($R_0 > 1$), stage of community transmission and the end of pandemic ($R_0 < 1$) (Chen *et al*., 2014a; Zhang *et al*., 2020; Chen *et al*., 2019; Cui *et al*., 2020).

The incubation and latent periods were substituted as 5.2 *days* and therefore, the term ω_P (or ω'_P) was taken as 0.1923 due to the 95% confidence level (Li *et al*., 2020a). On average, there was a delay of *5 days* before admitting any COVID-19 infected patients after they started complaining about symptoms of the pandemic (JMH, 2020; WHO, 2020c; 2020d). The parameters such as γ_P and δ_P were taken as 0.1724 (due to 95% confidence level (Li *et al*., 2020a)) and *0.5* (due to unavailability of the novel COVID-19 infected patients without symptoms), respectively. Both terms such as κ and c were set to *0.5*. Out of the

11 million population of the city, *0.3 million* population was tested for symptoms of the novel COVID-19 (NENVN, 2020). It was estimated that *0.2 million* population was travelling out from the city per day to celebrate the festive season during the outbreak of the pandemic. Therefore, n_P and m_P were set to *0.0018/day* (as *0.1* times the fraction *0.2/11*) (CBN, 2020; WG, 2020). It was believed that SARS-CoV2 could remain active in the atmosphere up to *10 days* in its host and therefore, the value of ε was assumed to be *0.1* and the pervasiveness of the SARS-CoV2 was assumed to be *0.00001* to the initial step of modeling (Chen *et al*., 2020). The above equations (3) of the simplified RP transmission network model were used to fetch the data of null COVID-19 spots $\left(\frac{\Lambda_P}{m_P},0,0,0,0,0\right)$. The next generation matrix (R_0) was calculated using Equation (4):

$$R_0 = FV^{-1} = \begin{bmatrix} 0 & \beta_P\dfrac{\Lambda_P}{m_P} & \beta_P\kappa\dfrac{\Lambda_P}{m_P} & \beta_W\dfrac{\Lambda_P}{m_P} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \dfrac{1}{\omega_P+m_P} & 0 & 0 & 0 \\ A & \dfrac{1}{\gamma_P+m_P} & 0 & 0 \\ B & 0 & \dfrac{1}{\gamma'_P+m_P} & 0 \\ D & E & G & \dfrac{1}{\varepsilon} \end{bmatrix} \qquad (4)$$

where,

$$A = \frac{(1-\delta_P)\omega_P}{(\omega_P+m_P)(\gamma_P+m_P)}, \quad B = \frac{\delta_P\omega_P}{(\omega_P+m_P)(\gamma'_P+m_P)}, \quad D = \frac{(1-\delta_P)\mu\omega_P}{(\omega_P+m_P)(\gamma_P+m_P)\varepsilon}$$

$$+\frac{\mu'\delta_P\omega_P}{(\omega_P+m_P)(\gamma'_P+m_P)\varepsilon}, \quad E = \frac{\mu}{(\gamma_P+m_P)\varepsilon}, and \; G = \frac{\mu'}{(\gamma'_P+m_P)\varepsilon}$$

The simplified RP transmission network model which was normalized further to provide the best fit to the curve (Fig. 1b) and it was found that the result of the model was in agreement with published data sources ($R^2 = 0.512$, $P < 0.001$). The values of R_0 were evaluated around *2.30* for those persons who were affected from reservoir and around *3.58* for those persons who were affected from community transmission (individual person to community population). On average, the value of R_0 of SARS-CoV2 was *2.9* (based on research in two such China's cities-Hong Kong and Beijing) and therefore, the

transmission of SARS coronavirus was estimated to be much higher than Middle East Respiratory Syndrome (MERS) coronavirus (Riley *et al*., 2003; Dye and Gay, 2003; Zhou and Yan, 2003; Peak *et al*., 2017).

Overall, the normalized RP transmission network model was based on the input data sources that were published for only a few countries during the outbreak of the novel COVID-19 and thus it might not fit well into the situations in other countries. However, it throws light on mapping the transmission of the novel COVID-19 pandemic during its initial outbreak in the city of patient zero.

The Concise Baseline Model Based on Individual Behavioral Response and the Control Measures Taken by the Government to Prevent the Spread of the Novel COVID-19

Lin *et al*. (2020) adopted the framework (population size, *N*) which was based on two key parameters such as (a) the general reaction of the public about novel COVID-19 infected patients (who were either seriously ill or about to die), represented as *D* and (b) the progressive cases of infected patients in the zone, represented as *C*. There were four categories of persons such as Susceptible (*S*), Exposed (*E*), Infected (*I*) and Removed persons (*R*). It was needed then to discuss the rate of transmission of the novel COVID-19 in a model as the report was showing the number of the infected patients such as (a) *81%* of the patients were having mild symptoms, (b) *14%* of the patients were seriously ill and they had breathing problems and (c) *5%* of the patients were identified with respiratory failure (Wu and McGoogan, 2020).

Lin *et al*. (2020) modeled the zoonotic transmission (period around December, 2019) using a function, *F* for the outbreak of the pandemic, which was first encountered in November, 2019. The transmission function was equated with zero when the Chinese government took the step to shutdown the Wuhan Seafood Market on 01st January, 2020 after the outbreak of the novel coronavirus (COVID-19) pandemic (WHO, 2020a). They modeled initially to map the community transmission (individual person to community population) of the novel COVID-19 before the government imposed a lockdown across the city, using the set of Equations (5):

$$S' = -\frac{\beta_0 SF}{N} - \frac{\beta(t)SI}{N} - \mu S,$$

$$E' = \frac{\beta_0 SF}{N} + \frac{\beta(t)SI}{N} - (\sigma + \mu)E,$$

$$I' = \sigma E - (\gamma + \mu)I,$$

$$R' = \gamma I - \mu R, \tag{5}$$

$$N' = -\mu N,$$

$$D' = d\gamma I - \lambda D, \text{ and}$$

$$C'' = \sigma E$$

The parameter, $\beta(t) = \beta_0 (1-\alpha)\left(1 - \frac{D}{N}\right)^{\kappa}$ was used to express the effect of (a) control measures taken by the government to prevent the spread of the novel

COVID-19 and (b) social distancing on the death tolls. The parameters such as *F*, *N*, *S*, *β*, *α*, κ, *μ*, σ^{-1}, γ^{-1}, *d* and λ^{-1} were used to express the count of the novel COVID-19 patients, the population length, suspected patients, the export rate initiative of the government to control the spread of the pandemic, the rate at which people were travelling into and out from the city, the latent time, the infectious time, the ratio of critical patients and the individual behavioral response, respectively. *5 million* emigrants (SCMP, 2020) were also involved in the modeling before the decision of lockdown was imposed. It was assumed that (a) the control measures were more effective from the fourth week of January, 2020 (α = 0.4249) until 29th January, 2020 and α = 0.8478 after 30th January, 2020) and (b) the population was travelling into and out from the capital city of Hubei province in between 31st December, 2019 and 22nd January, 2020.

Children aged between *0-17 years* are less critically affected by the novel COVID-19 so far. Only *10%* of the population thus, was not included in the modeling. The time between successive cases in the transmission chain of the pandemic and the incubation period were reported as *5 days* (Nishiura *et al*., 2020a; 2020b; Fine, 2003; SDT, 2012) and *4 days* (Guan *et al*., 2020), respectively. The infectious and latent periods were thus substituted as *4 and 3 days,* respectively. The results of the model were in good agreement with the previously published data (Zhao *et al*., 2020a; 2020b; Tuite and Fisman, 2020) as it involved real-time time-dependent data and critical cases instead of death rates only.

Lin *et al*. (2020) realized that the pandemic spread across the city at much higher rates Fig. 2 due to inadequate medical care infrastructure and health services. There was a delay of *14 days* between the first symptom of the novel COVID-19 and its official confirmation in the laboratory (Li *et al*., 2020b; Liu *et al*., 2020) for patients in the same age group (Fig. 3).

Lin *et al*. (2020) considered three different cases such as (a) when the government was not taking the outbreak of the novel COVID-19 pandemic seriously (α = 0) and there was then no individual behavioral response (*k* = 0), (b) when people were aware about the novel COVID-19 (thus, the official record of cumulative cases was trending down) and (c) when the government was on alert mode with all its task forces in action to prevent the spread and then the individual behavioral response reduced the cases of the novel COVID-19 patients (Fig. 4). They highlighted the third case which became a key element to break the transmission chain of the pandemic; and the estimated results of the simulation were in inline with the published data sources (Riou and Althaus, 2020; Bogoch *et al*., 2020; Imai *et al*., 2020; Mahase, 2020).
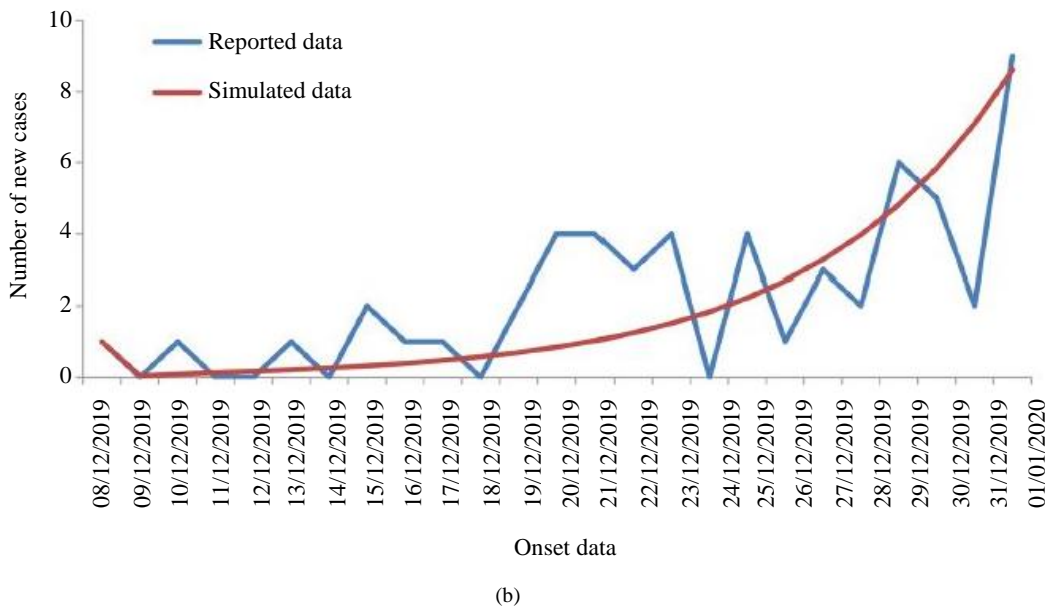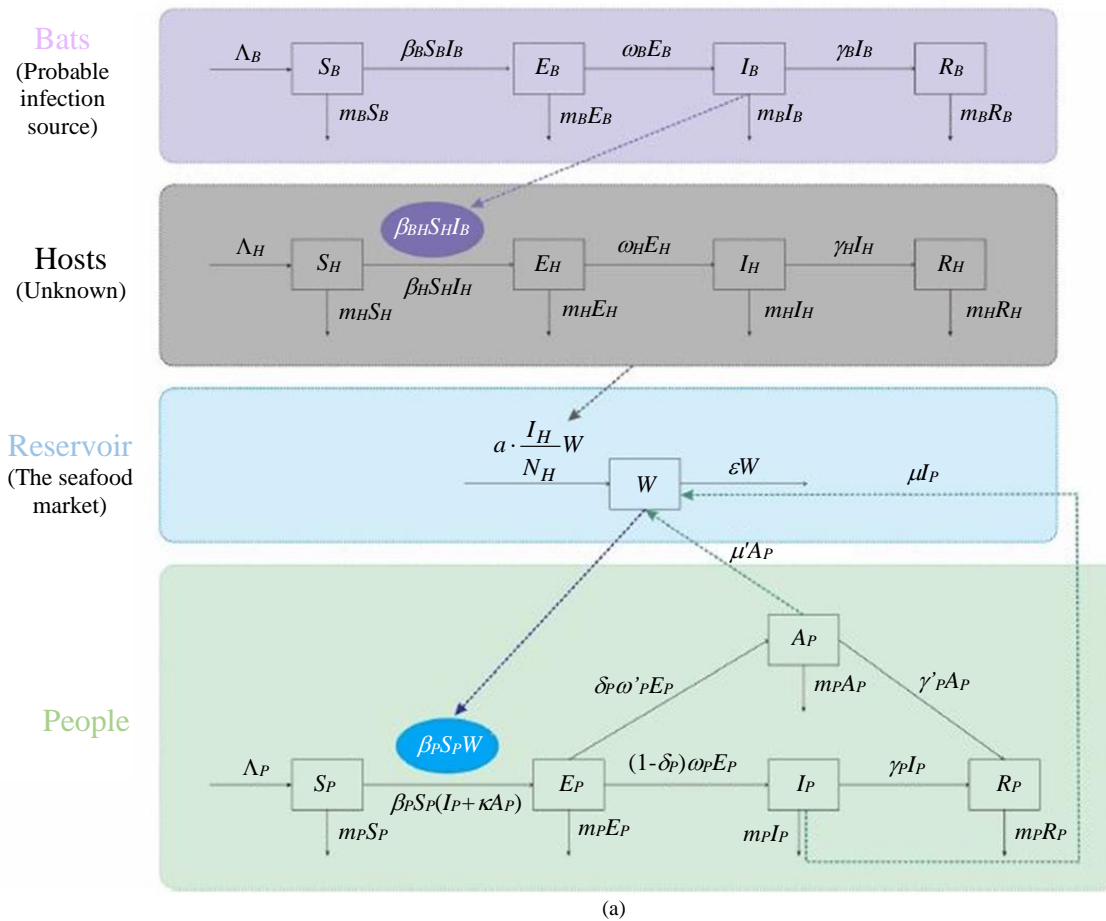
Fig. 1: The Bats-Hosts-Reservoir (Wuhan Seafood Market)-People (BHRP) transmission network model (Reprinted with permission from Ref. (Chen *et al*., 2020). Copyright 2020 Springer Nature). (a) The logic behind the transmission network model. (b) The response of simplified Reservoir (Wuhan Seafood Market)-People (RP) transmission network model
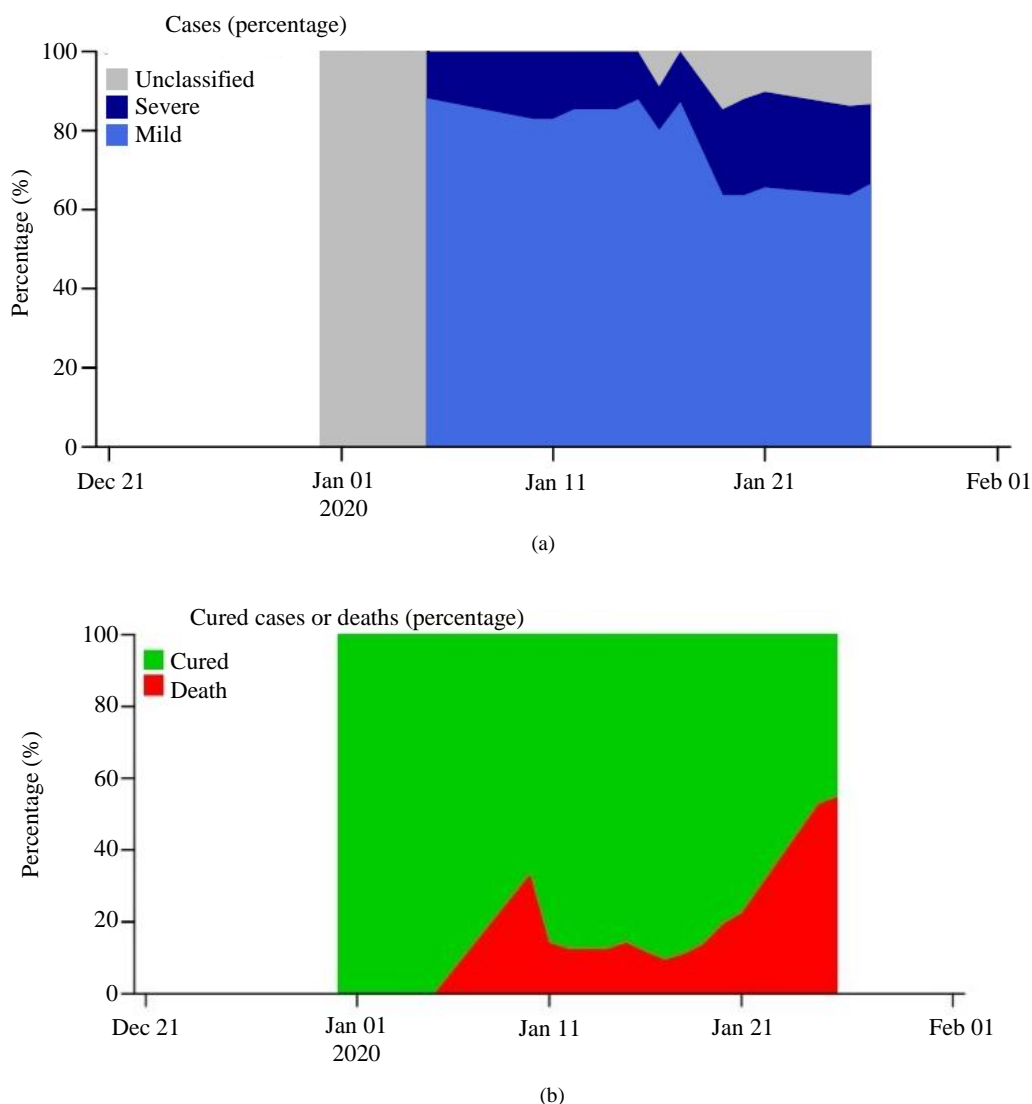
(a)

(b)

Fig. 2: The novel COVID-19 cases in Wuhan, China for the patients in the same age group (Reprinted with permission from Ref. (Lin *et al*., 2020). Copyright 2020 Elsevier). (a) The officially recorded severe and mild cases *(%)*. (b) The officially recorded cured and deaths cases

The concise baseline model did not rely on the conventional approach of fitting a curve to the dataset. It involved real-time time-dependent data which were based on testing facilities, availability of hospitals, etc. and thus, this framework was suitable for other countries including India as well.

The Epidemiological, Exponential and Susceptible-Infected-Recovered (SIR) Models to Investigate the Transmission of the Novel COVID-19 Outbreak in India

Ranjan (2020) estimated the basic Reproduction number (R_0) for India in the range between *1.4* and *3.9*

using exponential and classical Susceptible-Infected-Recovered (SIR) models (Hethcote, 2000). The exponential model (Ma, 2020) was used in previous pandemics to estimate the transmission rate of disease Equation (6):

$$\frac{dI}{dt} = rI$$

(6)

After integration, the above equation was expressed in its general form Equation (7):

$$I(t) = I_0 \exp(rt)$$

(7)

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The parameters, $I(t)$ and I were used to express the number of infected patients with time, t and the overall cumulative cases of cured and dead persons.

The other parameter, I_0 was evaluated using the conventional approach of fitting a curve to the dataset (Rao and Vazquez, 2020).
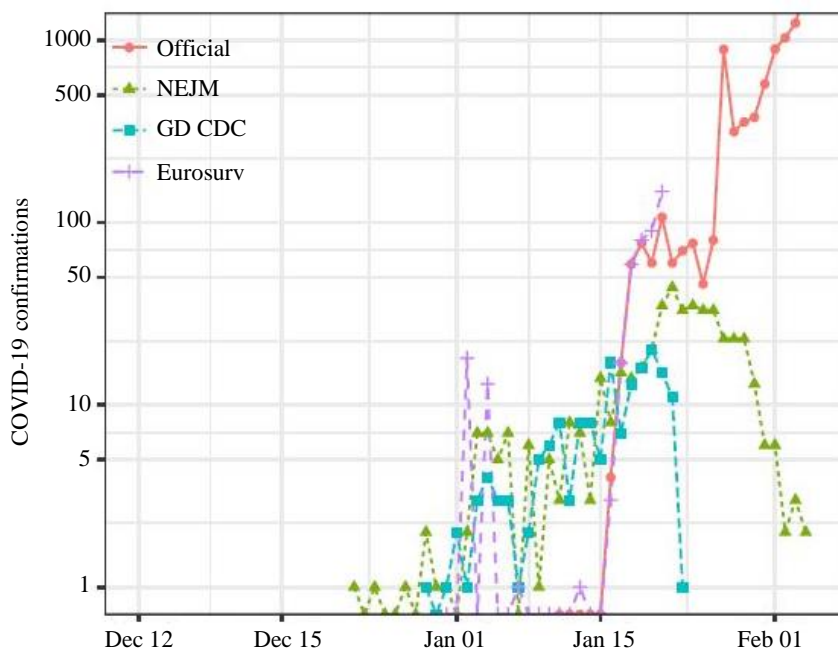

Fig. 3: The evaluation of previously published data such as (a) the officially recorded data was shown using red color (NHCPRC, 2020), (b) the data of (Li *et al*., 2020a) was shown using green color, (c) the data of (Liu *et al*., 2020) was shown using blue color and (d) the data of (Wu *et al*., 2020b) was shown using purple color (Reprinted with permission from Ref. (Lin *et al*., 2020). Copyright 2020 Elsevier)
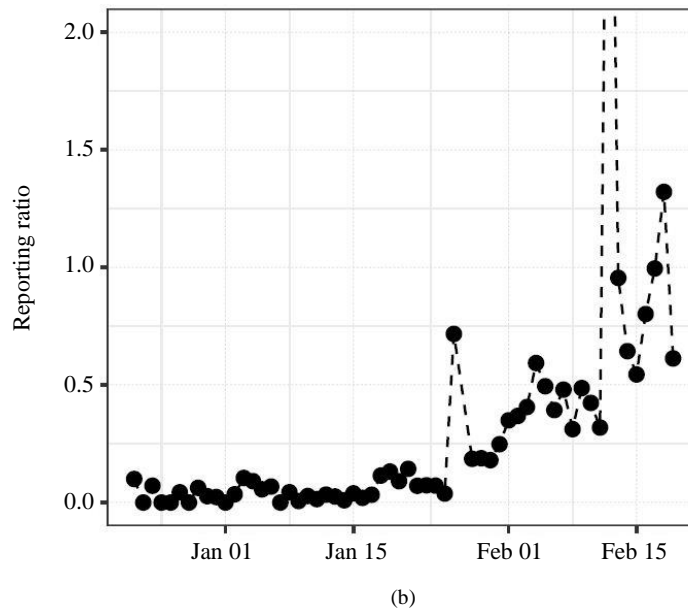

(a)

(b)
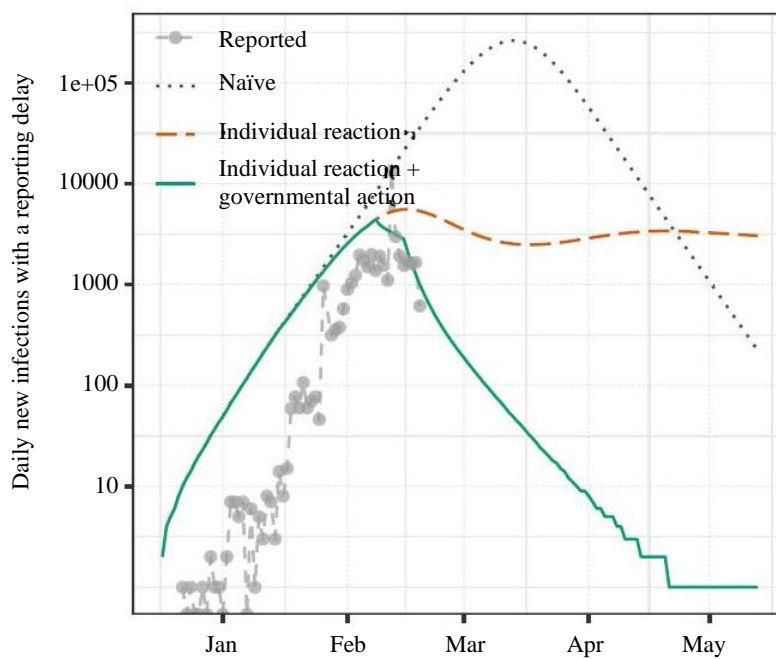
Fig. 4: The official and laboratory confirmation of the SARS-CoV2 test was delayed for two weeks after the onset of its symptoms (Reprinted with permission from Ref. (Lin *et al*., 2020). Copyright 2020 Elsevier). (a) The day-to-day reporting of new cases of the SARS-CoV2 was shown with three types of observational studies such as (i) when the government was not in action (shown using grey color), (ii) when there was individual behavioral response (shown using red color) and (iii) when the government was active and took initiatives to prevent spread of the pandemic and people were also aware about the novel COVID-19 (shown using green color); and the officially recorded data as well as data of Li *et al*. (2020a) was shown using dotted grey curve. (b) The graph was reconstructed on the basis of real-time time-dependent data such as the day-to-day number of tests, adequate medical care infrastructures and health services.

The epidemiological SIR model (evaluated using real-time time-dependent data) was based on three categories of persons such as Susceptible (*S*), Infected (*I*) and Recovered or Dead persons (R). The classical SIR model was expressed in its general form using the set of Equations (8):

$$\frac{dS(t)}{dt} = -\frac{\beta}{N} SI,$$

$$\frac{dI(t)}{dt} = \left(\frac{\beta}{N} S - \gamma\right) I, \text{ and} \qquad (8)$$

$$\frac{dR(t)}{dt} = \gamma I$$

The parameters, β and γ were used to express the spread rate and the mean recovered rate, respectively. The entire population at a specific time, *t* was expressed as $N = S + I + R$ and that was unchanged during the prediction of transmission rate using the classical SIR model. The parameter such as the basic Reproduction number (R_0) (for the next generation matrix) was calculated using Equation (9):

$$R_0 = \frac{\beta}{\gamma}\left(1 - \frac{I_0}{N}\right) \qquad (9)$$

Ranjan (2020) assessed the initial values of the parameters, β and γ at $R_0 = 0$ (Batista, 2020; McGee,

2020) as they assumed the equilibrium stage of the pandemic. They had used data available between 11th March, 2020 (*62* infected patients) and 23rd March, 2020 (*499* infected patients) for conducting the research using the exponential model. Furthermore, they had used data available from 10th March, 2020 to 30th March, 2020 (a period of *21 days*) for conducting the research using the classical SIR model. India has not entered the community transmission stage (third stage). The outcomes of the models were in good agreement with the first and second stages of the transmission of the pandemic. The transmission rate of India was the same as that of California and Washington (Fig. 5a). The variation in the trends of growth rates in different countries was due to the implementation of testing facilities to identify the patients. The exponential model was used to predict provisional and perpetual estimations about the novel COVID-19 cases in India. The values of I_0, r and the coefficient of determination, R^2 were *39.64, 0.1887 and 0.9768,* respectively. The existing case of the novel COVID-19 was plotted against the estimated cases up to 06th April, 2020 (Fig. 5b). The comparison was also made between India (*5000* infected patients by 06th April, 2020) and Washington in Fig. 5b. The exponential model was unable to deliver the perpetual estimation about the novel COVID-19 cases, i.e., up to 30th April,

2020 (Fig. 5c). The exponential model did not involve the initiatives (control measures such as lockdown imposed across the nation on 24th March, 2020 and social distancing was practiced as mitigatory measures) of the Indian government to break the transmission chain of SARS-CoV2 and that was why the estimation of the model was near to *0.5 million* cases by 30th April, 2020.

(a)

(b)

Fit:
$y = 39.64 \exp(0.1887x)$

(c)

$R_0 = 1.504 \; \beta = 0.43 \; \gamma = 0.285$

Infection rate
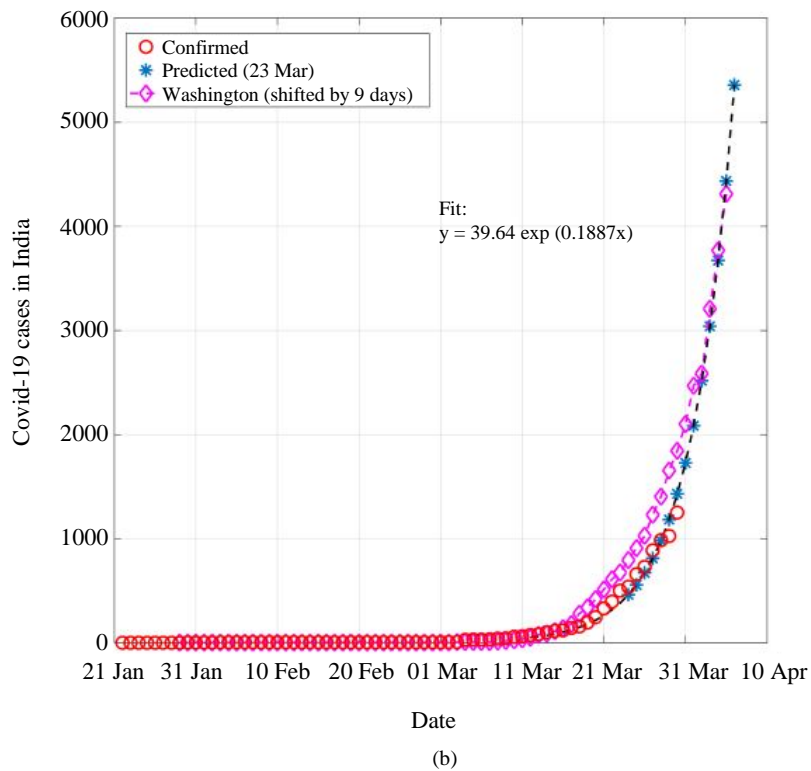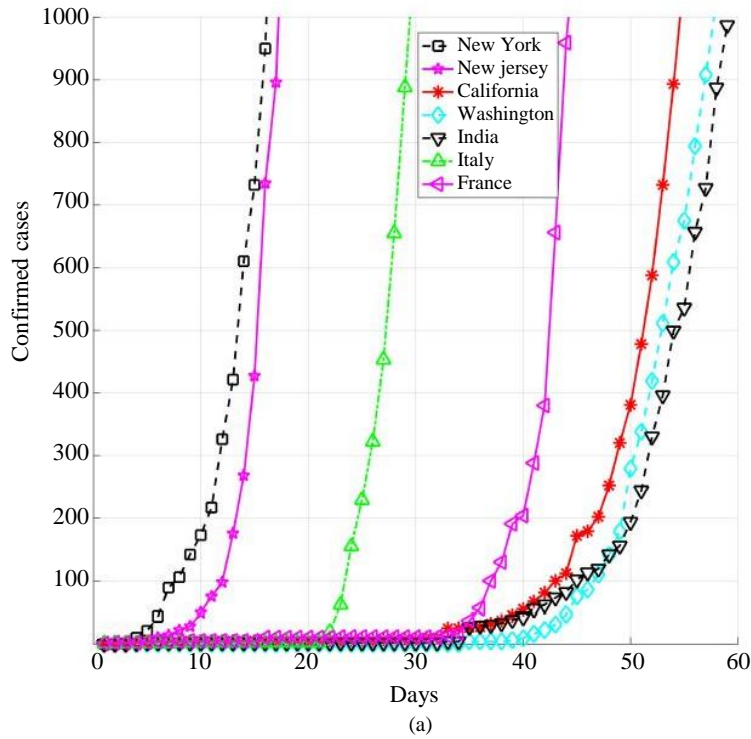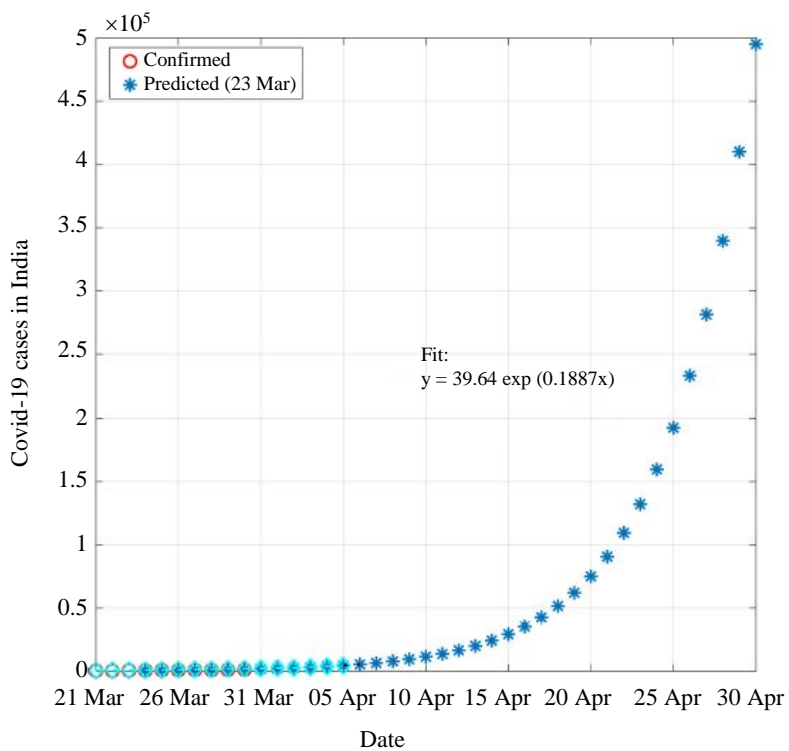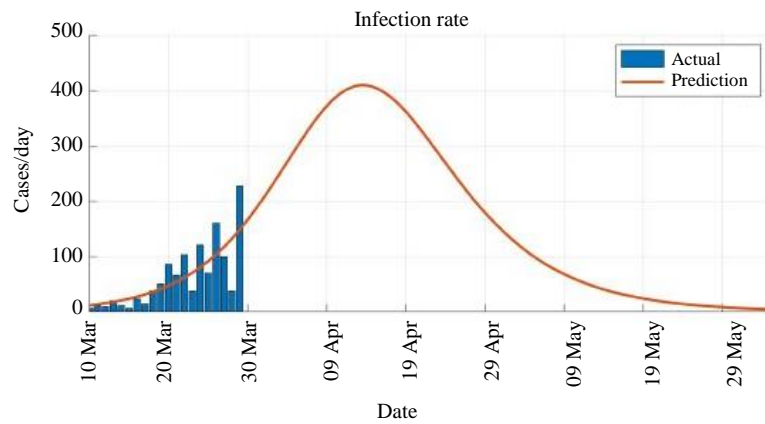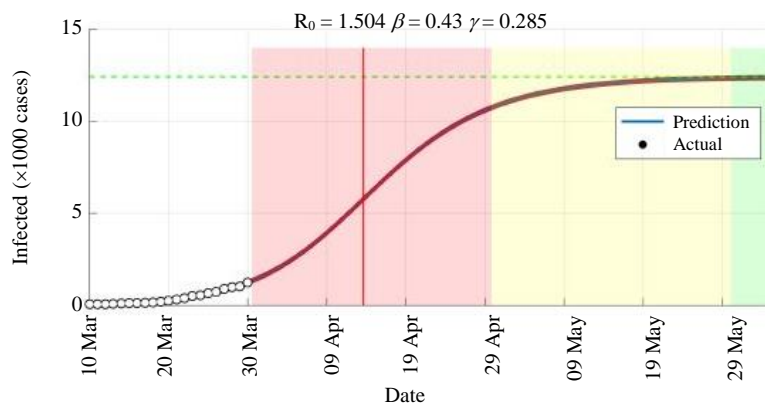
(d)

Fig. 5: The epidemiological exponential and SIR models (Reprinted with permission from Ref. (Ranjan, 2020). Copyright 2020 medRxiv). (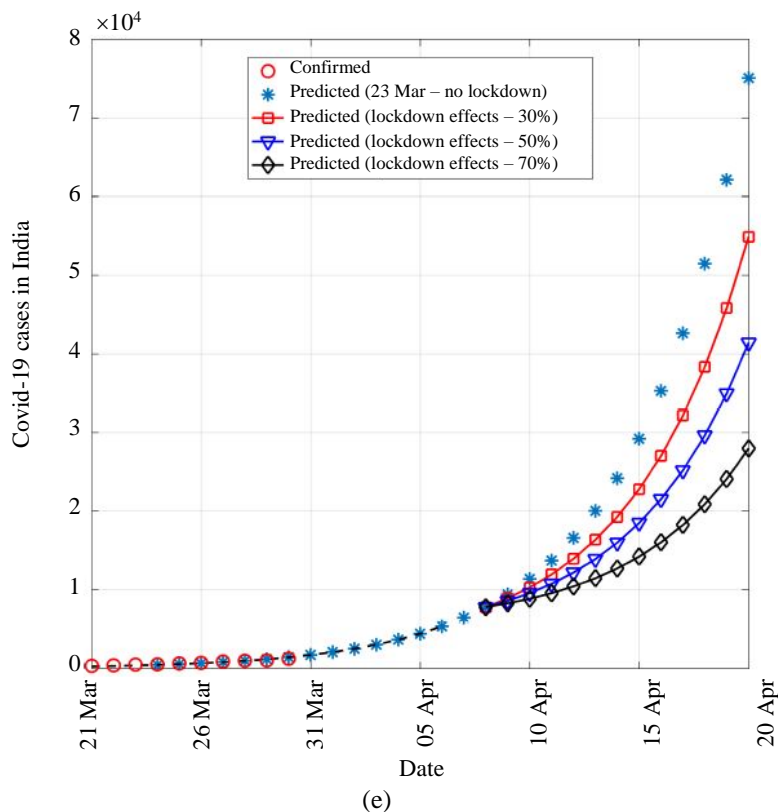a) The variation in trends of growth rates in different countries was due to their implementation of testing strategies. The growth rate of India was same as that of California and Washington using the exponential model. (b) The existing case of the SARS-CoV2 in India was plotted against the estimated cases up to 06th April, 2020. The comparison was also made between India (*5000* infected patients by 06th April, 2020) and Washington. (c) The exponential model did not involve the initiatives of the Indian government to break transmission chain of the SARS-CoV2 and that was why the estimation of the model was near to *0.5 million* cases by 30th April, 2020. (d) The classical SIR model was used to present a more realistic estimate of the SARS-CoV2. The effect of mitigatory social distancing was considered in the SIR model and the equilibrium stage of the pandemic was predicted around the last week of May, 2020. (e) The effects of mitigatory social distancing in few countries were outlined.

Ranjan (2020) therefore, switched over to the classical SIR model for the long term prediction of the novel COVID-19 cases and presented a more realistic estimate of the SARS-CoV2 (Fig. 5d) with the value of coefficient of determination, R^2 around *0.996*. The basic reproduction number (R_0) was estimated to be *1.504* (higher than the estimate of (Sahasranaman and Kumar, 2020); and close to the estimate of (Deb and Majumdar, 2020). Furthermore, the epidemiological SIR model considered the initiatives of the Indian government such as mitigatory social distancing to prevent the spread (Wu *et al*., 2020c) and suggested the equilibrium stage of the pandemic by the last week of May, 2020 (Fig. 5d). The impact of mitigatory social distancing Ridenhour *et al*., 2018; Chang *et al*., 2020; Mandal *et al*., 2020; Dhama *et al*., 2020) in a few countries was outlined in Fig. 5e.

The Analysis of Mitigatory Social Distancing to Investigate the Transmission of the Novel COVID-19 Outbreak in India using the Classical Susceptible-Infected-Recovered (SIR) Model

Singh and Adhikari (2020) studied the novel COVID-19 outbreak in India using the modified age-structured Susceptible-Infected-Recovered (SIR) model (Pontryagin, 1985; Box, 1976) by considering the initiative of the Indian government to implement mitigatory measures such as lockdown across the nation and social distancing (Ferguson *et al*., 2020; Bootsma and Ferguson, 2007; Hatchett *et al*., 2007; He *et al*., 2020) to prevent the pandemic. They assumed that persons within a specific age class (Prem *et al*., 2017) were equal with respect to their birth and death rates. The basic Reproduction number (R_0) was estimated on the basis of real-time time-dependent data, age groups and

mitigatory social distancing using the modified age-structured SIR model.

The persons were classified into different ages and thus in 'M' groups expressed as $i = 1,2,…M$. The persons within a specific age group were represented with 'i' and they were classified into susceptible patients (S_i), asymptomatic patients $\left(I_i^a\right)$, symptomatic patients $\left(I_i^s\right)$, and removed patients (R_i).

Therefore, the sum of all these was the total number of persons within a specified age group (i) and thus $N_i = S_i + I_i^a + I_i^s + R_i$ (Anderson and May, 1991; Keeling and Rohani, 2008; Towers and Feng, 2012; Ferguson *et al*., 2006).

Thus, each N_i was expressed as the total number of persons (thus a constant with respect to time) Equation (10):

$$N = \sum_{i=1}^{M} N_i \tag{10}$$

The rate of transmission of disease in susceptible patients within a specific age group (i) was expressed using Equation (11):

$$\lambda_i(t) = \beta \sum_{j=1}^{M} \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} \right), \; i, j = 1,…M \tag{11}$$

where, the term, β was the chance of transmission of the novel COVID-19 due to social contact and C_{ij}^a and C_{ij}^s were used to express the cases of social contact between asymptomatic patients within a specific age group (j) and susceptible patients within a specific age group (i), respectively.

The cured rate, γ was not dependent on age and was the same for both asymptomatic (ratio, α) and symptomatic patients (ratio, $\bar{\alpha} = 1 - \alpha$).

Therefore, the growth of the pandemic was expressed using the age-structured SIR model Equation (12):

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t) S_i, \\
\dot{I}_i^a &= \alpha \lambda_i(t) S_i - \gamma I_i^a, \\
\dot{I}_i^s &= \bar{\alpha} \lambda_i(t) S_i - \gamma I_i^s, \\
\dot{R}_i &= \gamma \left(I_i^a + I_i^s \right).
\end{aligned} \tag{12}$$

The age group of the persons was expressed as the ratio of Ni/N and social contact was expressed using C_{ij}^a, and C_{ij}^s matrices. Furthermore, the symptomatic patients were supposed to have less contact as compared to the asymptomatic patients and thus, $C_{ij}^s = fC_{ij}^a \equiv fC_{ij}$, (where, $0 \le f \le 1$).a

The people in self-isolation were supposed to remain in houses, work premises, school premises and other areas, thus the contact matrix was expressed using Equation (13):

$$C_{ij} = C_{ij}^H + C_{ij}^W + C_{ij}^S + C_{ij}^O \tag{13}$$

The contact matrix for a specific size of the population was expressed as $N_i C_{ij} = N_j C_{ji}$.

The mitigatory social distancing was modeled on a large-scale as a function of time, $u^W(t)$, $u^S(t)$ and $u^O(t)$, thus the time dependent contact matrix was expressed using Equation (14):

$$C_{ij}(t) = C_{ij}^H + u^W(t) C_{ij}^W + u^S(t) C_{ij}^S + u^O(t) C_{ij}^O. \tag{14}$$

During the lockdown across the nation, the social distancing measures were implemented effectively and thus a single household contact function was sufficient as shown using the linear Equation (15):

$$2u(t) = -\tanh\left(\frac{t - t_{on}}{t_w}\right) + \tanh\left(\frac{t - t_{off}}{t_w}\right) \tag{15}$$

The basic reproductive number was evaluated from null COVID-19 spots (where $S_i = N_i$) and infected persons were expressed using $2M \times 2M$ matrix, Equation (16):

$$J = \gamma(L - 1). \tag{16}$$

The next generation matrix, $2M \times 2M$ was expressed using Equation (17):

$$L = \begin{pmatrix} L^{aa} & L^{as} \\ L^{sa} & L^{ss} \end{pmatrix} \tag{17}$$

where, $L_{ij}^{aa} = \frac{\alpha\beta}{\gamma} C_{ij}^a \frac{N_i}{N_j}$, $L_{ij}^{as} = \frac{\alpha\beta}{\gamma} C_{ij}^s \frac{N_i}{N_j}$; and $L_{ij}^{sa} = \frac{\alpha\beta}{\gamma} C_{ij}^a \frac{N_i}{N_j}$, $L_{ij}^{ss} = \frac{\bar{\alpha}\beta}{\gamma} C_{ij}^s \frac{N_i}{N_j}$.

The identity matrix, I ($2M \times 2M$) was used to encompass both asymptomatic and symptomatic patients Equation (18):

$$I = \left(I^a, I^s\right) = \left(I_1^a,…,I_M^a, I_{1,…}^s I_M^s\right) \tag{18}$$

The dynamics of the above Equation (18) was expressed using Equation (19):

$$I(t) = \exp\left[\gamma(L-1)t\right]I(0) \tag{19}$$

where, L was used to evaluate the eigenvectors, V and the diagonal matrix of eigenvalues, $\Lambda = diag(\Lambda_1,\ldots,\Lambda_{2M})$ to calculate the equation, $\exp[\gamma(L-1)t] = V \, diag[\exp \gamma(\Lambda-1)t]V^{-1}$.

In general, the span of L had to be greater than one for the spread of the pandemic and thus the basic reproductive number was expressed using Equation (20) (Diekmann *et al.*, 2010):

$$R_0 \equiv \rho(L) = \max\left\{|\Lambda_1|,\ldots,|\Lambda_{2M}|\right\}. \tag{20}$$

The basic reproductive number was reasonably good to support the spread of the pandemic if the eigenvalue was real Equation (21):

$$\exp\left[\gamma(R_0-1)t\right] \tag{21}$$

The basic reproductive number was based on (a) the chance of transmission of disease on social contact, β, (b) the social contact matrix C_{ij} (c) the ratio of persons without and with symptoms of SARS-CoV2, α and (d) the ratio of symptomatic patients who were in self-isolation, f. The conversions such as (a) $N_i \rightarrow S_i(t)$ and (b) $C_{ij} \rightarrow C_{ij}(t)$ were done to transform the formulation into its linear form for time-based stability matrix, $L^{(t)}$. The time-based stability matrix, $L^{(t)}$ was expressed using Equation (22):

$$R_0^{eff}(t) \equiv \rho\left(L^{(t)}\right) = \max\left\{\left|\Lambda_1^{(t)}\right|,\ldots,\left|\Lambda_{2M}^{(t)}\right|\right\} \tag{22}$$

The cases of infected patients at any time, $t + \delta t$ were expressed Equation (23):

$$I(t+\delta t) = \exp\left[\gamma\left(L^{(t)}-1\right)\delta t\right]I(t) \tag{23}$$

The basic reproductive number played a significant role, $\left(\exp\left[\gamma(R_o^{eff}(t)-1)\delta t\right]\right)$, when the eigenvalue was real for its highest magnitude for the tremendous growth of the pandemic in a very short time, t. The end of the pandemic was shown with $R_0^{eff} < 1$. The rise and fall of the spread of the SARS-CoV2 outbreak were shown with time constants such as $\gamma(R_0-1)$ and $\gamma\left(R_0^{eff}(t_{on})-1\right)$, respectively.

The predictions of the SARS-CoV2 outbreak in India without and with implementation of social distancing measures using the age-structured epidemiological SIR models were shown in Fig. 6 and 7, respectively. In the absence of mitigatory measures such as locking down across the nation and thus social distancing; the results were frightening (Fig. 6). Singh and Adhikari (2020) thus, emphasized over the various schemes of mitigatory measures such as successive lockdowns of *21 days* and *28 days* Fig. 7b and further *21 days, 28 days* and *18 days* Fig. 7c (each scheme with a relaxation of some *5 days* and suggested to implement from 25th March, 2020); and if not possible then a single lock down of *49 days* starting from 25th March, 2020 would be required to impose across the nation to bring the equilibrium stage of the novel COVID-19 pandemic Fig. 7d.
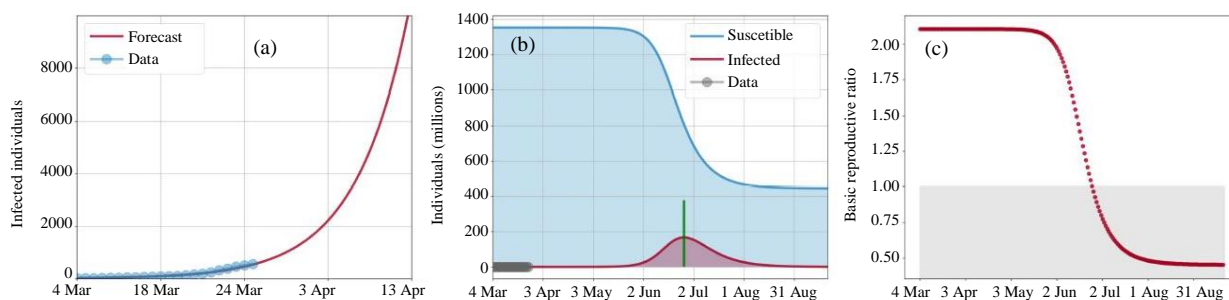

Fig. 6: The prediction of the SARS-CoV2 outbreak in India without implementation of social distancing measures using the age-structured epidemiological SIR model (Reprinted with permission from Ref. (Singh and Adhikari, 2020). Copyright 2020 arXiv). (a) The confirmed cases (shown using blue color) of the novel COVID-19 was plotted against the estimated cases (shown using red color) up to 25th March, 2020. (b) The prediction for the next five months, i.e., up to August, 2020 about the susceptible and infected cases was shown using blue and red colors, respectively. In the absence of mitigatory measures such as lock down across the nation and social distancing; the results were frightening (as shown using green bar). (c) The effective basic reproduction ratio was plotted against the time. *Note: All cases were assumed to be symptomatic during the prediction using the age-structured SIR model and thus $\bar{\alpha}=1$. The parameters such as β and γ were set to 0.0155 and 1/7, respectively*
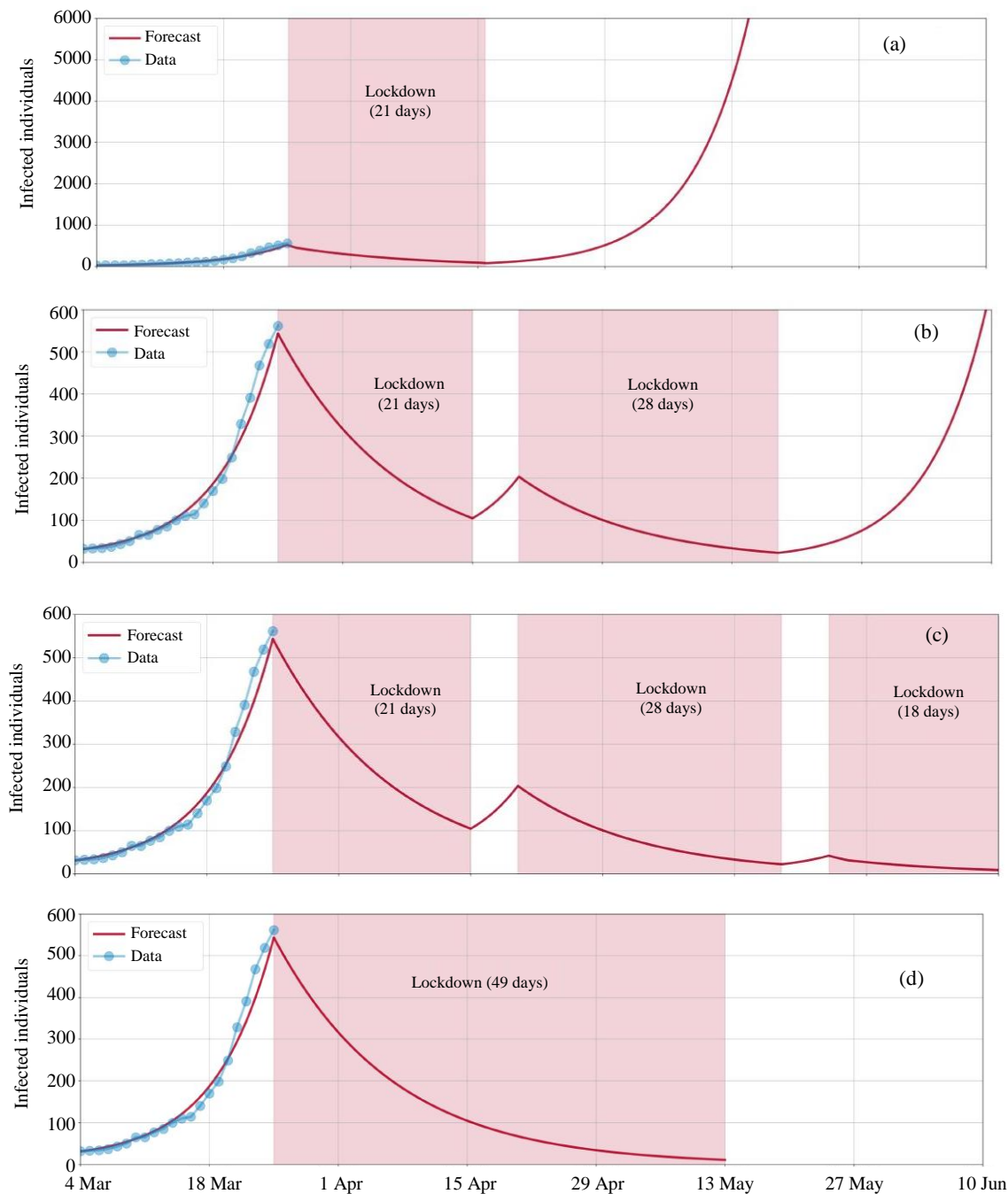
Fig. 7: The prediction of the SARS-CoV2 outbreak in India with effective implementation of social distancing measures using the age-structured epidemiological SIR model. The cases of infected patients were plotted against the various time intervals (Reprinted with permission from Ref. (Singh and Adhikari, 2020). Copyright 2020 arXiv). (a) A *21days* lockdown (from 25th March, 2020 until 14th April, 2020) was found to be insufficient after careful investigation to ensure the equilibrium stage of the pandemic by the end of May, 2020. (b) The outcome of the model was in favor of sustained lockdown with some relaxation for effective implementation of social distancing measures. It was found that the lockdown if imposed across the nation for further *28 days* after the relaxation period of *5 days* from 25th March, 2020, then the measure will be still insufficient to break transmission chain of the SARS-CoV2. (c) As per the scheme, it was found that three successive lockdowns with a gap of *5 days* as relaxation periods were required to bring the equilibrium stage of the pandemic. (d) An alternative scheme was also suggested herewith to impose a *49 days* lockdown across the nation to bring the number of infected cases below *10* or to ensure the equilibrium stage of the novel COVID-19 pandemic. *Note: All cases were assumed to be symptomatic during the prediction using the age-structured SIR model and thus $\bar{\alpha} = 1$. The parameters such as β and γ were set to 0.0155 and 1/7, respectively.*

The Scope and Limitation of the Mathematical Models Used to Investigate Transmission of the Novel COVID-19

Overall, the normalized RP transmission network model was based on the input data sources that were published for only a few countries during the outbreak of the novel COVID-19 and thus it might not fit well into the situations in other countries. The concise baseline model did not rely on the conventional approach of fitting a curve to the dataset. It involved real-time time-dependent data which were based on testing facilities, availability of hospitals, etc. and thus, this framework was suitable for other countries as well. However, the authors acknowledged that due to their limited knowledge of weather conditions, they could not connect it with the equations they have used in their concise modeling to understand the transmission of the pandemic. The exponential model was unable to deliver the perpetual estimation about the novel COVID-19 cases, i.e., up to 30th April, 2020 (section 4), as it did not involve the initiatives of the Indian government to break the transmission chain of the SARS-CoV2. The epidemiological SIR model will not be effective if India reaches the stage of community transmission due to poor implementation of the practice of social distancing. The modified age-structured epidemiological SIR model (section 5) was evaluated by considering both symptomatic and asymptomatic patients (Rothe *et al.*, 2020) of SARS-CoV2. The prediction of the age-structured epidemiological SIR model were suggested to vary region-wise as it was based on data such as day-to-day number of tests.

During investigation of the transmission network models useful in mapping the transmission of the pandemic from its source, we realize the need of machine learning algorithms to identify infected symptomatic and asymptomatic patients during the lockdown periods, quickly based on a web based (artificial intelligence framework) participatory surveillance of the novel COVID-19 pandemic (implemented in cases of previous infectious diseases) (Rao and Vazquez, 2020; Neill, 2013; Rajalakshmi *et al.*, 2018; Arabasadi *et al.*, 2017; Kumar *et al.*, 2013; Tomlinson *et al.*, 2009; Ballivian *et al.*, 2015; Braun *et al.*, 2013; Bastawrous and Armstrong, 2013; Paolotti *et al.*, 2014; Fabic *et al.*, 2012; Liang *et al.*, 2019).

Conclusion

The review finds the simplified Reservoir (Wuhan Seafood Market)-People (BHRP) transmission network model (section 2) as an effective tool to discuss the local transmission of the novel coronavirus disease (COVID-19). The simplified RP transmission network model was based on the next generation matrix (R_0). Using the

model, it was estimated that the transmission of SARS coronavirus was much higher than Middle East respiratory syndrome (MERS) coronavirus.

The concise baseline model (section 3) based on the individual behavioral response and the control measures taken by the government to prevent the spread of the novel COVID-19 was found in close agreement with the previously published data and thus it throws light on mapping the transmission of the novel COVID-19 pandemic. The model did not rely on the conventional approach of fitting a curve to the dataset.

The epidemiological exponential and SIR models (section 4) revealed a similar exponential trend for the transmission of the novel coronavirus disease (COVID-19) in India, Washington and California. The classical model was derived based on the inputs available till 30th March, 2020 to predict the equilibrium stage of the pandemic by the last week of May, 2020. The outcomes of these models were based on real-time time-dependent data (reported on day-to-day basis) and thus found reasonably well to understand the transmission of the novel COVID-19 outbreak in India. The model, however, will not be effective if India reaches the stage of community transmission due to poor implementation of the social distancing strategies.

The modified age-structured epidemiological SIR model (section 5) was based on age groups and effective implementation of social distancing measures. The outcomes of the model were emphasizing about sustained lockdown across the nation with some relaxation to prevent the transmission of the novel COVID-19 outbreak to India. A *21 days* lockdown was found to be insufficient after careful investigation to ensure the equilibrium stage of the pandemic in May, 2020, instead, the outcomes of the model were emphasizing about sustained lockdown with some relaxation of a few days for effective implementation of social distancing measures. It has clearly demonstrated about the need of mitigatory measures such as successive lockdowns of *21 days* and *28 days* and further *21 days, 28 days and 18 days* (each scheme with a relaxation of some *5 days and* suggested to implement from 25th March, 2020), or alternatively a single lock down of 49 days starting from 25th March, 2020; which are required to impose across the nation to bring the equilibrium stage of the novel COVID-19 pandemic.

Author's Contributions

Eva Gupta: She has reviewed papers on epidemiological models for simulating the transmissibility of the novel coronavirus disease 2019 (COVID-19) outbreak to prepare and develop the entire research work to its publication.

Nand Jee Kanu: He has critically reviewed papers on epidemiological models for simulating the transmissibility of the novel coronavirus disease 2019 (COVID-19) outbreak to prepare and develop the entire research work to its publication.

Conflicts of Interest

The authors declare that there are no conflicts of interest.

Planning and Motivation

We reviewed the relevant articles on the novel coronavirus (SARS-CoV2) published online within the past few months with the aim to join the battle against Coronavirus Disease (COVID-19). The idea behind was to study efficient epidemiological models for simulating the transmissibility of the novel Coronavirus Disease 2019 (COVID-19) outbreak across the globe and understand the effective mitigatory measures to break the transmission chain of the pandemic.

Ethics

The author does not see any ethical issues that may arise after the publication of this manuscript.

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