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Applying SEIR model without vaccination for COVID-19 in case of the United States, Russia, the United Kingdom, Brazil, France, and India

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Abstract

Objectives: Compartmental models are helpful tools to simulate and predict the spread of infectious diseases. In this work we use the SEIR model to discuss the spreading of COVID-19 pandemic for countries with the most confirmed cases up to the end of 2020, i.e. the United States, Russia, the United Kingdom, France, Brazil, and India. The simulation considers the susceptible, exposed, infective, and the recovered cases of the disease.

Method: We employ the order Runge–Kutta method to solve the SIER model equations-for modelling and forecasting the spread of the new coronavirus disease. The parameters used in this work are based on the confirmed cases from the real data available for the countries reporting most cases up to December 29, 2020.

Results: We extracted the coefficients of the exposed, infected, recovered and mortality rate of the SEIR model by fitting the collected real data of the new coronavirus disease up to December 29, 2020 in the countries with the most cases. We predict the dates of the peak of the infection and the basic reproduction number for the countries studied here. We foresee COVID-19 peaks in January-February 2021 in Brazil and the United Kingdom, and in February-March 2021 in France, Russia, and India, and in March-April 2021 in the United States. Also, we find that the average value of the SARS-CoV-2 basic reproduction number is 2.1460.

Conclusion: We find that the predicted peak infection of COVID-19 will happen in the first half of 2021 in the six considered countries. The basic SARS-CoV-19 reproduction number values range within 1.0158–3.6642 without vaccination.

Keywords: numerical simulation; pandemic; Runge–Kutta; SARS-CoV-2; SEIR model.

Introduction

Infections caused by SARS-CoV-2 disease were first reported at the end of 2019 in China. The disease spread quickly all over the world causing significance health threats in addition to social and economic difficulties. There are many models used in epidemiology for forecasting the spreading of infectious diseases, some with ordinary differential equations and others with fractional derivatives, and some take the vaccination and the deceased cases into account. Different researchers carried out many attempts using the epidemiologic

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models to study COVID-19 (Aabed and Lashin 2020; Adedire and Ndam 2021; Ali et al. 2020; Al-Raei 2018; Al-Raei 2020a, 2020b, 2020c; Bhadra, Mukerjee, and Sarkar 2020; Fang, Wang, and Pan 2020; Gao et al. 2007; Gupta, Banerjee, and Das 2020; Hamdan and Kilicman 2018; Kamara, Wang, and Mouanguissa 2020; Kermack 1927; Khan et al. 2020; Lifshits and Neklyudova 2020; Malavika et al. 2020; Osemwinyen et al. 2015; Rejaun Rahman, Islam, and Islam 2020; Roy, Bhunia, and Shit 2020; Santosh 2020; Tarabichi 2010; Zhu et al. 2019). Malavika et al. (2020) used SIR and logistic growth models for the forecasting of COVID-19 epidemic in India, while Lifshits and Neklyudova (2020) used a similar approach in Russia. Roy, Bhunia, and Shit (2020) employed ARIMA, autoregressive integrated moving average, model for the forecasting the disease in India and the same model was applied in Russia by Fang, Wang, and Pan (2020). Rejaun Rahman, Islam, and Islam (2020) employed geospatial modelling in Bangladesh, while geographical locations effects were discussed in India by Gupta, Banerjee, and Das (2020). Santosh (2020) discussed the prediction models with unexploited disease data, Adedire and Ndam (2021) developed a mathematical model of dual latency compartments to investigate the transmission dynamics of COVID-19 epidemic in Oyo state, Nigeria. While Aabed and Lashin (2020) discussed the analytical study of the forecasting factors on the spread of COVID-19, Ali et al. (2020) discussed the effects of the PM_{2.5} on its spreading. Khan et al. (2020) discussed the effects of underlying morbidities on the occurrence of deaths in COVID-19 patients. Al-Raei (2020a, 2020b, and 2020c) calculated fundamental SARS-CoV-2 reproduction number values for multiple countries with mortality based on fractional calculus and Bhadra, Mukerjee, and Sarkar (2020) discussed the effects of population density on the infection and the mortality of COVID-19 (Aabed and Lashin 2020; Adedire and Ndam 2021; Ali et al. 2020; Al-Raei 2018; Al-Raei 2020a, 2020b, 2020c; Bhadra, Mukerjee, and Sarkar 2020; Fang, Wang, and Pan 2020; Gao et al. 2007; Gupta, Banerjee, and Das 2020; Hamdan and Kilicman 2018; Kamara, Wang, and Mouanguissa 2020; Kermack 1927; Khan et al. 2020; Lifshits and Neklyudova 2020; Malavika et al. 2020; Osemwinyen et al. 2015; Rejaun Rahman, Islam, and Islam 2020; Roy, Bhunia, and Shit 2020; Santosh 2020; Tarabichi 2010; Zhu et al. 2019). In this work, we use the SEIR model, which takes the exposed cases into account, where we consider the ratio of fifty per-cents for infected-exposed. The SEIR model is composed of four differential equations; the first two equations of this model are non-linear and describe the change of the susceptible and the exposed cases concerning the time and these two equations are given as follows:

$$\frac{dS(t)}{dt} = -\frac{\eta_2}{N}I(t)S(t) + \eta_1[N - S(t)] \quad (1)$$

$$\frac{dE(t)}{dt} = -(\eta_1 + \eta_3)E(t) + \frac{\eta_2}{N}I(t)S(t) \quad (2)$$

While the other two equations of the model describe the change of the infectious and the recovered cases concerning the time and these two equations are given as follows:

$$\frac{dI(t)}{dt} = -(\eta_1 + \eta_4)I(t) + \eta_3E(t) \quad (3)$$

$$\frac{dR(t)}{dt} = -\eta_1R(t) + \eta_4I(t) \quad (4)$$

where N is the population number, η_1 , η_2 , η_3 and η_4 are parameters of the SEIR model and $S(t)$, $I(t)$, $R(t)$, and $E(t)$ are the susceptible, infectious, recovered, and the exposed cases of the pandemic respectively. In the following, we apply the SEIR model to study the spreading and forecasting of the new coronavirus disease in the United States, Russia, the United Kingdom, Brazil, France and India which are considered the countries with most cases of the new coronavirus disease up to the end of 2020 in worldwide. In Section “Computational implementations”, we illustrate the principle of the method used, and in Section “Results and discussion”, we present the results and the discussion while the last section (“Conclusions”) is the conclusion of the study.

Computational implementations

We applied the SIER epidemiological model to simulate the spreading and forecasting of the new coronavirus pandemic. First, we extract the coefficient of exposed, infected, recovered and the mortality of the SEIR model in case of COVID-19 by fitting the collected data of confirmed infected, recovered and the total cases of the new coronavirus up to date December 29, 2020 in the United States, Russia, Brazil, France, India, and the United Kingdom. After that, we used the computed coefficients to predict values for the infectious, recovered, and all cases of the pandemic using numerical simulations of the SEIR model, where we used the Runge–Kutta method for the calculations. Numerical equations used in the Runge–Kutta method are:

$$S(t_{n+1}) \approx S(t_n) + T \sum_{m=1}^{m=z} l_m^1 K_m^1 \quad (5)$$

$$I(t_{n+1}) \approx I(t_n) + T \sum_{m=1}^{m=z} l_m^2 K_m^2 \quad (6)$$

$$R(t_{n+1}) \approx R(t_n) + T \sum_{m=1}^{m=z} l_m^3 K_m^3 \quad (7)$$

$$E(t_{n+1}) \approx E(t_n) + T \sum_{m=1}^{m=z} l_m^4 K_m^4 \quad (8)$$

where the Runge–Kutta simulation functions are:

$$K_1^1 = f_1(t_n, S_n) \quad (9)$$

$$K_2^1 = f_1(t_n + c_2^1 T, S_n + T(a_{21}^1 K_1^1)) \quad (10)$$

$$K_Z^1 = f_1\left(t_n + c_Z^1 T, S_n + T\left(a_{Z1}^1 K_1^1 + a_{Z2}^1 K_2^1 + a_{Z3}^1 K_3^1 + \cdots + a_{Z,Z-1}^1 K_{Z,Z-1}^1\right)\right) \quad (11)$$

$$K_1^2 = f_2(t_n, I_n) \quad (12)$$

$$K_2^2 = f_2(t_n + c_2^2 T, I_n + T(a_{21}^2 K_1^2)) \quad (13)$$

$$K_Z^2 = f_2\left(t_n + c_Z^2 T, I_n + T\left(a_{Z1}^2 K_1^2 + a_{Z2}^2 K_2^2 + a_{Z3}^2 K_3^2 + \cdots + a_{Z,Z-1}^2 K_{Z,Z-1}^2\right)\right) \quad (14)$$

$$K_1^3 = f_3(t_n, R_n) \quad (15)$$

$$K_2^3 = f_3(t_n + c_2^3 T, R_n + T(a_{21}^3 K_1^3)) \quad (16)$$

$$K_Z^3 = f_3\left(t_n + c_Z^3 T, R_n + T\left(a_{Z1}^3 K_1^3 + a_{Z2}^3 K_2^3 + a_{Z3}^3 K_3^3 + \cdots + a_{Z,Z-1}^3 K_{Z,Z-1}^3\right)\right) \quad (17)$$

$$K_1^4 = f_4(t_n, E_n) \quad (18)$$

$$K_2^4 = f_4(t_n + c_2^4 T, E_n + T(a_{21}^4 K_1^4)) \quad (19)$$

$$K_Z^4 = f_4\left(t_n + c_Z^4 T, E_n + T\left(a_{Z1}^4 K_1^4 + a_{Z2}^4 K_2^4 + a_{Z3}^4 K_3^4 + \cdots + a_{Z,Z-1}^4 K_{Z,Z-1}^4\right)\right) \quad (20)$$

Figure 1: Schematic chart of the algorithm used in the study.

where T is the time step and $S(t_n)$, $I(t_n)$, $R(t_n)$, and $E(t_n)$ are the susceptible, infectious, recovered, and the exposed cases of the pandemic individual respectively at the moment t_n and $S(t_{n+1})$, $I(t_{n+1})$, $R(t_{n+1})$ and $E(t_{n+1})$ are the susceptible, infectious, recovered and the exposed cases of the pandemic individual respectively at the moment t_{n+1} . The coefficients l_m^j and c_u^j are the weights and the nodes of the expansion function and a_{qu}^j are the Runge–Kutta matrix coefficients, all the previous coefficients were found using Butcher tableau, and the weights are normalized to one under the following condition:

$$\sum_{m=1}^{m=z} l_m^j = 1 \quad (21)$$

In each step, we use the conservation of the total population condition, which is given as follows:

$$\frac{dS(t)}{dt} + \frac{dE(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} = 0 \quad (22)$$

The previous equations of the simulation method with the equations of the SEIR model were coded to implement the calculation. The numerical errors resulting from approximations used in Eqs. (5)–(20) and approximation calculations can be computed using this program. In Figure 1, we illustrate a schematic chart for the algorithm used for calculations.

Results and discussion

We calculated the coefficient of exposed, infected, recovered cases and mortality of the new coronavirus for the United States, Russia, the United Kingdom, Brazil, France, and India. The calculations are based on the reported collected data of all COVID-19 cases in each country. We used the initial values of the day a COVID-19

case was reported in each country, and those values plus the total COVID-19 cases up to date December 29, 2020 are illustrated in Table 1. We combined the collected results of the total cases from the formal sites, which count the total COVID-19 cases of a daily basis. The results of the coefficients of the SEIR model are shown in Table 2, which includes the coefficients in (per day) d^{-1} unit and the countries studied here. Based on the obtained coefficients, we calculated the predicted COVID-19 cases and based on these cases, we found the predicted dates of the infection's peak in Brazil, France, the United States, the United Kingdom, Russia, and India, the dates of which are listed in Table 3 for each country. Finally, we found the basic SARS-CoV-2 reproduction number in Brazil, France, the United States, the United Kingdom, Russia, and India, these values are listed in Table 4 for each country. The reason for choosing these countries is that these countries were the countries with the most COVID-19 cases up to the end of 2020. As shown in Table 3, the dates of the peak based on the SEIR model for the considered countries are expected in the first half of the year 2021, where we forecast a peak between January-February 2021 for Brazil and the United Kingdom and between February-March 2021 for Russia, France and India while the peak may appear between March-April 2021 for the United States. We see from Table 4 that the basic reproduction number value is 1.0158 for India which is the smallest value between the calculated values and 3.6642 for the United Kingdom, which is the largest one of the calculated values.

Table 1: The initial values of the COVID-19 cases, dates of the initial values, and the total number of cases reported by the end of 2020.

	Data of 1st report of COVID-19 cases	Cases reported on the 1st day	Total cases
United States	13-January 2020	1	19,484,710
Russia	31-January 2020	2	3,105,037
United Kingdom	31-January 2020	2	2,329,730
Brazil	26-February 2020	1	7,506,890
France	24-January 2020	3	2,562,646
India	30-January 2020	1	10,207,871

Table 2: The coefficient of cases exposed, the coefficient of infection, the coefficient of recovery, and the coefficient of mortality of the new coronavirus disease in the United States, Russia, the United Kingdom, Brazil, and Spain.

	$\eta_1 (d^{-1})$	$\eta_2 (d^{-1})$	$\eta_3 (d^{-1})$	$\eta_4 (d^{-1})$
United States	0.0615	0.5248	0.1125	0.0763
Russia	0.0084	0.6879	0.2500	0.4062
United Kingdom	0.2418	1.8049	0.3125	0.0359
Brazil	0.5646	3.4216	1.0000	1.2897
France	0.3580	2.2616	0.3906	0.0421
India	0.0502	0.3538	0.1250	0.1982

Table 3: The predicted infection peak of COVID-19 cases in most cases countries based on the total COVID-19 cases reported by the end of 2020.

Country	Date of predicted peak
United States	March–April 2021
Russia	February–March 2021
United Kingdom	January–February 2021
Brazil	January–February 2021
France	February–March 2021
India	February–March 2021

Table 4: The basic SARS-CoV-2 reproduction number in countries reporting the most cases.

	United States	India	France	Brazil	United Kingdom	Russia
R_0	2.4614	1.0158	2.9497	1.1794	3.6642	1.6057

Conclusions

We applied the SEIR model for demonstrating the spreading and forecasting of the new coronavirus pandemic in six countries with the disease, namely, the United States, Russia, the United Kingdom, Brazil, France, and India. We used the collected real COVID-19 data in those countries to find the coefficient of the SEIR model for each one of the studied countries. The Runge–Kutta method was employed for fitting the collected data. The same numerical method was employed to calculate the predicted values of the total COVID-19 cases, the infectious cases, and the recovered cases c in each country, and based on these values, we predicted the date of the peak in each country. We foresee COVID-19 peaking between February–March 2021 in Russia, France, and India, between March–April 2021 in the United States, and between January–February 2021 in Brazil and the United Kingdom without taking the vaccination into account. The values of the SARS-CoV-2 basic reproduction number are reported to vary between 1.0158, which returns to India, and 3.6642, which returns to the United Kingdom, based on the simulation method used.

The method applied in this work on selected countries with the most cases can be used for other countries to predict peaks in COVID-19 cases and to calculate the parameters of the disease, such as the basic reproduction number.

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