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Coronavirus pandemic: A predictive analysis of the peak outbreak epidemic in South Africa, Turkey, and Brazil

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Abstract

In this research, we are interested in predicting the epidemic peak outbreak of the Coronavirus in South Africa, Turkey, and Brazil. Until now, there is no known safe treatment, hence the immunity system of the individual has a crucial role in recovering from this contagious disease. In general, the aged individuals probably have the highest rate of mortality due to COVID-19. It is well known that this immunity system can be affected by the age of the individual, so it is wise to consider an age-structured SEIR system to model Coronavirus transmission. For the COVID-19 epidemic, the individuals in the incubation stage are capable of infecting the susceptible individuals. All the mentioned points are regarded in building the responsible predictive mathematical model. The investigated model allows us to predict the spread of COVID-19 in South Africa, Turkey, and Brazil. The epidemic peak outbreak in these countries is considered, and the estimated time of the end of infection is regarded by the help of some numerical simulations. Further, the influence of the isolation of the infected persons on the spread of COVID-19 disease is investigated.

Keywords: COVID-19, Age-structured, SIR model, Basic reproduction number, Peak epidemic, Computational epidemiology

1. Introduction

Coronaviruses are a large group of viruses that can infect animals and humans and cause respiratory distress; they may be as mild as a cold or as severe as pneumonia. In rare cases, animal coronaviruses infect humans and then spread through them. The SARS (Severe Acute Respiratory Syndrome) virus was an example of the coronavirus. It was transmitted from animals to humans between 2002 and 2003 [1,27]. Another important and newer breed is the Coronavirus MERS virus, which was discovered in 2012 in the Middle East. The virus was first transmitted from camels to humans. The virus is usually spread through coughing and sneezing, personal contact with an infected person, or touching infected surfaces and then touching the mouth, nose, and eyes. In the last days of 2019, a new coronavirus, called the new coronavirus, began to spread pneumonia from Wuhan to all over China and then around the world. The disease is currently the most important health threat to public health in the world. The epidemic of Covid-19 virus, caused by the coronavirus, is spreading rapidly around the world and has affected 76 countries since March 1, 2020. According to global statistics, the mortality rate is 0.9 for this disease. Early symptoms of Quad-19 include pneumonia, fever, muscle aches and fatigue. Prevention and control of infections and observance of hygienic principles by the people is the main health priority in dealing with this disease. Unfortunately, no vaccine has been developed to treat this disease. Because the source of the disease is a virus, antibiotics do not affect the pathogen. In medical centers, without any specific treatment for the disease, they usually treat the symptoms and make the patient feel more comfortable.

As it has been mentioned, the main method of transmission of the disease is the respiratory droplets that a person secretes when coughing. The risk of COVID-19 disease is diminished by someone asymptomatic. But many people with the disease have only slight symptoms. This is especially true in the early stages of the disease. Therefore, COVID-19 can be infected by a person who suffers from a mild cough and does not feel ill. WHO is assessing ongoing research on the transmission period of COVID-19 and the method of isolation and other measures for controlling the spread of COVID-19 [5,6,8,10–13,18,20,26,28]. In [32], it is obtained that an infected person that passes 60s has a 5.3% chance of dying due to COVID-19 disease. So we are interested in studying the influence of the age structure of the studied countries on the spread of COVID-19,
where the percentage of the aged individuals next to the total size of populations in South Africa, Turkey and Brazil are given in the following table:

To mention that the average incubation period is five days. Some western, traditional, or home medicines (such as the Chloroquine) may relieve or alleviate some of the symptoms of the COVID-19. There is no evidence that medications are currently in place to prevent or treat this disease. WHO does not recommend self-medication with any medicines, including antibiotics, either to prevent or treat the disease. However, there are several clinical trials under way that include both western and traditional medicines. WHO still continues to provide updated information in this regard when clinical results are available. On the other hand, by using declared infection cases in South Africa, Turkey and Brazil by WHO.

We draw the evolution of the infection and death cases in the studied countries, and it is highlighted in Fig. 1. Here, we are interested in predicting the epidemic peak outbreak in the studied countries with the help of the mathematical model obtained in the next section, where a proper interpretation of the model parameters is provided next to the method of approximation of the model parameters. The predictive results are obtained in sections 3, 4, and 5. The suggested measures are given in sections 6 and 7 where it is obtained that the restriction of the social movements and the isolation of the infected individuals are the most powerful tools for reducing the spread of the COVID-19 pandemic. The conclusion section have been included to highlight the achievements and provided some suggestions for reducing the outbreak of Coronavirus disease.

2. Mathematical model and preliminary results

In this section, we will construct the responsible mathematical model for our predictions of the spread of the COVID-19 epidemic. In the introduction section, we highlighted the effect of the age of individuals in mortality due to this infectious disease. In fact, was and still predicting natural behavior using mathematical models very useful for predicting the behavior of species (Human or animals or particles) we mention as epitome the papers [2–4,21–25].

In the mathematical epidemiology, the age-structured models play an important role in describing, modeling the spread of different infectious diseases. For instance we cite the papers [2–4,9,14,16,19].

The responsible model for our predictions is expressed as:

\[
\begin{align*}
\frac{dS(t,\theta)}{dt} + \frac{dS(t,\theta)}{d\omega} &= -\rho S(t,\theta) \big( \int_0^\infty I(t,\omega)d\omega + \int_0^\infty E(t,\omega)d\omega \big), \\
\frac{dE(t,\theta)}{dt} + \frac{dE(t,\theta)}{d\omega} &= \rho S(t,\theta) \big( \int_0^\infty I(t,\omega)d\omega + \int_0^\infty E(t,\omega)d\omega \big) - v E(t,\theta), \\
\frac{dI(t,\theta)}{dt} + \frac{dI(t,\theta)}{d\omega} &= v E(t,\theta) - (\mu + \eta(\theta)) I(t,\theta), \\
\frac{dR(t,\theta)}{dt} &= \mu \int_0^\infty I(t,\theta)d\theta, \\
S(t,0) &= 0, E(t,0) = 0, I(t,0) = 0, \\
S(0,\theta) &= S_0(\theta) \in L^1(0, +\infty), E(0,\theta) = E_0(\theta) \in L^1(0, +\infty), \\
I(0,\theta) &= I_0(\theta) \in L^1(0, +\infty). 
\end{align*}
\]

(1)

where \(0 \leq S(t,\theta), E(t,\theta), I(t,\theta) \leq 1\) stand respectively for the categories of the susceptible individuals, exposed individuals, infected individuals at the time \(t\) (measured in days) with the chronological age \(\theta\) (measured in years). \(R(t)\) is the recovered proportion from the COVID-19 at time \(t\). \(\rho\) is the transmission coefficient. The reason behind choosing a constant transmission rate hich not depend on the chronological age \(f\) individual is due to the method of transmission of this contagion disease, where in the introduction section we highlighted that the Coronavirus transmits through droplets generated by the infected individual on the surfaces and different public places which is not affected by the chronological age of the infected individual, so we can consider that the transmission rate is constant with respect to the age of the individuals. 
\(v\) is the rate of quitting the E-class, and interting into the I-class. For the COVID-19 infection, an individual in E-class will stay about five days in the exposed stage before becoming a fully infected individual, at this stage the Coronavirus reproduces in the host individual where it uses the humane cell to reproduce. Hence we can consider \(\frac{1}{5} = 5\) (days) which represents the period for recent infected individual remains in the E-class. At this stage, the mortality of the individual due to COVID-19 is not potential because the density of virus in the infected individual body is not fatal yet for this class. Besides, the COVID-19 has symptoms similar to
Fig. 2. The method of approximating $x_1$, $x_2$ and $x_3$ using the data in Tables 1, 2 for each country, wherein $t = 0$ stands for the date 15/04/2020.

influenza, and stays in the human body in a short time about $\frac{1}{\mu} \approx 15$ days which is the average of the infection period. In the model (1), the integral $\int_0^{+\infty} I(t, \omega)d\omega$ (resp. $\int_0^{+\infty} E(t, \omega)d\omega$) stands for the total fraction of the infected individuals (resp. exposed individuals) at instance $t$. A new researches are proved that the newborns individuals (that have age equal to zero) are not concerned by this infection where this result can be seen through the boundary conditions $E(t, 0) = 0$, $I(t, 0) = 0$, and $S(t, 0) = 0$. Also, the infection will stay a few mounts; thus, the newborn can be even neglected. Due to the research of [17], it is shown that COVID-19 is
Table 1
Population densities of different countries.

| Country     | South Africa | Turkey | Brazil | Total number of population (million) | Percentage of individuals with age over 60 |
|-------------|--------------|--------|--------|-------------------------------------|------------------------------------------|
|             | 57.78        | 82     | 209.5  | 12.89%                              | 17.60%                                   |
|             |              |        |        | 11.42%                              |                                          |

fatal for the individuals that passed their 60s, where there is a 5.3% chance of dying due to COVID-19. The responsible mortality functional \( \eta(\theta) \) can be expressed as:

\[
\eta(\theta) = \begin{cases} 
\eta_0 & \text{if } \theta \geq 60, \\
0 & \text{if } \theta < 60.
\end{cases}
\]

For the well possessiveness of our system, we assume that the initial conditions belong the space \( S = L^1(0, +\infty) \times L^1(0, +\infty) \times L^1(0, +\infty) \times \mathbb{R}^+ \), where \( L^1(0, +\infty) \) is the space of positive and Lebesque integral functionals, equipped with the norm

\[
||\{(\theta_1, \theta_2, \theta_3, \kappa)\}|| = \int_0^{+\infty} |\theta_1(a)| da + \int_0^{+\infty} |\theta_2(a)| da
+ \int_0^{+\infty} |\theta_3(a)| da + \kappa.
\]

The existence and uniqueness of a positive solution for the system (1) can be obtained by a similar way as considered by [2,7] for initial conditions \( (S_0, E_0, I_0, R_0) \in S \).

Now we are in a situation to calculate the basic reproduction number, which going to help prediction of the epidemic outbreak in the studied countries. For the model (1), we have

\[
R_0 = \beta s_0 \int_0^{+\infty} \exp^{-\nu a} \left( 1 + \frac{\nu}{\mu + \eta(\theta)} \right) da.
\]

with \( s_0 = \int_0^{+\infty} S(0, \theta) d\theta \). We can simplify the explicit formula of \( R_0 \) as

\[
R_0 = \frac{\rho s_0}{\nu} \left( \frac{\mu + \nu}{\mu + \eta_0 e^{-60}} \right).
\]

As expected, the critical value of the mortality for the aged individuals affects the value of the basic reproduction number. The value \( s_0 = \int_0^{+\infty} S(0, \theta) d\theta \) which is the total number of the susceptible individuals at \( t = 0 \). Now, it remains to determine the value of the transmission rate \( \rho \). By integration of the three first equations of the system (1) we

![Predictive results in South Africa](image-url)
get the following system

\[
\begin{align*}
\frac{ds(t)}{dt} &= -\rho s(t)(i(t) + e(t)), \\
\frac{di(t)}{dt} &= \rho s(t)(i(t) + e(t)) - ve(t), \\
\frac{de(t)}{dt} &= ve(t) - \mu i(t) - \int_{0}^{\infty} \delta(a)I(t, a)da,
\end{align*}
\]

with \( s(t) = \int_{0}^{\infty} S(t, a)da \), \( e(t) = \int_{0}^{\infty} E(t, a)da \), \( i(t) = \int_{0}^{\infty} I(t, a)da \). We expect that \( i(t) \) (the total proportion of infected individuals) has the following special form:

\[
i(t) = x_1 \exp^{k_1 t} - x_3.
\]

Using the values of \( x_1, x_2, x_3 \) found in Table 2, we can determine the value of the transmission rate \( \rho \), which by taking a look at (3) it is difficult to deduce it. Hence, using the fact that \( 0 \leq \delta(0) \leq \delta^* \) we can obtain that:

\[
\rho_1 \leq \rho \leq \rho_2,
\]

where \( \rho_1 = \frac{x_2 + \delta}{2(0)} \), \( \rho_2 = \frac{x_2(x_2 + \delta)}{2(0)(x_2 - \delta)} \). Besides, the choice of the transmission rate \( \rho \) is highlighted in Table 2.

### 3. Predictive results in South Africa

For obtaining an approximate number of the individuals in the exposed class we can calculate the number of the new infected individuals in five days, this gives us an approximation to the number of persons in the exposed stage. On the other hand, using Fig. 3 we can conclude that in South Africa, the infection will reach its higher rate at \( t = 50 \) starting from 15/04/2020, with 0.03141% of the total population which means that \( 1.8149 \times 10^4 \) active infection cases, this leads us to say that South Africa is in the way of controlling the spread of the COVID-19. Besides, from the two lower figures we can deduce that Coronavirus can infect all kinds of population of different ages. Further, we can also mention that COVID-19 will disappear from the South African community by the 100 days, starting from the date 15/04/2020.

### 4. Predictive results in Turkey

For obtaining an approximate number of the individuals in the exposed class we can calculate the number of the new infected individuals in five days. In Turkey, the infection will reach to
its higher percentage after 52 days starting from 15/04/2020, with 0.899% of the total population, which means that \(7.3718 \times 10^5\) active infection cases, this means that Turkey is in advance stage for the spread of the COVID-19 compering with South Africa, where a serious measure is needed before the infection cases become higher. Further, we can also mention that COVID-19 will disappear from the population in Turkey after 97 days, starting from the date 15/04/2020.

5. Predictive results in Brazil

In a similar way in the previous figure, we can obtain the proportion of the persons in the incubation stage. In Brazil, the epidemic peak outbreak will be reached at \(t=52\) starting from 15/04/2020, with 0.1443% of the total population which means that \(3.0231 \times 10^5\) active infection cases, this means that Brazil is in advance stage for the spread of COVID-19 where a governmental health intervention is needed for reducing the number of infection cases before becoming much higher. Besides, the two lower figures signify that all the population with its different stage structures are concerned by this infection. Further, we can also expect that COVID-19 will disappear from the population in Brazil after 100 days, starting from the date 15/04/2020 which means by the end of July.

6. Restriction of the social movements

Now, we are in a position to study the influence of the restriction strategy of the social interactions on reducing the pandemic peak outbreak. In fact, after considering this case of restriction, the contact between an infected and susceptible individuals will decrease brutally, which it can be chosen to be exponentially decreasing. Hence, it is wise to consider that the transmission rate is a decreasing functional in time. Based on the research [15], we assume that the transmission functional \(\eta(t)\) has the following special form:

\[
\eta(t) = \begin{cases} 
\eta_0 & \text{if } t \geq T \\
\eta_0 e^{-\kappa(t-N)} & \text{if } T < t.
\end{cases}
\]  

(5)

where \(\eta_0\) takes the values of \(\eta\) used in Table 2 also \(\mu = 0.16\) (see [15]), next, we presume that the time of restrictions is \(T = 40\) starting from 15/04/2020. As it has been shown in Fig. 6 we can see that this measure reduces the epidemic peak outbreak, where 35 days of restriction is able to get rid of the infection from populations of South Africa, Turkey, and Brazil.

Indeed, the blue curves are the infection cases highlighted in Fig. 3, 4, 5. The black curves are the proportion of the infection cases after the full restriction with the help of the transmission functional (5). The restriction measures are assumed to began after 40 days starting from 15/04/2020, where it is obtained that 35 days
of full restriction is able to stop the spread of COVID-19 in three samples of the studied countries.

7. The effect of the quarantine on the spread of COVID-19 in South Africa, Turkey, Brazil

In this section, we are interested in studying the influence of the quarantine on the spread of the COVID-19, wherein this case the quantity of tests for revealing the infected persons is crucial in reducing the active infected individuals. Note that the individuals in the quarantines can be considered as inactive infected individuals, which means that they can not infect susceptible individuals. The system (1) becomes in the presence of this class of individuals

$$\frac{dS(t, \theta)}{dt} + \frac{d\tilde{S}(t, \theta)}{dt} = -\rho S(t, \theta)\left(\int_0^\infty I(t, \omega) d\omega + \int_0^{+\infty} E(t, \omega) d\omega\right),$$

$$\frac{dE(t, \theta)}{dt} + \frac{d\tilde{E}(t, \theta)}{dt} = \rho S(t, \theta)\left(\int_0^\infty I(t, \omega) d\omega + \int_0^{+\infty} E(t, \omega) d\omega\right) - \nu E(t, \theta),$$

$$\frac{dI(t, \theta)}{dt} + \frac{d\tilde{I}(t, \theta)}{dt} = \nu E(t, \theta) - (\mu + q + \eta(\theta)) I(t, \theta),$$

$$\frac{dQ(t, \theta)}{dt} + \frac{d\tilde{Q}(t, \theta)}{dt} = qI(t, \theta) - (\mu + \eta(\theta)) Q(t, \theta),$$

$$\frac{d\theta}{dt} = \mu \int_0^{+\infty} I(t, \theta) d\theta,$$

$$S(t, 0) = 0, E(t, 0) = 0, I(t, 0) = 0, Q(t, 0) = 0,$$

$$S(0, \theta) = S_0(\theta) \in L^1(0, +\infty), E(0, \theta) = E_0(\theta) \in L^1(0, +\infty),$$

$$I(0, \theta) = I_0(\theta) \in L^1(0, +\infty), Q(0, \theta) = Q_0(\theta) \in L^1(0, +\infty).$$

(6)

where \(q\) represents the proportion of the revealed infected individuals and moved to the quarantine. Other parameters have the same interpretations as it has been mentioned in the introductions section. The real value of the parameter \(q\) is not known, where the quantity of tests is responsible for revealing the percentage of infected individuals that moved to the quarantine. So, we will use several values of the parameter \(q\) and see how it can influence the spread of the COVID-19 disease. The obtained results are highlighted in Fig. 7. To mention that \(q=0\) refers to the case of the absence of the quarantine. Hence the system (6) behaves in the same manner of (1).

Indeed, for \(q = 0\) (no isolation) the pandemic peak outbreak will reach as it has been obtained previously in sections 3, 4 and 5. However, for \(q = 0.3\) or \(q = 0.5\) (q=30% or q=50% of infected individuals are in isolation) this reduces the peak time and the number of infected individuals at this peak. So it is important to reveal the infected individuals and isolates them to reduce the transmission of this contagion disease.

8. Discussion and suggestions

In this research, we investigated with some data analysis for predicting the epidemic peak outbreak in South Africa, Turkey and Brazil using the declared infection and death cases by WHO [28–31]. An age structured model is used for determining the predictive results. The transmission of COVID-19 disease changes from one country to another. This leads to a change of the basic reproduction number \(R_0\) where for South Africa we obtained that \(R_0 = 1.6685\), Turkey \(R_0 = 1.9184\) and Brazil \(R_0 = 1.8882\).

In sections 3, 4, 5 we found the predictive pandemic peak outbreak of COVID-19 where in South Africa it will be reached at \(t=50\) with 18 149 active infection cases, this means that due to the small number of infection cases South Africa is in the way of controlling the spread of the COVID-19 disease. More strict measures are needed for reducing the number of infection cases, and we predict that the pandemic will disappear by the end of July. Besides, in Turkey, we expect that the highest number of infection cases will be achieved at \(t=52\) with 737 180 active infection cases, and we expect to be finished by the end of July. Turkey needs a serious
Fig. 7. The influence of the quarantine on the spread of COVID-19 where the blue color figure stands for the exposed class, red color one for the infected persons, the black one for the individuals in the quarantine.
measure for stopping the spread of this infectious disease as a full restriction. Indeed, 35 days of full restriction is capable of preventing the spread of the COVID-19 epidemic. Also, isolation of infected individuals can help to reduce the spread of Coronavirus disease where the quantity of tests can increase the number of infected individuals that moved to quarantine (see Fig. 7) this helps to reduce the number of active infected individuals (not in the quarantine). The same remark can be deduced for Brazil, where the highest number of infected individuals is predicted to be reached at \( t = 52 \) with 302 310 active infection cases. The restriction next to the isolation of infected individuals is the best strategy for reducing the number of infected individuals in Brazil.

To mention that the restriction has a bad influence on the economic system of the countries, but it is needed for reducing the number of infected persons. So, the advantage of the isolation of the infected individuals is for the possibility of using it without restriction (full or partial restriction), which means it allows the economic system (commercial transactions) of the countries to work with less danger of the spread of COVID-19 disease. The opposite for the restriction where it stops this kind of transitions, and the most of countries must start to work on augmenting the number of tests per day.

Thus, as a conclusion we can highlight that the quantity of tests for revealing the infected persons is essential tool for fighting Coronavirus disease, and the full restriction has a bad influence of the economic system of the studied countries. It can be avoided if the percentage of the isolated infected individuals is more than 50\% \( q=0.5 \) in Fig. 7, where for this case the number of the declared infection cases will decrease immediately.

Also to mention that it is been mentioned that 35 days of full restriction is able to eliminate the infection from the three samples of the countries. But in reality it is very difficult to conserve this restriction for 35 days in a row where supplying the citizens by the elementary equipments as food medicaments and others, which makes it very difficult of respecting this restriction. However, the isolation strategy of the infected individuals offered in section 7 is more proper strategy the can be considered by the governments for the purpose of reducing the epidemic peak outbreak where he quantity of tests has a crucial role in augmenting the number of isolated infected individuals. Furthermore, through section 7 we can highlight the huge sensitivity of our predictions due to the measures taken by the three governments.

**Compliance with Ethics Requirements**

This article does not contain any study with human or animal subjects.

**Declaration of Competing Interest**

The authors declare that they have no conflict of interest.

**CRediT authorship contribution statement**

**Salih Djilali:** Conceptualization, Data curation, Visualization, Investigation, Writing - review & editing. **Behzad Ghanbari:** Writing - original draft, Conceptualization, Methodology, Software, Supervision.

**Acknowledgments**

The first author is partially supported by the DGRSDT of Algeria.

**References**

[1] Anderson R, Fraser F, et al. Epidemiology, transmission dynamics and control of SARS: the 2002-2003 epidemic. Phil Trans Roy Soc B 2004;359:1091–490.
[2] Bentout S, Touaoula TM. Global analysis of an infection age model with a class of nonlinear incidence rates. J Math AnalAppl 2016;434(2):1211–39.
[3] Djilali S, Touaoula TM, Mini SEH. A heroin epidemic model: very general non linear incidence, treat-age, and global stability. Acta Math Appl 2017;152(1):171–94.
[4] Diekmann O, Heesterbeek JAP. Mathematical epidemiology of infectious diseases: model building, analysis and interpretation. Chichester, UK: Wiley; 2000.
[5] Fraser C, Riley S, Anderson R, Ferguson N. Factors that make an infectious disease outbreak controllable. Proc Natl Acad Sci USA 2004;101:6146–51.
[6] UK Government. 2020. Department of Health and Social Care. Coronavirus action plan. March 1, 2020. https://www.gov.uk/government/publications/coronavirus-covid-19-adult-social-care-action-plan (Accessed 02/05/2020).
[7] Hale JK. Asymptotic behavior of dissipative systems. Mathematical Surveys and Monographs 25, American Mathematical 1988:48. Society, Providence, RI.
[8] Hellewell J, Abbott S, Gimma A, et al. Feasibility of controlling COVID-19 outbreaks by isolation of cases and contacts. Lancet Glob Health (2020), published online Feb 28. 10.1016/s2214-109x(20)30074-7.
[9] Hethcote HW. An age-structured model for pertussis transmission. Mathematical Biosciences 1997;151(2):195–208.
[10] Imperial College London. MRC Centre for Global Infectious Disease Analysis. News COVID-19-report 3: transmissibility of 2019-nCoV 2020. https://www.imperial.ac.uk/mrc-global-infectious-disease-analysis/covid-19-report-3-transmissibility-of-covid-19/ (accessed May 2 2020).
[11] Keeling M., Hollingsworth T., Read J. The efficacy of contact tracing for the containment of the 2019 novel coronavirus (COVID-19). medRxiv 2020; published online Feb 17 (prepint). 10.1101/2020.02.14.20023036.
[12] Kunyova T. Prediction of the epidemic peak of coronavirus disease in Japan. J Clin Med 2020;9(3). doi:10.3390/jcm9030789.
[13] Li Q., Guan X., Wu P. et al. Early transmission dynamics in wuhan, china, of novel coronavirus-infected pneumonia. n engl j med. 2020. Published online Jan 29. doi:10.1056/NEJMoa2001316.
[14] Liu Z, Magal P, Seydi O, Webb G. Understanding unreported cases in the COVID-19 epidemic outbreak in wuhan, china, and the importance of major public health interventions. Biology 2020;9:50.
[15] Magal P, Webb G. Predicting the number of reported and unreported cases for the COVID-19 epidemic in south korea, Italy, France and Germany, medRxiv 2020. doi:10.1101/2020.03.21.20040154.
[16] Magal P, McCluskey C, Webb G. Lyapunov functional and global asymptotic stability for an infection-age model appl. Anal 2010;89(7):1109–40.
[17] Porcheddu R, Serra C, Kelvin D, Kelvin N, Rubino S. Similarity in case fatality rates (CFR) of COVID-19/SARS-COV-2 in italy and china. J Infect Dev Cities 2020;14:125–8. doi:10.3855/jidc.12600.
[18] Remuzzi A, Remuzzi G. COVID-19 and italy: what next? Health Policy 2020. doi:10.1016/j.ypmed.2020.03.019.
[19] Schniedz D. An age-structured model of propose- pre and post-vaccination measles transmission. Mathematical Medicine and Biology. A Journal of the IMA 1984;1(2):169–91. doi:10.1093/imanum/1.2.169.
[20] Sun H, Qiu Y, Yan H, Huang Y, Zhu Y, X Chen S. Tracking and predicting COVID-19 epidemic in china mainland. medRxive 2020. doi:10.1101/2020.02.17.20022577.
[21] Riaz MB, Atangana A, N I. Heat and mass transfer in Maxwell fluid in view of local and non-local differential operators. J Therm Anal Calorim 2020. doi:10.1007/s10973-020-09383-7.
[22] Djilali S. Spatiotemporal patterns induced by cross-diffusion in predator-prey model with prey herd shape effect. International J of Biomath 2020. doi:10.1142/S1793544420500308.
[23] Ghanbari B, Djilali S. Mathematical and numerical analysis of a three-species n predator-prey model with herd behavior and time fractional-order derivative. Math Meth Appl Sci 2019. doi:10.1002/mma.5999.
[24] Bonyah E, Atangana A, Elsadany AA. A fractional model for predator-prey with Lynxwore, Chaos 2019;29:031336.
[25] Djilali S. Impact of prey herd shape on the predator-prey interaction. Chaos, Solitons and Fractals 2019;120:135–48.
[26] Zhou L, Ruan F, Huang M, et al. SARS-cov-2 viral load in upper respiratory speci mens of infected patients. N Engl J Med 2020. doi:10.1056/NEJMc2001737. Published online Feb 19
[27] Zhu Y, Ce Q, Wei X. The research of the influence of SARS to the number of foreign tourists of china. Geographical Research 2003;22(5):551–9. 2003.
[28] https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports.
[29] https://en.wikipedia.org/wiki/2020_coronavirus_pandemic_in_South_Africa.
[30] https://en.wikipedia.org/wiki/2020_coronavirus_pandemic_in_Turkey.
[31] https://en.wikipedia.org/wiki/2020_coronavirus_pandemic_in_Brazil.
[32] https://www.cia.gov/library/publications/the-world-factbook/fields/141.html.