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Research Article

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Posted Date: June 2nd, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-30383/v1>

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A simple kinetic modelling of coronavirus infection in a system

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In this paper, provide an analysis of data on the characteristics of patients with confirmed COVID-19 infection throughout Iran and other countries such as China, S. Korea, USA, Italy, Spain, Germany, France, UK, Austria, and Argentina, and presented a kinetic modelling for prediction of infection, death, recovery and patients populations. The predict results of infection, death and recovery rate constants helps to interpret of public sentiment on disseminating related health information, and comparison different governments behavior to overcoming the outbreak of the coronavirus (COVID-19). Calculation results are in agreement with the census data of the coronavirus infection in many regions of the world.

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Keywords: Kinetic modelling, COVID-19, Coronavirus, Prediction, Analysis

Since December 2019, novel pneumonia cases were reported in China.¹ These cases have been identified as infections with a novel strain of coronavirus, called COVID-19 by the World Health Organization (WHO).²⁻⁶ In January 2020, the coronavirus spread over China and reached to other countries. Daily situation containing the infection and death cases were reported by WHO from January 21.

Common symptoms include fever, cough and shortness of breath. Other symptoms may include fatigue, muscle pain, diarrhea, sore throat, loss of smell and abdominal pain. While the majority of cases result in mild symptoms, some progress to viral pneumonia and multi-organ failure.⁷

In 19 February 2020, first cases of coronavirus infections in Iran were reported from Qom province.⁸ The number of infection cases to COVID-19 have spread exponentially since March, 2020 in most countries in Europe and USA. As of 16 April 2020, more than 2 million cases have been reported in more than 200 countries and territories, resulting in more than 95,800 deaths and more than 542,000 people have recovered.⁹

For many researchers and specialists it is crucial to understand the time profile of infection population. Therefore, analysis and modelling can inform predictions about potential future growth of infection.

Lin and et al. utilize Susceptible-Exposed-Infectious-Recovered (SEIR) modelling to forecast COVID-19 outbreak within and outside of China based on daily observations.¹⁰ Kucharski and co-workers reported a mathematical modelling study for dynamics of transmission and control of COVID-19.¹¹ Leung provide an impact assessment of the transmissibility and severity of COVID-19 during the first wave in mainland Chinese locations outside Hubei.¹² Also Bayham used data from the monthly releases of the US Current Population Survey to characterize the

family structure and probable within-household child-care options of US health-care workers by a modelling analysis.¹³ Koo and co-workers were adapted an influenza epidemic simulation model to estimate the likelihood of human-to-human transmission of severe acute respiratory syndrome coronavirus 2 in a simulated Singaporean population.¹⁴

In this work, kinetic modelling of coronavirus infection has been provided based on an autocatalytic behavior. The proposed model was used for data on cases of coronavirus disease (COVID-19) in China as a sample. The number of infection, death, recovery and patients (time-profile) were predicted for China cases by provided model. With regarding to very good adaptation of calculated and census data, model were used for Iran and other countries to estimate how transmission had varied over time during in January, 2020, and April, 2020.

Modelling

The scheme 1 shows an autocatalysis reaction, which is just the appearance of one of the products of the reaction as a reactant in the same (HV) or a coupled reaction. The following kinetic model (Scheme 1) adapted to coronavirus infection which can depict the dynamic of infection, recovery and death processes in one and two steps (one-wave and two-waves). In this model H, HV, R and D are number of health, infected, recovered and death cases, respectively. The mass balance and rate expressions equations of each component are given by Eqs. (1)–(6).

Scheme 1:One and two-wave infection scheme.

$$[H_0] - [H] = [HV] - [HV_0] \quad (1)$$

$$[H] = [X] \quad (2)$$

$$[HV]_{\text{tot}} = [H_0] + [HV_0] - [X] \quad (3)$$

$$d[X]/dt = k_1[X]([H_0] + [HV_0] - [X]) \quad (4)$$

$$d[R]/dt = k_2[HV] \quad (5)$$

$$d[D]/dt = k_3[HV] \quad (6)$$

$$[HV]_{\text{tot}} = [HV] + [D] + [R] \quad (7)$$

By dividing Eq.(6) to Eq.(5), Eq.(8) is obtained:

$$[D] = [R].k_3/k_2 \quad (8)$$

where $[H_0]$, $[HV_0]$ are the initial number of health and infected cases, $[HV]_{tot}$ and $[HV]$ are total number of infected and patients cases ($[P]$), k_1 , k_2 and k_3 are infection, recovery and death rate constants, respectively. By solving the differential Eq.(4):

$$\ln([H_0].[HV]/[HV_0].[H])/([H_0] + [HV_0]) = -k_1.t \quad (9)$$

or

$$[HV]_{tot} = A / \{ 1 + B \cdot \exp(-k_1 \cdot A \cdot t) \} \quad (10)$$

where $A = [H_0] + [HV_0]$ and $B = [H_0]/[HV_0]$

Equation (10) shows of number of infected–time profile with the sigmoid function behavior. Note that at $t=0$, $[HV]_{tot}$ just has its initial value $[HV_0]$ and levels off at value of long times to $[H_0] + [HV_0]$.

The number of recovery cases can be obtained by solving Eq.(5). By rearrangement of Eq.(7) and substituting in Eq.(5), Eq.(11) is obtained:

$$d[R]/dt = k_2 \cdot ([HV]_{tot} - [D] - [R]) \quad (11)$$

As can be seen from Eq.(11), the solving of differential equation seems to be difficult. Thus, by considering the assumption given in Eq.(12) and Eq.(8), Eq. (11) can be altered to Eq.(13).

$$[R] = \alpha \cdot [HV]_{\text{tot}} \quad (12)$$

$$d[R]/dt = [HV]_{\text{tot}} \cdot (k_2 - \alpha \cdot (k_3 + k_2)) \quad (13)$$

By substituting Eq.(10) in Eq.(13) and solving it, Eq.(14) is obtained:

$$[R] = (k_2 - \alpha(k_2 + k_3)) \cdot \{(\ln(B \cdot \exp(-k_1 \cdot A \cdot t)) - \ln(B + 1)) / (k_1 + A \cdot t)\} \quad (14)$$

With assumption similar to Eq.(12), [D] can be calculated by Eq.(15).

$$[D] = (k_3 - \beta(k_2 + k_3)) \cdot \{(\ln(B \cdot \exp(-k_1 \cdot A \cdot t)) - \ln(B + 1)) / (k_1 + A \cdot t)\} \quad (15)$$

$$\text{or } [D] = \beta \cdot [HV]_{\text{tot}} \quad (16)$$

By dividing Eq.(16) to Eq.(12), and substituting to Eq.(8), β is obtained:

$$\beta = \alpha \cdot k_3 / k_2 \quad (17)$$

where α and β are recovery and death fraction, respectively.

According to Eq.(7), Eq.(8), Eq.(10) and Eq.(14), number of patients can be calculating by Eq.(18):

$$[P] = [HV]_{\text{tot}} - [R] - [D] \quad (18)$$

The values of A, B and k_1 can be estimated by rearrangement of Eq.(10) and substituting first derivative of Eq.(10), Eq.(21) is obtained:

$$[HV]_{\text{tot}} + (B/A) \cdot \exp(-k_1 \cdot A \cdot t) = A \quad (19)$$

$$(d[HV]_{\text{tot}}/dt) / ([HV]_{\text{tot}}^2 \cdot k_1 \cdot A) = B \cdot \exp(-k_1 \cdot A \cdot t) \quad (20)$$

$$[HV]_{\text{tot}} = \{(d[HV]_{\text{tot}}/dt) / k_1 \cdot A\} + [HV]_{\text{tot}}^2 / A \quad (21)$$

By fitting of Eq.(21) in term of $[HV]_{\text{tot}}$ vs. $[HV]_{\text{tot}}^2$ in time interval that first derivative of function is constant ($t < \text{rise time}$ to $t \leq \text{levels off time}$), A and k_1 can be estimate from slope and intercept of regression.

The peak time or $t_{50\%}$ can be estimate by Eq.(22) for a single sigmoid function:

$$t_{50\%} = (\ln B) / (k_1 \cdot A) \quad (22)$$

With regarding to second wave of infection is probable after the first wave of infection, a two-wave model is shown in Scheme 1. In Scheme 1, k_1' is infection rate constant in second wave. The governing equations of the two-wave infection model are as follows:

$$[HV]_{\text{tot}} = A_1 / \{1 + B_1 \cdot \exp(-k_1 \cdot A_1 \cdot t)\} + A_2 / \{1 + B_2 \cdot \exp(-k_1' \cdot A_2 \cdot t)\} \quad (23)$$

where all variables are the same as for Eqs. (1-14), with the subscripts 1 and 2 referring to the two different kinetic waves. Two-wave model assumes that the total infection number on the infection process can be divided into two fractions with different rates and various coefficients and infection rate constants. The initial conditions are at time = 0:

$$[HV]_0 = A_1 / (1+B_1) + A_2 / (1+B_2) \quad (24)$$

$$A_1 = [H_{01}] + [HV_0] \quad \text{and} \quad A_2 = [H_{02}] \quad (25)$$

$$B_1 = [H_{01}] / [HV_0] \quad \text{and} \quad B_2 = [H_{02}] / [HV_0] \quad (26)$$

and at the long times, levels off times:

$$[HV]_{\text{tot}} = [H_{01}] + [H_{02}] + [HV_0] \quad (27)$$

where $[H_{01}]$ and $[H_{02}]$ are number of infection cases in wave 1 and wave 2, respectively.

Analysis and model validation

To show the feasibility of the proposed model for the description of coronavirus infection in a system, the number of infection, recovery, death, and patients of China as a sample set of data was used to compare with predictions by the model. Data is extracted from verified sources.¹⁵⁻

¹⁷The aim of this calculation was to demonstrate that model can be used to predict infection-time profiles over wider range of time. The Eq.(10) have three unknown parameters, which should be estimated: A = maximum number of infection, B = relative health cases that can be infected by other infected cases to initial infected cases, and k_1 = infection rate constant in first wave. The quasi first order infection rate constant ($k_1.A$) was estimated by the first-order conditional

estimation extended least squares method. This parameter was obtained from the slope of $\ln$ (number of infection cases) vs. time plot in the time interval, where $t \geq$ rise time (Fig. S1). The intercept of plot estimate the natural logarithm of the initial infection number ($[HV_0]$). The maximum number of infection ($A_{\max}$), can also be estimated by Eq.(19). In time interval that variation of cumulative infected number is linear vs. time, we can use slope of this dependency for fitting of Eq. (19) by a linear regression for estimation of A and k_1 from slope and intercept, respectively (Fig.S2). Kinetic estimated parameters are given in Table 1. Then refinements were obtained by choosing the best fit of proposed infection-time profiles by using the Excel Solver program. Kinetic parameters of Eqs.(7-15) such as k_1 , k_2 , k_3 α and β were computed by using least squares curve fit method for the given number of infection, recovery, death and patient cases, and which are given in Table 1.

In order to assess the performance of the obtained kinetic model, the number of infected coronavirus calculated from Eq.(10) were compared with the infection census data for China and is indicated in Fig. 1a. A comparison between the census data and predicted data indicates a very good correlation coefficient of kinetic model ($R^2 = 0.94-0.99$). The number of recovery, death and patient cases were also calculated from equations Eq.(14), Eq. (15) and Eq.(18), respectively and compared with the corresponding census data in Fig.1b, Fig.1c, and Fig.1d, respectively. The calculated kinetic parameters regression using kinetic model is summarized in Table 1.

An additional set of data containing infected, recovery, death and patients cases for other countries such as S. Korea, Iran, USA, Italy, China, Spain, Germany, France, UK, Austria and Argentina were used to compare with predictions of the kinetic model. Kinetic estimated parameters of

different countries are given in Table 1. The model was fitted with all the available census data (before 17 April, 2020) and kinetic parameters are shown in Table 1.

Figs. 2a show fits obtained using the one-wave infection model for S. Korea. As can be seen from Figs. 2a, the one-wave infection model does not completely describe the end part of infection curve. While the one-wave model predicts a plateau phase in long times, census data display a more gradual increase of the later part of the tail. The two-wave model, Eq. (23) did fit the overall shape of the infection curves very well (Figs. 2b). Apparently, we will in anticipation of a possible second wave in S. Korea. Results of the calculation of the infected, recovery, death and patient cases for S. Korea are shown in Fig. 2a, Fig. 2b, Fig. 2c, Fig. 2d and Fig. 2e, respectively.

Similarly as, the one wave model was used in predicting the number of coronavirus infection in Iran. When calculating the number of patients in Iran and other countries, the infected number-time profiles have not yet reached to their final values (plateau phase).

Typically, comparison of predicted and infection census data for Iran and USA are also shown in Fig. 3(a-d) and Fig. 4(a-d). The excellent match between the census and predicted results for different countries indicates that the proposed kinetic model in Scheme 1 represents the coronavirus infection satisfactorily. The results of prediction and calculated kinetic parameters are summarized in Table 1.

Discussion

Comparing results of model predict with census infection cases reported in China, show that the model predict good agreements results with census data reported before 17 April, 2020. The model also did predict the infection time-profile of other countries in different regions of the world. Typical results of observation and predicted infection-time profiles for other countries are

shown in Fig. 2(a-e), Fig. 3(a-d) and Fig.4(a-d) and supporting information figures. With the exception of S. Korea, other countries fit by one-wave kinetic model.

The results demonstrate that best fitting obtained for infection-time profiles ($R^2 \geq 0.98$) while death-time profiles fitted by lower correlation coefficients ($0.90 \leq R^2 < 0.98$). In some case such as Germany and Australia calculation death-time profile has a similar trend to observed data with a time delay. A time shift about 7-11 days caused improve correlation coefficient of fitting (Fig.S9c and 9c'). The main assumption of this kinetic model is the individual behaviors and governmental action, effect on kinetic parameters and is not affected on model validity.

As summarized in Table 1, the infection rate constants values (k_1) obtained by fitting of kinetic model cannot be compared simply for different countries. Therefore, for better comparison, a first order infection rate constant is obtained from the multiplication of $100k_1$ in A_{cal} where used as “corona”. A corona unit is defined 100 case/(day.case). According to corona unit definition, the highest value of first order infection rate constant belong to S. Korea and then to China. However, the highest value of first order recovery rate constant is also belongs to S. Korea.

The highest and lowest values of first order death rate constant belong to France and USA, respectively. However, the lowest value of first order recovery rate constant is also belongs to USA.

In conclusion, kinetic modelling of coronavirus infection based on autocatalytic chemical reaction idea can be applied for simulation of infection cases that originated in a system to estimate how transmission had varied over time during and not depended to region of infection. The merit of our model is that we predicted some essential parameters, including maximum number of infection, first and second order infection rate constants, recovery, death rate constants,

recovery and death fractions and plateau time of infection. Meanwhile, proposed model is relatively simple and our estimates for different countries are in good agreements with census data at during selected times. However, individual behaviors and governmental action, effect on deviation of calculation and census data, but these values compensate by kinetic parameters and is not affected on validity of model.

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Acknowledgements

This work dedicated to all coronavirus victims in the world. Financial support from the Research Council of Tarbiat Modares University and Iran National Science Foundation (INSF) is gratefully acknowledged. The author thanks Hussein Gharibi for helpful comments and Saeed Aghamiri for help to conversion of census reports to Excel data.

Author Contributions

N.A. analyzed data and wrote the manuscript.

Additional Information

Supplementary information accompanies this paper at <http://www.nature.com/srep>

Competing financial interests: The authors declare no competing financial interests

Figures

Figure 1

The number of cases–time profiles for the infection (a), recovery (b), death (c) and patients(d), with the symbols representing the census data and lines representing the predicted results using kinetic model for China (Jan. 22 - Mar. 22, 2020).

Figure 2

The number of cases–time profiles for the infection (a) for one wave and (b) for two wave, recocery (c), death (d) and patients(e), with the symbols representing the census data and lines representing the predicted results using kinetic model for S. Korea (Jan. 22 - Mar. 11, 2020).

Figure 3

The number of cases–time profiles for the infection (a), recovery (b), death (c) and patients(d), with the symbols representing the census data and lines representing the predicted results using kinetic model for Iran (Feb. 19 - Apr. 16, 2020).

Figure 4

The number of cases–time profiles for the infection (a), recovery (b), death (c) and patients(d), with the symbols representing the census data and lines representing the predicted results using kinetic model for USA (Jan. 22 - Apr. 16, 2020).

Supplementary Files

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