Mathematical model of transmission dynamics with mitigation and health measures for SARS-CoV-2 infection in European countries

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Abstract The pandemic of Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV-2) continue to pose a serious threat to global health resulting in disease COVID-19. No specific drug or vaccine is available against this infection. Therefore, the prevention is only way to reduce the spread of infection. The pandemic needs an enhanced mathematical model, therefore, we propose a SEIAJR compartmental mathematical model to estimate the basic reproduction number \( R_0 \) and the transmission dynamics of four European countries (Germany, United Kingdom, Switzerland and Spain). The proposed mathematical model incorporates mitigation and healthcare measures as recommended by ECDC (European Centre for Disease Prevention and Control). The simulation of proposed model is done in two phases. First-phase simulation estimates basic reproduction number and mitigation rate according to active infected cases in all four European countries. \( R_0 \) estimate 2.82 - 3.3 for considered European countries. Second-phase simulation predicts the dynamics of infection on the estimated \( R_0 \) with varying mitigation rate and constant healthcare rate. This study predicts that no more mitigation is required to invade the infection. The current mitigation and healthcare measures are enough to stop the propagation of infection, however, infection would last by end of July 2020. The developed mathematical model would also be applicable

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to portray the infection transmission dynamics for other geographical regions with varying parameters.

**Keywords** SARS-CoV-2 · mathematical model · mitigation rate · basic reproduction number

1 Introduction

In early December 2019, a novel coronavirus emerged as an outbreak in the city of Wuhan, Hubei Province, China and rapidly spread to other parts of China. Novel coronavirus causing disease COVID-19 and has progressively expanded to various parts of China and has stretched internationally including South Korea, Cambodia, Philippines, Russia, United Arab Emirates, Thailand, Vietnam, Malaysia, Singapore, Nepal, Australia, Canada, United States of America and European countries [23]. So far, the novel virus has infected more than 1,843,123 people and died 113,479 of them on 13 April 2020 (source: https://www.worldometers.info/coronavirus). Despite recent research efforts in pandemic novel coronavirus there is still no vaccine for coronavirus for use in humans. The world is completely unprepared in order to cope with swiftly and properly to this pandemic. The entire world is suffering from this SARS-CoV-2 infection, and WHO declared pandemic on 11 March 2020. European countries are highly widespread after China [4]. As per the 2nd March 2020, ECDC (European Centre for Disease Prevention and Control) Risk Assessment Report [4] suggested for community mitigation measures for prevention and control such as social distancing, travel-related and screenings of travellers, subsequently, 6th and 7th ECDC Risk Assessment Reports [3], [1] suggested some mitigation measures including social distancing, closing of schools and colleges, social gathering/meeting point etc. Due to the unavailability of vaccine and its control, the mitigation plays important role to stop the infection. Thus, mathematical modelling might be an attempt to understand the infection propagation and its also enable us to know the basic reproduction number (it is an average number of infections one case can generate over the course of the infectious period to uninfected population.), duration of European outbreak. It is observed that many epidemiological (pandemic) scenario used mathematical modelling with different approach on different scenario to estimate basic reproduction number, sensitive parameters and weight of control strategies to stop spreading of infection [17], [13], [19], [8]. The exhaustive literature review throws light that mathematical formulation is widely employed for vector-borne and direct human-to-human contact based viral infection [24], [21], [13], [5], and several researchers also incorporated environmental factor for their studies [22], [13]. In a study, a mathematical model is based on previous reported cases at Wuhan city, Hubei province, China which estimated basic reproduction number $R_0 = 2.82 \pm 0.11$ and suggested the epidemic end in the first week of April 2020 [28]. Another mathematical model was also developed for calculating the transitivity of the infection. Primarily, this model is based on Bats-Hosts-Reservoir-People model, later the model was rebuilt to
Reservoir-People model and estimated basic reproduction number\cite{11}. Several researchers are involved continuously on the development of mathematical modelling for pandemic COVID-19\cite{12}. In this research, an enhanced mathematical model for coronavirus dynamics and transmission is devised for prediction of infection scenario with incorporation of all possible parameters which is suggested by ECDC in 5th, 6th and 7th Risk Assessment Reports\cite{4},\cite{3},\cite{1}. Prediction of infection dynamics aims to estimate the basic reproduction number $R_0$, dynamics of active infected cases and outbreak period. In addition, the proposed mathematical model is developed for better understanding of disease transmission among people, the peak of infectiousness among population during the outbreak of novel coronavirus, severity of the infection and to sketch the effective interventions have been and ought to be. This model suggests to strictly implement mitigation measures. However, available severe acute respiratory illness data could be inaccurate, contain substantial uncertainty, for instance, the precise timing and natural history of cases. It is well-known that the estimation of this number may vary due to several methodological issues, including different assumptions and choice of parameters, utilized models, used datasets and estimation period.

2 Materials and Methods

2.1 Mathematical Model Construction

In this section, we construct a mathematical model of SARS-CoV-2 infection dynamics that is based on the SARS-CoV-2 Reservior-People model (RP model)\cite{11} and 2009 A/H1N1 influenza SEIAR mathematical model\cite{20}. RP model does not include transmission from asymptomatic population to symptomatic but a research showed that about 82.5% population getting symptoms from asymptomatic\cite{26}. As per the ECDC report mitigation measures is only way to prevent and control the infection. Therefore, we also include isolation of infected people who do not involve in the further infection propagation and other population is directly cut-off from susceptible due to the other mitigation measures as suggested by ECDC. Here, the total population $N$ is sub-divided in 6 compartmental population: susceptible for infection ($S$), latent infected such that a population which is involved in the transmission of infection but not infected ($E$), infected (symptomatic) population ($I$), asymptomatic population ($A$), Isolated from infected (the population which does not have role in the further transmission of infection) ($J$), recovered/death population ($R$). Although $I+J$ is total population is active infected case. It is assumed here, that the population is homogeneous-mixed and people have equal probability of acquiring the infection. Proposed Model does not consider the migration from one country to other country and new births or deaths by natural process. It considers only human-to-human transmission.
The proposed mathematical model is represented for SARS-CoV-2 based on SEIAJR compartmental structure as shown in Figure 1. The model is formulated for European countries for SARS-CoV-2 infection scenario in the system non-linear ordinary differential equations (1-6).

\[
\frac{dS}{dt} = -\alpha \frac{(E + I + A)}{N} S - \sigma S 
\]

\[
\frac{dE}{dt} = \alpha \frac{(E + I + A)}{N} S - \beta_1 E 
\]

\[
\frac{dI}{dt} = \beta_1 h E + \beta_2 r A - \psi q I - \gamma (1 - q) I
\]

\[
\frac{dA}{dt} = \beta_1 (1 - h) E - \beta_2 r A - \gamma (1 - r) A
\]

\[
\frac{dJ}{dt} = \psi q I - \gamma J
\]

\[
\frac{dR}{dt} = \gamma (1 - q) I + \gamma (1 - r) A + \gamma J
\]

The \(\alpha\) is the transmission rate of infection, \(\beta_1\) is the rate of latent infection, \(\beta_2\) is the rate of appearance the symptoms in the asymptomatic population, \(\psi\) is the rate of isolation for infected population, \(\sigma\) is the mitigation rate for susceptible individuals. Further, \(\gamma_1, \gamma_2, \gamma_3\) (all are assumed to be same level say \(\gamma\)) are the recovery rates from asymptomatic, symptomatic and isolated infected population, respectively, because period of infection is similar in symptomatic and asymptomatic SARS-CoV-2 infected population [10], [16].

The symbol \(h\) represents proportion of exposed population which shows symptoms in individuals those are at exposed stage, \(r\) shows proportion of population to get symptomatic infection from asymptomatic stage, \(q\) represents proportion of isolated population in infected individuals.
2.2 Basic Reproduction Number

Basic reproduction number ($R_0$) provides an average measure of infected population by single infected individual when whole population has been treated as susceptible [15]. It is an important threshold parameter which indicates the progression characteristic of the infection in a given population. The infection will spread if the value of $R_0$ is greater than one otherwise infection it will not be able to spread in the given population. In this section, we drive the formula of $R_0$ for the proposed model. For this purpose, we observed that at infection free stage $E = I = A = R = 0$ which imply $S = N$. Then the above system of equation can be reduced into the following linearized subsystem of equations:

\[
\begin{align*}
\frac{dE}{dt} &= \alpha(E + I + A) - \beta_1 E \\
\frac{dI}{dt} &= \beta_1 h E + \beta_2 r A - \psi q I - \gamma (1 - q) I \\
\frac{dA}{dt} &= \beta_1 (1 - h) E - \beta_2 r A - \gamma (1 - r) A \\
\frac{dJ}{dt} &= \psi q I - \gamma J
\end{align*}
\]  

Above system of equations can be written in the matrix form as follow:

\[
\frac{dX}{dt} = (T + \Sigma)X
\]

where \( X = \begin{bmatrix} E \\ I \\ A \\ J \end{bmatrix} \), \( T = \begin{bmatrix} \alpha & \alpha & \alpha & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \), and \( \Sigma = \begin{bmatrix} -\beta_1 & 0 & 0 & 0 \\ \beta_1 h & -\psi q - \gamma (1 - q) & \beta_2 & 0 \\ \beta_1 (1 - h) & 0 & -\beta_2 r - \gamma (1 - r) & 0 \\ \psi q & 0 & 0 & -\gamma \end{bmatrix} \).

Then we can compute the next-generation matrix:

\[
G = -T\Sigma^{-1} = \begin{bmatrix} \frac{\alpha}{\beta_1} + \frac{\alpha(1-h)}{D_1} & \frac{\alpha(\gamma h + \beta_2 r - \gamma hr)}{D_2} & \frac{\alpha}{D_2} + \frac{\alpha \beta_2 r}{D_2} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}
\]

where \( D_1 = \gamma + \beta_2 r - \gamma r \) and \( D_2 = D_1(\gamma - \gamma q + \psi q) \). The basic reproduction number of this modified model is given by spectral radius of matrix \( G \), and computed as:

\[
R_0 = \frac{\alpha}{\beta_1} + \frac{\alpha(1-h)}{D_1} - \frac{\alpha(\gamma h + \beta_2 r - \gamma hr)}{D_2}
\]  

(11)
Table 1: Initial value of state variables during the simulation

| State variable | Description | Initial value |
|----------------|-------------|---------------|
| S              | Susceptible | 90% of total population |
| E              | Exposed (Latent) | \( I + A \times f \) |
| I              | Confirmed Infected | \( I \times f \) |
| A              | Asymptomatic Infected | \( A \times f \) |
| J              | Isolated Infected | 0 |
| R              | Recovered | 0 |

Table 2: Parameters with definitions and values with their range

| Symbol | Description | Value | References |
|--------|-------------|-------|------------|
| h      | Proportion of exposed population showing symptoms directly | 0.1 | 
| \( \beta_1 \) | Rate of change to get symptoms | \( 1/7 \) | \([1]\) |
| \( \beta_2 \) | Rate of change to get symptoms from asymptomatic | \( 1/14 \) | \([1], [6]\) |
| \( \alpha \) | Transmission rate | Varying as per the state | |
| \( r \) | Proportion of population to get symptomatic infection from asymptomatic | 17.5% | \([26]\) |
| \( \psi \) | Rate of isolation from infected | 0.9 | 
| \( q \) | Proportion of population for isolation | 0.9 | 
| \( \gamma_1 \), \( \gamma_2 \), \( \gamma_3 \) | Recovery rate in asymptomatic, symptomatic, isolated | \( 1/14 \) | \([29]\) |

2.3 Sensitivity analysis of \( R_0 \)

To use the model as predictive tool, a knowledge about change in model output is required when the values of parameters involved in the model changes. This crucial knowledge may be obtained via the sensitivity tool. If alteration in the value of parameters gives a small change in the model output then parameters are less sensitive for model output. But, when the model output changes in a great magnitude with respect to the small perturbation in input parameters then model is known as highly sensitive with respect to these parameters. Sensitivity has been defined in several ways by many researchers and scientists \([9,27,7]\). Normalized sensitivity index (elasticity index; \( \Gamma \)) of an output variable \( y \) with respect to the input parameter \( p \) may be defined as:

\[
\Gamma_p^y = \frac{\partial y}{\partial p} \times \frac{p}{y}
\]  

We discussed in section 2.2 basic reproduction number is an important quantity which provide the information about the progression of the infection in the given population. Therefore, we did the sensitivity analysis of \( R_0 \) with respect to different parameters involved in its expression and listed in Table 4.

3 Results and Discussion

The heft of a mathematical model is only significant when the developed solution correlates with realistic data. In this research, we simulate a proposed SEIAJR mathematical model for four European countries including UK. At time of simulation, initial values for the compartmental population is assumed as per country current scenario according to ECDC database as listed in Table 1 and parameters are obtained from literature. The aforesaid parameters are based on physiological characteristics of SARS-CoV-2 in human, the values of the parameters are listed in Table 2. In Addition, few parameters are estimated which varies as per the geographical reasons, human-to-human interaction behavior and mitigation strategies as enumerated in Table 3.
The proposed model is simulated in two phases with respect to time. In the first phase, the model is deployed and best fitted with outbreak real data (Source: on 05 April 2020, https://www.worldometers.info/coronavirus). Through this simulation, we estimated infection transmission rate ($\alpha$), mitigation rate of susceptible population ($\sigma$) and basic reproduction number ($R_0$), as mentioned in Table 3. In the second phase, simulation predicts the infection dynamics on different rates of infection mitigation by assuming estimated basic reproduction number (same as estimated in first phase). The whole simulation as shown in detail in Figure 2a-2d for all 4 countries.

The simulation result showed $R_0$ of SARS-COV-2 was estimated 2.815, 2.981, 3.326 and 2.943 for Germany, United Kingdom, Switzerland and Spain respectively. In addition to this, $R_0$ was also similar in recent research studies [1], [25]. A small variation in $R_0$ values might be due to different method and assumption of modelling, it is also similar to china outbreak where it is commonly accepted $R_0 = 2.9$ [11]. Aforesaid, simulated results also showed mitigation rates 0.15, 0.135, 0.218 and 0.186 for Germany, United Kingdom, Switzerland and Spain.

The mitigation rate was estimated almost similar to all countries, however, it is highest in Switzerland. High mitigation rate means that they were following quickly implementation of mitigation measures. It could be easily visible through simulation that the impact is decreasing rapidly in Switzerland due to their high mitigation measures implementation as shown in Figure 2c.

Second-phase analysis depicts the peak of the infection found in the mid and last week of April 2020 in all 4 European countries and outbreak would last by end of July 2020. Although, simulation suggest that there is no more additional mitigation measures are required. The peak would reach on 9th-10th week of outbreak and it is again similar to china outbreak [28].

Furthermore, we have also done sensitivity analysis of $R_0$ with respect to other considered parameters. The basic reproduction number is directly correlated with transmission rate. It is observed through this analysis that there are two more parameters which are also sensitive for $R_0$ namely $\beta_1$ and $\beta_2$. The absolute value of index for $\beta_1 = 0.49$ and for $\beta_2 = 0.39$. This value implies that $\beta_1$ (based latent period) is second most sensitive parameter for propagation of infection. The proposed model as well as the literature both states that the latent period plays crucial role in terms of infection propagation [2]. The plot $R_0$ versus parameters can be seen in Figure 3a-3c. Blue and Yellow solid line in Figure 3a depict that $R_0$ would decrease by less than 1 only at values of $\alpha$ and $\beta_1$. Other all the parameter are can not decrease $R_0$ by less than 1 (see Figure 3a and 3b). Thus, the combined three dimension plot of $R_0$ versus $\alpha$ and $\beta_1$ is shown in Figure 3c.

The proposed mathematical model might be applicable for other European countries too by tuning only two parameters (i.e. transmission rate and mitigation rate). Apparently, the analysis could highlight the dynamical behavior of infection and estimates reproduction number, peak, infectious cases, the
estimated mitigation rate is suggested about the future preparedness to stop the invasion of infection.

Conclusions

We proposed SEIAJR mathematical model is develope to estimate the basic reproduction number and infection transmission dynamics with incorporation of mitigation measures for SARS-CoV-2. The model is deployed and fitted in 4 European countries outbreak real data with fixing infection transmission and mitigation rate. The basic reproduction number is estimated and lies between 2.8 to 3.3 for considered all 4 European countries, as noted by other
research studies and also reported in 7th rapid risk assessment report released by ECDC. Apparantly, this could be said that aforesaid report is validating the proposed mathematical model. Futhermore, the infection would last by end of July 2020 on the basis of estimated $R_0$ even though if no more additional mitigation measures implemented. The model predicts that the peak of infection reaches in the mid and last week of April 2020 which meets the other research studies hypothsis. The simulation of model suggests that the latent period is another highly sensitive parameter for infection transmission.
Table 3 Calculated value of reproduction number $R_0$ at best fitted parameters for different geographical regions.

| Symbol | Description                      | Germany | U. K. | Switzerland | Spain |
|--------|----------------------------------|---------|-------|-------------|-------|
| $\alpha$ | infection transmission rate | 0.22    | 0.233 | 0.26        | 0.23  |
| $\sigma$ | mitigation rate for susceptibles | 0.15    | 0.135 | 0.218       | 0.186 |
| $R_0$  | basic reproduction number       | 2.815   | 2.981 | 3.326       | 2.943 |

Table 4 Sensitivity elasticity expression and its value for basic reproduction number $R_0$ with respect to involved parameters ($h = 0.1, \beta_1 = 1/10, \beta_2 = 1/10, r = 1-0.175(0.825), \psi = 0.9, q = 0.9, \gamma = 1/14, \alpha = 0.22$).

| Parameter | Expression for elasticity index | Index value |
|-----------|---------------------------------|-------------|
| $h$       | $-\frac{\beta_1}{\gamma + \beta_2 - \gamma + \psi + q} (\gamma + \beta_2 - \gamma + \psi + q)$ | -0.05043314754 |
| $\beta_1$ | $\frac{1}{\gamma + \beta_2 - \gamma + \psi + q} (\gamma + \beta_2 - \gamma + \psi + q)$ | -0.4865578761 |
| $\beta_2$ | $\frac{1}{\gamma + \beta_2 - \gamma + \psi + q} (\gamma + \beta_2 - \gamma + \psi + q)$ | -0.3941746837 |
| $r$       | $\frac{1}{\psi q + (c + h + s + h - r) r}$ | -0.0793798343 |
| $\psi$    | $\frac{1}{\psi} q + (c + h + s + h - r) r$ | -0.0520337063 |
| $q$       | $\frac{1}{\psi} q + (c + h + s + h - r) r$ | -0.0479040468 |
| $\gamma$  | $\frac{1}{\gamma + \beta_2 - \gamma + \psi + q} (\gamma + \beta_2 - \gamma + \psi + q)$ | -0.4865578761 |
| $\alpha$  | $\frac{1}{\gamma + \beta_2 - \gamma + \psi + q} (\gamma + \beta_2 - \gamma + \psi + q)$ | 1 |

It means the untraced infected population could extend the outbreak as untraced infected population seems to spreading infection, which is also stated by the WHO situation report-73 on COVID-19. Thus, the model might be key role to understand European outbreak of SARS-CoV-2 and also for other geographical reasons with varying certain parameters. In addition, the deployment of proposed mathematical model would also helpful to evaluate the basic reproduction number which would suggest the weight of community mitigation measures implementation in near future.

Declaration

Availability of data and material

Not Applicable

Competing interests

The authors declare that they have no conflict of interest.
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Authors’ contributions

Dr. Shweta Sankhwar completed her M. Sc. And Ph.D. from Department of Information Technology, Babasaheb Bhimrao Ambedkar University (BBAU), Lucknow, India. Dr. Sankhwar has an outstanding academic background with a very sound academic and research experience. She has a research expertise in the areas of cyber security and internet security. She has published more than 15 research papers in international and national journals. She contributed as framing and writing the manuscript.

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References

1. Coronavirus disease 2019 (covid-19) pandemic: increased transmission in the eu/eea and the uk – seventh update, 25 march 2020. ECDC: Stockholm (2020)
2. Coronavirus disease 2019 (covid-19) situation report – 73, 2 april 2020. WHO (2020)
3. European centre for disease prevention and control. novel coronavirus disease 2019 (covid-19): increased transmission in the eu/eea and the uk – sixth update - 12 march 2020. ECDC: Stockholm (2020)

4. European centre for disease prevention and control. outbreak of novel coronavirus disease 2019 (covid-19): increased transmission globally – fifth update, 2 march 2020. ECDC: Stockholm (2020)

5. Andraud, M., Hens, N., Marais, C., Beutels, P.: Dynamic epidemiological models for dengue transmission: a systematic review of structural approaches. PloS one 7(11) (2012)

6. Backer, J.A., Klinkenberg, D., Wallinga, J.: Incubation period of 2019 novel coronavirus (2019-ncov) infections among travellers from wuhan, china, 20–28 january 2020. Eurosurveillance 25(5) (2020)

7. Blower, S.M., Dowlatabadi, H.: Sensitivity and uncertainty analysis of complex models of disease transmission: an hiv model, as an example. International Statistical Review/Revue Internationale de Statistique pp. 229–243 (1994)

8. Brauer, F.: Mathematical epidemiology: Past, present, and future. Infectious Disease Modelling 2(2), 113–127 (2017)

9. Cariboni, J., Gatelli, D., Liska, R., Saltelli, A.: The role of sensitivity analysis in ecological modelling. Ecological modelling 203(1-2), 167–182 (2007)

10. Cerdedo, D., Tirani, M., Rovida, F., Demicheli, V., Ajelli, M., Poletti, P., Merler, S.: The early phase of the covid-19 outbreak in lombardy, italy (2020)

11. Chen, T.M., Rui, J., Wang, Q.P., Zhao, Z.Y., Cui, J.A., Yin, L.: A mathematical model for simulating the phase-based transmissibility of a novel coronavirus. Infection Diseases of Poverty 9(1), 1–8 (2020)

12. Cherniha, R., Davydovych, V.: A mathematical model for the coronavirus covid-19 outbreak (2020)

13. da Cruz Ferreira, D.A., Degener, C.M., de Almeida Marques-Toledo, C., Bendati, M.M., Fetzer, L.O., Teixeira, C.P., Eiras, Á.E.: Meteorological variables and mosquito monitoring are good predictors for infestation trends of aedes aegypti, the vector of dengue, chikungunya and zika. Parasites & vectors 10(1), 78 (2017)

14. Daozhou, G., Yijun, L., Daihai, H., Travis, C., Yangk, K., Gerardo, C., Shigui, R.: Prevention and control of zika as a mosquito-borne and sexually transmitted disease: A mathematical modelling analysis. Scientific Reports 6, 28070 (2016)

15. Diekmann, O., Heesterbeek, J., Roberts, M.G.: The construction of next-generation matrices for compartmental epidemic models. Journal of the Royal Society Interface 7(47), 873–885 (2010)

16. Han, Y., Yang, H.: The transmission and diagnosis of 2019 novel coronavirus infection disease (covid-19): A chinese perspective. Journal of Medical Virology (2020)

17. Hays, J.N.: Epidemics and pandemics: their impacts on human history. Abc-clio (2005)

18. Hethcote, H.W.: Three basic epidemiological models. In: Applied mathematical ecology, pp. 119–144. Springer (1989)

19. Hethcote, H.W., Van Ark, J.W.: Modeling HIV transmission and AIDS in the United States, vol. 95. Springer Science & Business Media (2013)

20. Kim, S., Lee, J., Jung, E.: Mathematical model of transmission dynamics and optimal control strategies for 2009 a/h1n1 influenza in the republic of korea. Journal of theoretical biology 412, 74–85 (2017)

21. Kumar, N., Abdullah, M., Faizan, M.I., Ahmed, A., Albenaïd, H.A., Dohare, R., Parveen, S.: Progression dynamics of zika fever outbreak in el salvador during 2015–2016: a mathematical modeling approach. Future Virology 12(5), 271–281 (2017)

22. Kumar, N., Faizan, M.I., Parveen, S., Dohare, R.: Temperature and rainfall dependent mathematical modelling for progression of zika virus infection. International Journal of Mathematical Modelling and Numerical Optimisation 9(4), 339–365 (2019)

23. Lai, C.C., Shih, T.F., Ko, W.C., Tang, H.J., Hsieh, P.R.: Severe acute respiratory syndrome coronavirus 2 (sars-cov-2) and corona virus disease-2019 (covid-19): the epidemic and the challenges. International journal of antimicrobial agents p. 105924 (2020)

24. Lipsitch, M., Cohen, T., Robins, J., Ma, S., et al.: Transmission dynamics and control of severe acute respiratory syndrome. scienceexpress (2003)

25. Liu, Y., Gayle, A.A., Wilder-Smith, A., Rocklov, J.: The reproductive number of covid-19 is higher compared to sars coronavirus. Journal of travel medicine (2020)
26. Mizumoto, K., Kagaya, K., Zarebski, A., Chowell, G.: Estimating the asymptomatic proportion of coronavirus disease 2019 (covid-19) cases on board the diamond princess cruise ship, yokohama, japan, 2020. Eurosurveillance 25(10) (2020)

27. Sanchez, M.A., Blower, S.M.: Uncertainty and sensitivity analysis of the basic reproductive rate: tuberculosis as an example. American journal of epidemiology 145(12), 1127–1137 (1997)

28. Wang, M., Qi, J.: A deterministic epidemic model for the emergence of covid-19 in china. medRxiv (2020)

29. Wang, W., Tang, J., Wei, F.: Updated understanding of the outbreak of 2019 novel coronavirus (2019-ncov) in wuhan, china. Journal of medical virology 92(4), 441–447 (2020)