

**MODELLING THE EFFECT OF SOCIAL DISTANCING
ON THE SPREAD OF COVID-19**

Amira Rachah

SINTEF Industry, S P Andersens vei 3
Trondheim - 7031, NORWAY

Abstract: The highly contagious infectious disease COVID-19 virus has spread around the world infecting millions of people with high number of deaths, causing profound health, social and economic distress around the world. Mathematical models can provide new insights into the transmission dynamics of the virus and suggest criteria for the design of efficient control strategies. In this work, we use epidemiological modelling to assess the effect of physical distancing measures on the spread of the virus. The mathematical model describing the epidemic progression includes COVID-19 treatment and vaccination. The numerical resolution of the model shows its suitability for describing the Tunisian COVID-19 outbreak. We show the impact of application of social distancing measures with and without vaccination on the epidemic peak. We found that vaccination against COVID-19 is crucial in controlling the virus, but it is important to back this up with social control measures.

AMS Subject Classification: 49K15, 92D25, 92D30

Key Words: modelling; epidemiology; transmission dynamics; Covid-19

1. Introduction

Mathematical modelling and simulation of infectious disease dynamics have a crucial role in quantifying infectious disease control measures, [1, 10]. Modelling is a powerful tool for understanding and predicting infectious diseases

progression in order to prevent a rapid spread of the disease and provide useful control measures [2, 3]. COVID-19 is a viral infectious disease caused by the severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), [29]. On March 2020, the COVID-19 outbreak was announced as a pandemic by the World Health Organization. The basic symptoms for COVID-19 are fever, tiredness, cough, headache, sore throat and loss of appetite and taste. More severe symptoms include difficulty breathing or shortness of breath, severe cough, and chest pain. The transmission between humans can take place with direct and indirect contact with an infected person by shaking hands or through the air when coughing or sneezing, [12]. The virus remains active for several hours (or even days) on a different surface. The virus transmits by touching a surface contaminated with the virus and then touching the body. The main difference in characteristics between COVID-19 and its close relative SARS, is the absence of symptoms on the patients during the incubation period of COVID-19, [28].

Since first identified, the COVID-19 virus has caused a large number of deaths worldwide and has also taken a serious toll on the global economy. The healthcare sector is fighting a large number of hospitalizations, equipment shortages and lack of effective medications. On top of this, the novelty of the virus means that no accurate data regarding contagiousness, incubation period, rates of serious disease or fatality rate, exist. In this uncertain situation, national and local authorities cope with several unknowns when they make important decisions both regarding appropriate delay strategies (social distancing, isolation, travel restriction, quarantine, school closures etc.), resource allocation and prioritization within the healthcare sector.

Since the transmission of the virus occurs through indirect and direct contact, the social physical distancing and reducing contact in population was used to control the epidemic. Social physical distancing and behavioral change of individuals have been applied in order to reduce the risk of the virus, [25]. Vaccination against COVID-19 represents a fundamental step towards ending the pandemic, protecting health systems and helping to restore global economies, [5]. Recently, different vaccine candidates created via differing approaches, [15, 23, 26]. Mathematical modelling has been utilized for a wide range of infectious diseases, [4]. It has a crucial role in the process of vaccine development by assessing the effect of vaccine candidates on the population-level, [14, 24].

The virus is characterized by a long incubation period and an epidemic trend which depends on local medical resources and quarantine measures, make it hard to describe, [6, 7, 13, 22]. Recently, different epidemiological models, such as SIR and SEIR models, have been used to describe the transmission dynamics of COVID-19 despite several artificial factors that exist in the features of the

virus, [11, 18, 21].

Mathematical description of the virus transmission dynamics with an application of social control measures in presence of vaccination play a crucial role for efficient allocation of resources and public health planning. In this work, we describe COVID-19 dynamics with application of social distancing measures and vaccination using compartmental model. In Section 2 of the paper, we present the mathematical formulation of the model. In Section 3, we present a qualitative analysis of the model. The numerical simulations and the parameters of the model used in the Tunisian epidemic are illustrated Section 4. A study of the impact of social distancing measures is presented Section 5. In Section 6, we study the efficacy of vaccination with and without social control measures. We end with Section 7 of conclusions and discussion.

2. Model formulation

Based on a 2018 model [1] and taking into account the epidemiological features of COVID-19, we use a compartmental model that includes COVID-19 treatment and vaccination. The total population is divided up into eight epidemiological categories or components: (S) which is equal to susceptible people who could potentially catch the disease, (V) which is equal to vaccinated people, (E_1) which represents latent undetectable, (E_2) which is equal to latent detectable people, infective people (I) which is equal to people who have the disease and can infect others, (T) which is equal to people who require COVID-19 treatment, (D) which represents people who are dead but have not been buried so they can transmit the virus during funerals; and (R) for people who have already caught to the disease and have now recovered from the disease. Then $S + V + E_1 + E_2 + I + T + D + R = N$, where N is equal to the total population. In the model, susceptible people who come into contact with

infectious people, become infected and latent at the rate $\frac{(\beta I + \beta \mu T + \beta' D)}{N}$,

where β is equal to the mean daily transmission rate, and μ represents the relative transmissibility of individuals who need COVID-19 treatment compared to infectious symptomatic patients who are not getting treatment. β' is equal to the funerals transmission rate. ρ is the rate of vaccination of susceptible people. λ represents the effectiveness of immunization. σ_1 is the rate at which people from latent undetectable category E_1 enter the latent detectable category E_2 . σ_2 is the rate at which people from E_2 move to the infectious symptomatic group. People from latent detectable class are detected and treated at the rate

θ . $\tau = \frac{\theta}{\theta + \sigma_2}$ is equal to the fraction of treated patients among latent detectable individuals exiting the class. α is the rate at which infectious people are treated, where γ is the rate at which they are recovered. People who require treatment are recovered at a rate γ_r . Figure 1 shows the flow between the different categories.

The mathematical description of transmission dynamics of the virus is based on a system of nonlinear ordinary differential equations:

$$\begin{aligned}
 \frac{dS}{dt} &= -\frac{(\beta I + \beta\mu T + \beta' D) S}{N} - \rho S, \\
 \frac{dV}{dt} &= \rho S - \frac{(\beta I + \beta\mu T + \beta' D) \lambda V}{N}, \\
 \frac{dE_1}{dt} &= \frac{(\beta I + \beta\mu T + \beta' D) (S + \lambda V)}{N} - \sigma_1 E_1, \\
 \frac{dE_2}{dt} &= \sigma_1 E_1 - (\sigma_2 + \theta) E_2, \\
 \frac{dI}{dt} &= \sigma_2 E_2 - (\alpha + \gamma) I, \\
 \frac{dT}{dt} &= \theta E_2 + \alpha I - \gamma_r T, \\
 \frac{dD}{dt} &= \delta \gamma I + \delta \gamma_r T - \gamma_d D, \\
 \frac{dR}{dt} &= (1 - \delta) \gamma I + (1 - \delta) \gamma_r T.
 \end{aligned} \tag{1}$$

The description of the model parameters is given in Table 1.

3. Qualitative analysis of the model

In this section, we present a qualitative analysis of the epidemiological model (1).

Lemma 1. *If we assume that initial states $S(0)$, $V(0)$, $E_1(0)$, $E_2(0)$, $I(0)$, $T(0)$, $D(0)$, $R(0)$ of the model (1) are nonnegative. Then, the solution of (1) will remain nonnegative for all $t > 0$.*

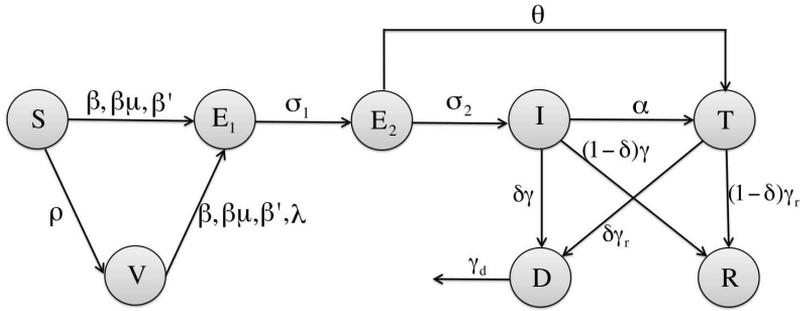


Figure 1: Flow diagram of the transmission dynamics of COVID-19

Table 1: Model parameters and their description.

Parameter	Description
β	Coefficient of transmission from group of infected people
μ	Relative transmissibility of treated individuals
β'	Rate of transmission during funeral
ρ	Vaccination rate
λ	The efficacy of vaccination
σ_1	Rate at which Latent undetectable become detectable
σ_2	Rate at which latent detectable become infected
θ	Rate at which latent detectable individuals progress to treated class
α	Rate at which infectious individuals progress to treated class
δ	The case fatality rate
γ	Rate at which infected individuals are removed by recovery or disease induced death
$\frac{1}{\gamma_d}$	Mean time from death to traditional burial
$\frac{1}{\gamma_r}$	Mean time that treated individuals are removed by recovery or disease induced death

Proof. The proof for the nonnegativity is explained in [10], (Theorem A4).

□

The basic reproduction number R_0 which indicates how contagious an infectious disease is, has the ability to quantify virus invasion or extinction in the population [19]. In the absence of effective vaccine ($\rho = \lambda = 0$), R_0 is equal to the spectral radius of FV^{-1} matrix based on next generation matrix method, [20]:

$$\begin{aligned} R_0 &= \rho(FV^{-1}) \\ &= (1 - \tau) \cdot \beta \cdot \frac{1}{\alpha + \gamma} + \beta\mu \left[(1 - \tau) \cdot \frac{\alpha}{\alpha + \gamma} \cdot \frac{1}{\gamma_r} + \tau \cdot \frac{1}{\gamma_r} \right] \\ &\quad + \delta \cdot \beta' \cdot \frac{1}{\gamma_d} \\ &= R_{0I} + R_{0T} + R_{0D}, \end{aligned} \tag{2}$$

where ρ is the spectral radius and

$$F = \begin{bmatrix} 0 & 0 & \beta & \beta\mu & \beta' \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \quad V = \begin{bmatrix} \sigma_1 & 0 & 0 & 0 & 0 \\ -\sigma_1 & \sigma_2 + \theta & 0 & 0 & 0 \\ 0 & -\sigma_2 & \alpha + \gamma & 0 & 0 \\ 0 & -\theta & -\alpha & \gamma_r & 0 \\ 0 & 0 & -\delta\gamma & -\delta\gamma_r & \gamma_d \end{bmatrix} \tag{3}$$

By including vaccination ($\rho > 0$, $\lambda > 0$), the reproduction number is equal to $R_{0V} = \lambda R_0$.

4. Numerical resolution

In this section, we present the numerical resolution of the model compared with the real data published by World Statistics [16, 17]. Our numerical simulations starts on 4 December 2020 after a first wave of the virus published by the tunisian authorities. Tunisia experienced its first case on March 2nd, 2020. The strict lockdown imposed early on by the Tunisian authorities had an important role in limitation on the propagation of the virus in parallel of its spread in Wuhan. After a first wave of the epidemic which spread until the end of June 2020, Tunisia experienced a respite during the month of July, followed by another wave later.

Using data of Tunisia from December 4th 2020 to February 21st 2021, the values of the model parameters are given in Table 2. We study first the transmission dynamics of the virus without vaccination because no vaccine was available before March, 2021. Then we focus on the impact of vaccination

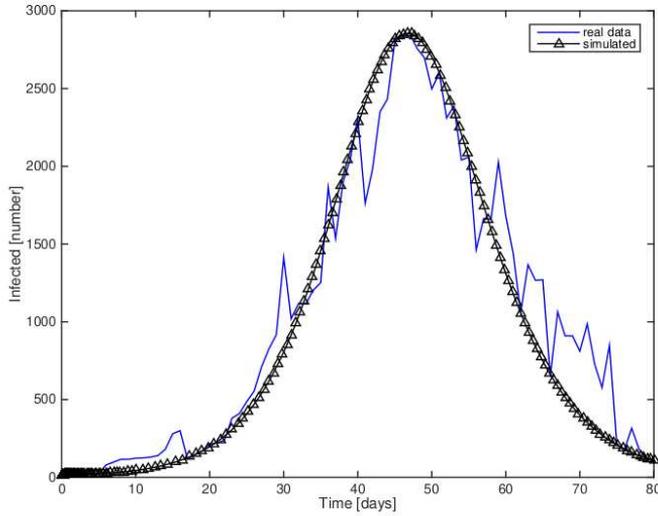


Figure 2: Plot shows the number of infected $I(t)$ obtained from numerical resolution of the model (1) and the real data

in Tunisia where Tunisian authorities started COVID-19 vaccination campaign since then. By using the Tunisian real data for $\rho = \lambda = 0$, we solve numerically the model (1) by using the Matlab solver ode45 and a fixed initial conditions $S_0 = N - E_2(0) - I_0$, $V_0 = 0$, $E_1(0) = 0$, $E_2(0) = 100$, $I_0 = 10$, $T_0 = 0$, $D_0 = 0$, $R_0 = 0$, where N is the total population of Tunisia which is about 11 million.

We plotted the simulated infected individuals in Figure 2 and the simulated dead in Figure 3 compared with the real data. A subset of the parameters of the model are assumed based on biological study of the virus [8, 9] and the other subset is obtained via estimation using real data (Table 2). Then, R_0 is equal to 3.1189. The numbers R_{0I} , R_{0T} and R_{0D} that mirror the contribution to new infection from the group (I), group of people who need COVID-19 treatment (T), and the dead class (D), are equal to 0.9131, 2.2017, and 0.0041 respectively. The numerical solution of the model (1) shows a good fit to the real data of infected and deaths groups as presented in Figures 2 and 3.

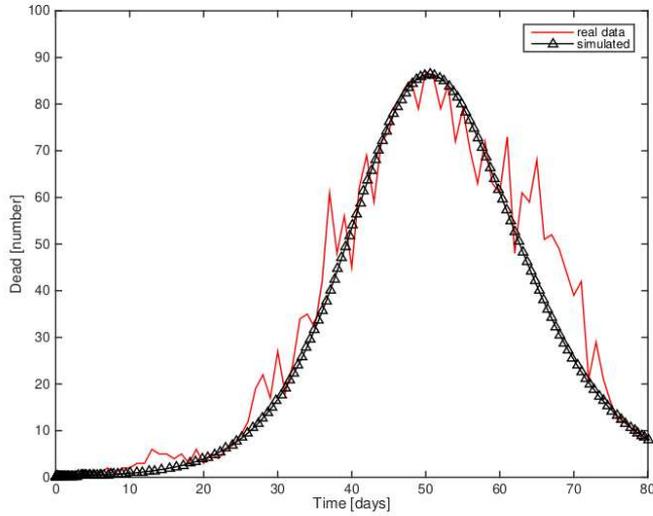


Figure 3: Plot shows the number of dead $D(t)$ obtained from numerical resolution of the model (1) and the real data.

Table 2: Values of model parameters for the case of Tunisia.

Parameter	Value
β	1.21
μ	0.4202
β'	0.1669
σ_1	0.25
σ_2	0.3333
θ	0.8291
α	0.18
δ	0.0124
γ	0.2
γ_d	0.5
γ_r	0.1961

5. Impact of social distancing measures

Since the spread of COVID19 occurs via direct and indirect interaction, physical distancing and keeping distance to others were applied in Tunisia and most countries to reduce the spread of the epidemic. By using the model (1), we add the parameter u which describes the social distancing phenomenon to obtain the following system of differential equations:

$$\begin{aligned}
 \frac{dS}{dt} &= -(1 - u) \frac{(\beta I + \beta \mu T + \beta' D) S}{N} - \rho S, \\
 \frac{dV}{dt} &= \rho S - \frac{(\beta I + \beta \mu T + \beta' D) \lambda V}{N}, \\
 \frac{dE_1}{dt} &= (1 - u) \frac{(\beta I + \beta \mu T + \beta' D) (S + \lambda V)}{N} - \sigma_1 E_1, \\
 \frac{dE_2}{dt} &= \sigma_1 E_1 - (\sigma_2 + \theta) E_2, \\
 \frac{dI}{dt} &= \sigma_2 E_2 - (\alpha + \gamma) I, \\
 \frac{dT}{dt} &= \theta E_2 + \alpha I - \gamma_r T, \\
 \frac{dD}{dt} &= \delta \gamma I + \delta \gamma_r T - \gamma_d D, \\
 \frac{dR}{dt} &= (1 - \delta) \gamma I + (1 - \delta) \gamma_r T.
 \end{aligned}
 \tag{4}$$

The value of the social distancing u is between 0 and 1. When $u = 1$, the term $(1 - u) \frac{(\beta I + \beta \mu T + \beta' D) S}{N} = 0$, that means there is no transmission of the infection because there is no contact.

By solving numerically the model (4) for different values of u , we can see how social distancing affects the dynamics of the virus. In the numerical resolution of (4), we used $\rho = \lambda = 0$ since vaccination campaign started after February, 2021 in Tunisia.

We plotted the number of infected individuals for different values of social distancing. The numerical simulation shows that social distancing strategy flattens the curve and delays the epidemic peak (see Figure 4). The peak of infected individuals I decreases from 2494 at day 51 for $u = 0.1$, to 2093 at day 58 for $u = 0.2$ and to 1694 at day 67 for $u = 0.4$, whereas the peak is equal to

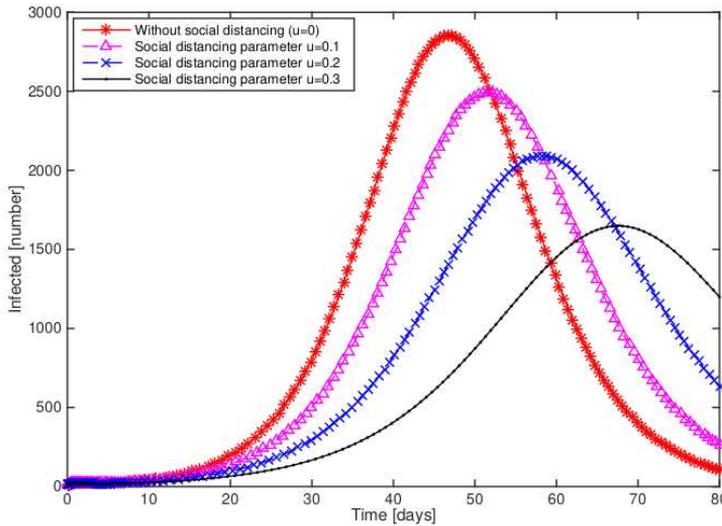


Figure 4: Plot shows the number of Infected $I(t)$ obtained from numerical resolution of (4) for different values of social distancing parameter.

2855 cases at day 46 without application of social distancing measures.

6. Impact of vaccination

Modelling the effect of vaccination in addition to understanding the transmission dynamics of the virus play a crucial role for resource allocation strategy for public health planning. Currently, the important challenge of describing mathematically vaccination against COVID-19 is the large number of unknown factors. Therefore different types of vaccine are currently under test to check their efficacy in eradicating the virus. In the aim of studying the effect of vaccination on COVID-19 spread, we test in this section different values of vaccination rate $\rho > 0$. The system of equations (1) of the model are solved numerically using ode45 solver in Matlab.

Because of unavailable vaccination, the epidemic peak is 2855 infected cases at day 46. Figure 5 shows an epidemic peak with 1753 infected cases at day 51 for a vaccine rate equal to 0.01. The peak has been reduced to 998 cases

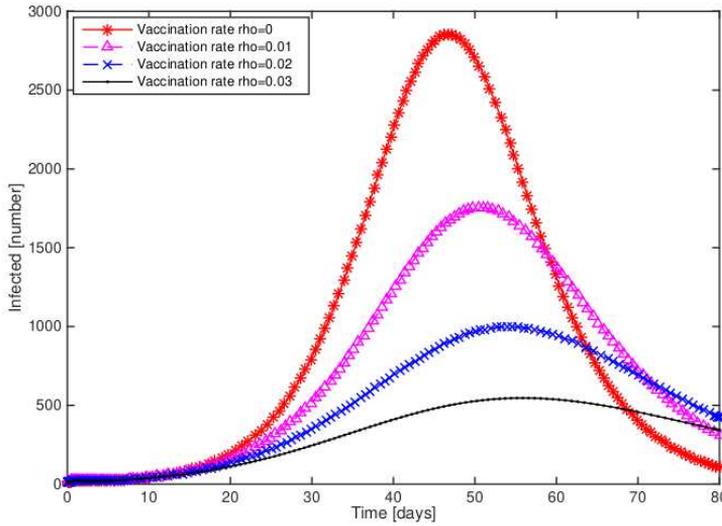


Figure 5: Number of infected individuals per day obtained by dumerical resolution of the system (1) for different values of vaccination rate ρ .

at day 54 and 546 cases at day 56 by increasing vaccine rate from 0.01 to 0.02 and 0.03 respectively. The results show the ability of vaccine in reducing the transmission of the virus. The basic reproductive number decreased from 3.1189 to 0.9357. Increasing the rate of vaccination flattens more the epidemic curve.

Let us now study the effect of applying social distancing control measures in addition to vaccination. Figure 6 shows the plot of infected individuals for different rates of application of social distancing measures in case of vaccination ($\rho = 0.03$). Applying physical distancing strategy in addition to vaccination has the ability to flatten the epidemic peak (Figure 6). The number of infected cases can be decreased from 546 without social distancing practices to 140 cases in case of application of social distancing using $u = 0.3$.

7. Conclusions and discussion

Modelling the effect of human behaviour on the propagation of coronaviruses is important for diseases control and prevention. In this work, we described

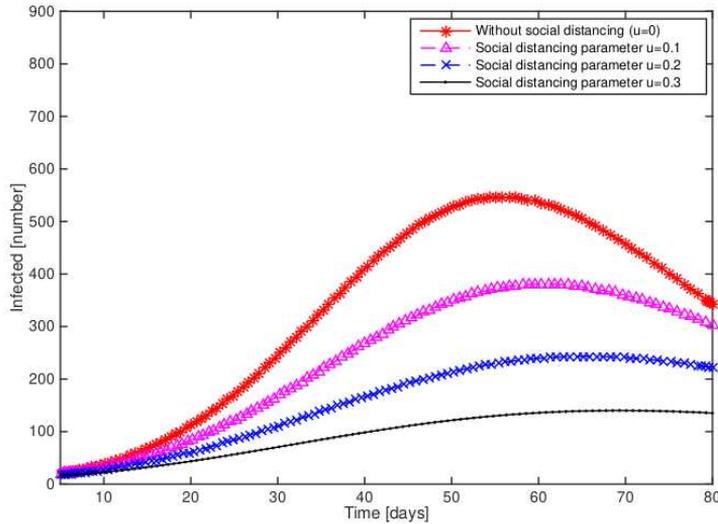


Figure 6: Number of infected individuals per day obtained by numerical resolution of the system (4) for different values of social distancing parameter in case of vaccination rate $\rho = 0.03$.

the transmission dynamics of COVID-19 using compartmental model based on nonlinear differential equations. The model takes into account COVID-19 treatment in addition to availability of vaccination. The model fits the real number of infected individuals and deaths during the 80 days outbreak (from December 4th, 2020 to February 21st, 2021) in Tunisia (Figures 2, 3), and shows a good description of the dynamics of the virus.

Since COVID19 dynamics depends on the contact network, we used the model to include social distancing phenomena in order to study its ability in reducing the severity of the transmission of the virus. We found that social distancing is one of the best strategies that is able to flatten the curve and to delay the peak of infected class (Figure 4). We showed that the transmission of the virus can be reduced by minimizing contact between potentially infected individuals and healthy individuals, or between population groups with high rates of transmission and population groups with low levels of transmission. Vaccination has an impact in reducing the susceptibility of individuals to infection as well as the chances of infected individuals passing the infection to

others. In this work, we studied vaccination strategy by testing different rates of vaccination in the model in order to predict how vaccination could control the epidemic. The results show that vaccination against COVID-19 is important in reducing the transmission of the virus, but it is important to back this up with social control practices.

References

- [1] A. Rachah, A mathematical model with isolation for the dynamics of Ebola virus, *Journal of Physics: Conference Series*, **1132** (2018), 12-58.
- [2] A. Rachah, D. FM. Torres, Dynamics and optimal control of Ebola transmission, *Mathematics in Computer Science*, **10** (2016), 331-342.
- [3] A. Rachah, D. FM. Torres, Predicting and controlling the Ebola infection, *Mathematical Methods in the Applied Sciences*, **40** (2017), 6155-6164.
- [4] A. Rachah, D. FM. Torres, Analysis, simulation and optimal control of a SEIR model for Ebola virus with demographic effects, *Communications Fac. of Sci. Univ. of Ankara Ser. A1: Math. and Stat.*, **67** (2018), 179-197.
- [5] AR. McLean, SM. Blower, Modelling HIV vaccination, *Trends in Microbiology*, **3** (1995), 458-463.
- [6] D. Fisman, E. Khoo, A. Tuite, Early epidemic dynamics of the West African 2014 Ebola outbreak: estimates derived with a simple two-parameter model, *PLoS Currents*, **6** (2014).
- [7] F. Brauer, C. Castillo-Chavez, Z. Feng, *Mathematical Models in Epidemiology*, Springer (2019).
- [8] FP. Polack, SJ. Thomas, N. Kitchin, J. Absalon, Safety and efficacy of the BNT162b2 mRNA Covid-19 vaccine, *New England J. of Medicine*, **383** (2020), 2603-2615.
- [9] G. Evensen, J. Amezcua, M. Bocquet, A. Carrassi, A. Farchi, A. Fowler, PL. Houtekamer, CK. Jones, RJ. de Moraes, M. Pulido, C. Sampson, FC. Vossepoel, An international assessment of the COVID-19 pandemic using ensemble data assimilation, *medRxiv*, 2020.
- [10] HR. Thieme, *Mathematics in Population Biology*, Princeton University Press (2018).

- [11] I. Cooper, A. Mondal, CG. Antonopoulos, A SIR model assumption for the spread of COVID-19 in different communities, *Chaos, Solitons and Fractals*, **139** (2020), Art. 110057.
- [12] JFW. Chan, S. Yuan, KH. Kok, KKW. To, H. Chu, J. Yang, A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster, *The Lancet*, **395** (2020), 514-523.
- [13] KJ. Stehl', N. Voirin, A. Barrat, C. Cattuto, V. Colizza, L. Isella, C. Régis, JF. Pinton, N. Khanafer, W. Van den Broeck, Simulation of an SEIR infectious disease model on the dynamic contact network of conference attendees, *Environmental Sci. & Technology Letters*, **9** (2011), 1-15.
- [14] KM. Andersson, AD. Paltiel, DK. Owens, The potential impact of an HIV vaccine with rapidly waning protection on the epidemic in Southern Africa: examining the RV144 trial results, *Vaccine*, **29** (2011), 6107-6112.
- [15] K. Thomas, New Pfizer results: Coronavirus vaccine is safe and 95% effective, *The New York Times*, 2020.
- [16] M. Dhafer, Covid19data. Website, *medRxiv*, 2020.
- [17] M. Dhafer, World Statistics,
URL: <https://covid19data.website>, 2020.
- [18] M. Ivanova, L. Dospatliev, Data analytics and SIR modeling of Covid-19 in Bulgaria, *International Journal of Applied Mathematics*, **33**, No 6, 2020, 1099-1114; DOI: 10.12732/ijam.v33i6.10.
- [19] P. Van den Driessche, Reproduction numbers of infectious disease models, *Infectious Disease Modelling*, **2** (2017), 288-303.
- [20] P. Van den Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, *Mathematical Biosciences*, **180** (2002), 29-48.
- [21] R. Ghostine, M. Gharamti, S. Hassrouny, I. Hoteit, An extended seir model with vaccination for forecasting the covid-19 pandemic in saudi arabia using an ensemble Kalman filter, *Mathematics*, **9** (2021), Art. 636.
- [22] S. Zhao, H. Chen, Modeling the epidemic dynamics and control of COVID-19 outbreak in China, *Quantitative Biology*, **2020**, 1-9.

- [23] SA. Madhi, V. Baillie, CL. Cutland, M. Voysey, AL. Koen, L. Fairlie, SD. Padayachee, K. Dheda, SL. Barnabas, QE. Bhorat, Efficacy of the ChAdOx1 nCoV-19 Covid-19 vaccine against the B. 1.351 variant, *New England J. of Medicine*, 2011.
- [24] SM. Blower, AR. McLean, Prophylactic vaccines, risk behavior change, and the probability of eradicating HIV in San Francisco, *Science*, **265** (1994), 1451-1454.
- [25] TC. Reluga, Game theory of social distancing in response to an epidemic, *PLoS Computational Biology*, **6** (2010).
- [26] WC. Koff, SF. Berkley, A universal coronavirus vaccine, *Science* (2021).
- [27] WHO, Novel coronavirus (2019 nCoV): situation report, *World Health Organization*, 2020.
- [28] X. Ma, S. Li, S. Yu, Y. Ouyang, L. Zeng, X. Li, H. Li, Emergency management of the prevention and control of novel coronavirus pneumonia in specialized branches of hospitals, *Academic Emergency Medicine*, **27** (2020), 312-316.
- [29] ZJ. Cheng, J. Shan, 2019 Novel coronavirus: where we are and what we know, *Infection*, **48** (2020), 155-163.

