MATHEMATICAL MODEL FOR PREDICTIONS
OF COVID-19 DYNAMICS

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Abstract: COVID19 outbreak presents the biggest global health creases in last century. Its pandemic spread and influence in everyday social life, economics and health is in central interest of concern for all governments in the world. This pandemic is the worst global disasters since the World Wars and pandemic from 1918, which completely change normal life of people. The combat against Covid-19 is playing a central role in all branches in each country in order to minimize the damage caused by this pandemic. Mathematical modelling of spread of infection and predictions that derived from the models can be used as efficient tool in this combat and can give precise direction to authorities to implement new or balance the already implemented restrictions and measures in order to decrease harmful consequences from epidemic. In this paper we are implementing new modified SEIRS-D model on Republic of North Macedonia epidemic situation, using AnyLogic software. Using this model, we give prediction of spread of disease with or without restriction measures.

1. Introduction

COVID-19 name derived from Corona (CO), Virus (VI), Disease (D) and year

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2019 (19), because COVID-19 first appeared in 2019 in Wuhan, Hubei Province of China. COVID-19 proved to be very contagious disease and was declared as a pandemic on March 12th, 2020 by WHO (World Health Organization), when confirmed cases were reported from countries and regions from all over the world. Pandemic presents very infectious disease which is widely spread almost in all countries in the world (see [1]). World pandemic is popularly called the killer of normal life. It leaves a lasting mark on people's lives. Covid 19 is on scale that people have not seen before. Namely the biggest world crisis in the world in the last tens of years. The number of infected is growing daily and that poses a threat to the further life and survival of certain institutions, mainly development and the economy (see [2],[3], [4]). Like every novel virus, COVID 19 and its infections among people is a of big public health concern, especially in the beginning when there is a little or no knowledge about the characteristics of the virus, its spreading between people, its consequences and treatments (see [5], [6]). Fast progression of disease and the overwhelming number of COVID-19 infection, worldwide, created an emergency situation among the governments and WHO was determined to recommend governments to take drastic measures for slowing down the propagation of the disease and flattering the epidemiology curve down to the lowest treatment capacity of the health system in each country, by pooling the resources and handling the epidemic at all levels. Because of the pandemic, the economy system is dealing with a lot of consequences, the governments had issued regulation with drastic measures for education, business, sports, culture, and people (see [7]). There were created new and special rules such as social distancing for communities and people, avoiding meetings in groups, wearing masks and gloves in public places, and isolation at home Lockdowns and online working from home became "new normal (see [8]). The symptoms caused by the COVID-19 virus usually might have large variations Consequences from the virus can be different for every human being. Some people can only have mild to moderate respiratory illnesses and some people can develop complications of respiratory system or other organs failure. Based on clinical data, more affected by the virus are elderly group who usually experienced severe symptoms with higher mortality rate compared to younger group of patients. Also, some people can be infected with virus but are asymptomatic carriers. They have no symptoms but are still have some chance to transport the virus to other people. People who once already have recovered from COVID-19 are more likely to be temporary resistant to the virus. But still, in rare cases, there have been clinical reports that shows patients who have recovered from the disease have been tested positive again (see [9], [10]). In order to find additional resources for

fighting the pandemic, researchers use mathematics and statistical modelling as a useful tool in creating forecasts for virus spreading. These modelling can include estimation of the severity of the disease, which can help public health officials and governments to implement special restrictions and protection measures and to prepare adequate medical care and include other resources which are needed to combat the pandemic (see [11]-[15]). Models used by now by researchers for infections spread and epidemic prognosis can be divided in two larger groups: statistical and mechanistic models, (see [16]). Statistical models, which are data-driven based, in order to predict infection outcomes, usually use statistical and machine learning methods. Results obtained from these models can forecast outcomes, such as number of new cases, deaths and can help in dealing with hospital demands and managements. These methods also include auto-regressive time series techniques, Bayesian techniques and deep learning techniques (see [17]-[22]). On the other hand mechanistic group of models are based on theoretical principles on how the disease spreads (see [18], [23]-[35]). These models use mechanistic or algorithmic and procedural methods in order to explain and describe the progression of disease through a population. The most popular and most used models of these group are the SIR based type models, and its variations. In other cases, researchers use hybrid models in which they apply algorithmic models in a combination with machine learning approaches (see [36]). In this paper we use modification version of SIR models, SEIRS-D model, in which not only susceptible, infected and recovered, but also exposed and deaths are included. First, we give mathematical explanation of the model, and then we include case studies from the epidemic of COVID 19 in North Macedonia. We apply this model implementation in AnyLogic, for the prediction of scenario of disease spread in North Macedonia. And at the end we give our conclusion and remarks based on results obtained from this modelling.

2. Modelling COVID-19 using SEIRS-D model

Many infectious diseases in populations can be described by appropriate mathematical models. The mathematical modelling is crucial for understanding of the infectious diseases spread at the individual and population levels. The simplest model for the spread of an infection is the SIR model, which tracks the fraction of a population in each of three groups: susceptible, infectious, and recovered (see [37], [38]). The most epidemiological models descend from the classical SIR model of Kermack and McKendrick model (see [39]). The difference between the classical SIR model and SEIRS model is the period of immunity. In the

SIR model it is assumed that the patients have carried lifelong immunity to a disease upon recovery. In SEIRS model it is assumed that the recovered individuals can return into a susceptible state. The contribution to a susceptible state, ignoring vaccination creates an open epidemic (see [40]). If there is no possibility for returning of the recovered in the suspectable, SEIR model is used (see [41]). In this paper we modify SEIRS model by introducing the Death condition in which are all the individuals who died, as consequence of the infection during the pandemic. The obtained model in this way is denoted by SEIRS-D. In Figure 1 is presented Schematic representation of SEIRS-D model with its parameters.
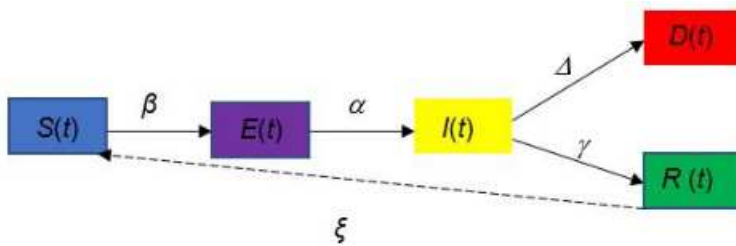
Figure 1: Schematic representation of SEIRS-D model.

SEIRS-D model is the most effective model for explaining how an epidemic is spreading. In the SEIR-D model is assumed that the totally population is susceptible at the initial time of pandemic $-t_0$. In the SEIRS-D model, the total considered population of N individuals is split in 5 categories: susceptible (S), exposed (E), infected (I), recovered (R), and death (D). Thus, at a given time t, $I(t), E(t), S(t)$ are the number of infected people, number of exposed people and the number of susceptible people, that were not infected yet, respectively. $R(t)$ is the number of recovered people and $D(t)$ the number of people who have died because of the infection. Therefore, at any time t, $S(t)+E(t)+I(t)+R(t)+D(t) = N$, where N is the fixed value of the total number of the population. The SEIRS-D model aim is to explain the variation of $S(t), E(t), I(t), R(t), D(t)$ during the time. In the conditions when no vaccine is available the people from different groups move from one group to another with appropriate rate. The

SEIRS-D model is represented with following differential equations:

$$\frac{dS(t)}{dt} = \xi R(t) - \frac{\beta}{N-D}I(t)S(t),$$

$$\frac{dE(t)}{dt} = \frac{\beta}{N-D(t)}I(t)S(t) - \alpha E(t),$$

$$\frac{dI(t)}{dt} = \alpha E(t) - \gamma I(t) - \Delta I(t),$$

$$\frac{dR(t)}{dt} = \gamma I(t) - \xi R(t),$$

$$\frac{dD(t)}{dt} = \Delta I(t).$$

The parameter β is the transmissions rate, i.e., the rate of the virus spread which represents the probability for disease transmission between a susceptible people and infected people. The parameter α is an incubation rate, i.e., the rate by which the latent patients becoming infectious. Therefore, the incubation time $\tau_{incubation} = \frac{1}{\alpha}$. While the parameter γ is a recovery rate and the recovery time is $\tau_{recovery} = \frac{1}{\gamma}$. The parameter ξ is the rate by which the recovered people return to the susceptible group due the loss of immunity and $\tau_{immunity} = \frac{1}{\xi}$. And parameter Δ is a rate of death.

The differential equations which described the model can be explained as follows:

• At the starting point of the pandemic, the whole population is susceptible to the infection, so all the population belong to the group S. If one individual is exposed on the virus, all other people around can become also exposed, so they are moving from the group S in the group E with rate β. One the other side, if recovered people loss immunity, then with parameter ξ going from group R in the group S.

• The number of the exposed people expand when susceptible people get exposed. With a rate α, with time of incubation $\tau_{incubation} = \frac{1}{\alpha}$, the exposed people move from the group E into the group I.

• The number of the infected people expand when susceptible people get infected. With a rate γ, the infected people move from the group I into the group R. And with death rate Δ infected people move from the group I into the group D.

• The group R contains the people who recovered after infection. Also, if recovered people loss the immunity, then with parameter ξ move from group R in the group of susceptible S.

• The group D contains the death people as consequence from virus infection.

An important epidemiological characteristic is the basic reproduction number $R_0 = \frac{\beta}{\gamma}$. The reproduction number shows the number of health people

who can be infected form one infected person. When no vaccine is available, the isolation of diagnosed infectives and social distancing are the only control measures available. The control action which should be taken by the governments is the key factor which impact of the number of the infected people. The value of the reproduction number shows the pandemic condition. If $R_0 \leq 1$, the pandemic will disappear spontaneously, while with $R_0 > 1$ it will continue spreading.

Scientists use the SIR model for a variety of purposes, most of them nowadays related to the Corona: for modelling the spread of COVID-19 (see [27], [28], [29], [30]) and modelling the epidemic of influenza (see [42]). The modifications of the basic SIR model, like SEIR and SEIRS model is also used in the recent period for modelling and representation of COVID-19 virus in different countries and regions around the world (see [18], [31]-[35]). In many papers there are different analysis about the factors which increases the spread of COVID-10 virus (see [43]). In the next section we used the modified SEIRS-D model to analyse the situation with COVID-19 virus in North Macedonia.

3. Case studies

We are using Republic of North Macedonia to apply the SEIRS-D model in order to show how the model works in the real situation. The Institute of Public Health in North Macedonia does not provide much detailed information for the COVID-19 situation, but with the available data we have modified the SEIRS model with adding the Death Cases. Republic of North Macedonia is a small and developing country at Balkan in which the first confirmed case of COVID-19 virus was reported on 26.02.2020 in women who arrived from Italy, which in that period was in red zone of COVID-19 virus. North Macedonia has around 2 000 000 citizens, but the public health system is not good organized and modernized. At the beginning of the March 2020 the country accepts the situation very serious, so, on the 11th of March 2020, the first restrictions were takeover to stop the transmission of the virus. The schools and other educational institutions were closed, and all the activities were transferred at the internet with online teaching and learning. But, after one month later on 22nd of March 2020 was confirmed the first death case from COVID-19. At the beginning the testing were performed only to the suspicious patients. The government decide to put in quarantine all the passengers who arrived from abroad. In that way, in the first three months of 2020 the ministry of health has control on the situation, because they accomplished the surveys of the

infected patients for the citizens with who they have contacts. But although these restrictions were taken, because of the bad health system at the end of May 2020 in the country were registered 133 deaths from COVID-19.

The following Figure 2 shows the simulations of the Infected, Recovered, Exposed, Susceptible and Death Cases in the first 100 days, from March to May 2020. The graphics are obtained from SEIRS-D model in AnyLogic Simulation Modelling Software. In this period the Fatality Rate is very high 0.7. The incubation period is 5 days, and the period of recovery is assumed to be 14 days. In this period the reproduction number $R_0 = 2$, which means that one infected person with the virus infected two others. Because of that the number of infected and death cases in this period increases exponentially.
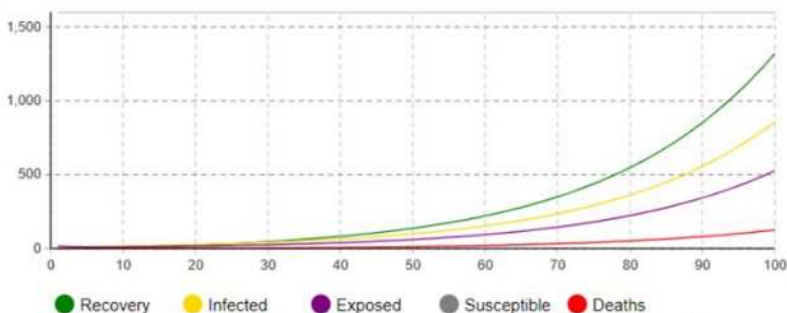

Figure 2: The initial fitting of the SEIRS-D Model in the first 100 days of COVID-19 virus in Republic of North Macedonia

In order to describe the situation in Republic of North Macedonia in conditions when no control actions are performed from the government, we have assumed the following values, but taking into account the worst values of the parameters which appeared in some period in North of Macedonia.

Parameter	Value
Population in North of Macedonia	2000000
Reproduction number	$R_0 = 3.3$
Incubation time	$\tau_{incub} = 5.1$ days
The incubation rate	$\alpha = \frac{1}{\tau_{incub}} = 0.196$
Fatality rate	$\Delta = 0.03$
Recovery period	$\tau_{recov} = 18.8$ days
Recovery rate	$\gamma = \frac{1}{\tau_{recov}} = 0.053$
Immunity period	$\tau_{immunity} = 90$ days

At the beginning the number of infected cases is 1, i.e. $I(0) = 1$, and the number of the exposed cases $E(0) = 20I(0) = 20$. In the initial moment as susceptible is taken the total population in North of Macedonia. The simulation of the SEIRS-D model for these assumed values are given at Figure 3.
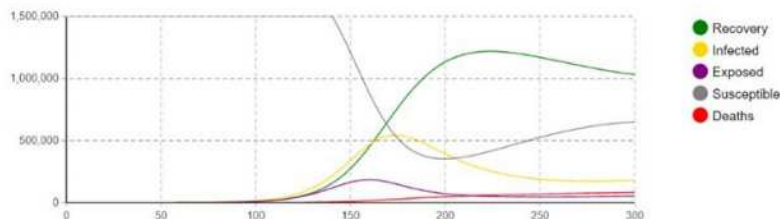

Figure 3: Projection of the SEIRS-D model in 300 days for COVID-19 virus in Republic of North Macedonia, when no control action is taken

According of this assumed situation, most of the population will be infected and recovered from COVID-19 virus. Also, the number of the death cases is very high because of the high death rate. The infected cases will take the maximum value and after that because of the high rate of recovery, the number of recovered cases will increase enormously. Next, we will describe the situation in Republic of North Macedonia in conditions when the control actions are introduced, according with mitigation and preventive measures that need be taken by the government. We assumed that the reproduction number is decremented from $R_0 = 3.3$ to $R_0 = 0.96$. Because of that, and transmission rate will be decremented from $\beta = 0.175$ to $\beta = 0.051$. Also, we assumed that the control action was introduced after 50 days from the first confirmed case.

The simulation of the SEIRS-D model for these assumed values with control action are given at Figure 4.

By comparing Figure 3 and Figure 4, we can conclude that the number of infected cases will be significantly decreased. Additionally, with modelling in Any-Logic we got that the number of total infected cases is reduced from about 1,2 million cases to about 4000 cases. One of the most frequently appointed questions about COVID-19 is whether recovered patients can be reinfected again? In North Macedonia there have been patients who have been recovered from the virus and reinfected again. But the question which is appointed here is whether the patients move from symptomatic cases in asymptomatic cases or again they are infected with the virus. Also, on the other hand, health author-
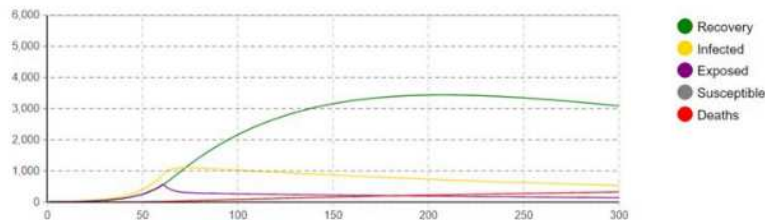
Figure 4: Projection of the SEIRS-D model in 300 days for COVID-19 virus in Republic of North Macedonia, with control action

ities think that the recovered patients developed an immunity for a COVID-19 virus. The immunity period of this infection is still not determined. There is a doubt is the obtained immunity on short-term or on a long term. For these reasons, we executed the case study on North Macedonia in conditions without control action, with assumption that the patients develop temporal immunity $\tau_\xi = 30, 60, 90, 360$ days. Appropriately, immunity rate will be 0.033, 0. 0,0167, 0.011 and 0.0027 (Figure 5).
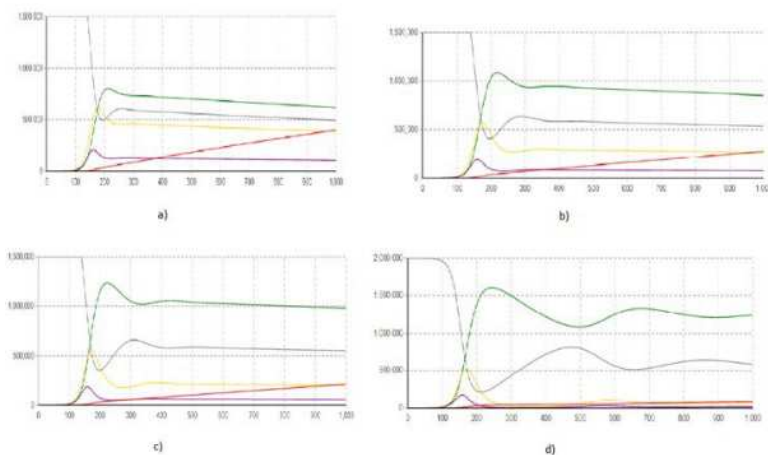

Figure 5: Projection of the SEIRS-D model in 300 days for COVID-19 virus in Republic of North Macedonia, when no control action is taken, with difference immunity of a) 30 days, b) 60 days. c) 90 days and d) 360 days.

From Figure 5, we can conclude that number of infected cases will be decreased if the immunity time is increased. For the result shown in Figure 5 d) where the immunity period is 360 days, it could also be used to show the situation where the COVID-19 virus may exhibit similar characteristics as the seasonal flu or the pandemic influenza A (pH1N1) that it is most likely active during certain seasons of the year, e.g., autumn/winter for the seasonal flu and spring/summer for the pH1N1, in which case an annual vaccine administration is necessary (see [44], [45]). Another question that is often appointed is how long period of recovery is. According to some health authorities the recovery time is 14 days, according to others 21 days. In our model, we assume that the recovery time is 18.8 days. To see how the recovery time affects, we executed the case study on North Macedonia without control action, with assumption that the recovery time is 14, 21 and 30 days. The results are shown in Figure 6.
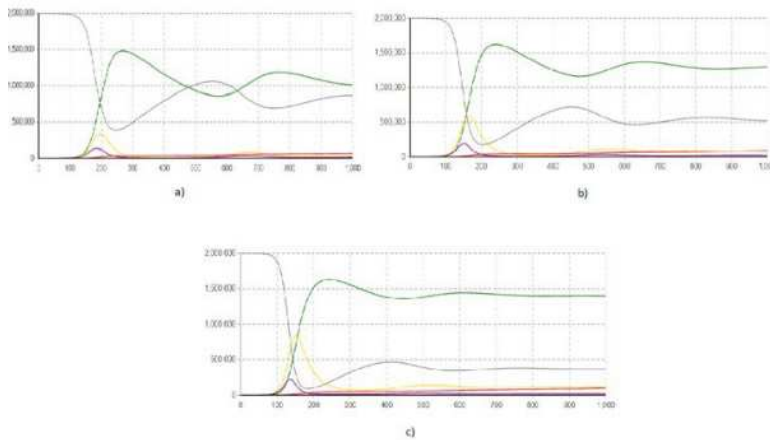

Figure 6: Projection of the SEIRS-D model in 300 days for COVID-19 virus in Republic of North Macedonia, when no control action is taken, with difference recovery period a) 14 days, b) 21 days and c) 30 days.

From Figure 6, it can be concluded that the number of infected cases will be decreased if the recovery period is decreased which is usually the case.

4. Conclusion

COVID 19 as a global crisis completely attracts the attention of many researchers in order to help authorities to minimize the fatal consequences from uncontrolled spreading of the disease. Mathematical modelling and simulations for this purpose have proven to be quite useful in many countries. In this paper, a new modified SEIRS-D mathematical model describing the evolution of the COVID-19 is presented, taking into account real situation of this infection in Republic of North Macedonia. According to the results presented, isolation of the infected people can greatly reduce the risk of future COVID-19 spread. The reproductive number, that shows the impact of interaction of infected people to susceptible population can be reduced, by controlling the contact rate. Therefore, control action taken from authorities are crucial for decreasing number of infected and number of deaths. According to results from projections and predictions, another important factor in reduction of spread of virus is immunity period of those who have already been infected. If immunity period is longer the number of new cases, especially fatal cases will be lower. In this manner, vaccination can play crucial role in increasing of immunity period. And other parameter which can help controlling the spread of infections is recovery period. If recovery period is lower, the number of infected and fatal cases will be drastically decreased.

The aim of this paper, making these predictions, is to find a way to help authorities in North Macedonia to adjust the measures of restrictions in order to control reproductive number and most painlessly to win the battle with COVID 19.

References

[1] S. Sugiyanto, M. Abrori, A mathematical model of the Covid-19 cases in Indonesia (Under and without lockdown enforcement), *Biol. Med. Nat. Prod. Chem.*, **9**, No 1 (2020), 1519.

[2] N. Mohapatra, Understanding the corona virus pandemic: From a sociological perspective, *Int. J. Sci. Res. Publ.*, **10**, No 06 (2020), 149-152.

[3] A. Dogra, B. Goyal, A.M. Sharma, Corona virus: A novel outbreak, *Biomed. Pharmacol. J.*, **13**, No 1 (2020), 05-10.

[4] A. Zeb, E. Alzahrani, V.S. Erturk, G. Zaman, Mathematical model for

coronavirus disease 2019 (COVID-19) containing isolation class, *Biomed. Res. Int.*, **2020** (2020), Article ID 3452402.

[5] T. Singhal, A review of corona virus disease-2019 (COVID-19), *Indian J. of Pediatrics*, **87**, No 4 (2020), 281-286.

[6] H. Song, Z. Jia, Z. Jin, Estimation of COVID-19 outbreak size in Harbin, China, (2020), 1-10.

[7] A. Anirudh, Mathematical modeling and the transmission dynamics in predicting the Covid-19 - What next in combating the pandemic, *Infect. Dis. Model.*, **5** (2020), 366-374.

[8] M.O.F. Barriguete, S.A. Zarasvand, Quarantine and COVID-19, *J. Heal. Med. Nurs.*, **85** (2021), 7374.

[9] K.Y. Ng, M.M. Gui, COVID-19: Development of a robust mathematical model and simulation package with consideration for ageing population and time delay for control action and resusceptibility, *Phys. D Nonlinear Phenom.*, **411** (2020), Article 132599.

[10] K. Sharma, R.L. Sharma, V. Sharma, Corona virus epidemiology: A review article, *Int. J. Community Med. Public Heal.*, **7**, No 12 (2020), 5219-5224.

[11] O. Zakary, S. Bidah, M. Rachik, H. Ferjouchia, Mathematical model to estimate and predict the COVID-19 infections in Morocco: Optimal control strategy, *J. Appl. Math.*, **2020** (2020), Article ID 9813926.

[12] B. Ivorra, M.R. Ferrndez, M. Vela-Prez, A.M. Ramos, Mathematical modeling of the spread of the coronavirus disease 2019 (COVID-19) taking into account the undetected infections. The case of China, *Commun. Nonlinear Sci. Numer. Simul.*, **88** (2020), Article 105303.

[13] S. Melliani, A. El Allaoui, L.S. Chadli, A simple mathematical model for Coronavirus (COVID-19), *medRxiv* (2020), 1-6.

[14] J. Wang, Mathematical models for COVID-19: applications, limitations, and potentials, *J. Public Heal. Emerg.*, **4**, No 9 (2020), 1-6.

[15] Y. Tang, S. Tang, S. Wang, The values and limitations of mathematical modelling to COVID-19 in the world: a follow up report, *Emerg. Microbes Infect.*, **9**, No 1 (2020), 2465-2473.

[16] A. Adiga, D. Dubhashi, B. Lewis, M. Marathe, S. Venkatramanan, A. Vullikanti, Mathematical models for COVID-19 pandemic: a comparative analysis, *J. of the Indian Institute of Science*, **100**, No 4 (2020), 793-807.

[17] B. Adhikari, X. Xu, N. Ramakrishnan, B. Aditya Prakash, Epideep: Exploiting embeddings for epidemic forecasting, In: *Proc. of the ACM SIGKDD Internat. Conf. on Knowledge Discovery and Data Mining (2019)*, 577586.

[18] A.N. Desai et al., Real-time epidemic forecasting: challenges and opportunities, *Heal. Secur.*, **17**, No 4 (2019), 268-275.

[19] S. Funk, A. Camacho, A.J. Kucharski, R.M. Eggo, W.J. Edmunds, Real-time forecasting of infectious disease dynamics with a stochastic semi-mechanistic model, *Epidemics*, **22** (2018), 56-61.

[20] C.J.L. Murray, Forecasting the impact of the first wave of the COVID-19 pandemic on hospital demand and deaths for the USA and European Economic Area countries, *medRxiv* (2020); doi: 10.1101/2020.04.21.20074732.

[21] G. Perone, An ARIMA model to forecast the spread and the final size of COVID-2019 epidemic in Italy, *medRxiv* (2020); doi: 10.1101/2020.04.27.20081539.

[22] N.G. Reich et al., Accuracy of real-time multi-model ensemble forecasts for seasonal influenza in the U.S., *PLoS Comput. Biol.*, **15**, No 11 (2019); doi: 10.1371/journal.pcbi.1007486.

[23] F. Brauer, Mathematical epidemiology: Past, present, and future, *Infectious Disease Modelling*, **2**, No 2 (2017); doi: 10.1016/j.idm.2017.02.001.

[24] S. Eubank, V. Anil Kumar, M. Marathe, A. Srinivasan, N. Wang, Structure of social contact networks and their impact on epidemics, *DIMACS Ser. in Discrete Mathematics and Theoretical Computer Science* (2007), 1-32.

[25] M.V. Marathe, N. Ramakrishnan, Recent advances in computational epidemiology, *IEEE Intell. Syst.*, **28**, No 4 (2013); doi: 10.1109/MIS.2013.114.

[26] M.E.J. Newman, The structure and function of complex networks, *SIAM Review*, **45**, No 2 (2003);
doi: 10.1137/S003614450342480.

[27] A. Palladino et al., Modelling the spread of Covid19 in Italy using a revised version of the SIR model, *arXiv* (2020), arXiv:2005.08724.

[28] S. Moein et al., Inefficiency of SIR models in forecasting COVID-19 epidemic: A case study of Isfahan, *Sci. Rep.*, **11**, No 1 (2021); doi: 10.1038/s41598-021-84055-6.

[29] M. Ivanova, L. Dospatliev, Data analytics and SIR modeling of COVID-19 in Bulgaria, *International Journal of Applied Mathematics*, **33**, No 6 (2020); doi: 10.12732/ijam.v33i6.10.

[30] A. Simha, R.V. Prasad, S. Narayana, A simple stochastic SIR model for COVID-19 infection dynamics for Karnataka after interventions Learning from European trends, *arXiv* (2020), arXiv:2003.11920.

[31] O.N. Bjrnstad, K. Shea, M. Krzywinski, N. Altman, Modeling infectious epidemics, *Nat. Methods*, **17**, No 5 (2020); doi: 10.1038/s41592-020-0822-z.

[32] M.B. Trawicki, Deterministic seirs epidemic model for modeling vital dynamics, vaccinations, and temporary immunity, *Mathematics*, **5**, No 1 (2017); doi: 10.3390/math5010007.

[33] J.M. Carcione, J.E. Santos, C. Bagaini, J. Ba, A simulation of a COVID-19 epidemic based on a deterministic SEIR model, *Front. Public Heal.*, **8** (2020); doi: 10.3389/fpubh.2020.00230.

[34] H. M. Youssef, N. A. Alghamdi, M. A. Ezzat, A. A. El-Bary, A. M. Shawky, A modified SEIR model applied to the data of COVID-19 spread in Saudi Arabia, *AIP Adv.*, **10**, No 12 (2020); doi: 10.1063/5.0029698.

[35] A. Rădulescu, C. Williams, K. Cavanagh, Management strategies in a SEIR-type model of COVID 19 community spread, *Sci. Rep.*, **10**, No 1 (2020); doi: 10.1038/s41598-020-77628-4.

[36] L. Wang, J. Chen, M. Marathe, TDEFSI: Theory-guided deep learning-based epidemic forecasting with synthetic information, *ACM Trans. Spat. Algorithms Syst.*, **6**, No 3 (2020); doi: 10.1145/3380971.

[37] P.M. Kaye, *Infectious Diseases of Humans: Dynamics and Control.* Roy M. Anderson and Robert M. May, Oxford University Press (1992).

[38] O.N. Bjrnstad, *Epidemics: Models and Data using R*, Springer Nature, Switzerland (2018).

[39] W.O. Kermack, A.G. McKendrick, Contributions to the mathematical theory of epidemics-I, *Bull. Math. Biol.*, **53**, No 12 (1991); doi: 10.1007/BF02464423.

[40] O.N. Bjrnstad, K. Shea, M. Krzywinski, N. Altman, The SEIRS model for infectious disease dynamics, *Nat. Methods*, **17**, No 6 (2020); doi: 10.1038/s41592-020-0856-2.

[41] A. Rachah, M. Saidi, Mathematical modeling and optimal control of Ebola virus transmission dynamics, *International Journal of Applied Mathematics*, **34**, No 3 (2021); doi:10.12732/ijam.v34i3.9.

[42] D. Osthus, K.S. Hickmann, P.C. Caragea, D. Higdon, S.Y. Del Valle, Forecasting seasonal influenza with a state-space SIR model, *Ann. Appl. Stat.*, **11**, No 1 (2017); doi: 10.1214/16-AOAS1000.

[43] E. Hincal, B. Kaymakamzade, N. Gokbulut, Humidity level on Covid-19 with control strategies, *International Journal of Applied Mathematics*, **34**, No 4 (2021); doi: 10.12732/ijam.v34i4.14.

[44] H. Kelly, K. Grant, Interim analysis of pandemic influenza (H1N1) 2009 in Australia: surveillance trends, age of infection and effectiveness of seasonal vaccination., *Euro Surveill.*, **14**, No 31 (2009); doi: 10.2807/ese.14.31.19288-en.

[45] S. Cook, C. Conrad, A.L. Fowlkes, M.H. Mohebbi, Assessing Google Flu trends performance in the United States during the 2009 influenza virus A (H1N1) pandemic, *PLoS One*, **6**, No 8 (2011); doi: 10.1371/journal.pone.0023610.