Communications in Mathematics and Applications
Vol. 13, No. 2, pp. 661–669, 2022
ISSN 0975-8607 (online); 0976-5905 (print)
Published by RGN Publications
DOI: 10.26713/cma.v13i2.1729

http://www.rgnpublications.com

Research Article

An SIR Model for COVID-19 Outbreak in India

S. Sweatha[1], P. Monisha[1] and S. Sindu Devi*[2]

[1] *Department of Mathematics, SRM Institute of Science and Technology, Ramapuram, Chennai, India*
[2] *Department of Mathematics, Faculty of Engineering and Technology, SRM Institute of Science and Technology, Ramapuram, Chennai 60089, India*
*__Corresponding author:__ sindudes@srmist.edu.in

Received: November 9, 2021 **Accepted:** April 21, 2022

Abstract. In this paper, we have proposed a SIR fuzzy epidemic model by taking the transmission rate and recovery rate as fuzzy numbers. The basic reproduction number and the fuzzy basic reproduction number have been computed. Further by considering the initial values for the susceptible, infected and recovered population the numerical simulation has been carried out using Runge-Kutta method. We can predict the transmission of the virus and prevent the COVID-19 outbreak in India with the results obtained from the proposed SIR model.

Keywords. Reproduction number, Fuzzy basic reproduction number, Runge-Kutta method

Mathematics Subject Classification (2020). 65L12, 34A067

1. Introduction

The noble coronavirus disease 2019 called Covid-19 has affected millions of people in the world this virus has made a great impact on the whole world as it spread to other persons very easily. The virus was first identified in Wuhan city of China in December 2019. Coronavirus was declared as an outbreak pandemic by World Health Organisation (WHO) in March 2020. Fever, cold, cough, bone pain and respiratory problems are the most common symptoms of this infection. Apart from these symptoms like loss of smell or taste, fatigue muscle pain and sore throat where are also observed in corona patients. Vaccines are the safe and effective tool to end this pandemic. Being vaccinated does not mean that we can throw caution to the wind and put ourselves and others at risk, particularly because research is still on going into how much vaccines protect not only against the disease but also against infection and transmission[1]. A mathematical model is a powerful tool which is used to analyse the spread of the virus and control the disease. Among many models which are used to predict Covid-19, the first model was conducted using Richard's method and GLM method [13]. In this modern era, there are many models which have been developed to describe about the epidemic process the first paper which emerged under the strength is given by Kermack and McKendrick [8]. In [4] prediction of the total number of Covid-19 cases is discussed and examples are presented using the measured data in Austria, France and Poland. Youssef *et al.* [15] have constructed SEIR model and have used the real data of Covid-19 of Saudi Arabia for numerical analysis and complex analysis. Jing *et al.* [2] proposed and SIR model to predict the epidemic trends of Covid-19 especially for USA-New York and Italy. By considering two parameters of SIR model Kudryashov *et al.* [9] analysed the infection expansion based on the first integrals for Covid-19. A mathematical model is constructed by considering 8 parameters by Ndaïrou *et al.* [11, 12] where they have included super spreaders class which is a different feature from other Covid-19 models. The SIR model is very useful for future prediction, end peak of epidemic disease and other related activity of outbreak disease.

Among the various paradigm exchanges in science and mathematics in the century one such change concerns the concept of uncertainty the first stage of transition from the traditional view to the modern view of uncertainty began in 19th century, and there came the introduction of Fuzzy by Zadeh; the introduction of uncertainty in biological model was given by Zadeh [16]. By considering different degrees of infectivity and transmission coefficient as fuzzy set De Barros *et al.* [3] constructed SI epidemiological model and applied the fuzzy technique. The transmission and the treatment control parameter where considered as fuzzy number by Mondal *et al.* [10] and they have modified the SIS epidemic model. Abdy *et al.* [1] have constructed an SIR model for COVID-19 and computed simulation results by considering data of Indonesia. In this study we have constructed an SIR model by considering the transmission rate and the recovery rate as fuzzy parameters, for the which we have compute the graph using Covid-19 data of India. By computing the graph, we can predict the future and peak of this Covid-19 epidemic disease.

2. Preliminaries

2.1 Fuzzy Set

Let X be a nonempty crisp sets. A fuzzy subset S of X is denoted by $\widetilde{S}$ and is defined as

$$\widetilde{S} = \{(x, \mu_{S(x)}) : x \in X\}$$

where $\mu_S : X \to [0,1]$ is a membership function associated with a fuzzy set $\widetilde{S}$ which describes the degree of belongingness of x with X.

Here we use the membership function $\mu(x)$ to indicate the fuzzy subsets $\tilde{S}$. Also, $\mu(x)$ is called fuzzy number if X is the set of real numbers.

[1]World Health Organisation (WHO), *Coronavirus disease (COVID-19) pandemic*, URL: https://www.who.int/emergencies/diseases/novel-coronavirus-2019.

2.2 Triangular Fuzzy Number

A *Fuzzy set* is called *Triangular fuzzy number* if the membership value can be represented by a *Triangular Function*. This function by a three parameters $F(x:a,b,c)$ [5] such as:

$$F(x:a,b,c)=\begin{cases}0 & x<a\\ \dfrac{x-a}{b-a} & a\le x<b\\ \dfrac{c-x}{c-b} & b\le x\le c\\ 0 & x>c\end{cases}$$

2.3 Fuzzy Measure and Fuzzy Expected Value

Let Ω be a nonempty set and $P(\Omega)$ denote the set of all subsets of Ω. Then $\mu:\Omega\to[0,1]$ is a fuzzy measure [5], if

(i) $\mu(\phi)=0$ and $\mu(\Omega)=1$,

(ii) for $A,B\in P(\Omega)$, $\mu(A)\le\mu(B)$ if $A\subset B$.

Let $\mu:\Omega\to[0,1]$ be an uncertain variable, i.e., μ is a fuzzy subset and μ a fuzzy measure on Ω. Then fuzzy expected value (FEV) of μ is the real number, defined by the sugeno measure [10].

$$FEV(\mu)=\int \mu d\mu=\sup\{\min(\alpha,k(\alpha))\},\quad 0\le\alpha\le 1$$

where $k(\alpha)=\mu\{\omega\in\Omega:\mu(\omega)\ge\alpha\}$.

3. Fuzzy System

In this paper, we propose an SIR model by incorporating the transmission rate and recovery rate as the fuzzy numbers. This model describes the susceptible, infected, and recovered population of Covid-19 in India. The model consists of three compartments of non-linear ordinary differential equations. The following is the fuzzy SIR model for COVID-19

$$\frac{ds}{dt}=-\beta(v)SI,$$

$$\frac{dI}{dt}=\beta(v)SI-\gamma(v)I,$$

$$\frac{dR}{dt}=\gamma(v)I,$$

where $S+I+R=N$.

In the above equations, S is the susceptible population, I is the infected population, R is the recovered population, and N is the total population, whereas the fuzzy numbers β represents the transmission rate of the disease and γ represents the recovery rate of the disease. v is considered as the virus load.

4. Analysis of Fuzzy System

Let $\beta = \beta(v)$ be the transmission rate which depend on the amount of virus load v given by [3]

$$\beta(v) = \begin{cases} 0, & \text{if } v < v_{\min}, \\ \dfrac{v - v_{\min}}{v_M - v_{\min}}, & \text{if } v_{\min} \le v \le v_M, \\ 1, & \text{if } v_M \le v \le v_{\max}. \end{cases}$$

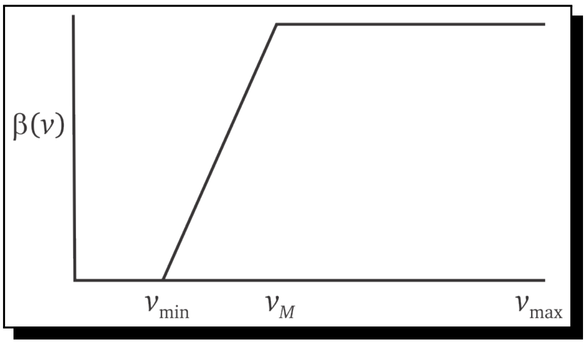

Figure 1. Membership of $\beta = \beta(v)$

The minimum amount of virus which is needed for transmission of the disease is represented as $v_{\min}$. The chance of transmission is negligible when the virus load is less than $v_{\min}$.For a certain amount of viruses say v_M The transmission rate is equal to 1. The amount of virus in an individual is always limited by $v_{\max}$. Figure 1 represents the membership function of $\beta(v)$.

Let $\gamma = \gamma(v)$ represent the recovery rate. The higher the virus load, the longer it will take to recover from the infection. The following is the fuzzy membership function of $\gamma(v)$ [14]

$$\gamma(v) = \frac{(\gamma_0 - 1)}{v_M}\gamma + 1, \quad \text{if } 0 \le v \le v_M,$$

where the lowest recovery rate is $0 < \gamma_0 < 1$. Figure 2 is the representation of $\gamma = \gamma(v)$.

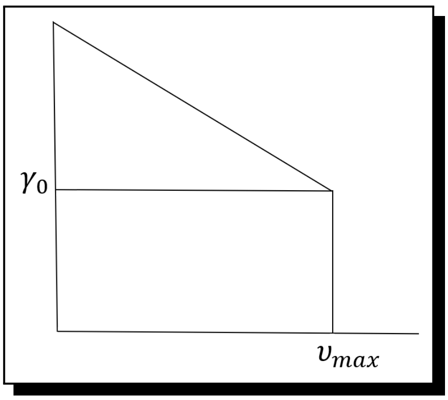

Figure 2. Membership of $\gamma = \gamma(v)$

We assume that for different individuals, the amount of virus we may be different. So, by the classification given by the expert, it can be seen as a linguistic variable such as weak, medium, and strong. Each classification of the linguistic variable with membership function $\Gamma(v)$ is given by [14]

$$\Gamma(v)=\begin{cases}0, & \text{if } v<\overline{v}-\delta,\\ \dfrac{v-\overline{v}+\delta}{\delta}, & \text{if } \overline{v}-\delta\le v\le\overline{v},\\ \dfrac{-(v-\overline{v}-\delta)}{\delta}, & \text{if } \overline{v}<v\le\overline{v}+\delta,\\ 1, & \text{if } v>\overline{v}+\delta.\end{cases}$$

Here $\overline{v}$ is the representation of the central value, δ is called the dispersion of each one of the fuzzy set assumed by v. Figure 3 is a representation of $\Gamma(v)$.

5. Reproduction Number

Basic reproduction number is defined as the average number of secondary infections caused by a single infectious individual during their entire infectious lifetime the number is denoted by R_0 [6, 7]:

$$R_0=\frac{\beta}{\gamma}.$$

6. Fuzzy Basic Reproduction Number

The basic reproduction number is $R_0=\frac{\beta}{\gamma}$, which increases with increase in the virus load and this cannot be a fuzzy set as it can be greater than 1. Thus $0\le\gamma_0R_0(v)\le1$, where $\gamma_0 R_0(v)$ is a fuzzy set and hence $FEV[\gamma_0R_0(v)]$ is well defined. In this view we introduce the fuzzy basic reproduction number.

The *fuzzy basic reproduction number* is given by

$$R_0^f=\frac{1}{\gamma_0}FEV(\gamma_0R_0(v))$$

here $FEV(\gamma_0R_0(v))=\sup\{\inf(\alpha,k(\alpha))\}$, $0\le\alpha\le1$, where $k(\alpha)=\mu\{v:\gamma_0R_0(v)\ge\alpha\}=\mu(X)$, is a fuzzy measure. To obtain $FEV(\gamma_0R_0(v))$ we need to define fuzzy measure μ. For which the possibility measure is given by

$$\mu(X)=\sup\Gamma(v),\quad \forall\, v\in X,\ X\subset R.$$

Since $R_0(v)$ is not decreasing with v, we have $X=[\overline{v},v_{\max}]$, from $FEV[\gamma_0R_0(v)]$ and $\overline{v}$ is the solution of the following equation

$$\gamma_0\frac{\beta}{\gamma}=\alpha.$$

Thus,

$$k(\alpha)=\mu[v',v_{\max}]=\sup\Gamma(v)\ \text{ with }\ v'\le v\le v_{\max},$$

where $k(0)=1$ and $k(1)=\Gamma(v_{\max})$.

The amount of virus v in the population which was assumed as a linguistic meaning is classified into three cases and all of them has fuzzy behaviour. They are weak virus load ($v_{\min}$), medium virus load (v_M) and strong virus load ($v_{\max}$).

Case 1: Weak virus load ($v_{\min}$)
(i.e.) when $\overline{\chi}+\delta \le \chi_{\min}$, we have

$$FEV(\gamma_0 R_0(v)) = 0 < \gamma_0 \quad \Leftrightarrow \quad R_0^f < 1.$$

Thus, we can conclude that corona will be extinct.

Case 2: Medium virus load (v_M)
(i.e.) when $\overline{v}-\delta \ge v_{\min}$ and $\overline{v}+\delta \le v_M$

$$k(\alpha)=\begin{cases} 1, & \text{if } 0<\alpha \le \gamma_0 R_0(\overline{v}), \\ \Gamma(v'), & \text{if } \gamma_0 R_0(\overline{v}) < \alpha \le \gamma_0 R_0(\overline{v}+\delta), \\ 0, & \text{if } \gamma_0 R_0(\overline{v}+\delta) < \alpha \le 1. \end{cases}$$

So, if $\delta > 0$, $k(\alpha)$ is continuous and decreasing function with $k(0) = 1$ and $k(1) = 0$. Hence, $FEV(\gamma_0 R_0(v))$ is the fixed point of k and

$$\gamma_0 R_0(\overline{v}) \le FEV(\gamma_0 R_0(v)) \le \gamma_0 R_0(\overline{v}+\delta),$$
$$R_0(\overline{v}) \le R_0^f \le R_0(\overline{v}+\delta).$$

As the function $R_0(\overline{v})$ is increasing and continuous function then by the intermediate value theorem there exists v with $\overline{v} < v < \overline{v}+\delta$ such that

$$R_0^f = R_0(v) > R_0(\overline{v}).$$

There exists virus load v such that R_0^f and $R_0(v)$ coincide. Furthermore, the average number of secondary cases R_0^f is higher than the number of secondary cases $R_0(\overline{v})$ due to the medium amount of virus.

Case 3: Strong virus load ($v_{\max}$)
(i.e.) when $\overline{v}+\delta \le v_M$ and $\overline{v}+\delta \le v_{\max}$, then

$$k(\alpha)=\begin{cases} 1, & \text{if } 0<\alpha \le \gamma_0 R_0(\overline{v}), \\ \Gamma(v'), & \text{if } \gamma_0 R_0(\overline{v}) < \alpha \le \gamma_0 R_0(\overline{v}+\delta), \\ 0, & \text{if } \gamma_0 R_0(\overline{v}+\delta) < \alpha \le 1. \end{cases}$$

Similar to Case 2, we have

$$\gamma_0 R_0(\overline{v}) \le FEV(\gamma_0 R_0(v)) \le \gamma_0 R_0(\overline{v}+\delta),$$
$$R_0(\overline{v}) \le R_0^f \le R_0(\overline{v}+\delta).$$

Thus, $R_0^f > 1$; we can conclude that corona will be endemic.

7. Numerical Simulation

From the data collected from[2], $S_0 = 13.57410$, $I_0 = 0.56340$, $R_0 = 0.18430$, $\beta = 0.03156$, $\gamma = 0.0714$, $\Delta t = 0.1407$.

The values have been calculated by Runge-Kutta method, considering the initial values of the susceptible, infected and, recovered population.

As the virus load increases the number of susceptible decreases. There is a decrease in the curve as the infection starts to spread. Figure 3 shows the susceptible population.

[2] R.S. Yadav, Mathematical modeling and simulation of SIR model for COVID-2019 epidemic outbreak: A case study of India, *medRxiv* (2020), DOI: 10.1101/2020.05.15.20103077.

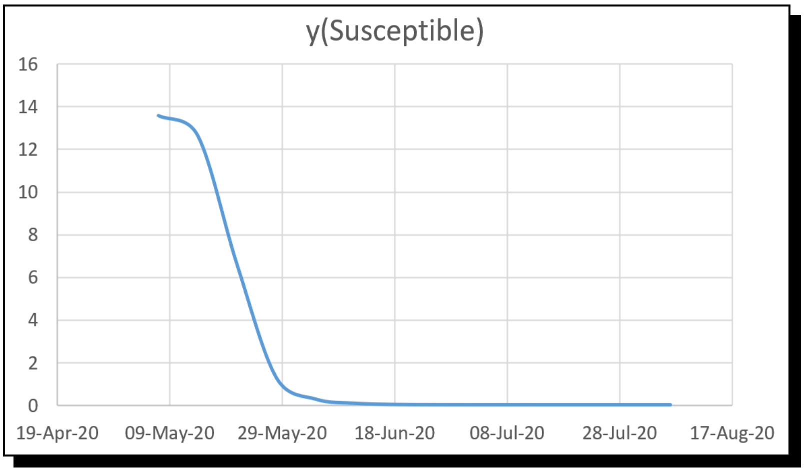

Figure 3. Susceptible population

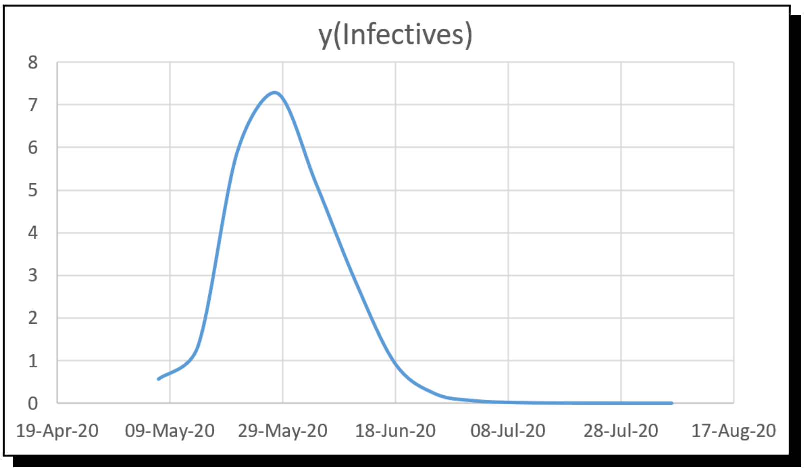

Figure 4. Infected population

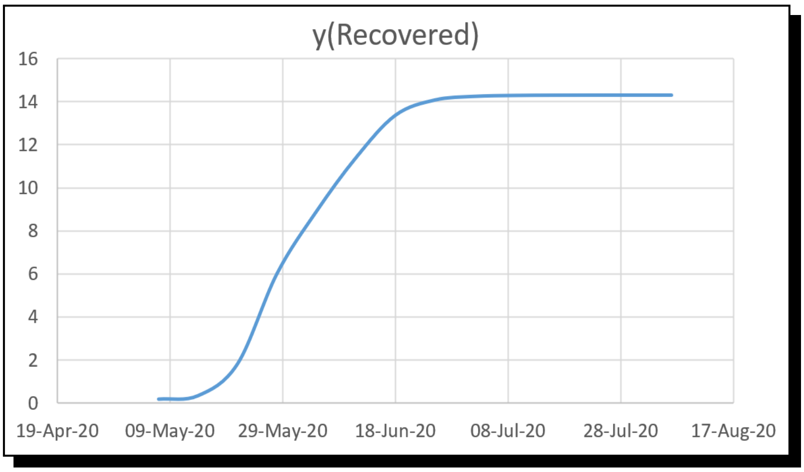

Figure 5. Recovered population

Initially when the virus has entered the community of people it starts spreading slowly and later when the infected population increases the rate of infection also increases. Figure 4 shows the infected population.

When the virus is newly entering into the community, the number of infected persons is relatively low and thus there is no recovered population whereas in the later stage when the infected population increases and when they undergo treatments the recovered population becomes higher. Figure 5 shows the recovered population.

Figure 6 is the representation of the dynamical behaviours of the system.

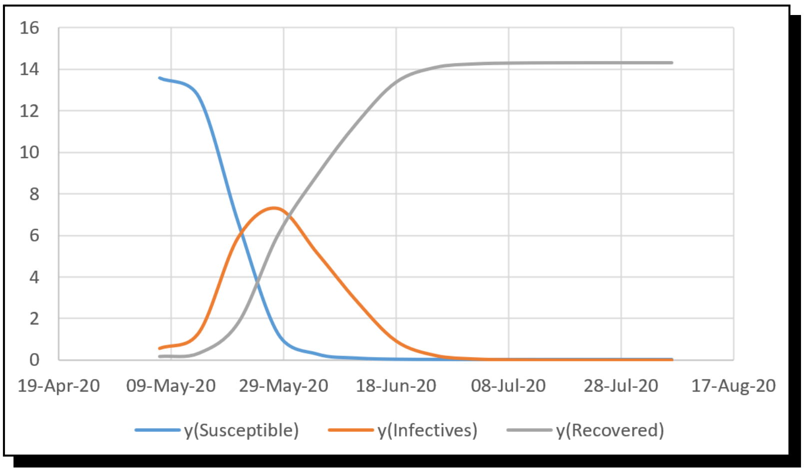

Figure 6. Dynamical behaviour of the system

8. Conclusion

According to the data it is predicted that the rate of transmission of the coronavirus increases during the months of May, and June and slowly starts decreasing in the month of July. The graph has been predicted using Runge-Kutta method. Runge-Kutta method gives the more accurate solutions. This study shows that abiding by the rules of government we can prevent the further spread of the disease.

Acknowledgement

We thank SRM Institute of Science and Technology, Ramapuram, Chennai for their continuous support.

Competing Interests

The authors declare that they have no competing interests.

Authors' Contributions

All the authors contributed significantly in writing this article. The authors read and approved the final manuscript.

References

[1] M. Abdy, S. Side, S. Annas, W. Nur and W. Sanusi, An SIR epidemic model for COVID-19 spread with fuzzy parameter: the case of Indonesia, *Advances in Difference Equations* **2021** (2021), Article number: 105, DOI: 10.1186/s13662-021-03263-6.

[2] J.L. Aron and I.B. Schwartz, Seasonality and period-doubling bifurcations in an epidemic model, *Journal of Theoretical Biology* **110**(4) (1984), 665 – 679, DOI: 10.1016/S0022-5193(84)80150-2.

[3] L.C. DE Barros, M.B.F. Leite and R.C. Bassanez, The SI epidemiological models with a fuzzy transmission parameter, *Computers & Mathematics with Applications* **45** (2003), 1619 – 1628, DOI: 10.1016/s0898-1221(03)00141-x.

[4] R. Cherniha and V. Davydovych, A mathematical model for the COVID-19 outbreak and its applications, *Symmetry* **12**(6) (2020), 990, DOI: 10.3390/sym12060990.

[5] S.S. Devi and K. Ganesan, A new approach for the solution of fuzzy initial value problems through Runge-Kutta method, *Journal of Informatics and Mathematical Sciences* **12**(2) (2020), 149 – 157, DOI: 10.26713/jims.v12i2.1144.

[6] O. Diekmann, J.A.P. Heesterbeek and J.A.J. Metz, On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations, *Journal of Mathematical Biology* **28** (1990), 365 – 382, DOI: 10.1007/bf00178324.

[7] P. van den Driessche and J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, *Mathematical Bioscience* **180**(1–2) (2002), 29 – 48, DOI: 10.1016/s0025-5564(02)00108-6.

[8] W.O. Kermack and A.G. McKendrick, Contributions to the mathematical theory of epidemics–I, *Bulletin of Mathematical Biology* **53** (1991), 33 – 55, DOI: 10.1007/bf02464423.

[9] N.A. Kudryashov, M.A. Chmykhov and M. Vigdorowitsch, Analytical features of the SIR model and their applications to COVID-19, *Applied Mathematical Modelling* **90** (2021), 466 – 473, DOI: 10.1016/j.apm.2020.08.057.

[10] P.K. Mondal, S. Jana, P. Haldar and T.K. Kar, Dynamical behavior of an epidemic model in a fuzzy transmission, *International Journal of Uncertainty, Fuzziness and Knowledge-Based Systems* **23**(5) (2015), 651 – 665, DOI: 10.1142/S0218488515500282.

[11] F. Ndaïrou, I. Area, J.J. Nieto and D.F. Torres, Corrigendum to "Mathematical modeling of COVID-19 transmission dynamics with a case study of Wuhan" [Chaos Solitons Fractals 135 (2020), 109846], *Chaos, Solitons & Fractals*, **141** (2020), 110311, DOI: 10.1016/j.chaos.2020.110311.

[12] F. Ndaïrou, I. Area, J.J. Nieto and D.F. Torres, Mathematical modeling of COVID-19 transmission dynamics with a case study of Wuhan, *Chaos, Solitons & Fractals* **135** (2020), 109846, DOI: 10.1016/j.chaos.2020.109846.

[13] K. Roosa, Y. Lee, R. Luo, A. Kirpich, R. Rothenberg, J.M. Hyman, P. Yan and G. Chowell, Short-term forecasts of the COVID-19 epidemic in Guangdong and Zhejiang, China: February 13–23, 2020, *Journal of Clinical Medicine* **9**(2) (2020), 596, DOI: 10.3390/jcm9020596.

[14] R. Verma, S.P. Tiwari and R.K. Upadhyay, Dynamical behaviour of fuzzy SIR epidemic model, in: *Advances in Fuzzy Logic and Technology*, Springer International Publishing (2017), 482 – 492, DOI: 10.1007/978-3-319-66827-7_45.

[15] H.M. Youssef, N.A. Alghamdi, M.A. Ezzat, A.A. El-Bary and A.M. Shawky, A modified SEIR model applied to the data of COVID-19 spread in Saudi Arabia, *AIP Advances* **10**(12) (2020), 125210, DOI: 10.1063/5.0029698.

[16] L.A. Zadeh, Fuzzy sets, *Information and Control* **8** (1965), 338 – 353, DOI: 10.1016/S0019-9958(65)90241-X.