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Research article

On stiff, fuzzy IRD-14 day average transmission model of COVID-19 pandemic disease

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Abstract: COVID-19, a new pandemic disease is becoming one of the major threats for surviving. Many new models are arrived to study the disease mathematically. Here we are introducing a new model in which instead of studying a day by day changes we are studying the average of 14 day transmission because its life or the patients incubation period is about an average of 14 days. Also, since this is pandemic, and being not aware of susceptible population among the world's population, we considered the model without S-susceptible population. i.e., IRD- Infectious, Recovered, Death-model. In this new model, we are also introducing a new method of calculating new number called N_0-average transmission number. This is used to study the average spread of infection instead of basic reproduction number R_0. The motto of this paper is not to predict the daily cases but to control the current spread of disease and deaths by identifying the threshold number, exceeding which will increase the spread of infection and number of deaths due to this pandemic. Also if the 14 day average IRD-populations are maintained under this threshold number, will definitely control this pandemic disease globally. Stability analysis and test for stiff system of differential equations are studied. Our main aim is to present the medical world, a threshold population of infected, recovered and death cases for every average of 14 days to quickly overcome this pandemic disease COVID-19.

Keywords: COVID-19; equilibrium points; stability analysis; basic reproduction number; average transmission number; IRD-model; fuzzy differential equations; stiff differential equations; threshold population

1. Introduction

People always love to live healthy. But it was not expected all the time. Over many years, many diseases have been evolved. The root of many diseases are not still known. Some of the natural elements being spoiled by mankind, spoil the mankind in turn. Sometimes, diseases emerge naturally and in sometimes, it may be by a human error. Whatever it is, once a disease has arrived among the mankind, it will spread to maximum number of people irrespective of age, gender, country, etc. Today, mankind is facing one such deadly disease called coronavirus. Coronavirus is not an exception in causing major loss to the society as well as mankind. Its time to quarantine our self to save our precious life. Coronaviruses are actually a group of same kind of viruses. They affect birds and mammals highly. In human beings, these coronaviruses are causing toughness to breath. The respiratory infections caused by COVID-19 may be light, like common cold, or may be severe, like SARS, MERS, and novel corona. The medical world is still struggling to find the medicine that can treat these diseases. The spread of coronaviruses from one human to other is believed to spread among the close communities by means of sneezing or coughing or even by touching. The first human infecting coronaviruses were discovered during 1960. The very first one was found in chickens called as infectious-bronchitis-virus. The other two were found in human beings with common cold. It was named as human coronaviruses 229E and human coronaviruses OC43 later. Also, there are other lists of this coronavirus. They are SARS-CoV which was found in 2003. In the year 2004, HCoV NL63 was found. In the next year, 2005 HKU1 was found. MERS-CoV found in the year of 2012, and SARS-CoV-2 which was well known to be 2019-nCoV, found recently in the year 2019. Still new viruses are persisting in the globe. Most of these viruses have involved very serious problems such as respiratory problems and inner organ failure. Coronaviruses are classified in to four types and they are Alpha-coronaviruses, Beta-coronaviruses, Gamma-coronaviruses, and Delta-coronaviruses. From the observations, the bats, birds and all hot blooded creatures are the only hosts for the alpha and beta coronaviruses, and birds are common to gamma and delta coronaviruses for the evolution and spreading of these viruses. All coronaviruses may change in terms of their risk factor. More than 30% of those infected (such as MERS-CoV) may die and some others such as fever, dry cough and sore throat from swollen adenoids, occurring mostly in the winter and in spring seasons are less harmful. Coronaviruses are able to cause pneumonia and bronchitis. The most threaten human coronavirus was discovered in the year 2003, (SARS-CoV), which causes a severe acute respiratory syndrome called SARS. It has very unique pathogenesis infecting both upper and lower respiratory tracts. During the years of 2002–2004, it was found as 774 people had died of SARS-CoV. In 2012, 2015 and 2018 the MERS-CoV respectively caused over 400, 36 and 41 deaths. Now, during 2019 to 2020, coronavirus pandemic was considered as a global threat with at least 30,935 deaths till March 29 2020.

1.1. Coronavirus disease 2019 (COVID-19)

During December 2019, It was reported in Wuhan, China , a pneumonia type of disease outbreak. On 31 September 2019, that was traced and identified as a novel coronavirus. The World Health Organization (WHO) called it as 2019-nCoV. Later, the International Committee on Taxonomy of viruses called it as SARS-CoV-2. Since, March 29, 2020, there have been found at least 30,935 confirmed deaths and more than 492,571 confirmed cases in the coronavirus pandemic over 199 countries and territories around the world and two international conveyances, one is the Diamond

Princess cruise ship of Japan and the other is Holland America's MS Zaandam Cruise ship. The Wuhan novel strain has been identified as a new type of Beta coronavirus and it was from group 2B with approximately 70% genetic similarity with SARS-CoV. As this virus has a 96% of similarity to bat coronaviruses, it was believed that these viruses start from bats. This pandemic has resulted in travel restrictions. Also worldwide, we can see lock-downs in several countries. Since modeling of any pandemic or epidemic disease spread is uncertain, there will be vagueness always. To overcome this vagueness and to study uncertainty, fuzzy sets was first introduced individually by Lofti A. Zadeh in 1965 [1]. Today randomness, vagueness and uncertainty problems were mostly studied everywhere like signal processing, artificial intelligence, population dynamics, optics, oriental medicine, by Engineers, Doctors and Scientists etc. Fuzzy sets, fuzzy differential equations, fuzzy logic are considered to be their important tools to study them. The imprecise nature of medical concepts are always defined with the help of fuzzy logic.

In [1] and [2], L.A. Zadeh, presented fuzzy sets, fuzzy mapping and control. In [3], J.J. Bukley and T. Feuring, in [4], D. Dubois and H. Prade, in [5], Lupulescu, in [6] and in [7], Kaleva did a great research on fuzzy differential equations. In [8], Ma, Friedman and Kandel, and in [9], seikkala, provided a great contribution to fuzzy differential equations, fuzzy differential calculus, fuzzy initial value problem and seikkala dervative is the predominant work of Seikkala in the fields of fuzzy differential equations. In [10], Diamond and Kloedan analyzed metric spaces of fuzzy sets in 1984. In [11], Y. Chalco-Cano and H. Roman-Flores, defined, analyzed and studied new solutions of fuzzy differential equations. In [12] and [13], S. Abbasbandy and T. Allahviranloo, studied numerical solution of fuzzy differential equation by Taylor method and by Runge-Kutta method. In [14], C.F. Curtiss, J.O. Hirschfelder, studied integration of stiff equations. In [15], Gustaff Soderlind, Laurent Jay and Manual Calvo, published a work on Stiffness. In [16], L. Shampine, provided evaluation of a test set for stiff ODE solvers. In [17], D.J. Higham and L.N Trefethen studied stiffness of ODEs. In [18], M.N. Spijker, evaluated stiffness in numerical initial value problems.

In [19], W.O. Kermack and A.G. Mckendrick, gave the first contribution to the mathematical theory of epidemics. In [20], P. Palese and J.F. Young, studied variation of Influenza A, B, and C. In [21], Allen LJS gave an introduction to mathematical biology in 2007. In [22], Sha He, Sanyi Tang and Libinin Rong, framed a discrete stochastic model for COVID-19 outbreak: forecast and control. In [23], Weike zhou, Aili Wang, Fan Xia, Yanni Xiao and Sanyi Tang reported the effects of media on mitigating spread of COVID-19 in the early phase of the outbreak. In [24], Fuliyan Yin, Jiahui Lv, Xiaojian Zhang, Xinyu Xia, and Jianhong Wu, presented COVID-19 information propagation dynamics in the chinese sina-microblog. In [25], Chenxi Dai, Jing Yang and Kaifa Wang, did evaluation of control interventions on the epidemic of coronavirus disease 2019 in Chongqing and Guizhou Provinces. In [26], Xinmiao Rong, Liu Yang, Huidi Chu and Meng Fan, analyzed the effect of delay in diagnosis on spread of coronavirus. In [27], Jingjing Tian, Jiabing wu, Yunting Bao, Xiaoyu Weng, Lei Shi, Binbin Liu, Xinya Yu, did modeling analysis of COVID-19 in Anhui, China. In [28], Chentong Li, Jinhu Xu, Jiawei Liu and Yicang Zhou, particularly studied the within-host viral kinetics COVID-19. In [29], Vitaly Volpert, Malay Banerjee and Sergei Petrovskii, gave their tremendous work on a quarantine model of coronavirus infection along with data analysis. In [30], Biao Tang, Nicola Luigi Bragazzi, Qian Li, Sanyi Tang, Yanni Xiao and Jianhong Wu analysed and provided an updated estimation of the novel coronavirus transmission. Zifeng Yang et al. analysed modified SEIR and AI prediction of the epidemics trend of COVID-19 in China under public health

interventions in [31]. ShreshthTuli, Shikhar Tuli et al. predicted the growth and trend of COVID-19 pandemic using machine learning and cloud computing in [32]. Chintamani Pai et al. investigated the dynamics of COVID-19 pandemic in India under lockdown in [33]. Matheus Henrique Dal Molin Ribeiro et al. focused on short-term forecasting COVID-19 cumulative confirmed cases: perspectives for Brazil in [34]. Muhammad Altaf Khan and Abdon Atangana, have modeled the dynamics of novel coronavirus (2019-nCov) with fractional derivative in [35]. In [36], [37], [38] and [39], authors like Muhammad Altaf Khan regularly studied SEIR, dengue and also presented the numerical solution of the competition model among bank data in Caputo-Fabrizio derivative. Authors of [40], [41] and [42] have regularly studied numerical solutions of fuzzy differential equations.

The paper contains preliminaries, which are essential to create some basic knowledge about the study to the readers, in section 2. The remainder of the paper is structured as follows. The formulation of models in terms of ordinary differential equations and in terms of fuzzy differential equations are given in section 3. Stability analysis and test for given system to be stiff differential equations are performed in section 4. Numerical simulation of infected, recovered and death cases are presented in terms of both ordinary differential equations and fuzzy differential equations in section 5.

2. Preliminaries

Before proceeding to some of the prerequisites necessary for the study, we are now presenting the novelty, new contributions and new objectives in this paper which will motivate the readers and researchers. This is the first paper in which the epidemic modeling without considering the susceptible population was framed. This is the first paper in which the stiff differential equations and fuzzy properties are used to frame and study such a model. Many papers are emerging daily to predict the daily cases but this is the first paper in which a new idea called maintaining the 14 day average-infectious, recovered and death populations under threshold populations is given to control the spread and human loss. Also in this paper since susceptible population was not considered, we are introducing the new number called average transmission number-N_0 instead of basic reproduction number R_0. For each country this modeling could be applied as here we are studying globally. In mathematical biology point of view, the advantage of models framed by stiff fuzzy differential equations is used to analyze the model in which the stiffness (stiffness is defined below) arise can be set under fuzzy boundary so that values are predicted at crisp set values and analyzed at the fuzzy set values. That will help us to set the boundary of our analyze to two extreme (minimum and maximum) values and also to the in between values (partial member values). All these are explained in detail below.

2.1. Stiff differential equations

Though stiff differential equations are most important field of research in mathematical modeling, a rigorous, efficient, meaningful and computationally relevant properties or definition of stiffness is still not well defined. Since many years, many different numerical methods and software codes have been designed for the efficient solution of stiff initial value problem. The seminal paper of curtiss and Hirchfelder [14] first opened this field, stiffness. But it was not yet properly defined. According to Shampine [16], "A major difficulty is that stiffness is a complex of related phenomena, so that it is not easy to define what stiffness is".

Stiff equations are some of the problems in ordinary differential equations for which explicit type of numerical methods does not work. The explicit type of numerical methods may struggle a lot when applied to the IVP's (initial value problems) $\dot{y} = f(y)$, $y(0) = y_0$. It is always not possible to solve, when $f'(y)$ is very large. Similarly in non linear equations, fixed point iteration $y^{m+1} = f(y^m)$ does not converge for problems whose $f'(y)$ is large. Curtiss and Hirchfelder [14] are the two people who introduced the notation stiffness for which the explicit methods for numerical solutions of ordinary differential equations failed. There is no unique definition of stiffness is found in the literature. But one can call the system of ordinary differential equations is called stiff if Lipschits constant L defined for solution over the interval is $L(y_0, y_n) >> 1$.

The following is the definition of stiff system of fuzzy differential equations.

Definition 2.1 (Stiff system of fuzzy differential equations)**.** *The linear system of fuzzy differential equations $\tilde{y}'(x) = A\tilde{y}(x)$, $A \in R^{n\times n}$, is known as fuzzy stiff, if all eigenvalues λ_i posses a negative real part and if*

$$q = \frac{max|(Re(\lambda_i))|, i = 1, 2, ..., n}{min|(Re(\lambda_i))|, i = 1, 2, ..., n} >> 1$$

Remarks:

1. The stiff differential equations are numerically known to be unstable unless the step size is extremely very very small.
2. Stiff differential equations are also characterized as one for which exact solution possessed to have a term of the form e^{-kt}, where k is a large positive constant.
3. Large derivatives of e^{-kt} always give error terms and that will always dominate the solutions.

2.2. Fuzzy differential equations

We are interested to study the model in fuzzy differential equations because, it only studies the system completely as non-member, partial members and full member. If y_0 is a fuzzy number found with α-level of intervals $[y_0]^\alpha = [\underline{y}^\alpha, \overline{y}^\alpha]$, $0 \le \alpha \le 1$. The extension principle of Zadeh leads us to the following definition of $\tilde{f}(t, y(t))$ when y is a fuzzy number.

It follows that

$$\tilde{f}(t, y(t)) = \begin{cases} \min f(t, u) : u(\underline{y}_t^\alpha, \overline{y}_t^\alpha), & u \in E \\ \max f(t, u) : u(\underline{y}_t^\alpha, \overline{y}_t^\alpha), \end{cases} \tag{2.1}$$

for $y \in E$ with α- level sets $[y]_\alpha = [\underline{y}_t^\alpha, \overline{y}_t^\alpha]$, $0 \le \alpha \le 1$
since the fuzzy derivative $y'(t)$ of a fuzzy process, $y : R_+ \to E$ is defined by $[y'(t)]_\alpha = [(\underline{y}^\alpha)'(t), (\overline{y}^\alpha)'(t)], 0 \le \alpha \le 1$.

We call $\overline{y} : R_+ \to E$ a fuzzy solution of (2.1) on the interval $I = [0, t]$ if

$$\begin{cases} (\underline{y}^\alpha)'(t) = \min\{f(t, u) : u \in [\underline{y}_t^\alpha, \overline{y}_t^\alpha], & \underline{y}(t_0) = \underline{y}_0\} \\ (\overline{y}^\alpha)'(t) = \max\{f(t, u) : u \in [\underline{y}_t^\alpha, \overline{y}_t^\alpha], & \overline{y}(t_0) = \overline{y}_0\} \end{cases} \tag{2.2}$$

for $t \in I$ and $0 \le \alpha \le 1$. Thus for fixed α we have an initial value problem in R^2. If we can solve it, we have only to verify that intervals $[\underline{y}_t^\alpha, \overline{y}_t^\alpha]$, $0 \le \alpha \le 1$, define a fuzzy number $y(t) \in E$.

3. Model formulation

As COVID-19 is pandemic and spreads in several countries of the world very quickly, we are unable to know the exact count of susceptible population. The infected, recovered and dead populations were taken from various online resources like [43]. In order to frame the model, we have taken the data from March 10 to March 23, 2020. All the existing mathematical models deals with growth of the disease day by day and there is no model yet without susceptible population, also they require the susceptible population to calculate the basic reproduction number. Here we take 14 days data of the whole world's COVID-19 cases and take their average as the initial population. The worlds population is very high and the disease is spreading in a very fast manner. so the population of infected, recovered and dead was also increasing day by day. We have to keep in mind that the worlds total population cannot be taken as susceptible. Anyone with common symptoms of the disease but not yet infected is what exactly susceptible population mean. Due to lack of awareness about the symptoms no one can visit the hospital. In such situation its not possible to record the exact population of susceptible cases as recording the exact population of infected, recovered and dead. So we are interested to create a model called IRD-Infected, Recovered and Dead. Since the disease has an average life of 14 days we are also interested to study the average cases of IRD population over 14 days mean. It is quite interesting to study such new way of modeling. In future many researchers may interested to study the model like this. The main advantage of studying this average transmission model is one can easily estimate the average change in population for any years. But the average number should be the life of virus. Before presenting the model, the data from March 10 to March 23, 2020 are presented.

Let β, μ, γ and ζ be the rate of infected $I(t)$, recovered $R(t)$, Death $D(t)$ and the total cases $T(t)$ respectively. We know that the rate of total case is always 100. i.e., $\zeta = 100$.

Table 1. COVID-19, 14 days population and rates [43].

Date(t)	I(t)	β	R(t)	μ	D(t)	γ	T(t)
Mar23	260277	68.70	102069	26.94	16514	4.36	378860
Mar22	224221	66.44	98627	29.22	14641	4.34	337489
Mar21	196523	64.43	95500	31.31	13013	4.26	305036
Mar20	172637	62.64	91573	33.23	11387	4.13	275597
Mar19	146740	59.91	88162	35.99	10031	4.10	244933
Mar18	124538	56.91	85333	39.00	8951	4.09	218822
Mar17	107637	54.30	82623	41.68	7978	4.02	198238
Mar16	95701	52.44	79628	43.64	7161	3.92	182490
Mar15	85622	50.49	77452	45.67	6519	3.84	169593
Mar14	74888	47.81	75932	48.47	5833	3.72	156653
Mar13	67447	46.36	72607	49.91	5429	3.73	145483
Mar12	592212	44.00	70383	52.30	4981	3.70	134576
Mar11	53279	42.21	68307	54.12	4628	3.67	126214
Mar10	48031	40.38	66621	56.01	4296	3.61	118948
Sum	1616753	757.02	1154817	587.49	121362	55.49	2892932
Average	115482.36	54.07	82486.93	41.97	8668.71	3.96	206638

From the above table it was found that $I(t)$, $R(t)$ and $D(t)$ increases rapidly and also it is clear that $I(t) > R(t) > D(t)$ and obviously $\beta > \mu > \gamma$. But without considering from the table we shall calculate β, μ and γ using separate forumalae later. So the COVID-19 model is the exponentially growing model. Since the spread of this pandemic disease is not coming to an end or any proper medicine was not yet found it is not a right way to go for the logistic growth model. If so, what will be the carrying capacity, as total population and susceptible population are not clearly known? Biologist and Doctors says the average life of this COVID-19 is 14 days. At least we can check whether its average population model is growing exponentially or not. If this is not growing exponentially then we can suggest doctors to maintain this average initial populations as threshold numbers. Exceeding this may lead to loss the control of infections and deaths. Through out the paper, Δ represents rate of change in population of Infected, Recovered and Dead cases with respect to time t and D represents death population. With these ideas the following model is made.

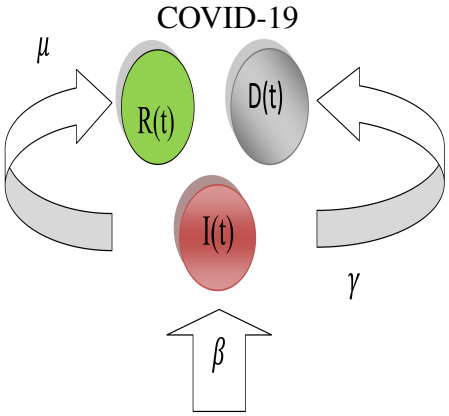

Figure 1. Model formulation.

$$\begin{aligned} \Delta I(t) &= (\beta I(t) - \mu I(t)R(t) - \gamma I(t)D(t) \\ \Delta R(t) &= (\mu I(t)R(t) - \beta I(t)R(t) - \gamma R(t)D(t)) \\ \Delta D(t) &= (\gamma D(t) - \mu R(t)D(t)) \end{aligned} \tag{3.1}$$

3.1. Description of the model

As already discussed, β, μ and γ be the rate of healthy become infected ($I(t)$), infected become recovered ($R(t)$), infected become death ($D(t)$) respectively. Mathematically death is similar to recovered because both are infection free. The average rate of infectious become death are given by $\gamma I(t)D(t)$. The average rate of infectious become recovered and recovered become infectious are given by $\mu I(t)R(t)$ and $\beta I(t)R(t)$. The average rate of recovered become death are represented in two ways as $\gamma R(t)D(t)$ to study death during infection or partial recovery and $\mu R(t)D(t)$ to study death after being recovered, i.e., natural death.

The exact solutions of (3.1) is found to be

$$I(t) = ce^{\int_{t_0}^{t_n} \beta - \mu R(t) - \gamma D(t) dt}.$$

$$R(t) = ce^{\int_{t_0}^{t_n} \mu I(t) - \beta I(t) - \gamma D(t) dt}.$$

$$D(t) = ce^{\int_{t_0}^{t_n} \gamma - \mu R(t) dt}.$$

For any value $t_0 \leq t \leq t_n$, $\beta - \mu R(t) - \gamma D(t) < 0$, $\mu I(t) - \beta I(t) - \gamma D(t) < 0$, $\gamma - \mu R(t) < 0$ which produces $ce^{(-ve)}$ values as the solutions of (3.1). Thus we call the model (3.1) as system of stiff differential equations. We shall present the test later to confirm it. Now fuzzy system of stiff differential equation are given in (3.2).

$$\begin{aligned} \Delta\tilde{I}(t) &= (\beta\tilde{I}(t) - \mu\tilde{I}(t)\tilde{R}(t) - \gamma\tilde{I}(t)\tilde{D}(t)) \\ \Delta\tilde{R}(t) &= (\mu\tilde{I}(t)\tilde{R}(t) - \beta\tilde{I}(t)\tilde{R}(t) - \gamma\tilde{R}(t)\tilde{D}(t)) \\ \Delta\tilde{D}(t) &= (\gamma\tilde{D}(t) - \mu\tilde{R}(t)\tilde{D}(t)) \end{aligned} \tag{3.2}$$

where, $\tilde{f}(t) = (0.75 + 0.25r, 1.125 - 0.125r)f(t)$ is the fuzzy number with $r \in [0, 1]$.

The initial conditions are the average populations, we presented in Table 1. Since the population cannot be a fractional number we take

$$I(t_0) = I_0 = m_1 = 115482,\ t = t_0,$$

$$R(t_0) = R_0 = m_2 = 82487,\ t = t_0,$$

$$D(t_0) = D_0 = m_3 = 8669,\ t = t_0.$$

The rate of infection, recovered and death are also found by average of ratios of 14 days. Instead of taking β, μ and γ from the Table 1, we are calculating them using more appropriate formulae given below.
$\beta \rightarrow$the rate of infection=Infected case$\times\zeta$ / total case
$\mu \rightarrow$ the rate of recovery=Recovered case$\times\zeta$/ total case
$\gamma \rightarrow$ the rate of death=death case$\times\zeta$/total case
$\zeta \rightarrow$ the rate of total case.
The total case $T(t)$=Infected case $I(t)$+Recovered case $R(t)$+Death case $D(t)$=206638 at $t = t_0$
$T'(t) = I'(t) + R'(t) + D'(t)$
Now we consider the average of those 14 days rate as the required rate.
We found that $\beta = 56$, $\mu = 40$, $\gamma = 4$ and $\zeta = 100$.

4. Stability analysis and stiff system test

4.1. Equilibrium points

The equilibrium points are found by setting $\Delta\tilde{I}(t) = 0$, $\Delta\tilde{R}(t) = 0$ and $\Delta\tilde{D}(t) = 0$. The disease free equilibrium points are $(0, 0, 0)$ and the disease depending equilibrium points are given by $(\frac{\gamma-\beta}{\mu-\beta}, \frac{\gamma}{\mu}, 1 - \frac{\beta}{\gamma})$ thus the values of disease depending equilibrium points are $(3.25, 0.1, -13)$.

4.2. Average transmission number: N_0

The average transmission number is the number telling the average spread of disease from one to others. Though it is similar to basic reproduction number R_0, we are not using susceptible population here. That's why we are calling it by a different name "average transmission number N_0". The

calculation of basic reproduction number requires the population of susceptible case. Since we are not aware of susceptible population, we are introducing this new method for calculating this new number called average transmission number. It is a two step method.

- Calculate $N*$ from setting $\Delta\tilde{D}(t) = 0$, which implies $N* = R = \gamma/\mu$
- Assuming no one are newly infected, few are recovered and few are dead. We have to keep in mind only infected people will infect others and not the dead or recovered people. Also if recovered become infect again they will also spread the disease. The outcome of any epidemic/pandemic disease is the sum of the death case and recovered case. (total case-outcome) = (infected case). But we consider (rate of infected case-rate of outcome) and (rate of total case-sum of rates of infected and death). Multiplying these numbers with $N*$ will constitute the left and right limits of N_0. We use their rates in the form of following formula to calculate the average transmission number N_0.

$$(\beta - \mu - \gamma)N* \leq N_0 \leq (\zeta - \beta - \gamma)N* \tag{4.1}$$

By our calculation,

$$[56 - (40 + 4)]\frac{\gamma}{\mu} \leq N_0 \leq [100 - (56 + 4)]\frac{\gamma}{\mu}$$

$$1.2 \leq N_0 \leq 4.0$$

From the above average transmission number, we can easily assert that this 14 day average pandemic COVID-19 is spreading from infected one to at least 1 person or to at most 4 persons. This number N_0 found from this new method matches with universally accepted basic reproduction number R_0 of COVID-19.

4.3. Stability analysis using eigen values

Theorem 4.1. *When all the eigen values of linearized form of* (3.2) *are* < 0*. Then the model considered is asymptotically stable.*

Proof. Let us first linearize the model (3.2) in the form of Jacobian matrix and name it as A

$$A = \begin{pmatrix} (\beta - \mu\tilde{R}(t) - \gamma\tilde{D}(t)) & -\mu\tilde{I}(t) & \gamma\tilde{I}(t) \\ \mu\tilde{R}(t) - \beta\tilde{R}(t) & (\mu\tilde{I}(t) - \beta\tilde{I}(t) - \gamma\tilde{D}(t)) & -\gamma\tilde{R}(t) \\ 0 & -\mu\tilde{D}(t) & \gamma - \mu\tilde{R}(t) \end{pmatrix} \tag{4.2}$$

On substituting the values of all the parameters and solving (4.2), the characteristic polynomial was found to be $\lambda^3 + 8515964\lambda^2 + 17276845232848\lambda + 422461568851044800 = 0$
The corresponding eigen values are given by

$$\lambda_1 = (-24753.6 + i(1.5522 \times 10^{-10})),$$

$$\lambda_2 = (-5.22464 \times 10^6) + i(1.16415 \times 10^{-10}),$$

$$\lambda_3 = (-3.26657 \times 10^6) - i(4.65661 \times 10^{-10}).$$

Since all the eigen values have the negative real parts, the system we considered is asymptotically stable. □

4.4. Stiff system of fuzzy differential equation-test

Theorem 4.2. *Stiffness test by eigen values*
By the definiton 2.1, a linear fuzzy system or a linearized form of a non linear fuzzy system posses negative real parts in all its eigen values and satisfying

$$q = \frac{max|(Re(\lambda_i))|, i = 1, 2, ..., n}{min|(Re(\lambda_i))|, i = 1, 2, ..., n} >> 1$$

is called stiff system of fuzzy differential equation.

Proof. Let us take (4.2), which is the linerized form of (3.2). We found the eigen values as

$$\lambda_1 = (-24753.6 + i(1.5522 \times 10^{-10})),$$

$$\lambda_2 = (-5.22464 \times 10^6) + i(1.16415 \times 10^{-10}),$$

$$\lambda_3 = (-3.26657 \times 10^6) - i(4.65661 \times 10^{-10}).$$

All are complex numbers whose real part is negative,
Now, calculating the value of q,

$$q = \frac{max|(Re(\lambda_i))|, i = 1, 2, ..., n}{min|(Re(\lambda_i))|, i = 1, 2, ..., n} >> 1,$$

$$q = \frac{24753.6}{3.26657} \approx 7577.8569 >> 1.$$

The (4.2) satisfied the theorem and hence our model (3.2) is the stiff system of fuzzy differential equations which obviously establishes that (3.1) is the stiff system of differential equations. □

5. Numerical simulations

Since the model we considered is a stiff system of differential equations, we do not prefer to use Runge-Kutta methods or any other numerical methods. As already discussed the exact solutions of $\tilde{I}(t)$, $\tilde{R}(t)$, $\tilde{D}(t)$ are in the form $e^{(-ve)value}$. Also those negative values are high requiring very precise small step size which will lead to more number of iterations. So it was found that numerical methods like Runge-Kutta methods are not stable to study any stiff differential equations like (3.1).

So going for software is the better option. Software like Mathematica, Matlab, Maple etc., having build in functions are effective to provide best approximate solutions. We obtain the numerical solutions of both ordinary and fuzzy valued model by using the NDSolve technique of Mathematica software to solve differential equations.

The following plots will be useful to check the average of 14 days pandemic transmission. The plots for March 10 to March 23 are not provided since seeing the table itself we can understand that all the cases like susceptible, infected and recovered are increasing like exponential growth. Without any logistic term to control the growth, the average population itself is giving the stable graphs, which means they are our threshold populations. The graphical representations are given for very minimum time span i.e., 0.00001 days or 0.864 seconds in order to zoom and show how the spread of diseases and each population changes are decreased. Also the main idea is to set a threshold population up to which the spread is under control and possible to completely remove the infection from the globe.

$I(t)$ for $t \in [0, 0.00001]$ and $r = 1$

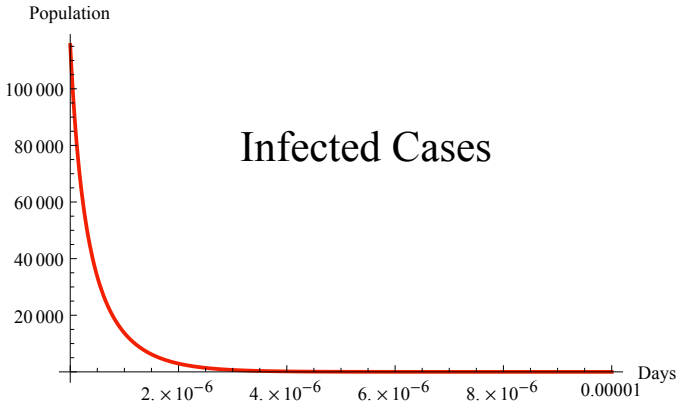

Figure 2. Infected case for every 0.864 seconds (0.00001 days).

$R(t)$ for $t \in [0, 0.00001]$ and $r = 1$

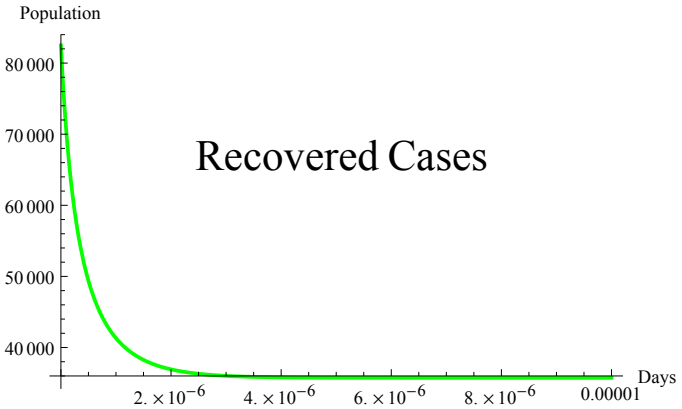

Figure 3. Recovered case for every 0.864 seconds (0.00001 days).

$D(t)$ for $t \in [0, 0.00001]$ and $r = 1$

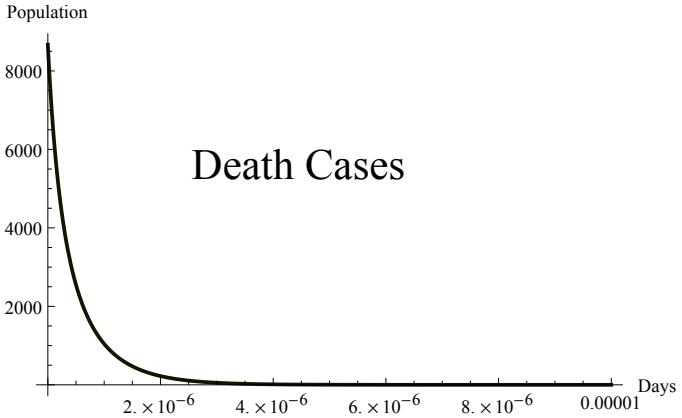

Figure 4. Death case for every 0.864 seconds (0.00001 days).

$\tilde{I}(t)$ for $t \in [0, 1]$ and $r \in [0, 1]$

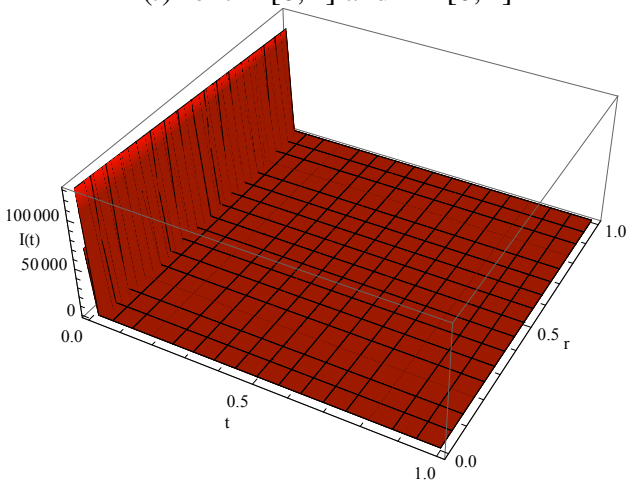

Figure 5. Infected case for every 86400 seconds (1 day).

$\tilde{R}(t)$ for $t \in [0, 1]$ and $r \in [0, 1]$

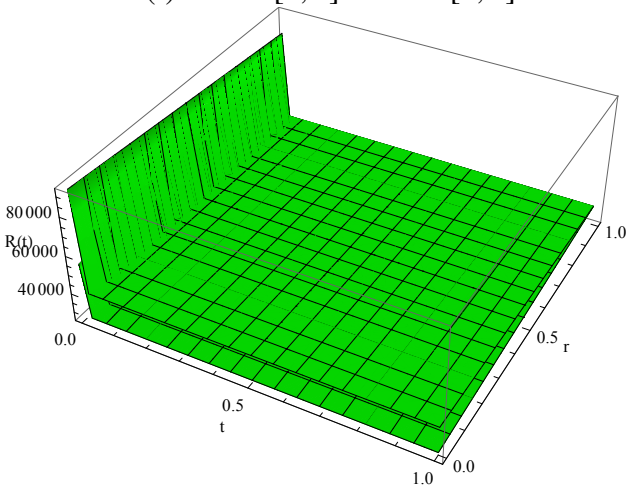

Figure 6. Recovered case for every 86400 seconds (1 day).

$\tilde{D}(t)$ for $t \in [0, 1]$ and $r \in [0, 1]$

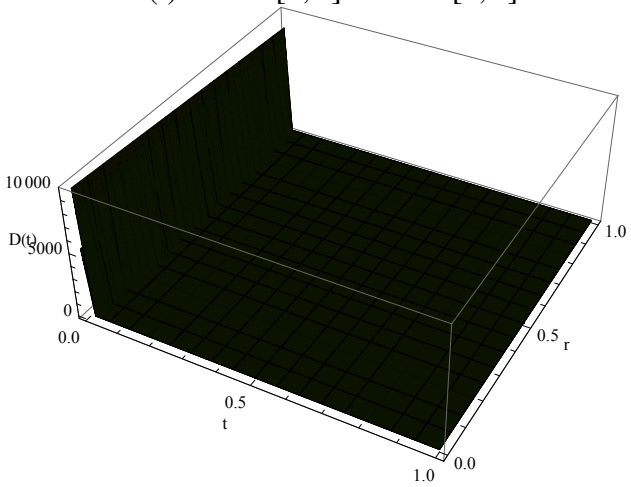

Figure 7. Dead case for every 86400 seconds (1 day).

6. Concluding remarks

Without susceptible population a new model, say IRD-Infection-Recovered and Death model of 14 day average transmission of COVID 19 pandemic system was formulated. It was reformulated as fuzzy system of differential equations. The equilibrium points have been found and stability analysis was done by studying the eigen values. We have given the new method for calculating the new number called average transmission number N_0 which matches with existing result of basic reproduction number R_0. Also we proved that the system considered was stiff system of differential equations as well as stiff system of fuzzy differential equations. From the Table 1, we can see the system is exponentially growing day by day. As a sample, we took the data from March 10, 2020 to March 23, 2020. Since $\tilde{I}(t)$, $\tilde{R}(t)$ and $\tilde{D}(t)$ are growing exponentially, we took the average of those 14 days as our initial populations, say $\tilde{I}(t_0)$, $\tilde{R}(t_0)$ and $\tilde{D}(t_0)$. Also their respective rates are found. From the plots Figures 2–4, we have shown in 0.00001 days (0.864 seconds) in average of 14 days, the cases approaching zero. This means for these initial populations the system produces a stable graph and approaches to zero in every 0.864 seconds per day of 14 day average is clearly noticed in plots. This study makes us to suggest the medical world to fix the threshold population of infectious, recovered and death cases under $I(t) = 115482$, $R(t) = 82487$ and $D(t) = 8669$ and their rates under $\beta = 56$, $\mu = 40$ and $\gamma = 4$. So that, the whole world will easily overcome this deadly disease COVID-19. If the next 14 day average exceeds this threshold population, then it will make the disease to quickly spread and infect everyone in the globe. The respective fuzzy plots were given in Figures 5–7 for 86400 seconds. i.e., for a day.

In this work, instead of prediction we had founded the threshold numbers maintaining under which will reduce the spread of disease and the number of deaths due to it. But as a future work we are going to predict and compare the growth of new daily cases using commonly used metrics for comparison like mean average precision error, regularized R squared values. This stiff fuzzy model is used here to bound the unbound disease growth by setting $0 \leq \alpha \leq 1$ depending on which the stiff model will actively work with the boundary framed by $0 \leq \alpha \leq 1$. This is not the predictive analysis or comparison tool with daily cases data. This stiff fuzzy model is used to analyze the present spread of disease as three cases such as inactive hosts, partially active hosts and completely active hosts. It will be thus useful to confidently propose the threshold number from which medical world and government will get benefited by setting the every 14 day average IRD populations under this threshold number to control the disease and the deaths due to this pandemic disease COVID-19.

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Conflict of interest

All authors declare no conflict of interest.

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