Stability Analysis of Fuzzy Mathematical Measles Model

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Keywords: Stability Analysis, Basic Reproduction Number, Fuzzy Basic Reproduction Number, Euler Method.

Abstract: The well-known susceptible-infected-recovered (SIR) mathematical model is used in this work to investigate the disease's spread utilising fuzzy parameters. We have demonstrated that when the reproduction number is less than unity, the disease-free equilibrium point is locally asymptotically stable. In order to extend the concept of basic reproduction number, we are creating a fuzzy basic reproduction number. We are examining the approximate numerical solution of the fuzzy non-linear differential equation applying Euler method and the outcome is examined with the basic reproduction number.

1 INTRODUCTION

One of the most aggressive bacterial illnesses, measles is brought on by the measles virus, which is found in the snot of affected people's throats and noses. Among all animal species, this virus is solely present in the human body and belongs to the paramyxovirus family (genus morbilivirus). The infected person's spitting and blowing can directly transmit this virus from one person to another. High fever, coughing, cataracts, allergies, little white spots on the body, and a rash are the early symptoms of measles in infected individuals. More vulnerable populations include people over the age of 20 and those under the age of five who are more at risk from this illness. Infections in the ears and sinuses, oral ulcers, diarrhoea, and malnutrition are among the consequences.

Measles outbreaks were reported on multiple occasions in various locations throughout Bangladesh, one of the South East Asia Region (SEAR) countries, between 2000 and 2016. In Bangladesh during this time, there were 33,213 recorded incidents and approximately 70,273 reported cases of the measles14. Despite the fact that the Expanded Program of Immunization (EPI) began in Bangladesh in 1979 to control and prevent measles. The government has continued these efforts in 2014 with the introduction of the combined treatment of the measles-containing vaccine (MCV2), with the goal of eradicating the disease nationwide by 2018. As a result, during the past few decades, measles cases have decreased by up to 84%. However, since 2016, there has been an increase in measles cases across the country. Considering certain already-existing obstacles, Rohingya refugees provide yet again another difficulty in the fight against measles.

The study of communicable diseases epidemiologic is heavily reliant on mathematical modelling and simulation. A key factor in the rigorous investigation, dissemination, and treatment of the disease is the use of mathematical models. Applying contemporary processing capabilities is a straightforward way to achieve the desired results. This is utilized to solve problems in many different fields. The authors have created a model that increases awareness through interactions with the aware population and public awareness campaigns (Agaba al. 2017). The developed framework is predicted to be advantageous to the researchers and medical professionals engaged in respiratory cancer charities. Making plans and making decisions for lung cancer prevention and treatment may help to identify the underlying causes of lung cancer and take the necessary steps to control them, thus enhancing global public health (Ahmed et al. 2021). The model's simulation results, according to the authors, shows that, under certain circumstances, brucellosis will entirely vanish or see a discernible drop throughout the whole population of the Democratic People's Republic of Congo (DRC) (Kasereka et al. 2020). Using data on pulmonary tuberculosis in Malang, the results of hypothesis assessment and

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computation showed that cases spiked briefly before declining in Makassar (Side et al. 2018). The simulation results show that COVID-19 transmission varies with corona virus load. The effects of vaccination and adherence to rules governing health have an equal influence on slowing or stopping the spread of COVID-19 in Indonesia (Abdy et al. 2021). The infected cases in India that a time series projections model is utilized for, as well as the time series predictions of actual cases against expected instances in India, were both examined by Bimal Kumar Mishra et al. (Mishra et al. 2021), as well as a time series forecasting model for India's case fatality rate. The major goal of this research is to restrict the propagation of the viral by estimating the reproduction number. The researchers have created the SEIR-SEI mathematical model by taking a few characteristics into consideration as fuzzy numbers by sweatha.et.al (Sweatha et al. 2022) The presence of backward bifurcation, as stated in Fuzzy SIR-epidemic model for transmission of measels by zaman.et.al (Zaman et al. 2017) The major goals of this paper are to investigate the fuzzy SIR model for malaria using stability analysis and backward bifurcation by Yuyang Chen.et.al (Joshua et al. 2020, Isaac et al. 2015, Kaiming et al. 2020).

2 PRELIMINARIES

2.1 Fuzzy Set

Let X be a nonempty crisp sets. A fuzzy subset S of X is denoted by and is defined as:

$$\tilde{S} = \{(x, \mu_{S(x)}) : x \epsilon\, X\}$$

Where μ_S: X$\rightarrow$ [0,1] is a membership function associated with a fuzzy set $\tilde{S}$ 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.

2.2 Fuzzy Measure

Let Ω be a non-empty set and P(Ω) denote the set of all subsets of Ω. Then μ: Ω $\rightarrow$ [0,1] is a fuzzy measure if (Zaman et al. 2017):

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

2) for A,B P(Ω) ,μ(A) $\leq$ μ(B) if A$\subset$ B

Let μ: Ω $\rightarrow$ [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.

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

Where

$$k(\alpha) = \mu\{\omega\epsilon\Omega : \mu(\omega) \geq \alpha\}$$

2.3 Fuzzy Mathematical Model

The core SIR model splits the population contributing to the transmission of an ailment into three epidemiology classes: Susceptible covers persons who have the ability to contract the illness, infected people who are contagious, and removed people who have previously been associated with the disease's spread. The SIR model's equation system is listed below:

Susceptible: They are the people who are exposed to the spread of the disease out of the overall population (N).

Infected: People who exhibit infectious disease symptoms are classified as to the infected population. They can transmit the disease because they are also contagious.

Recovered: Persons who have undergone treatment or taken vaccination and recovered from the infectious disease are termed as recovered population. When developing the model for the transmission of measles among people with the entire population, the system of nonlinear ordinary differential equations is taken into account (Zaman et al. 2017). Let says that π is the virus load.

$$ds/dt = -\alpha(\pi)SI + \mu R \qquad (1)$$

$$dI/dt = \alpha(\pi)SI - \beta(\pi)I \qquad (2)$$

$$dR/dt = \beta(\pi)I - \mu R \qquad (3)$$

Where

- α is the rate of transmission
- β is the recovery rate
- μ is the rate of losing immunity
- π is the virus load

2.4 Analysis of Fuzzy System

$\alpha = \alpha(\pi)$ be the membership function this is a rising function because as the population of people who are susceptible grows, the risk of infection will also grow. The transmission rate is selected to be fuzzy membership function because it is more appropriate than the alternatives. In order to build a fuzzy membership function, we assume that the virus load of the disease in an individual is quite low (π_{min}),

making the possibility of transmission negligible. The least amount of virus load required to transmit the disease is π_0. When the virus load is at its highest, the viral spread rate reaches its optimum level and reaches one. However, we presume that π_{max} is the maximum permitted viral load that an individual can have. We define $\alpha(\pi)$ as follows and fig:1 describes the membership function of $\alpha(\pi)$ as follows (Sweatha et al. 2022):

$$\alpha(\pi) = \begin{cases} 0, & if \ \pi < \pi_{min}, \\ \frac{1-\alpha_0}{\pi_{max}}\pi + \alpha_0, & if \ \pi_{min} \leq \pi \leq \pi_0, \\ 1, & if \ \pi_0 \leq \pi \leq \pi_{max} \end{cases} \quad (4)$$

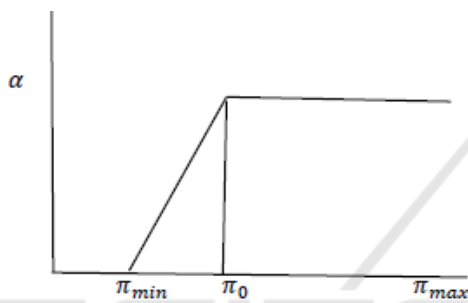Where $\pi_0 > 0$ is the lowest infection rate.

Figure 1.

And $\beta = \beta(\pi)$ is the fuzzy membership function for the recovery rate. It is a decreasing function since a higher viral load makes recovery from infection take longer. The fuzzy membership function of $\beta = \beta(\pi)$ is represented in the following equation

$$\beta(\pi) = \frac{(\pi_{min}-1)}{\pi_{max}}\pi + 1 \ if \ 0 < \pi < \pi_{max}$$

The recovery rate that is lowest is $\pi_{min} > 1$. Figure 2 illustrates how the membership function $\beta(\pi)$ works.
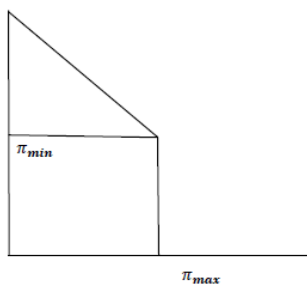

Figure 2.

2.5 Membership Function of $\Gamma(\pi)$

Additionally, as virus load is regarded as a linguistic variable, we take into account the fact that different individuals have varying viral loads. The members of the linguistic variable are listed below (Sweatha et al. 2022):

$$\Gamma(\pi) = \begin{cases} 0, & if \ \pi < \bar{\pi} - \delta \\ \frac{\pi - \bar{\pi} + \delta}{\delta}, & if \ \bar{\pi} - \delta \leq \pi \leq \bar{\pi} \\ \frac{-(\pi - \bar{\pi} + \delta)}{\delta}, & if \ \bar{\pi} \leq \pi \leq \bar{\pi} + \delta \\ 0, & if \ \pi > \bar{\pi} + \delta \end{cases}$$
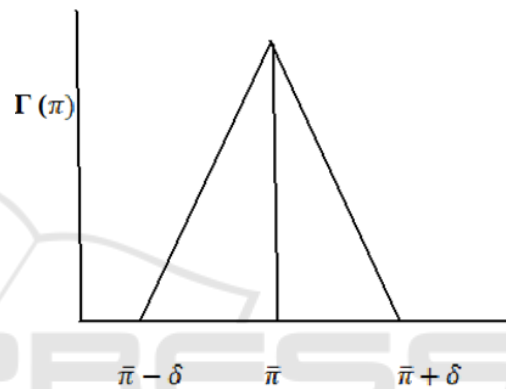

Figure 3: Membership function of $\Gamma(\pi)$.

The symbols $\bar{\pi}$ and δ stand for the centre value and dispersion of each fuzzy set assumed. There are three levels for the linguistic variable: weak, medium, and high. Every classification can be seen as a triangular-shaped fuzzy number. The following graphic provides a diagrammatic representation of the membership function $\Gamma(\pi)$. The figure 3 is the membership function of $\Gamma(\pi)$.

Equilibrium Points
The disease free equilibrium and endemic equilibrium are the two equilibrium points in the model. In order to find these two equilibrium points each of the equations in (1),(2),(3) must equals zero.

Disease Free Equilibrium Points
The points of DFE implies that there is no transmission of the disease, namely I = I_0 = 0 and R = R_0 = 0. Thus the DFE is
S = S_0 = 0
$R_0 = (S_0, I_0, R_0) = (0, 0, 0)$

Basic Reproduction Number

BRN is the average number of secondary infections carried on by a single infectious person throughout the lifetime of an infection. The BRN is determined using next generation matrix method (Isaac et al. 2015, Kaiming et al. 2020).

$$F = \alpha(\pi)S \qquad V = \beta(\pi)$$

$$V^{-1} = \frac{1}{\beta(\pi)}$$

$$R_0(\pi) = \frac{\alpha(\pi)S}{\beta(\pi)} \qquad (5)$$

3 STABILITY ANALYSIS

Theorem 1:

The DFE of our model is locally asymptotically stable when $R_0 < 1$

Proof:

The Jacobian matrix is

$$J = \begin{bmatrix} -\alpha I & -\alpha S & \mu \\ \alpha I & \alpha S - \beta & 0 \\ 0 & \beta & -\mu \end{bmatrix}$$

At DFE

$$J_0 = \begin{bmatrix} 0 & 0 & \mu \\ 0 & -\beta & 0 \\ 0 & \beta & -\mu \end{bmatrix}$$

The characteristic equation at the disease-free equilibrium point is

$$\lambda^3 + (\beta + \mu)\lambda^2 + \beta\mu\lambda = 0 \qquad (6)$$

According to Routh-Hurwitz criteria the disease-free equilibrium point is said to be asymptotically stable.

Global Stability

While considering Lyapunov function $g_a(t, S, I, R) = AI'$ by substituting the value of I' we found that the lypnov function is 0 iff I is 0. Hence by Lasalle's invariance principle the disease is globally asymptotically stable.

Fuzzy Basic Reproduction Number

The **fuzzy basic reproduction number** is given by (Zaman et al. 2017),

$$R_0{}^f = \frac{1}{\beta_0} FEV(\beta_0 R_0(\pi))$$

where $FEV(\beta_0 R_0(\pi)) = \sup \{\inf(\tau, k(\tau))\}, 0 \le \tau \le 1$,
$k(\tau) = \mu\{\tau : \beta_0 R0(\pi) \ge \tau\} = \mu(X)$, which is a fuzzy measure. To obtain $FEV(\beta_0 R_0(\pi))$ we need to define fuzzy measure μ which is given by

$$\mu(X) = \sup \Gamma(\pi), \forall \pi \in X, X \subset R$$

From $FEV(\beta_0 R_0(\pi))$, here $R_0(\pi)$ is not diminishing with, where the set, $X = [\bar{\pi}, \pi_{max}]$, and π is the solution to the underlying expression

$$\frac{\alpha(\pi)S}{\beta_0(\pi)} = \pi$$

Thus, $k(\pi) = \mu [\bar{\pi}, \pi_{max}] = \sup \Gamma(\pi)$ with $\bar{\pi} \le \pi_{max}$ where $k(0) = 1$ and $k(1) = \Gamma(\pi_{max})$.

The amount of virus π 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(π_{min}), medium virus load (π_0) and strong virus load (π_{max}).

Case 1: Weak virus load (π_{min})
(i.e.) when $\bar{\pi} + \delta \le \pi_{min}$, we have

$$FEV(\beta_0 R_0(\pi)) = 0 < \beta_0 \Leftrightarrow R_0{}^f < 1$$

Thus, we can conclude that the disease will be extinct.

Case 2: Medium virus load (π_0)
(i.e.) when $\bar{\pi} - \delta \ge \sigma_{min}$ and $\bar{\pi} + \delta \le \pi_0$
Therefore,

$$k(\pi) = \begin{cases} 1, & if \ 0 < \pi \le \beta_0 R0(\bar{\pi}), \\ \Gamma(\sigma'), & if \ \beta_0 R0(\bar{\pi}), < \alpha \le \beta_0 R0(\bar{\pi} + \delta), \\ 0, & if \ \beta_0 R0(\bar{\pi} + \delta) < \pi \le 1 \end{cases}$$

So, if $\delta > 0$, $k(\pi)$ is continuous and diminishing function with $k(0) = 1$ and $k(1) = 0$. Hence, $FEV(\beta_0 R0(\pi))$ is the fixed point of k and

$$\beta_0 R0(\bar{\pi}) \le FEV(\beta_0 R0(\pi)) \le \beta_0 R0(\bar{\pi} + \delta)$$
$$R0(\bar{\pi}) \le R_0{}^f \le R0(\bar{\pi} + \delta)$$

As the function R0 $(\bar{\pi})$ is increasing and continuous function then by the intermediate value theorem there exists π with $\bar{\pi} < \sigma < \bar{\pi} + \delta$ such that

$$R_0{}^f = R_0(\pi) > R_0(\bar{\pi})$$

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

Case 3: Strong virus load (π_{max})
(i.e.) when $\bar{\pi} + \delta \leq \pi_0$ and $\bar{\pi} + \delta \leq \pi_{max}$, then

$$k(\pi) = \begin{cases} 1, & if \ \ 0 < \pi \leq \beta_0 \ R0 \ (\bar{\pi}), \\ \Gamma(\bar{\pi}), & if \ \beta_0 \ R0 \ (\bar{\pi}) < \pi \leq \beta_0 \ R0 \ (\bar{\pi} + \delta), \\ 0, & if \ \ \beta_0 \ R0 \ (\bar{\pi} + \delta), < \pi \leq 1 \end{cases}$$

Similar to case 2, we have

$\beta_0 \ R0 \ (\bar{\pi}) \leq \ FEV(\gamma_0 \ R_0(\sigma)) \leq \ \beta_0 \ R0 \ (\bar{\pi} + \delta)$,
$R0 \ (\bar{\pi}) \leq \ R_0{}^f \leq R0 \ (\bar{\pi} + \delta)$

Thus, $R_0{}^f > 1$; we can infer that the illness will be widespread.

3.1 Numerical Simulation

In order to solve the numerical simulation, we made the following assumptions: S = 500, I = 100, R = 0, α = 0.00000181, β = 0.0009, μ = 0.2
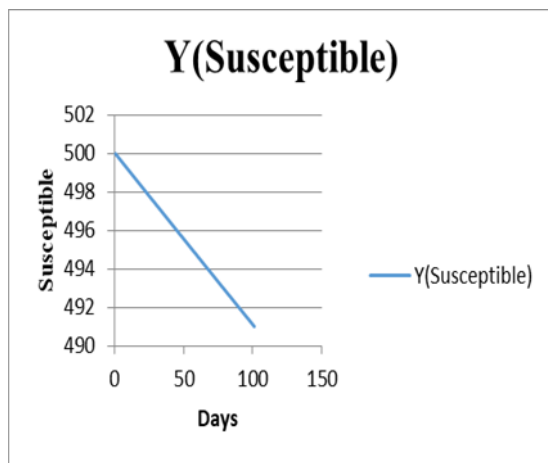
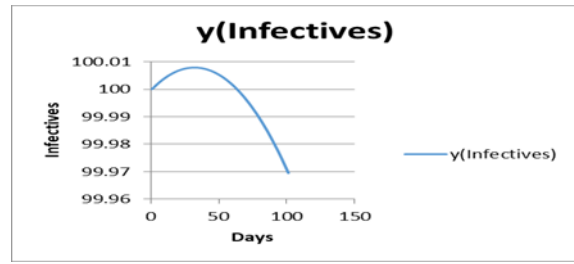Figure 4: Susceptible population using Euler.

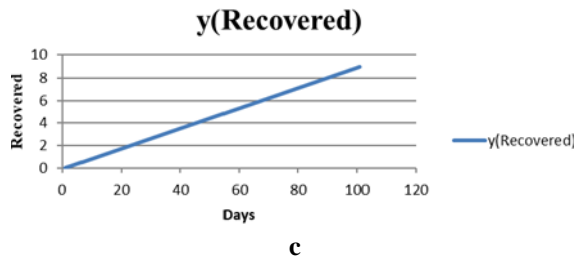Figure 5: Infected population using Euler's method.
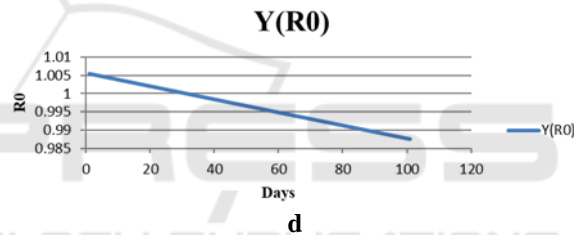
Figure 6: Recovered population using Euler's method.

Figure 7: represents the graph for basic reproduction number.

The figures 4, 5, 6 are the susceptible, infected and recovered population which is depicted using Euler's method. Figure d shows the dynamical behaviour of basic reproduction number. It also shows that when R0 value less than unity, that is around 30 days infection graph in fig b also falls down after 30 days

In order to solve the numerical simulation, we made the following assumptions: S = 500, I = 100, R = 0, α = 0.00000181, β = 0.0009, μ = 0.2. Using Euler method we found first 20 values in the similar manner we can find for next consecutive days.
In order to solve the numerical simulation, we made the following assumptions:
S = 500, I = 100, R = 0, = 0.00000181, = 0.0009, = 0.2

4 CONCLUSION

The compartmental SIR epidemic model has been utilized in this paper to examine the population spread. We

Table 1: is calculated using Euler's meth.

X (Date)	Y (R0)	Y (Susceptible)	Y (Infectives)	Y (Recovered)
0	1.005555556	500	100	0
1	1.00537355	499.9095	100.0005	0.09
2	1.005191577	499.8190161	100.0009836	0.18000027
3	1.005009636	499.7285483	100.0014509	0.270000795
4	1.004827728	499.6380967	100.0019017	0.360001561
5	1.004645852	499.5476612	100.0023362	0.450002553
6	1.004464009	499.4572419	100.0027544	0.540003755
7	1.004282198	499.3668387	100.0031562	0.630005154
8	1.00410042	499.2764517	100.0035416	0.720006735
9	1.003918674	499.1860809	100.0039106	0.810008482
10	1.003736961	499.0957263	100.0042633	0.900010382
11	1.00355528	499.0053879	100.0045997	0.990012419
12	1.003373632	498.9150658	100.0049196	1.080014578
13	1.003192017	498.8247599	100.0052233	1.170016846
14	1.003010435	498.7344702	100.0055106	1.260019207
15	1.002828885	498.6441968	100.0057815	1.350021646
16	1.002647368	498.5539397	100.0060361	1.44002415
17	1.002465883	498.4636989	100.0062744	1.530026702
18	1.002284432	498.3734743	100.0064964	1.620029289
19	1.002103013	498.2832661	100.006702	1.710031896
20	1.001921627	498.1930742	100.0068913	1.800034507

determined the membership function and derived the fuzzy parameters as a function of viral load. We have identified the conditions for the local stability of the endemic equilibrium and the disease-free equilibrium of our model. Figure 7 shows the dynamical behaviour of basic reproduction number. It also shows that when R0 value less than unity, that is around 30 days infection graph in fig. 5 also falls down after 30 days. That is around 35 days the infection rate reduced to 20% in the meantime recovery rate gradually increases around 2%.

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