### Article

# Fuzzy modeling for the spread of influenza virus and its possible control

# Renu Verma, S.P. Tiwari, Ranjit Kumar Upadhyay

Department of Applied Mathematics, Indian Institute of Technology (ISM) Dhanbad-826004, India E-mail: renuismmaths@gmail.com, sptiwarimaths@gmail.com, ranjit\_ism@yahoo.com

Received 11 November 2017; Accepted 20 December 2017; Published 1 March 2018

#### Abstract

In this paper, we analyze a model of Influenza spread with an asymptotic transmission rate, wherein the disease transmission rate and death rate are considered as fuzzy sets. Comparative studies of the equilibrium points of the disease for the classical and fuzzy models are performed. Using the concept of probability measure and fuzzy expected value, we obtain the fuzzy basic reproduction number for groups of infected individuals with different virus loads. Further, a basic reproduction number for the classical and the fuzzy model are compared. Finally, a program based on the basic reproduction value of disease control is suggested and the numerical simulations are carried out to illustrate the analytical results.

Keywords influenza virus; fuzzy expected value; fuzzy basic reproduction number; bifurcation; stability.

Computational Ecology and Software ISSN 2220-721X URL: http://www.iaees.org/publications/journals/ces/online-version.asp RSS: http://www.iaees.org/publications/journals/ces/rss.xml E-mail: ces@iaees.org Editor-in-Chief: WenJun Zhang Publisher: International Academy of Ecology and Environmental Sciences

#### **1** Introduction

Influenza epidemics are observed worldwide with excessive morbidity and mortality, and influenza happen to a problem of public health. Spanish flu (1918-1919) was the most prominent and fatal outbreak, caused by influenza A virus (H1N1). Influenza, a contagious disease, burst out during 1918-1920 (Spanish flu), 1957-1958 (Asian flu), 1968-1969 (Hong Kong flu), 2002-2003 (SARS) and 2009-2010 (A/H1N1), and killed tens of millions of people. A number of researchers have studied mathematical modeling of influenza from different point of views (Qiu et al., 2010; Ruan et al., 2003; Sattenspiel et al., 2003; Tang et al., 2010). Also, a number of deterministic epidemic models have been proposed to perceive the transmission dynamics of influenza (Alexander et al., 2004; Chong et al., 2014; Gonzâlez-Parra et al., 2011; Gumel, 2009; Samsuzzoha et al., 2011). Influenza virus is a member of the Orthomyxoviridae family, which precisely consists of four genera: Influenza A virus, Influenza B virus, Influenza C virus, and Thogoto virus. Influenza A viruses, infect humans, avian species, swine, and other mammalian species, while, influenza B and C viruses infect humans (Gillim-Ross and Subbarao, 2006). Influenza is representative transmitted across the air by coughs or sneezes, creating aerosols containing the virus.

Behavior turn under influences of consciousness of infection risk have been analyzed (D'Onofrio and Manfredi, 2009; Epstein et al., 2008; Funk et al., 2010; Kiss et al., 2010; Poletti et al., 2009; Su and Wang, 2015). In these works, mathematical models divide human population into a group with the lower infection risk and a group with the higher infection risk, analyzes the transfer of behavior attribute as an outcome of social interaction, and analyzes how these behavior riposte effect of disease transmission in dynamics. It has been described that behavior alteration can persuade rich dynamical criterion involving sustained oscillations and multiple waves of infections. Gao et al. (2006), Kaddar (2009), Ruan and Wang (2003), Zhang (2016, 2018), and Zhang et al. (2011) analyzed several types of epidemic models, most of which have explored the transmission rate of susceptible individuals who have been reveal to infected individuals. Different incidence functions have been utilized in epidemic models, of which the most common are bilinear and saturated incidences. The bilinear (or mass-action) incidence rate is originated by  $\beta SI$ , where  $\beta$  is a positive constant, and S and I are the number of susceptible and infected individuals, respectively by Zhang et al. (2008) and Zhou and Liu (2003). Both susceptibility and infectiousness being intrinsically vague concepts become ideal subjects for fuzzy logic analysis. The fuzzy logic approach considers health and disease as, at least partially; complementary states (Zadeh, 1999). Uncertainty in epidemiology is not restricted to random variations. Actually, there are two kinds of uncertainty (Ferson and Ginsburg, 1996). One kind arises as variability resulting from heterogeneity or stochasticity, while the other arises as partial ignorance resulting from systematic measurement errors or subjective (epistemic) uncertainty. Therefore, variability and ignorance should be treated separately, the former by probability theory and the latter by Bayesian analysis and/or multivalued fuzzy logic.

After introduction of the concept of fuzzy sets by (Zadeh, 1965), a broad effort has been dedicated to the development of various aspects of the theory and applications of fuzzy systems, in particular to the theory of differential equations with uncertainty. (Barros et al., 2003; Barros and Bassanezi, 1999; Bassanezi and Barros, 1995) proposed a new approach to treat an ecological model using fuzzy parameters in differential equations that describes the dynamical system. In this case, the solution of the set of equations is found to be so-called fuzzy expected value. Applying that approach in epidemiological systems is not easy because several details should be treated carefully. In order to investigate, how fuzzy logic could treat epidemic systems in a more realistic way (Sugeno, 1974) in his doctoral work, presented a linguistic fuzzy model applied to the canine rabies problem of São Paulo City.

Some epidemic model by considering uncertainty of the parameter space and heterogeneity in the population were introduced and studied by Massad et al. (2008), while Ortega et al. (2000) have studied the fuzzy dynamical systems in epidemic model and Farahi and Barati (2011) studied the fuzzy time delay dynamical systems by applying a fuzzy theory approach. In different directions, the recent study on fuzzy parameter (Massad et al., 2008; Mishra and Pandey, 2010; Pal et al., 2013) described interval valued parameter set in a harvested prey-predator model and an epidemic model with fuzzy parameters which they have studied for computer network. Recently, Mondal et al. (2015) have studied the dynamical behavior of an epidemic model with fuzzy transmission. The fuzzy epidemic models for human infectious diseases were studied (Barros and Bassanezi, 2003; Jafelice et al., 2004; Massad et al., 1999; Massad et al., 2008; Ortega et al., 2000).

In this paper, we study a model recently proposed by Upadhyay et al. (2014) in which the individuals are considered, assuming that they infect according to their viral charge (that is limited). In this case, the transmission rate (contact rate) and death rate has been considered as fuzzy sets which depend on the viral charge. The paper is organized as follows: In Section 2, we recall the dynamical behavior of the crisp system. In Section 3, we analyze the fuzzy system and describe the transmission coefficient of the disease and disease-

induced mortality as fuzzy number. We present a new definition of the fuzzy basic reproduction value which is different from the classical model and provides some conditions for the disease control in fuzzy epidemic system. In Section 4, numerical simulations have been presented to illustrate the analytical results. Lastly, a brief discussion and conclusions have been given in Section 5.

We close this section by recalling some basic notions related to fuzzy sets and fuzzy expected value. For details on fuzzy sets, we refer Barros et al. (2003) and Klir and Yuan (1995).

**Definition 1.1** For a nonempty set X, a fuzzy set F in X is a map  $F : X \to [0,1]$ . For a nonempty set X, we shall denote by F(X), the collection of all fuzzy sets in X. For  $F \in F(X)$  and  $\alpha \in [0,1]$ , the set  ${}^{\alpha}F = \{x \in X : F(X) > \alpha\}$  is called the  $\alpha$ -cut of F.

**Definition 1.2** Let X be a nonempty set and P(X) be the power set of X. The function  $\mu: P(X) \to [0,1]$  is called a fuzzy measure if

- (i)  $\mu(\phi) = 0$  and  $\mu(X) = 1$ , and
- (ii)  $\mu(\mathbf{A}) \leq \mu(\mathbf{B})$  if  $\mathbf{A} \subseteq \mathbf{B}$ .

**Definition 1.3** The fuzzy expected value of a fuzzy set *F* is a map  $FEV : F(X) \rightarrow [0,1]$  such that  $FEV(F) = \sup_{0 \le \alpha \le 1} \inf[\alpha, k(\alpha)]$ , where  $k(\alpha) = \mu\{x \in X : F(x) \ge \alpha\}$  and  $\mu$  is a fuzzy measure.

**Remark 1.1** It is easy to see that k(0) = 1 and k(1) = 0.

**Definition 1.4** A fuzzy set F in the set of real is called a fuzzy number if

- (i) F must be a normal fuzzy set, i.e.,  $F(\mathbf{x}_0) = 1$ , for some  $x_0 \in \mathbf{x}_0$ ,
- (ii)  ${}^{\alpha}F$  is a closed interval for every  $\alpha \in [0,1]$ , and
- (iii) the support of F is bounded.

## 2 Model for Influenza Virus with Equilibrium and Stability Criteria

Recently, Upadhyay et al. (2014) have proposed a simple model of influenza spread with an asymptotic transmission rate. In the *SI* model, it has been described that the dynamics of directly transmitted diseases with interaction between susceptible and infected individuals in the absence of vital dynamics (i.e., the rates of birth and mortality are not considered). Following is the system of differential equations describing the proposed model.

$$\frac{dS}{dt} = \frac{S}{N} \left( b(N) - d(N) \right) - \frac{\beta SI}{N+c},$$
  
$$\frac{dI}{dt} = \frac{\beta SI}{S+I+c} - aI$$
(1b)

with initial condition  $S(0) = S_0$ ,  $I(0) = I_0$ .

Here S is the proportion of susceptible individuals, I is the proportion of infected individuals at each instant,  $\beta$  denotes the contact rate between infective and susceptible, a denotes the disease-induced mortality, r is the intrinsic growth rate of susceptible individuals and K > 0 the carrying capacity, c represents half saturation constant (see the derivation of a Holling type (II) functional response in prey-predator models).

Following is towards equilibrium and stability criteria of model (1).

**Theorem 2.1** The system has three equilibrium points, namely, the trivial equilibrium point  $E_0 = (0,0)$ , disease- free equilibrium  $E_1 = (1,0)$ , and the nontrivial equilibrium point  $E^*(S^*, I^*)$ .

**Theorem 2.2** The disease-free equilibrium (1,0) is locally asymptotically stable when  $\Re_0 < 1$  and unstable when  $\Re_0 > 1$ .

**Theorem 2.3** If  $\mathfrak{R}_0 > \frac{c+K}{K}$  hold, the endemic equilibrium  $E^*(S^*, I^*)$  is always locally asymptotically stable.

**Remark 2.1** In the model system (1) the basic reproduction number is defined by  $\Re_0 = \frac{\beta}{a}$ . The disease will be successfully invade when  $\Re_0 > 1$  but will die out when  $\Re_0 < 1$ .  $\Re_0 = 1$  is usually a threshold whether the disease becomes endemic or goes to extinction. We may consider that the system undergoes a bifurcation around the disease free equilibrium for  $\Re_0 = 1$ .

In the model (1), both the concepts of susceptible and infectious may be uncertain in the perception that there may be different degrees among the individuals of population. The population groups have their different habits and customs, different degrees of resistance, etc. In this way, to make the model more realistic, we consider the parameter  $\beta$  and a both as a fuzzy numbers and called the system as a fuzzy model system, which we have to study in the next sections. Also, we consider the populations in normalized form and hence S(t) + I(t) = 1. (2)

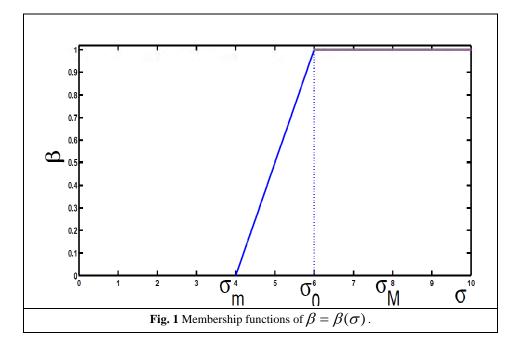
# 3 Analysis of the Fuzzy Model System

In this section, we consider the two important parameters of the model, i.e., the contact rate between infective and susceptible  $\beta$  and death- induced mortality a is fuzzy numbers. We assume that they are the function of virus load  $\sigma$  and their fuzzy membership functions are defined. We study the concepts of contact rate  $\beta(\sigma)$ , death-induced mortality  $a(\sigma)$  and virus-load  $\sigma$ . Towards the end, we provide an analysis and interpretation of the system.

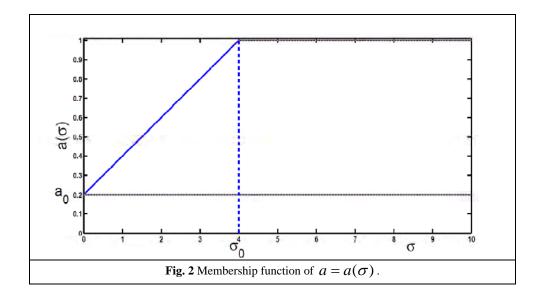
We assume that the population in this fuzzy model is given by the infected individuals and diseaseinduced mortality as the function of the accessible virus. Let  $\beta = \beta(\sigma)$  be the chance of transmission to turn out in a meeting between a susceptible and an infected individuals with the amount of virus  $\sigma$ . Then there will be the maximum chance of disease transmission when the virus-load is maximum. From (Barros et al., 2003), fuzzy membership function of the transmission parameter  $\beta(\sigma)$  is given by

$$\beta(\sigma) = \begin{cases} 0 & \text{if } \sigma < \sigma_m \\ \frac{\sigma - \sigma_m}{\sigma_0 - \sigma_m} & \text{if } \sigma_m \le \sigma \le \sigma_0 \\ 1 & \text{if } \sigma_0 < \sigma < \sigma_M \end{cases}$$

From above, it is clear that if the virus-load is low then the disease transmission will be negligible and that there is a minimum virus-load  $\sigma_m$  is required. Moreover, there should be a certain amount of virus say,  $\sigma_0$  where the transmission rate is maximum and equal to unity. Again, the amount of virus is always limited by  $\sigma_M$  for each disease. The diagram for membership function of  $\beta(\sigma)$  is given in Fig. 1.



The death rate can also be assumed to be a fuzzy number as it occurs due to the infection of the disease. When the disease transmission is negligible for low virus load, there is only natural death. So there is no transmission of disease due to infection say,  $a_0$ . Also, it is an increasing function of  $\sigma$ . When the amount of virus is at its highest level, i.e.,  $\sigma_0 < \sigma$ , the death will be higher. In view of this, the fuzzy membership function of  $a(\sigma)$  is given by



$$a(\sigma) = \begin{cases} \frac{1-a_0}{\sigma_0}\sigma + a_0 & \text{if } 0 \le \sigma \le \sigma_0\\ 1 & \text{if } \sigma_0 < \sigma \end{cases}$$

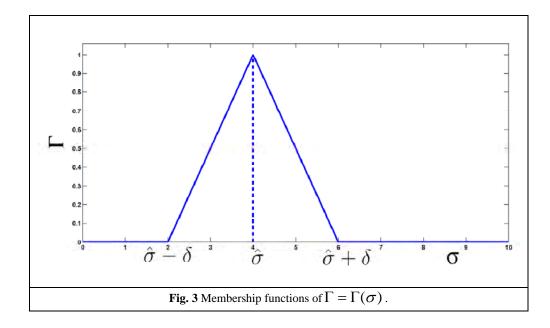
where  $0 < a_0 < 1$ , is the lowest death rate. The diagram for membership function of death rate  $a(\sigma)$  is given in Fig. 2.

We also assume that the virus load of the studied group  $\Gamma$  may be different for different individuals and so,  $\Gamma$  can be viewed as a linguistic variable with classification given by an expert according to the studied group. Each classification is modeled by a fuzzy number whose membership function is given as under.

$$\Gamma(\sigma) = \begin{cases} 0 & \text{if } \sigma < \hat{\sigma} - \delta \\ \frac{\sigma - \hat{\sigma} + \delta}{\delta} & \text{if } \hat{\sigma} - \delta \le \sigma \le \hat{\sigma} \\ -\frac{\sigma - \hat{\sigma} - \delta}{\delta} & \text{if } \hat{\sigma} < \sigma \le \hat{\sigma} + \delta \\ 1 & \text{if } \sigma > \hat{\sigma} + \delta \end{cases}$$

Here, the parameter  $\hat{\sigma}$  is a central value and  $\delta$  gives the dispersion of each one of the fuzzy sets assumed by  $\sigma$ . For fixed  $\hat{\sigma}$ ,  $\Gamma(\sigma)$  can have a linguistic meaning, given by an expert, such as weak, medium and high. From (Barros et al., 2003), the diagram for membership function of  $\Gamma$  is given in Fig. 3.

For each value of  $\sigma$ ,  $I(\sigma,t)$  can be interpreted as a family of solutions of model (1), which provide the number of infected individuals created by the contact between susceptible and infected individuals with an amount of virus load  $\sigma$  at time t. It is clear that  $I(\sigma,t)$  is a fuzzy number for each fixed time t. Since, from (2) we have  $0 \le I(\sigma,t) \le 1$ .



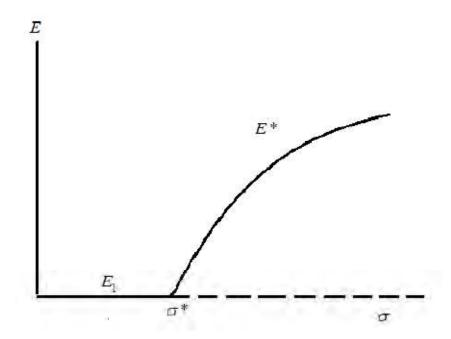


Fig. 4 Bifurcation diagrams (Barros et al., 2003).

#### 3.1 Bifurcation and fuzzy basic reproduction number

The basic reproduction number  $\Re_0$  may vary significant for different infectious diseases but also for the same disease in different populations. The threshold result of epidemic theory associates the outbreaks of epidemics and the persistence of endemic levels with basic reproduction numbers greater than one and the disease dies out when its value is less than unity. The stability of the disease-free equilibrium changes from unstable to stable while the basic reproduction number increases through 1 but when  $\Re_0 = 1$ , the system obtains a bifurcation at the disease-free equilibrium. Now, we consider the bifurcation value at  $\sigma^*$ , where  $\sigma^*$  (Fig. 4) is

given by 
$$\sigma^* = \frac{\sigma_0 \sigma_m + a_0 \sigma_0 (\sigma_0 - \sigma_m)}{\sigma_0 - (1 - a_0)(\sigma_0 - \sigma_m)}$$
, where  $\sigma_m \le \sigma^* \le \sigma_0$ .

The fuzzy basic reproduction number is given by  $\Re_0^f = \frac{1}{a_0} FEV(a_0 \Re_0(\sigma))$ , where  $\Re_0(\sigma) = \frac{\beta(\sigma)}{a(\sigma)}$ .

Now, from the definition of *FEV*, we have  $FEV(a_0\Re_0(\sigma)) = \sup_{0 \le \alpha \le 1} \inf(\alpha, k(\alpha))$ , where

$$k(\alpha) = \mu \{ x \in A : a_0 \Re_0(\sigma) \ge \alpha \}.$$

Further, to obtain  $FEV(a_0\mathfrak{R}_0(\sigma))$ , we have to define a fuzzy measure  $\mu$ . For this purpose, the possibility measure is given by

$$\mu(\mathbf{A}) = \sup_{\sigma \in X} \Gamma(\sigma), \quad \mathbf{A} \subset \mathbb{R}.$$

IAEES

From  $FEV(a_0\mathfrak{R}_0(\sigma))$ , it is clear that  $\frac{\beta(\sigma)}{a(\sigma)}$  is not decreasing with  $\sigma$ , whereby the set X is an interval of

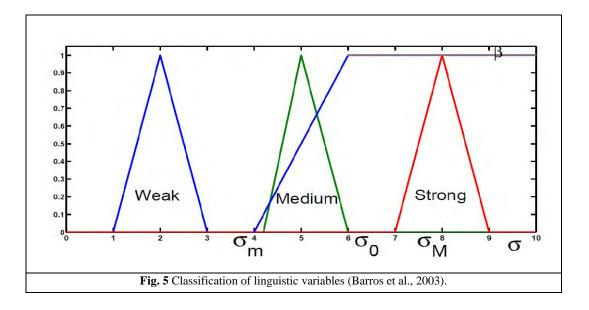
the form  $\left[\sigma', \sigma_{M}\right]$ , where  $\sigma'$  is the solution of the following equation  $a_{0} \frac{\beta(\sigma)}{a(\sigma)} = \alpha$ .

Thus

$$k(\alpha) = \mu \left[ \sigma', \sigma_M \right] = \sup_{\sigma' \le \sigma \le \sigma_M} \Gamma(\sigma), \qquad (3)$$

where k(0) = 1 and  $k(1) = \Gamma(\sigma_M)$ 

This measure indicates that the infectivity of a group is the one presented by the individual belonging to the group with the maximal infectivity. Now, in order to determine  $FEV(a_0\mathfrak{R}_0(\sigma))$  we assume that the amount of the virus-load  $\Gamma$  of a group of individuals is a linguistic and is divided into three classes: "weak  $(\Gamma_-)$ ", "medium $(\Gamma_-^+)$ ", and "strong $(\Gamma^+)$ ". Each classification is a fuzzy number based on the values  $\sigma_m$ ,  $\sigma_0$  and  $\sigma_M$  that come into view in the definition of  $\beta$  (see Fig. 5).



**Case** (a) Weak virus load ( $\Gamma_{-}$ ) is defined for  $\hat{\sigma} + \delta < \sigma_{m}$ . As  $\hat{\sigma} + \delta < \sigma$ , we have  $k(\alpha) = \sup_{\sigma \le \sigma \le \sigma_{M}} \Gamma(\sigma) = 0$ ,

 $\forall \alpha \in [0,1] \text{ and } FEV(a_0 \Re_0(\sigma)) = 0 < a_0 \Leftrightarrow \Re_0^f < 1,$ 

which makes it possible to conclude that the disease will be extinct.

**Case (b)** Strong virus load ( $\Gamma^+$ ) is defined for  $\hat{\sigma} - \delta > \sigma_0$  and  $\hat{\sigma} + \delta < \sigma_M$ . Thus from equation (3), we have

$$k(\alpha) = \begin{cases} 1 & \text{if } 0 \le \alpha < \frac{a_0}{a(\hat{\sigma})}, \\ \Gamma(\sigma') & \text{if } \frac{a_0}{a(\hat{\sigma})} \le \alpha < \frac{a_0}{a(\hat{\sigma}+\delta)} \\ 0 & \text{if } \frac{a_0}{a(\hat{\sigma}+\delta)} \le \alpha \le 1. \end{cases}$$

Obviously, if  $\delta > 0$ , k is continuous and decreasing function with k(0) = 1 and k(1) = 0. Hence

 $FEV(a_0\mathfrak{R}_0(\sigma)) \text{ is the fixed point of } k \text{ and } \frac{a_0}{a(\hat{\sigma})} < FEV(a_0\mathfrak{R}_0(\sigma)) < \frac{a_0}{a(\hat{\sigma}+\delta)}$   $\frac{1}{a(\hat{\sigma})} < \mathfrak{R}_0^f < \frac{1}{a(\hat{\sigma}+\delta)}$ , or that  $\mathfrak{R}_0^f > 1$ , which indicates that the disease will be endemic.

**Case** (c) Medium virus load  $(\Gamma_{-}^{+})$  is defined for  $\hat{\sigma} - \delta > \sigma_{m}$  and  $\hat{\sigma} + \delta < \sigma_{0}$ . Therefore again from (3),

$$k(\alpha) = \begin{cases} 1 & \text{if } 0 < \alpha \le a_0 \frac{\beta(\hat{\sigma})}{a(\hat{\sigma})} \\ \Gamma(\sigma') & \text{if } a_0 \frac{\beta(\hat{\sigma})}{a(\hat{\sigma})} < \alpha \le \frac{\beta(\hat{\sigma} + \delta)}{a(\hat{\sigma} + \delta)}, \\ 0 & \text{if } a_0 \frac{\beta(\hat{\sigma} + \delta)}{a(\hat{\sigma} + \delta)} < \alpha \le 1. \end{cases}$$

Similar to case (b), we have

$$\frac{\beta(\hat{\sigma})}{a(\hat{\sigma})} < \Re_0^f < \frac{\beta(\hat{\sigma}+\delta)}{a(\hat{\sigma}+\delta)}$$

Thus in any case, we have

$$a_0 \frac{\beta(\hat{\sigma})}{a(\hat{\sigma})} < FEV(a_0 \Re_0(\sigma)) < a_0 \frac{\beta(\hat{\sigma} + \delta)}{a(\hat{\sigma} + \delta)}$$

or

$$\frac{\beta(\hat{\sigma})}{a(\hat{\sigma})} < \frac{FEV(a_0 \Re_q(\sigma))}{a_0} < \frac{\beta(\hat{\sigma} + \delta)}{a(\hat{\sigma} + \delta)}$$

or  $\mathfrak{R}_0(\hat{\sigma}) < \mathfrak{R}_0^f < \mathfrak{R}_0(\hat{\sigma} + \delta)$ .

$$\Re_0(\sigma) = \frac{\beta(\sigma)}{a(\sigma)}$$
 is an increasing and continuous function, from Intermediate Value Theorem (Stewart, 1999),

there exists a unique  $\overline{\sigma}$  with  $\hat{\sigma} < \overline{\sigma} < (\hat{\sigma} + \delta)$  such that  $\Re_0^f = \Re_0(\overline{\sigma}) > \Re_0(\hat{\sigma})$ ,

or that, there exists only one virus load  $\bar{\sigma}$  such that the basic reproduction number  $\Re_0$  and the fuzzy basic reproduction number  $\Re_0^f$  coincide. Furthermore, the average number of secondary cases  $\Re_0^f$  is higher than the number of secondary cases  $\Re_0(\hat{\sigma})$  due to the medium amount of infection.

# 3.2 Disease control in fuzzy epidemic system

In this section, we analyze the control of the estimation of the disease in the population using the fuzzy basic reproduction number  $\Re_0^f = \Re_0(\overline{\sigma})$ . In the fuzzy system, spread of disease depends not only on the variable  $\sigma$  but also on the contact rate  $\beta$  as well as the death-mortality rate a. In the following, we describe some of the following cases about the existence and stability of the disease in the system. It is to be pointed out here that the proposed fuzzy system represents a family of systems depending on the parameter  $\sigma$ . In order to simplify this family of systems by a unique system of equations with the same outcome, our result shows that there is one value of  $\sigma$ , i.e., the bifurcation value  $\sigma^*$ .

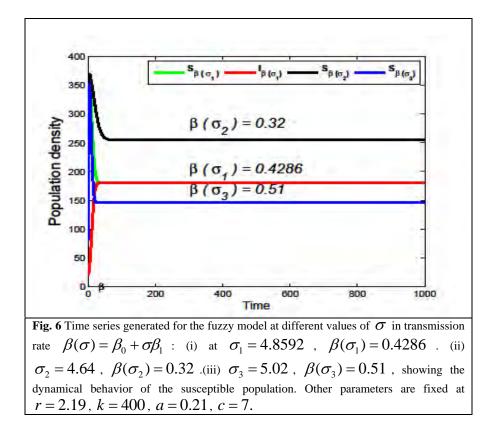
- (1) Weak amount of infection: In this case  $\overline{\sigma} < \hat{\sigma} + \delta \le \sigma_m$ , whereby the fuzzy basic reproduction number  $\Re_0^f$  is zero and the disease will be vanish in the population.
- (2) Medium amount of infection: In this case,
- (a) If  $\sigma^* > \sigma$ , then fuzzy basic reproduction number  $\Re_0^f$  is less than the unity and the system will be free from disease; and
- (b) If  $\sigma^* < \sigma$ , then fuzzy basic reproduction  $\Re_0^f$  is greater than the unity and the system will become endemic in the population.
- (3) Strong amount of infection: In this case  $\overline{\sigma} > \hat{\sigma} > \hat{\sigma} + \delta \ge \sigma_0$ , whereby the fuzzy basic reproduction number  $\Re_0^f(\sigma) = \frac{1}{a(\hat{\sigma})} > 1$  and the disease will invade.

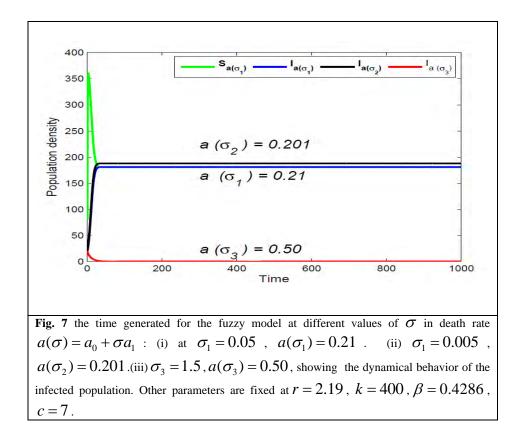
Now, the assumption of  $\mathfrak{R}_0^f$  is related to control policies to stop the spread of influenza;

- (1)  $\mathfrak{R}_0^f$  can be reduced by increasing  $\sigma_m$  (or, increasing  $\sigma^*$ ).
- (2) Since  $\overline{\sigma} \in (\hat{\sigma}, \hat{\sigma} + \delta)$ , if the amount of median virus load is very less than the value of  $\mathfrak{R}_0^f$  can reduce. For example, by using the medicine or separation of infected individuals (decreasing  $\delta$ ).

### **4** Numerical Solution

In this section, the dynamical behavior of the system is investigated numerically. In the fuzzy model, analysis depends directly on those parameters which define the rates at which individuals move from one stage to another, such as contact rate  $\beta(\sigma)$  and death rate  $a(\sigma)$ . The dynamics of the susceptible and infected is observed at the parameter values r = 2.19, k = 400 and c = 7. As we increase the value of the parameter  $\beta(\sigma)$  (res.  $a(\sigma)$ ) for the susceptible (res. infected) population, the susceptible (res. infected) decreases and as we decrease the value of  $\beta$  (res. a), the susceptible (resp. infected) increases (see Figs. 6, 7).





#### **5** Discussion and Conclusion

The purpose of the paper is to use fuzzy set theory in epidemiology, which is a recent area of research. We have studied the effect of two important fuzzy parameters, e.g., transmission rate  $\beta$  and the death rate a as a function of the virus load  $\sigma$  on the dynamics of the model system. Interestingly, the fuzzy basic reproduction number  $\Re_0^f$  is a function of disease spreading virus, while in case of crisp system basic reproduction number is not a direct function of virus. From the simulation results, we observed that the value of the control parameters  $\beta(\sigma)$  the transmission rate and  $a(\sigma)$  the death rate, at which both the populations (susceptible as well as infected) coincides or matches at 0.4286 and 0.21 respectively, i.e., the death rate of infected population is approximately the half of its transmission rate. For controlling the spread of influenza virus in the population proper management of  $\beta(\sigma)$  and  $a(\sigma)$  is required.

### Acknowledgments

The first author acknowledge with thanks the support received through a research grant, provided by the Council of Scientific and Industrial Research (CSIR) (Grant No. 09/085(0113)/2015-EMR-1), New Delhi, under which this work has been carried out.

#### References

- Alexander ME, Bowman C, Moghadas SM, Summers R, Gumel AB, Sahai BM. 2004. A vaccination model for transmission dynamics of influenza. SIAM Journal of Applied Dynamical System, 3: 503-524
- Bassanezi RC, Barros LC. 1995. A simple model of life expectancy with subjective parameters. Kybernets, 24: 91-98
- Barros LC, Bassanezi RC. 1997. About fuzzy dynamical systems: Theory and applications. PhD Thesis. University of Campinas, Sâo Paulo, Brazil
- Barros LC, Bassanezi RC. 1992. Deterministic models with subjective parameters. Ms Thesis. University of Campinas, Sâo Paulo, Brazil
- Barros LC, Bassanezi RC, Leite MBF. 2003. The SI epidemiological models with a fuzzy transmission parameter. Computer and Mathematics with Applications, 45: 1619-1628
- Chong NS, Tchuenche JM, Smith RJ. 2014. A mathematical model of avian influenza with half saturated incidence. Theory in Biosciences, 133: 23-38
- D'Onofrio A. Manfredi P. 2009. Information-related changes in contact patterns may trigger oscillations in the endemic prevalence of infectious diseases. Journal of Theoretical Biology, 256: 473-478
- Epstein JM, Parker J,Cumming D, Hammond RA. 2008. Coupled contagion dynamics of fear and disease: mathematical and computational explorations. Plos One, 3: e3955
- Farahi MH, Barati S. 2011. Fuzzy time-delay dynamical systems. The Journal of Mathematics and Computer Science, 2: 44-53
- Ferson S. Ginsburg LR. 1996. Different methods are need to propagate ignorance and variability. Reliability Engineering and System Safety, 54: 133-144
- Funk S. Gilad E. Jansen VAA. 2010. Endemic disease, awareness and local behavioral response. Journal of Theoretical Biology, 264: 501-509
- Gao S, Chen L, Nieto J, Torres A. 2006. Analysis of a delayed epidemic model with pulse vaccination and saturation incidence. Vaccine, 24: 6037-6045

- Gillim-Ross L, Subbarao K. 2006. Emerging respiratory viruses: challenges and vaccine strategies. Clinical Microbiology Reviews, 19: 614-636
- Gonzâlez-parra, Arenas AJ, Aranda DF, Segovia L. 2011. Modeling the epidemic waves of AH1N1/09 influenza around the world. Spatial and Spatio-temporal Epidemiology, 2: 219-226
- Gumel AB. 2009. Global dynamics of a two-strain avian influenza model. International Journal of Computer Mathematics, 86: 85-108
- Jafelice R, Barros LC, Bassanezei RC, Gomide F. 2004. Fuzzy modeling in symptomatic HIV virus infected population. Bulletin of Mathematical Biology, 66: 1597-1620
- Kaddar A. 2009. On the dynamics of a delayed SIR epidemic model with a modified saturated incidence rate. Electronic Journal of Differential Equations, 133: 1-7
- Kiss IZ, Cassell J, Recker M, Simon PL. 2010. The impact of information transmission on epidemic outbreaks. Mathematical Biosciences, 225: 1-10
- Klir GL, Yuan B. 1995. Fuzzy Sets and Fuzzy Logic. Prentice Hall, Upper Saddle River, USA
- Massad E, Burattini MN, Ortega NRS. 1999. Fuzzy logic and measles vaccination: designing a control strategy. International Journal of Epidemiology, 28: 550-557
- Massad E, Ortega NRS, Barros LC, Struchiner CJ. 2008. Fuzzy Logic in Action: Application and Epidemiology and Beyond. Studied in Fuzziness and Soft Computing, 232
- Mishra BK, Pandey SK. 2010. Fuzzy epidemic model for the transmission of worms in computer network. Nonlinear Analysis: Real World Applications, 11: 4335-4341
- Ortega NRS, Sallum PC, Massad E. 2000. Fuzzy dynamical systems in epidemic modeling. Kybernetes, 29: 201-218
- Mondal PK, Jana S, Haldar P, Kar TK. 2015. Dynamical behavior of an epidemic model in a fuzzy transmission. International Journal of Uncertainty, Fuzziness and Knowledge-Based Systems, 23: 651-665
- Pal D, Mahaptra GS, Samanta GP. 2013. Optimal harvesting of prey-predator system with interval biological parameters: a bioeconomic model. Mathematical Biosciences, 241: 181-187
- Poletti P, Caprile B, Ajelli M, Pugliese A, Merler S. 2009. Spontaneous behavioral changes in response to epidemics. Journal of Theoretical Biology, 260: 31-40
- Qiu Z, Feng Z. 2010. Transmission dynamics of an influenza model with vaccination and antiviral treatment. Bulletin of Mathematical Biology, 72: 1-33
- Ruan S, Wang W. 2003. Dynamical behavior of an epidemic model with a nonlinear incidence rate. Journal of Differential Equations, 188: 135-163
- Samsuzzoha M, Singh M, Lucy D. 2011. Numerical study of a diffusive epidemic model of influenza with variable transmission coefficient. Applied Mathematical Modelling, 35: 5507-5523
- Sattenspiel L, Herring DA. 2003. Simulating the effect of quarantine on spread of the 1918-19 flue in central Canada. Bulletin of Mathematical Biology, 65: 1-26
- Stewart J. 1999. Calculus-Early Transcendental. Books/ Cole Publishing Company, USA
- Su M, Wang H. 2015. Modeling at the interface of ecology and epidemiology. Computational Ecology and Software, 5(4): 367-379
- Sugeno M. 1974. Theory of Fuzzy Integrals and its Applications. PhD Thesis. Tokyo Institute of Technology, Japan
- Tang S, Xiao Y, Yang Y, Zhou Y, Wu J, Ma Z. 2010. Community based measures for mitigating the 2009 H1N1 pandemic in China. Plos One, 5: e10911

- Upadhyay RK, Roy P, Rai V. 2014. Deciphering dynamics of epidemic spread: the case of influenza virus. International Journal of Bifurcation and Chaos, 24: 145-164
- Yager RR, Filev DP. 1994. Essentials of Fuzzy Modeling and Control. Wiley-Interscience, New York, USA

Yen J, Langari R. 1999. Fuzzy Logic: Intelligence, Control, and Information, Prentice-Hall, New Jersey, USA

- Zadeh KS. 1999. Fundamentals of clinical methodology: 3. Nosology. Artificial Intelligence in Medicine, 17: 87-108
- Zadeh LA. 1965. Fuzzy sets. Information Control, 8: 338-353
- Zhang F, Li Z, Zhang F. 2008. Global stability of a SIR epidemic model with constant infectious period. Applied Mathematics and Computation, 1999: 285-291
- Zhang WJ. 2016. Selforganizology: The Science of Self-Organization. World Scientific, Singapore
- Zhang WJ. 2018. Fundamentals of Network Biology. World Scientific, Singapore
- Zhang WJ, Wopke van der Werf, Pang Y. 2011. A simulation model for vegetable-insect pest-insect nucleopolyhedrovirus epidemic system. Journal of Environmental Entomology, 33(3): 283-301
- Zhou Y, Liu H. 2003. Stability of periodic solutions for a *SIS* model with pulse vaccination. Mathematical and Computer Modeling, 38: 299-308