Chapter 10
Biomathematical Modeling in a Fuzzy Environment

As far as the laws of mathematics refer to reality, they are not certain; as far as they are certain, they do not refer to reality.
(Albert Einstein)

Abstract This chapter looks at the influence of the environment in a population as a whole, that is, it looks at processes in which the environment affects all individuals equally. We illustrate this phenomenon via four models.

Chapter 9 stated that the methods of incorporating uncertainties in mathematical models are quite varied and mentioned that there two such ways of incorporating fuzzy uncertainty, environmental fuzziness and demographic fuzziness. Whereas the aim of Chap. 9 was the incorporation of demographic fuzziness in models, this chapter focuses on environmental fuzziness. Thus, for pedagogical and didactic purposes and for clarity, we have distinguished these two types of fuzziness inherent in modeling biomathematical systems: *demographic fuzziness* (Chap. 9) and *environmental fuzziness*, this chapter. These terms, demographic and environmental fuzziness, have their origin in dynamic population modeling (see [1–3]). "Demographic stochasticity (or 'within-individual variability', - ... individuals who are apparently identical have different life spans and produce different numbers of offspring. ... Environmental stochasticity - Environments vary unpredictably through time in ways that affect all individuals equally" (Turelli [3], p. 321).

The estimation of the entity such as the future "number of descendents" in a population, already inherently exhibits stochastic or fuzzy uncertainty properties because of the existence of perturbations in the conditions surrounding any population as a whole. Examples of this nature are abundant - how the cost of living in a particular locality influences the life expectancy in a group of people, how, in a predator-prey model, the natural surroundings favor either the predator or the prey, how in a survival of the fittest model nature is favorable to one or another of the competitors at various periods of time. Through translation of rules, environmental fuzziness may be changed into a parameters or demographic fuzziness in biomathematical models. In this chapter we study how to model with environmental fuzziness and compare

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this type of fuzzy model with the deterministic and stochastic ones. Details of similar types of models can be found in [4, 5]. Recall that what we have called environmental fuziness is fuzziness in the parameters of model.

The models we treat next can, from the mathematical point of view, be treated by classical methods without the necessity of new concepts of mathematics to model the evolution of uncertainty in them. For example, if the phenomenon were modeled with differential equations and the rate of change in the differential equation were uncertain, the differential equation may be understood as a family of classical differential equations dependent on the parameters governing the uncertain rates of change (the derivatives) so that the theory of stochastic differential equations may be used. These types of equations are called *random dynamical equations* (see [6]).

Most of the models with uncertainty of interest to us have both types of uncertainties present (demographic and environmental fuzziness) and, in these cases, the modeling is not very different than what has been developed in the previous chapters of this book. However, depending on the purpose of the model, environmental fuzziness can be treated as demographic fuzziness. For this, however, we need to transform all the uncertainty of the variables into the parameters of the mathematical model assuming that such a process makes sense. Let us begin with an example in which environmental fuzziness appears in the model.

10.1 Life Expectancy and Poverty

We can use various indicators to model *poverty,* for example, caloric intake, vitamin intake, basic sanitation, and so on. For this presentation, we will use income of the relevant group we are studying [5].

10.1.1 The Model

Suppose that A is a closed group (no in-migration or out-migration) with $n(t)$ individuals at instant t. Assuming that poverty, here evaluated as the income level, is one factor in the reduction of the number of years of life of all the individuals in A, we can consider that

$$\begin{cases} \dfrac{\mathrm{d}n}{\mathrm{d}t} = -\left[\lambda_1 + \beta(r)\lambda_2\right] n \\ n_0 = n(0) \end{cases}, \tag{10.1}$$

where:

- λ_1 is the natural death rate (obtained from a group who is under favorable survival conditions);
- $\beta(r)\lambda_2$ indicates the influence of poverty on the increase on the natural death rate λ_1;

- $\beta(r)$ indicates the level to which an individual with income r belongs to the fuzzy set *poverty*, that is, β is a membership function.

We note that the maximum mortality rate is $\lambda_1 + \lambda_2$ which is obtained when $\beta(r) = 1$.

The solution to the differential equation (10.1) is

$$n(t) = n_0 e^{-[\lambda_1 + \beta(r)\lambda_2]t}.$$

The membership function β can be represented by a function that is decreasing in r and, here, we think it convenient to adopt a family of curves (see Example 1.5)

$$\beta_k(r) = \begin{cases} [1 - (\frac{r}{r_0})^2]^k & \text{if } 0 < r < r_0 \\ 0 & \text{if } r \geq r_0 \end{cases}, \tag{10.2}$$

where k is a parameter that supplies some characteristics of the group *poverty*.

Recall, from our previous models, the larger the value of k, the smaller the dependence of the individual has in relation to income, that is, the smaller the influence that income has on *poverty*. In this way, intuitively, k reveals if the environment in which the group lives is more or is less favorable to life expectancy.

Observe that (10.1) is a family of ordinary differential equations. Thus, $n(.)$ is a family of solutions of the differential equation indexed by r, that is, for each fixed r, $n(.)$ is a solution of the differential equation corresponding to this r. This set forms the solution of the fuzzy problem (10.1). In this way, suppose that r has a statistical distribution, then $n(t)$ is a random variable for each fixed t. If we wish to select precisely one curve to represent the evolution of the number of individuals over time, a strong candidate is the one that gives us numbers at the midpoint of $n(t)$ for each t. This "mid-curve" is obtained calculating the expectation in the same way as it is done in stochastics/statistics.

Our object in what follows is to obtain an expectation of life expectancy of the group by means of classical mathematical and fuzzy expectation according to the concepts we have seen in Chap. 7.

10.1.2 Statistical Expectation: E[n(t)]

Statistical expectation is given by

$$E[n(t)] = \int_{-\infty}^{\infty} n(t)h(r)dr, \tag{10.3}$$

where $h(r)$ is the probability density function of income.

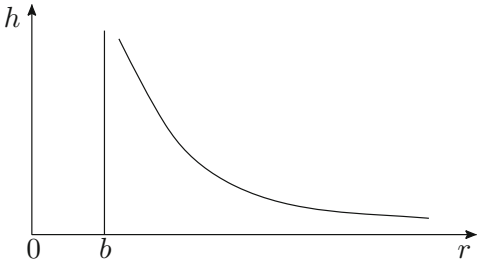

Fig. 10.1 Probability density function of income - Pareto distribution

The Pareto distribution for developing countries (see [7]) with parameters a and b,

$$h(r) = \begin{cases} ab^a r^{-(a+1)} & \text{if } r \geq b \\ 0 & \text{if } r < b \end{cases}.$$

is used for our specific case (Fig. 10.1).

Therefore,

$$E[n(t)] = n(0)e^{-\lambda_1 t} ab^a \int_b^\infty e^{-\beta_k(r)\lambda_2 t} r^{-(a+1)} dr$$

or

$$E\left[\frac{n(t)}{n(0)}\right] = e^{-\lambda_1 t} ab^a \int_b^\infty e^{-\beta_k(r)\lambda_2 t} r^{-(a+1)} dr. \tag{10.4}$$

- If $r_0 \leq b$, then $\beta_k(r) = 0$ for $r \geq b$ and

$$E[n(t)] = n(0)e^{-\lambda_1 t} ab^a \int_b^\infty r^{-(a+1)} dr = n(0)e^{-\lambda_1 t}.$$

  This means that $E[\frac{n(t)}{n(0)}] = e^{-\lambda_1 t}$ for all $a > 0$, that is, in this case the value of b is sufficiently large so that there is no affect of poverty on the life expectancy of the group.

- If $r_0 > b$, we have that $ab^a \int_b^\infty e^{-\beta_k(r)\lambda_2 t} r^{-(a+1)} dr < 1$, so that $E[n(t)] < n(0)e^{-\lambda_1 t}$. This means that we can interpret the number

$$ab^a \int_b^\infty e^{-\beta_k(r)\lambda_2 t} r^{-(a+1)} dr$$

  as a factor of reduction in the life expectancy due to poverty.

What follows is the calculation of fuzzy expectation in order for us to compare it with the statistical expectation given above.

10.1.3 Fuzzy Expectation Value: $FEV\left[\frac{n(t)}{n(0)}\right]$

Let us consider $Y_t(r) = \frac{n(t)}{n_0}$ a membership function of a fuzzy set since we have $\frac{n(t)}{n_0} \in [0, 1]$. Let us next obtain $FEV\left[\frac{n(t)}{n(0)}\right]$ using Theorem 7.1 applying the function

$$\begin{aligned} H(\alpha) &= P\{r : Y_t(r) = \frac{n(t)}{n(0)} \geq \alpha\} = P\{r : e^{-(\lambda_1+\lambda_2\beta_k(r))t} \geq \alpha\} \\ &= P\{r : e^{-\lambda_2\beta_k(r)t} \geq \alpha e^{\lambda_1 t}\}, \end{aligned} \tag{10.5}$$

where P is a probability defined by the density function for income $h(r)$.
Thus, $H(\alpha) = 0$ if $\alpha > e^{-\lambda_1 t}$. On the other hand, if $\alpha \leq e^{-\lambda_1 t}$,

$$H(\alpha) = P\{r : \alpha \leq e^{-(\lambda_1+\lambda_2\beta_k(r))t} < e^{-\lambda_1 t}\} + P\{r : r \geq r_0\}$$

which, with a little algebraic manipulation, we arrive at

$$H(\alpha) = \begin{cases} 1 & \text{if } 0 \leq \alpha \leq e^{-(\lambda_1+\lambda_2\beta_k(b))t} \\ \left[\dfrac{b}{r_0\sqrt{1-(-(\frac{\ln\alpha}{\lambda_2 t}+\frac{\lambda_1}{\lambda_2}))^{\frac{1}{k}}}}\right]^a & \text{if } e^{-(\lambda_1+\lambda_2\beta_k(b))t} < \alpha \leq e^{-\lambda_1 t} \\ 0 & \text{if } e^{-\lambda_1 t} < \alpha \leq 1 \end{cases}. \tag{10.6}$$

It is easy to see that $H(\alpha)$ is continuous over $[0, 1]$, except when $\alpha = e^{-\lambda_1 t}$ and H has a fixed point between $Y_t(b)$ and $e^{-\lambda_1 t}$, that is,

$$Y_t(b) = e^{-(\lambda_1+\lambda_2\beta_k(b))t} \leq FEV\left[\frac{n(t)}{n(0)}\right] \leq e^{-\lambda_1 t} (Fig.\ 10.2).$$

Some conclusions can quickly be made which are different than that of statistical expectation. Specifically, if

$$\left(\frac{b}{r_0}\right)^a \geq e^{-\lambda_1 t},$$

then

$$FEV\left[\frac{n(t)}{n(0)}\right] = e^{-\lambda_1 t} = FEV[e^{-\lambda_1 t}].$$

In particular, we have if $b \geq r_0$, then poverty does not affect life expectancy. This was the case with the results that were obtained using statistic expectation. However, fuzzy expectation indicates more. In order for poverty to have no effect on life expectancy, what is of interest is the relationship $\left[\left(\frac{b}{r_0}\right)^a \geq e^{-\lambda_1 t}\right]$ between individual income and the minimal group income. For example, an individual can

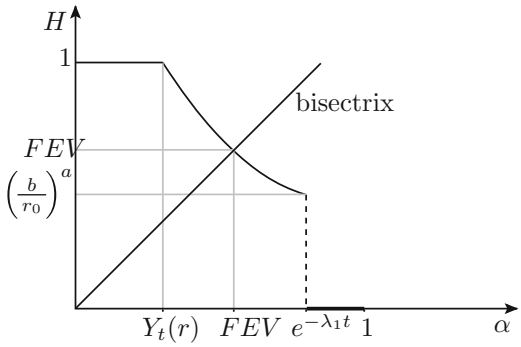

Fig. 10.2 $H(\alpha)$ and Fuzzy Expectation (FEV)

have a relatively small income ($b < r_0$) and even so, not have it interfere with his/her life expectancy. For this to occur, we just need that $\left(\frac{b}{r_0}\right)^a \geq e^{-\lambda_1 t}$. This is the typical case of a single person who has all the infrastructure to survive.

We want to emphasize that, from a technical point of view, it is harder to obtain $E(n(t))$, since it is not integrable in closed form, whereas $FEV\left[\frac{n(t)}{n(0)}\right]$ whose value is the fixed point of H, can be obtained by the Banach Fixed Point Theorem (see [8, 9]). If $\left(\frac{b}{r_0}\right)^a < e^{-\lambda_1 t}$, we can compute the value of $FEV\left[\frac{n(t)}{n(0)}\right]$ determined by the fixed point of H once this function is continuous and decreasing for $\alpha < e^{-\lambda_1 t}$. We observe that H has the same fixed point as its inverse, that is, as

$$H^{-1}(\alpha) = \exp\left\{-\left[\lambda_1 + \lambda_2 \beta_k\left(\frac{b}{\alpha^{1/a}}\right)\right]\right\} t, \text{ if } \left(\frac{b}{r_0}\right)^a < \alpha < 1.$$

This model of poverty was used to evaluate the life expectancy of a group of metal workers in the city of Recife (see Tables 10.1 and 10.2), the capital of the state of the northeast state of Pernambuco in Brazil. For this group we had some information about the income and the calculation of life expectancy using classical statistical methods thus permitting us to compare the statistical methods to the fuzzy methods.

10.1.4 Application: Life Expectancy of a Group of Metal Workers in Recife, Pernambuco - Brazil

We can determine the values of the parameter a and b of the income variable from Table 10.1 for a Pareto distribution $h(r)$. Now consider the cumulative distribution of income

$$F(r) = \int_b^r h(x)dx = \int_b^r ab^a x^{-a-1}dx = 1 - b^a r^{-a} = R.$$

Table 10.1 Workers' distribution by minimum wage ranges. Recife, 1988 Source: DIEESE

Minimal salary range	Populational distribution		% of total of payment
	n^0	%	
0 to 2	4003	45.0	21.1
2 to 3	2099	23.6	18.8
3 to 4	933	10.5	12.0
4 to 5	670	7.5	11.0
5 to 6	300	3.4	6.0
6 to 7	264	303.0	6.2
7 to 10	367	4.1	11.1
10 to 15	171	1.9	7.8
over 15	81	0.9	6.1

Table 10.2 Source: Carvalho and Wood (1977)

Income class	Income Cr$	Life expectance(years)
1	1 to 150	40.0
2	151 to 300	45.9
3	301 to 500	50.8
4	over 500	54.4

This means that,

$$\ln(1-R) = a\ln b - a\ln r.$$

Linearizing the data from Table 10.1, we obtain an approximation of $a \approxeq 2.031$ and $b \approxeq 1.726$. Thus,

$$h(r) = \begin{cases} 6.15r^{-3031} & \text{if } r \geq 1.726 \\ 0 & \text{if } r < 1.726 \end{cases}.$$

The table for life expectancy in the northeast of Brazil in 1977, in urban areas, where the minimum salary (which we denote S) was Cr$ 156.00 per month, is given in Table 10.2.

Suppose that income r is proportional to a power of the minimum salary S of the group we are studying, $r = S^m$, where m is a constant. Then, we have

$$\beta_k(S^m) = \begin{cases} [1 - \left(\frac{S}{S_0}\right)^{2m}]^k & \text{if } 0 < S < S_0 \\ 0 & \text{if } S \geq S_0 \end{cases}.$$

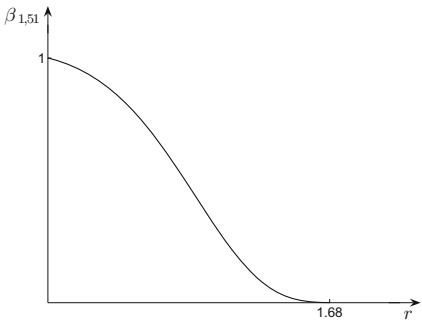

Fig. 10.3 Membership function of poor for $k = 1.51$

Life expectancy, independent of family income was 54.4 years. From this, the natural mortality rate is $\lambda_1 = \frac{1}{54.4}$. On the other hand, $\lambda_1 + \lambda_2$ is the highest rate of mortality of the group which is 40, that is,

$$\lambda_1 + \lambda_2 = \frac{1}{40} \Longrightarrow \lambda_2 = \frac{1}{40} - \frac{1}{54.4} = 6.618 \times 10^{-3}.$$

Let us consider that the minimum livable wage in 1977 was Cr$ 500.00 per month which is equivalent to $S_0 = \frac{500}{156} = 3.2$ minimum salaries. From Table 10.2 we have two values for life expectancy

$$\begin{array}{l} \text{If } S = 1 \Longrightarrow \frac{1}{\lambda_1 + \lambda_2 \beta_k(1)} = 45.9 \\ \text{If } S = 2 \Longrightarrow \frac{1}{\lambda_1 + \lambda_2 \beta_k(2^m)} = 50.8 \end{array} \Longrightarrow$$

$$\begin{array}{l} \lambda_2 \beta_k(1) = \frac{1}{45.9} - \frac{1}{54.4} = 3.404 \times 10^{-3} \\ \lambda_2 \beta_k(2^m) = \frac{1}{50.8} - \frac{1}{54.4} = 1.303 \times 10^{-3}. \end{array}$$

Since $\lambda_2 = 6.618 \times 10^{-3}$, we have

$$\begin{array}{l} \beta_k(1) = 0.514 \Longrightarrow \left[1 - (\frac{1}{S_0})^{2m}\right]^k = 0.514 \\ \beta_k(2^m) = 0.197 \Longrightarrow \left[1 - (\frac{2}{S_0})^{2m}\right]^k = 0.197. \end{array}$$

Then, $m = 0.4435$ and $k = 1.51$. Since $S_0 = 3.2$, it must be that $r_0 = (3.2)^{0.4435} \simeq 1.68$ which means the membership function of the fuzzy set $\beta_k(r)$ (Fig. 10.3) is given by

$$\beta_k(r) = \begin{cases} \left[1 - \left(\frac{r}{3.2}\right)^{0.887}\right]^{1.51} & \text{if } 0 < r < 1.68 \\ 0 & \text{if } r \geq 1.68 \end{cases}. \tag{10.7}$$

Table 10.3 Statistical expectation and fuzzy of number of workers and difference between two methodology

t	$E\left[\frac{n(t)}{n(0)}\right]$	$EF\left[\frac{n(t)}{n(0)}\right]$	$\left\lvert E\left[\frac{n(t)}{n(0)}\right] - EF\left[\frac{n(t)}{n(0)}\right]\right\rvert \times 10^3$
1	0.9810872	0.9800555	1.0317
2	0.9625352	0.9605718	1.9634
3	0.9443294	0.941537	2.7924
4	0.9264697	0.9229397	3.5300
5	0.908949	0.9047686	4.1804
10	0.8261962	0.8199376	6.2486
20	0.682632	0.6766003	6.0317
40	0.4660586	0.4687494	2.6908

10.1.5 Comparisons of the Statistical Expected Value and the Fuzzy Expected Value

We have, in hand, the membership function of the set *poverty* ($\beta_{1.51}$), so that we can calculate the average for the metal workers that we have been studying in Sect. 10.1.4, year by year, utilizing the results obtained in Sects. 10.1.2 and 10.1.3. Table 10.3 illustrate these values.

The fourth column of Table 10.3 shows us the various differences between the two methods to calculate life expectancy. In a general manner, Corollary 7.3 guarantees us that the differences are no greater than 0.25. For the values of the table, the largest difference in life expectancy is on the order of 0.63 %.

Moreover, for this specific example, it is easy to see that $FEV\left[\frac{n(t)}{n(0)}\right]$ is in fact between $Y(cb^m)$ and $e^{-\lambda_1 t}$. Thus,

$$\lim_{t\to\infty}\left|E\left[\frac{n(t)}{n(0)}\right] - FEV\left[\frac{n(t)}{n(0)}\right]\right| = 0,$$

that is, $E\left[\frac{n(t)}{n(0)}\right] \simeq FEV\left[\frac{n(t)}{n(0)}\right]$ for t sufficiently large.

Now, as an example, let us suppose that income are given as fixed and let us use Theorem 7.5. Moreover, suppose that the group of workers A have 150 individuals, that is, $\#A = 150 = n_0$ and income is distributed in the following manner:

1. $n_1 = 100$ individuals receive an income of about $r = 2.0$ minimum salaries $\rightarrow$ $Y(2) = e^{-0.0013t}e^{-\lambda_1 t}$;
2. $n_2 = 40$ individuals receive an income of about $r = 2.5$ minimum salaries $\rightarrow$ $Y(2.5) = e^{-0.00057t}e^{-\lambda_1 t}$;

3. $n_3 = 10$ individuals receive an income of about $r = 3.5$ minimum salaries $\rightarrow$ $Y(3.5) = e^{-\lambda_1 t}$.

We can consider that

$$P\{n\,|Y > \alpha\} = \frac{\#\{n\,|Y > \alpha\}}{\#A}.$$

Then,

$$\text{if } Y(2.5) < \alpha \leq Y(3.5) \Longrightarrow \frac{n_2}{\#A} = \frac{10}{150} = 0.0667;$$
$$\text{if } Y(2.0) < \alpha \leq Y(2.5) \Longrightarrow \frac{n_2 + n_1}{\#A} = \frac{50}{150} = 0.333.$$

If we now use the fuzzy expected value at time t of $Y(r)$, we have,

$$\begin{aligned} FEV[Y_t(r)] &= \sup_{0\leq\alpha\leq 1} \inf\left[\alpha, P\{n\,|Y > \alpha\}\right] \\ &= \text{median}\left\{0.0667;\, 0.333;\, e^{-0.0013t-\lambda_1 t};\, e^{-0.00057t-\lambda_1 t};\, e^{-\lambda_1 t}\right\} \\ &= e^{-0.0013t}e^{-\lambda_1 t}. \end{aligned}$$

Observe that for $t = 1$ we have $FEF(Y_1(r)) \approxeq 0.9987e^{-\lambda_1}$.

On the other hand, if we take the classical average for these same data we obtain

$$E[Y_t] = \frac{100Y_1 + 40Y_2 + 10Y_3}{150} = \frac{e^{-\lambda_1 t}}{150}(100e^{-0.0013t} + 40e^{-0.00057t} + 10)$$

so that for $t = 1$

$$E[Y_1] \approxeq 0.9998e^{-\lambda_1}.$$

That is, the values $FEF(Y_1(r))$ and $E(Y_1)$ are similar. This corroborates that, in general, $FEV[Y]$ and $E[Y]$ are similar for normalized random variable.

The two following examples have similar characteristics in mathematical models and as such are treated as analogous mathematical tools in terms of building blocks in general biomathematical models. The principal similarity between the two examples as we shall see, is the fact that their uncertainties have their origin in the state variables and so we treat the uncertainty as environmental fuzziness. However, we will "transform" this uncertainty into uncertainty in the parameters. This procedure results in the reduction of complexity in the associated solution methods. To be specific, to treat demographic fuzziness, we will need to use rule-based systems which is generally more complex than if the uncertainty is all in the parameters - environmental fuzziness. However, it is clear that we cannot always use this process of transforming demographic fuzziness to environmental fuzziness. It depends on the situation being modeled.

10.2 The SI Epidemiological Model

The simplest mathematical model to describe the dynamics of directly transmitted illnesses where there is interaction between susceptible individuals and infected individuals is the *SI* model type and it can be represented by the compartmental model depicted by Fig. 10.4.

The classical differential equations that describe the dynamics are given by:

$$\begin{cases} \dfrac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI \\ \dfrac{\mathrm{d}I}{\mathrm{d}t} = \beta SI \end{cases}, \tag{10.8}$$

where S is the proportion of susceptible individuals, I is the proportion of infected individuals and β is the coefficient of transmission of the disease. Taking into account that the model is normalized, that is, $S + I = 1$, the number of infected individuals is obtained by the solution to the logistic equation

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta(1 - I)I.$$

whose solution is given by:

$$I = \frac{I_0 e^{\beta t}}{S_0 + I_0 e^{\beta t}}, \tag{10.9}$$

where S_0 and I_0 are the initial proportions of susceptible and infected individuals respectively.

The *SI* model (10.8) is a part of a group of direct disease transmission models. These models are formulated as differential equations and are based on the *law of mass action* whose origin is in kinematic chemistry. The law of mass action postulates that the rate of formation of composites is proportional to the concentration of the reactants. The acceptance of this law is based on the fact that each particle of the reactants are moving independently with respect to all the other particles which means that the mixture is homogeneous so that each particle has the same chance of encountering the other particles. The translation of this law to biomathematical models is made considering that the *encounter* between the variables of the model is their product. Lotka and Volterra, in the same epoch also used this formulation to model the interaction between animal species.

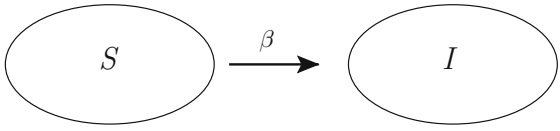

Fig. 10.4 Compartimental diagram of *SI* model

The incorporation of this law into epidemiological models was first made by Kermack-Mackendric (see [10, 11]) based on the hypothesis that infected individuals are homogeneously distributed in the entire population and each infected individual has the same potential to transmit the illness. This is a rather considerable assumption for epidemiological models since there are heterogeneous sources that interfere or accelerate the propagation of an illness, for example, age and/or social class, health habits (washing hands or quarantine, for example).

The model that we are going to propose uses the law of mass action, that is, each infected individual has the same chance of encountering a susceptible individual. This notwithstanding, let us also consider that the chance of new cases of the illness varies from individual to individual. In particular let us consider that a new infection can only occur if a minimal number of viruses (or another pathogenetic agent) is transmitted by the host. In this way, we will take as a factor, the viral (or other pathogen) load as a factor in the propagation of an illness where our assumption is that individuals with a large viral load have a greater chance of transmitting an illness than an individual with a lower viral load (see [12]). Thus, the *SI* model that we present next takes into consideration viral load as a relevant property of an infected individual.

10.2.1 The Fuzzy SI Model

With the heterogeneity in the population described above in mind as we build SI model, we will consider that the higher the viral load, the higher the chance of transmitting the disease. In other words, we will assume that $\beta = \beta(v)$, where v denotes the viral load which will be a non-decreasing function in v. On the other hand, we expect that when the viral load is very low, there is no chance of transmission occurring. That is, we assume that there is a minimum viral load, $v_{mín}$, necessary for there to be the possibility of transmission of the illness. Moreover, after a viral load of v_M, the chance chance of infection is maximum. Lastly, we suppose the there is an upper bound to the viral load which we denote as $v_{\max}$.

We choose, keeping the above in mind, for β the following membership function,

$$\beta(v) = \begin{cases} 0 & \text{if } v \leq v_{\min} \\ \dfrac{v - v_{\min}}{v_M - v_{\min}} & \text{if } v_{\min} < v \leq v_M \\ 1 & \text{if } v_M < v \leq v_{\max} \\ 0 & \text{if } v > v_{\max} \end{cases}. \tag{10.10}$$

The parameter $v_{\min}$, as was mentioned, represents the minimal quantity of virus (pathogens) necessary for there to be a transmission of the illness. This parameter could be interpreted as the threshold value of susceptibility of the group in question. In fact, the larger the value of $v_{\min}$, the larger the quantity of virus necessary for a transmission of the disease to occur and this means that the group in question has

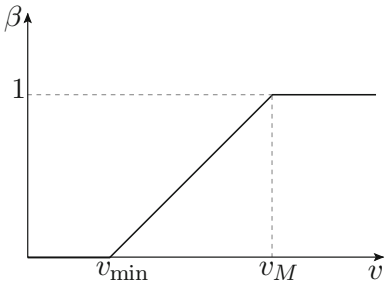

Fig. 10.5 Fuzzy transmission coefficient β [4]

low susceptibility to the illness. In other words, the larger that $v_{\min}$ is, the larger the resistance of the susceptible individuals. Whereas the parameter v_M represents the viral load above which the chance of transmission is maximum, that is, $\beta(v) = 1$. Obviously, this does not mean that a transmission of the disease will occur in fact when $\beta(v) = 1$, just that the chance of transmission is the greatest at this value.

Since $\beta(v) \in [0, 1]$, we can interpret β as a membership function of some fuzzy set whose domain is the viral load (see Example 7.6) (Fig. 10.5).

Fuzzy Solution

System (10.8), incorporating viral lood, can be seen as a family of ordinary differential equations that has as a solution the functions

$$I(v, t) = \frac{I_0 e^{\beta(v)t}}{S_o + I_0 e^{\beta(v)t}} \tag{10.11}$$

for each fixed v. Now, for each fixed $t > 0$, $I(v, t)$ is a set of real numbers and this means that for each instant t, a solution (10.11) of the fuzzy problem (10.8) is a distribution of possible values for the number of infected individuals whose range lies in the interval [0, 1]. Thus,

$$I(v, t) = I_t(v) \in [0, 1]$$

may be interpreted as a membership function of a fuzzy set. If for some reason it is necessary to adopt a single real-value to represent the number in infected individuals, we should choose some defuzzification. We could use, for example, the average at every instant of time t by way of the fuzzy expected value $FEV[I(V, t)]$ using as our defuzzier of the fuzzy set $I(v, t)$. To make a comparison between the classical and fuzzy *SI* models we are calculating the statistic expected value $E[I(V, t)]$ and the fuzzy expected value $FEV[I(V, t)]$. To do this, let us consider that the viral load V is a linguistic variable that can be considered *weak* (V_-), *medium* (V_-^+) or *strong* (V_+), where each of these classifications is a fuzzy set whose membership function is a triangular fuzzy number dependent on actual viral load associated with the disease being studied,

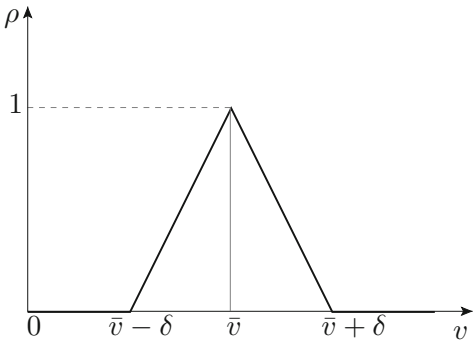

Fig. 10.6 Possibility distribution of viral load ρ [4]

$$\rho(v) = \begin{cases} 1 - \frac{|v-\bar{v}|}{\delta} & \text{if } v \in [\bar{v}-\delta, \bar{v}+\delta] \\ 0 & \text{if } v \notin [\bar{v}-\delta, \bar{v}+\delta] \end{cases}. \tag{10.12}$$

Note that $\rho(v)$ may be viewed as a possibility of occurrence $V = v$ and, in this case ρ becomes a possibility distribution for the variable V. For a fuller interpretation of possibility (say of a fuzzy set like ρ) see Example 7.6 of Chap. 7 (Fig. 10.6).

The parameter $\bar{v}$ is an average value around which each one of the fuzzy sets generated by V distributes itself, whereas δ is half of the distance of the base of the triangles. This triangular fuzzy number may be considered as an ideal dispersion around the average $\bar{v}$. The fuzzy sets generated by the linguistic variable V are classified based on the parameters $v_{\min}$ and v_M that appear in the definition of β.

10.2.2 Expected Value of the Number of Infected Individuals

This section calculates the average number of infected individuals in the distinct cases corresponding to the distributions of the viral load of the group. Since in Chap. 7 we have already defined the fuzzy expected value *FEV*, we now use this definition to define the expected value of the fuzzy set $I(V,t)$ as follows

$$FEV[I(V,t)] = \sup_{0\le\alpha\le 1} \min[\alpha, \mu\{I(v,t) \ge \alpha\}],$$

where $\mu\{v : I(v,t) \ge \alpha\}$ is the classical measure of the $\alpha - level\ [I(V,t)]^{\alpha}$, which is a classical set. In this way, for each t, the function $H(\alpha)$, whose fixed point is the value of $FEV[I(V,t)]$ according to Theorem 7.1 is given by

$$H(\alpha) = \mu\{v : I(v,t) \ge \alpha\} = \int_{[I(v,t)]^{\alpha}} \rho(v)\mathrm{d}v = 1 - \mu\{v : I(v,t) < \alpha\}.$$

First, observe that $H(0) = 1$ and $H(1) = 0$. For $0 < \alpha < 1$, and setting $k = \frac{S_0}{I_0}$ we have

$$H(\alpha) = 1 - \mu\{v : I(v,t) < \alpha\} = 1 - \mu\{v : \beta(v) < \ln\left(\frac{\alpha k}{1-\alpha}\right)^{\frac{1}{t}}\} =$$

$$= \begin{cases} 1 & \text{if } \ln(\frac{\alpha k}{1-\alpha})^{\frac{1}{t}} \leq 0 \\ \mu\{v \in [0, B)\} & \text{if } 0 < \ln(\frac{\alpha k}{1-\alpha})^{\frac{1}{t}} < 1 \\ 0 & \text{if } \ln(\frac{\alpha k}{1-\alpha})^{\frac{1}{t}} \geq 1 \end{cases} =$$

$$= \begin{cases} 1 & \text{if } 0 \leq \alpha \leq I_0 \\ \mu\{v \in [0, B)\} & \text{if } I_0 < \alpha < \frac{I_0 e^t}{S_0 + I_0 e^t} \\ 0 & \text{if } \frac{I_0 e^t}{S_0 + I_0 e^t} \leq \alpha \leq 1 \end{cases},$$

where $B = v_{\min} + (v_M - v_{\min}) \ln(\frac{\alpha k}{1-\alpha})^{\frac{1}{t}}$. Note that $v_{\min} < B \leq v_M$.

To calculate the fuzzy expectation, any measure can be used not necessarily a σ-additive one. To this end, in our case, let us adopt a fuzzy measure

$$\mu(A) = \frac{1}{\delta} \int_A \rho(v) \mathrm{d}v = \int_A \frac{\rho(v)}{\delta} \mathrm{d}v,$$

which is also a probability measure where in that case, $\frac{\rho(v)}{\delta}$ is the probability density function and we note that $\int_A \frac{\rho(v)}{\delta} \mathrm{d}v = 1$. With the aim of giving the example of the cases where the viral load is *weak, medium,* or *strong,* let us calculate the fuzzy expectation $FEV[I(V,t)]$ for the three distinct cases according to Fig. 10.7.

- **Weak viral load** (V_-).

This case $B > v_{\min} > \bar{v} + \delta$ and we have $\mu\{v \in [0, B]\} = 1$ and thus,

$$H(\alpha) = \begin{cases} 1 & \text{if } 0 \leq \alpha \leq I_0 \\ 0 & \text{if } I_0 < \alpha \leq 1 \end{cases}.$$

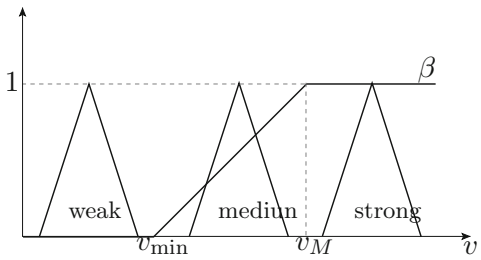

Fig. 10.7 Classification of viral load [4]

Therefore,

$$FEV[I(V,t)] = I_0.$$

The number if infected at each instant of time t remains the same as at the initial state and so the disease does not propagate. This result is concordant with the fact that in this interval, $\beta(v) = 0$.

- **Strong viral load** (V^+).
  This case $B \leq v_M \leq \bar{v} - \delta$ and we obtain $\mu\{v \in [0, B]\} = 0$. As a result

$$H(\alpha) = \begin{cases} 1 & \text{if } 0 \leq \alpha \leq \frac{I_0 e^t}{S_0 + I_0 e^t} \\ 0 & \text{if } \frac{I_0 e^t}{S_0 + I_0 e^t} < \alpha \leq 1 \end{cases}$$

and therefore,

$$FEV[I(V,t)] = \frac{I_0 e^t}{S_0 + I_0 e^t}.$$

  In addition, we obtain the classical solution when $\beta = 1$.

- **Medium viral load** (V_-^+). This case has $v_{\min} < \bar{v} - \delta < \bar{v} + \delta < v_M$ and a direct calculation, though it requires quite a bit of work, gives us the following,

$$H(\alpha) = \begin{cases} 1 & \text{if } 0 \leq \alpha \leq I(\bar{v} - \delta, t) \\ 1 - \frac{1}{2}\left(\frac{B - \bar{v}}{\delta} + 1\right)^2 & \text{if } I(\bar{v} - \delta, t) < \alpha \leq I(\bar{v}, t) \\ \frac{1}{2}\left(\frac{\bar{v} - B}{\delta} + 1\right)^2 & \text{if } I(\bar{v}, t) < \alpha \leq I(\bar{v} + \delta, t) \\ 0 & \text{if } I(\bar{v} + \delta, t) < \alpha \leq 1 \end{cases}. \tag{10.13}$$

In accordance with expression (10.13) and the above figure, we can conclude that $H(\alpha)$ is continuous and decreasing with $H(0) = 1$ and $H(1) = 0$. Consequently, H has one and only one fixed point that coincides with $FEV[I(V,t)]$ (Theorem 7.1). Once give the values of the parameters δ, $\bar{v}$, $v_{\min}$ and v_M are used to obtain $FEV[I(V,t)]$ (Fig. 10.8).

It is not hard to see that for each $t > 0$, if $v \in [v - \delta, v + \delta]$ then $I(\bar{v} - \delta, t)$ and $I(\bar{v} + \delta, t)$ are, respectively, the left and right endpoints of a real-valued interval. We also have that if $v_2 \geq v_1$, then $I(v_2, t) \geq I(v_1, t)$. In this way, by the Intermediate-Value Theorem (see [13, 14]), for each $t > 0$ there exists a unique $v = v(t) \in [v - \delta, v + \delta]$ such that

$$FEV[I(V,t)] = I(v(t), t) = \frac{I_0 e^{\beta(v(t))t}}{S_0 + I_0 e^{\beta(v(t))t}}.$$

Therefore, the expectation of the solutions $FEV[I(V,t)]$ does not coincide with any of the solution curves (10.11) of the model. What we have is that for each t, the

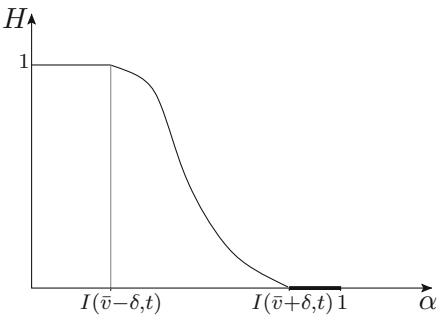

Fig. 10.8 Level function $H(\alpha)$ for the medium viral load [4]

value of $FEV[I(V,t)]$ coincides with $I(v,t)$ for some v. Consequently, changing the instant t, also will change the curve $I(v,t)$, since $FEV[I(V,t)] = I(v(t),t)$ and $v = v(t)$ varies with time. In other words, a curve $FEV[I(V,t)] = I(v(t),t)$ is not a solution of the original autonomous differential equation

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta(1-I)I.$$

We make several observations based on what we presented above.

• While there are susceptible individuals and $\bar{v} - \delta - v_{\min} > 0$, the expectation of the infected $FEV[I(V,t)]$ grow with respect to t, because

$$\lim_{t\to\infty} FEV[I(V,t)] \geq \lim_{t\to\infty} I(\bar{v}-\delta,t) = 1.$$

• The disease can be controlled by $I(\bar{v}+\delta,t)$, that is, making $\bar{v} + \delta - v_{\min} \leq 0$, the average number of infected cannot grow since

$$\lim_{t\to\infty} FEV[I(V,t)] \leq \lim_{t\to\infty} I(\bar{v}+\delta,t) = I_0.$$

10.2.3 Statistical Expected Values of the Number in Infected

The way we have considered the parameter $\beta = \beta(v)$, the classical statistical expected value of the number of infected individuals, $E[I(V,t)]$, is given by

$$E[I(V,t)] = \int_{-\infty}^{+\infty} I(v,t)\frac{\rho(v)}{\delta}dv = \frac{1}{\delta}\int_{\bar{v}-\delta}^{\bar{v}+\delta} I(v,t)\rho(v)dv, \tag{10.14}$$

since $\rho(v) = 0$ outside the interval $[\bar{v} - \delta, \bar{v} + \delta]$. So, we have

$$I(\bar{v} - \delta, t) \leq E[I(v, t)] \leq I(\bar{v} + \delta, t).$$

Since there exist various ways for us to calculate the expected value as a function of the parameters, we choose the three particular cases already analyzed using the fuzzy expected value (*FEV*).

Weak viral load: $v_{\min} > \bar{v} + \delta$.

In this case, for all the infected individuals, the transmission coefficient $\beta(v)$ is zero. Substituting $\beta(v) = 0$ and $I(V, t)$ given by (10.11) in (10.14), we obtain:

$$E[I(V, t)] = \frac{1}{\delta} \int_{\bar{v}-\delta}^{\bar{v}+\delta} I(v, t)\rho(v)dv = I_0.$$

Therefore, since all the infected individuals exhibit a viral load less than $v_{\min}$, that is, no individual possesses a minimal viral load necessary for transmission, there occurs no propagation of the disease. We may interpret this situation as one in which the group of individuals is highly resistant ($v_{\min}$ is high), that in turn makes the susceptibility to the disease low. In this case the number of infected remains unaltered from I_0.

Strong viral load: $v_M < \bar{v} - \delta$.

In this case, the coefficient of transmission is maximum for all the infected individuals, that is, $\beta(v) = 1$. After some calculations we obtain

$$E[I(V, t)] = \frac{1}{\delta} \int_{\bar{v}-\delta}^{\bar{v}+\delta} I(v, t)\rho(v)dv = \frac{I_0 e^t}{S_0 + I_0 e^t}. \tag{10.15}$$

Observe that (10.15) coincides with the classical model when we consider the transmission coefficient as constant, that is, $\beta = 1$.

Medium viral load: $\bar{v} - \delta > v_{\min}$ and $\bar{v} + \delta < v_M$.

In this case, similar to we saw for the fuzzy expectation, here also the coefficient of transmission is variable for all infected individuals. All the distribution, the support of the distribution of V is in the region where $\beta(v) = \frac{v - v_{\min}}{v_M - v_{\min}}$. So, to obtain $E[I(V, t)]$ it is necessary to know the values of all the parameters: δ, $\bar{v}$, $v_{\min}$, v_M and $v_{\max}$.

Analogous observations that were made about the propagation of the disease made for the fuzzy expected value also apply here remembering that

$$I(\bar{v} - \delta, t) \leq E[I(v, t)] \leq I(\bar{v} + \delta, t),$$

$$\lim_{t\to\infty} E[I(V, t)] \geq \lim_{t\to\infty} I(\bar{v} - \delta, t) = 1$$

and

$$\lim_{t\to\infty} E[I(V,t)] \leq \lim_{t\to\infty} I(\bar{v}+\delta,t) = I_0.$$

For the statistic expectation, we also have

$$E[I(V,t)] = I(v(t),t)),$$

for some function $v = v(t)$.

To conclude this section we would like to emphasize that unlike the statistic expectation, we could have utilized other fuzzy measures to obtain the fuzzy expectation. This possibility to choose different measures, according to the phenomenon being studied, is what makes the fuzzy expectation a powerful tool in applications. For example, instead of using the measure

$$\mu(A) = \frac{1}{\delta}\int \rho(v)dv,$$

we could have used the **possibilistic measure** (see Chap. 7)

$$\mu(A) = \sup_{v\in A} \rho(v).$$

In our view, this is a very reasonable measure to use for our example if we want to be very conservative in the following sense. It may be that for a particular disease, a group A of infected individuals is evaluated by the one person with the greatest viral load. The expectation of the number of infected individuals, $FEV[I(V,t)]$, could be evaluated with this more conservative measure and from this, mechanisms applied to control the disease could be made according to this figure. To be specific, for the possibility measure, we arrive at a very similar conclusion for the three cases previously analyzed where in the possibilistic measure case the function H becomes

$$H(\alpha) = \begin{cases} 1 & \text{if } 0 \leq \alpha \leq I_0 \\ \sup\limits_{v\in[a,v_{\max}]} \rho(v) & \text{if } I_0 < \alpha \leq \frac{I_0 e^t}{S_0+I_0 e^t} \\ 0 & \text{if } \frac{I_0 e^t}{S_0+I_0 e^t} < \alpha \leq 1 \end{cases} \tag{10.16}$$

and $FEV[I(V,t)]$ is the fixed point of the function H.

Let us do a comparative study between the approaches taken above and the deterministic method with the aim of exploring a little more this example.

10.2.4 $I(FEV[V], t)$ Versus $FEV[I(V, t)]$

This section will compare the trajectories of the three cases we have been studying previously above of the curve $FEV[I(V, t)]$, that is, $I(FEV[V], t) = I(\bar{v}, t)$. From the expression of H (10.16), we can conclude that $H(I(\bar{v}, t)) = \frac{1}{2}$ for all t. Thus $FEV[I(V, t)] = I(\bar{v}, t)$ only when $I(\bar{v}, t) = \frac{1}{2}$.

On the other hand, once $FEV[I(V, t)]$ is a fixed point of H we have

$$\begin{array}{l} FEV[I(V,t)] > I(\bar{v},t) \text{ if } I(\bar{v},t) < \frac{1}{2} \\ FEV[I(V,t)] < I(\bar{v},t) \text{ if } I(\bar{v},t) > \frac{1}{2} \end{array}.$$

In this way, a trajectory due to a medium viral load ($\bar{v}$), does not produce the medium number of infected individuals, as given by $FEV[I(V, t)]$, at every instant. Therefore, from our point of view, it is not correct to adopt an average or modal viral load, $\bar{v}$, to study the evolution of the disease in a population as a whole since $FEV[I(V, t)] = I(\bar{v}, t)$ only at the instant $\bar{t} = \frac{v_M - v_{\min}}{\bar{v} - v_{\min}} \ln(\frac{S_0}{I_0}), S_0 \geq I_0$. We observe that $\bar{t}$ is the inflection point of $I(\bar{v}, t)$ and that $I(\bar{v}, \bar{t}) = \frac{1}{2}$, that is, at the instant $\bar{t}$, the increment of the rate of increase of $I(\bar{v}, t)$ is larger than $I(\bar{v}, \bar{t}) = \frac{1}{2}$ (see Fig. 10.9). Starting with Jensen's inequality [15], we obtain similar results as those commented upon above for the classical expectation, $E(I(V, t))$, by only changing the time $\bar{t}$ at which the curve $I(\bar{v}, t)$ lies above $E(I(V, t))$.

These facts reveal that, for heterogeneous systems, two distinct instants of time can appear in which the uncertainties of the model can induce different values for the system as a whole. If we adopt a **deterministic model** to study the system above, it leads us to adopt $I(\bar{v}, t)$ as a solution since in this case, all the uncertainty should be extracted right at the beginning of the mathematical model which in our case is, $V = \bar{v}$. On the other hand, the **fuzzy model** allows the uncertainties, in this case inherent in the phenomenon, to be extracted in a desired (future) moment resulting in the solution $FEV[I(V, t)]$ or $E[I(V, t)]$ which is more representative of the system as a whole.

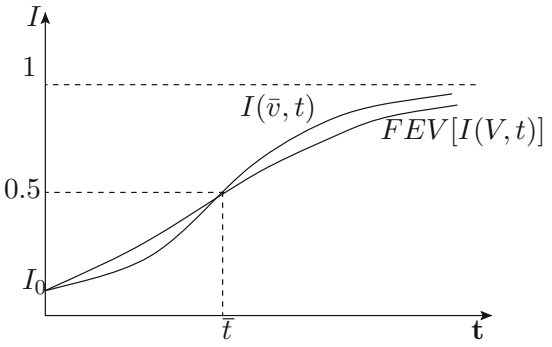

Fig. 10.9 Deterministic solution $I(\bar{v}, t)$ with $\bar{v}$ and the fuzzy expected value $FEV[I(V, t)]$ [4]

Mathematical models of epidemics are studied, in large part, with the aim of the implementation of policies or strategies to control the disease. We further illustrate this by studying a fuzzy *SI* model.

10.2.5 Control of Epidemics and the Basic Reproductive Number

The discussion in this section is based on the properties of the fuzzy *SI* model, keeping in mind the curve given by the fuzzy expectation $FEV[I(V,t)]$. In our previous development, we obtained conclusions based on the curve $E[I(V,t)]$ [4, 16]. In our previous discussions we saw the following facts.

- If $S_0 > I_0$, while $t < \bar{t} = \frac{v_M - v_{\min}}{\bar{v} - v_{\min}} \ln(\frac{S_0}{I_0})$, then $FEV[I(V,t)] > I(\bar{v},t)$. Beginning with $t = \bar{t}$ we have that $FEV[I(V,t)] < I(\bar{v},t)$. In this way we can say that the deterministic model underestimates the number of infected individuals at the beginning of the illness and overestimates the number of infected individuals beginning with $\bar{t}$ (see Fig. 10.9).
- If $S_0 \leq I_0$ then $FEV[I(V,t)] \leq I(\bar{v},t)$ for all $t > 0$ and in this case, the deterministic model overestimates the number of infected individuals.

Therefore, at the beginning of the illness when $t < \bar{t} = \frac{v_M - v_{\min}}{\bar{v} - v_{\min}} \ln(\frac{S_0}{I_0})$ and $S_0 >> I_0$, we have

$$I(\bar{v},t) \leq FEV[I(V,t)] \leq I(\bar{v}+\delta,t)$$

and thus, $v(t) \in [\bar{v}, \bar{v}+\delta]$.

Once $FEV[I(V,t)] = I(v(t),t)$ increases with the increase in $v(t)$, we can say that the larger the medium viral load the larger the average number of infected individuals $FEV[I(V,t)]$. Also, the larger the dispersal δ, the larger will be $FEV[I(V,t)]$ and the larger $v_{\min}$ is, the smaller $FEV[I(V,t)]$ will be.

An essential parameter, for epidemiological classical models, is the *basic reproductive number* R_0, which gives the number of secondary cases caused by an infected individual introduced in a population that is totally susceptible [10, 17]. In this way, this parameter indicates under what conditions the disease is propagated in a population. If an infected individual causes more than one new case, that is, if $R_0 > 1$ then the disease will propagate. On the other hand, when $R_0 < 1$ the disease will be extinguished.

The expression for the parameter R_0, for the more simple epidemiological models can be obtained beginning with the condition $\mathrm{d}I/\mathrm{d}t > 0$, that is, the condition that there occurs an increase in the number of infected. In this case, for the classical normalized *SI* model where $I + S = 1$, we will have

$$\frac{\mathrm{d}I}{\mathrm{d}t} > 0 \Longleftrightarrow \beta SI = \beta(1-I)I > 0,$$

which holds as long as there exist susceptible individuals in the populations since $\beta > 0$. In other words we will always have $R_0 > 1$ when $\beta > 0$ and $I < 1$. However, when we use a fuzzy set to describe the parameter β this cannot occur. In our case, according to the analysis we made above, it is easy to verify that a sufficient condition for there to be no transmission of the disease is that no infected individual possesses the minimum or higher viral load. That is, the condition $\bar{v} + \delta < v_{\min}$ should be satisfied. We can therefore define the *fuzzy basic reproductive number* as being the value

$$R_0^{\text{fuzzy}} = \frac{\bar{v} + \delta}{v_{\min}}. \tag{10.17}$$

Classical epidemiological models use, as a prevention control mechanism, the policy of reducing the value of the parameter R_0 in such a way that $R_0 < 1$ so that the disease will not propagate. But for the classical *SI* model this is not possible since the number of susceptible individuals is always positive as we have seen above.

However, if we consider the number of susceptible individuals was a fuzzy set, that is, $\beta = \beta(v)$ in (10.8), even in this simple model, we will garner additional information about the dynamics of the disease. For example, it is possible to interfere in the illness' transmission by reducing the value of the fuzzy parameter R_0^{fuzzy}. This can be done in two ways: (1) Increasing the value of $v_{\min}$, which means that we increase the resistance of the susceptible individuals (decrease the susceptibility); Increasing the value of $v_{\min}$ could be done through, for example, vaccination, basic sanitation, etc. In this sense, by the fact that the parameter $v_{\min}$ is related to the susceptible individuals, the way to reduce the value of R_0 is referred to as methods of control; (2) the second way to reduce R_0 would be to diminish the value of $\bar{v} + \delta$, by reducing the value of $\bar{v}$ and/or δ. The reduction of the value of δ could be done by means of control of the infected population as in, for example, quarantine or **isolation**. The reduction in $\bar{v}$ is related to measures of **treatment** of the infected individuals.

We finish our discussion of this application by emphasizing that unlike the classical *SI* model that is quite simple as we presented it, and inadequate for most diseases, even the simple fuzzy *SI* model is more inclusive whose results are more closely associated with more complex models in which the class of infected are divided into subclasses in accordance with the intensity of the infected (see [18]). A more detailed study of the fuzzy *SI* models can be found in [4] and fuzzy *SIS* models in [11, 16, 19].

10.3 A Fuzzy Model of the Transference from Asymptomatic to Symptomatic in HIV$^+$ Patients

The model that we present next can be found in [20, 21]. When we analyze the evolution of a population of individuals from asymptomatic *HIV*$^+$ to a class of symptomatic ones, many factors are involved in the process since the rate at which the

transference occurs is subject to the factors responsible for the change in the stages of HIV^+. Some of these factors are more crucial and influential than others. For example, the viral load of an individual and the level of $CD4^+$ are fundamental to the determining the next state in a HIV^+ the patient. What we exhibit with this example is to show how we can study a phenomenon, that is typically modeled deterministically, as a fuzzy model that explicitly and effectively uses inexact variables and parameters as they occur in the data and model statement. We demonstrate the transformation of the subjective, uncertain, and inexact variables and parameters into a fuzzy model via environmental fuzziness. To this end, the demographic fuzziness (fuzzy variables) are transformed into environmental (parameters) fuzziness. This being the case, we will consider the rate of transference, from asymptomatic to symptomatic, subjectively dependent on the viral load and the level $CD4^+$. In this way, we can express the rate of transference by a fuzzy set, that is, we express the transference rate via a linguistic variable as developed and studied in Chap. 5. However, to begin, we review the classical deterministic case.

10.3.1 The Classical Model

In 1986 Anderson et al. [22] proposed the following model for the transference of asymptomatic individuals to symptomatic HIV^+ ones,

$$\begin{cases} \dfrac{\mathrm{d}x}{\mathrm{d}t} = -\lambda(t)x \text{ with } x(0) = 1 \\ \dfrac{\mathrm{d}y}{\mathrm{d}t} = \lambda(t)x \text{ with } y(0) = 0 \end{cases}, \tag{10.18}$$

where the function $\lambda(.)$ represents the rate of transference of infected asymptomatic individuals with HIV^+ into symptomatic ones. The state variable x is the proportion of the infected individuals who still do not have symptoms indicative of *AIDS* and y is the proportion of the individuals that possess clear symptoms of *AIDS*. As a first approximation, Anderson proposes that this rate be given as a linear function

$$\lambda(t) = at, \text{ with } a > 0,$$

which means that the solution of the deterministic system (10.18) is

$$x(t) = e^{-\frac{at^2}{2}} \text{ and } y(t) = 1 - e^{-\frac{at^2}{2}}.$$

10.3.2 The Fuzzy Model

Let us now consider the rate of transference to be dependent on *viral load* v and the *level of* $CD4^+$ c, that is,

$$\lambda = \lambda(v, c).$$

Using the analogous deterministic model given by Anderson, we can write the model as:

$$\begin{cases} \dfrac{\mathrm{d}x}{\mathrm{d}t} = -\lambda(v, c)x \\ x(0) = 1 \end{cases} \tag{10.19}$$

or as its complementary/dual equation in terms of the variable y,

$$\frac{\mathrm{d}y}{\mathrm{d}t} = \lambda(v, c)x = k\lambda(v, c)(1 - y) \text{ with } y(0) = 0.$$

The difference in the fuzzy model and the deterministic one is that now the rate of transference λ has a clear biological and linguistical meaning whereas with the deterministic case, this rate was a adjustable parameter. The fuzzy model solution is

$$x(t) = e^{-\lambda(v,c)t} \text{ or } y(t) = 1 - e^{-\lambda(v,c)t}.$$

Each solution can be understood as an element of a family of curves which has initial value equal to 1,

$$x(t) = e^{-\lambda(v,c)t}, \text{ with } t > 0,$$

where λ assumes values dependent on the viral load and the level of $CD4^+$ present in the blood. The values v and c of variables, are characteristic properties of the infected population. The analytic definition of the parameter λ is obtained through a combination of the linguistic meaning of the variables V and $CD4^+$ and a rule base as developed in Chap. 5.

Medical knowledge and research seems to indicate that the parameter most used to control the transference from asymptomatic HIV^+ to symptomatic ones is the value of $CD4^+$. In this way we can simply use $\lambda = \lambda(c)$ as the transference rate in the fuzzy model (10.19). If for every viral load v we have $\lambda = \lambda(c)$, then its graph is approximately the decreasing curve depicted by Fig. 10.10. The equation that defines $\lambda = \lambda(c)$ given next and depicted in Fig. 10.10, was chosen taking in consideration arguments similar to those of the models previously presented (see Chap. 5, Subsect. 5.6.2 for more technical justification) is,

$$\lambda(c) = \begin{cases} 1 & \text{if } c < c_{\min} \\ \dfrac{c_M - c}{c_M - c_{\min}} & \text{if } c_{\min} \le c \le c_M, \\ 0 & \text{if } c > c_M \end{cases} \tag{10.20}$$

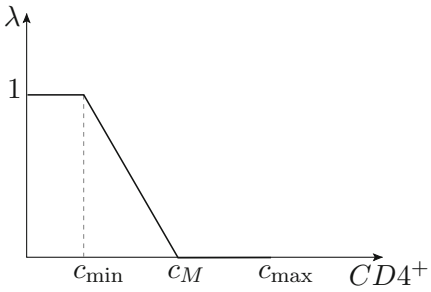

Fig. 10.10 Transference rate $\lambda = \lambda(c)$ [21]

where $c_{\min}$ represents the minimal level of $CD4^+$ required for an individual to become symptomatic and c_M represents the level of $CD4^+$ after which the chance of an infected individual becoming symptomatic is minimal or none.

10.3.3 The Fuzzy Expectation of the Asymptomatic Individuals

The fuzzy expected value provides a type of average value for the values of $x(t, c)$ at each instant of time, since it is a type of defuzzification of the fuzzy set of asymptomatic individuals

$$x(t, c) = e^{-\lambda(c)t}.$$

As we have seen in Chap. 7, to define fuzzy expectation we initially need to choose a fuzzy measure μ. Once this is done, the value of the fuzzy expectation of the asymptomatic individuals $x(t, c)$ is given by

$$FEV\,[x] = \sup_{0 \le \alpha \le 1} \inf\left[\alpha, \mu\left\{x \ge \alpha\right\}\right],$$

where $\{x \ge \alpha\} = \{c : x(c) \ge \alpha\}$ and μ is a fuzzy measure. Here, we have, recalling Theorem 7.1, $H(\alpha) = \mu\{c : x(c) \ge \alpha\}$ for each $t > 0$. For this case, a direct calculation results in the following expression of the function H:

$$H(\alpha) = \begin{cases} \mu\,[c_M, c_{\max}] & \text{if } \alpha = 1 \\ \mu\,[B, c_{\max}] & \text{if } e^{-t} \le \alpha < 1\,, \\ 1 & \text{if } \alpha \le e^{-t} \end{cases} \tag{10.21}$$

where $B = c_M - (c_M - c_{\min})(\frac{\ln \alpha}{t}) \Longrightarrow c_{\min} < B \le c_M$.

The fuzzy measure that we choose is a distribution of levels of $CD4^+$ with different associated possibilities of occurrence. We will assume that the levels of $CD4^+$ has a

triangular distribution given by,

$$\rho(c) = \begin{cases} 1 - \frac{|c-\bar{c}|}{\delta} & \text{if } c \in [\bar{c}-\delta, \bar{c}+\delta] \\ 0 & \text{if } c \notin [\bar{c}-\delta, \bar{c}+\delta] \end{cases}. \tag{10.22}$$

Here, we take $\bar{c}$ to be the modal or median value in $[0, c_{\max}]$, with $c_{\max}$ as a maximum limit of viral load in an individual and δ being the dispersion of the levels of $CD4^+$ within the population of interest (those infected with HIV). Thus, with this in mind, we suggest to use the following fuzzy measure μ

$$\mu(A) = \begin{cases} \sup_{c \in A} \rho(c) & \text{if } A \neq \emptyset \\ 0 & \text{if } A = \emptyset \end{cases},$$

where A is a subset of real numbers, containing the domain of possible values of $CD4^+$ (Fig. 10.11).

The subsets A of real numbers of interest are the intervals $A = [B, c_{\max}]$, where $B = c_M - (c_M - c_{\min})(\frac{-\ln \alpha}{t}) \Longrightarrow c_{\min} < B \leq c_M$. Observe that μ is an optimistic measure in the sense that the level of $CD4^+$ of a group is evaluated as being the best level of the individuals of this group.

Consider the level of $CD4^+$ as a linguistic variable with values *low*, *medium* and *high*, each one of these being characterized by a triangular fuzzy set according to the membership function ρ (see Fig. 10.12).

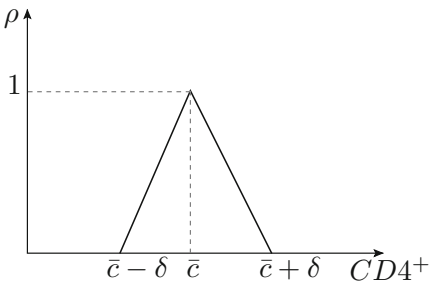

Fig. 10.11 Possibility distribution of $CD4^+$ [21]

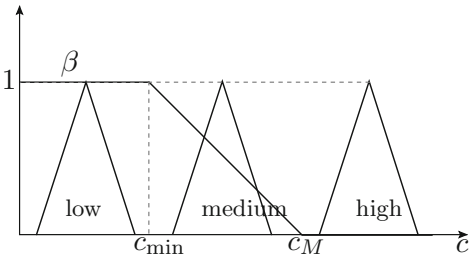

Fig. 10.12 Values of the linguistic variable "level of $CD4^+$" [21]

Case 1: The level of $CD4^+$ ***low*** (C_-).

In this case, we take $c_{\min} > \bar{c} + \delta$. Since $B > c_{\min}$ we have that $\mu[c_M, c_{\max}] = 0$ and $\mu[B, c_{\max}] = 0$. Thus,

$$H(\alpha) = \begin{cases} 1 & \text{if } \alpha \leq e^{-t} \\ 0 & \text{if } e^{-t} < \alpha \leq 1 \end{cases}$$

so that we obtain $FEV[x] = e^{-t}$ which means that the average number of transferences from asymptomatic to symptomatic has an exponential decay since the expected value of individuals with no HIV symptoms, x, goes to zero exponentially and the transference to symptomatic is an exponential decay.

Case 2: The level of $CD4^+$ ***high*** $(C+)$.

In this case, we take $c_M \leq \bar{c} - \delta$ and $\bar{c} + \delta \leq c_{\max}$. Thus, we have $B \leq c_M$ and therefore $\mu[c_M, c_{min}] = 1$ and $\mu[B, c_{\max}] = 1$ which yields

$$H(\alpha) = \begin{cases} 1 & \text{if } \alpha = 0 \\ 0 & \text{if } \alpha > 0 \end{cases}.$$

This means that $FEV[x] = 1$, so that if in the group, the level of $CD4^+$ is high, then there is no transference of asymptomatic individuals to symptomatic ones.

Case 3: The level of $CD4^+$ ***medium*** (C_-^+).

In this case, we take $\bar{c} - \delta > c_{\min}$ and $\bar{c} + \delta < c_M$ which implies that $\mu[c_M, c_{\max}] = 1$. After a few calculations we have that

$$H(\alpha) = \begin{cases} 1 & \text{if } 0 \leq \alpha \leq e^{-\lambda(\bar{c})t} \\ \rho(B) & \text{if } e^{-\lambda(\bar{c})t} < \alpha < e^{-\lambda(\bar{c}+\delta)t} \\ 0 & \text{if } e^{-\lambda(\bar{c}+\delta)t} \leq \alpha \leq 1 \end{cases},$$

where $\rho(B) = \frac{1}{\delta}[-c_M - (c_M - c_{\min})(\frac{\ln \alpha}{t}) + \bar{c} + \delta]$. Since $H(\alpha)$ is a continuous decreasing function with $H(0) = 1$ and $H(1) = 0$, H has a unique fixed point that coincides with $FEV[x]$ (see Chap. 7). Figure 10.13 illustrates this fact.
Thus,

$$e^{-\lambda(\bar{c})t} < FEV[x] < e^{-\lambda(\bar{c}+\delta)t}.$$

We observe that for the three cases of low/medium/high, we always have the inequality

$$e^{-EF[\lambda]t} \leq e^{-\lambda(\bar{c})t} \leq FEV[x].$$

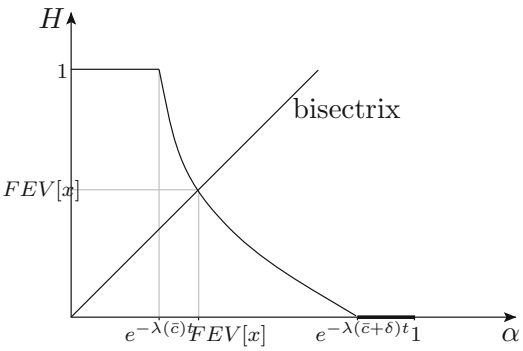

Fig. 10.13 Representation of $FEV[x]$ [21]

This means that the expected value of the asymptomatic population, at each instant, is larger than the deterministic model which considers the rate of transference (from asymptomatic to symptomatic) as a constant $\lambda(\bar{c}) = \bar{\lambda}$.

10.4 Population Dynamics and Migration of Blow Flies

We close this chapter with the presentation of a two-dimensional model that represents a competition and migration of flies. This model was developed by Castanho et al. [23]. The model comes from a discrete two-dimensional system where the parameters were determined by means of a rule base. This is a environmental fuzziness case because in the model, the uncertainties are all in the parameters. The uncertainties in the parameters are treated by means of fuzzy set theory and the values obtained are via fuzzy controllers.

A deterministic model used by Godoy [24] to analyze the establishment of colonies of blow flies has its foundation based on the incorporation of deterministic models of Prout and McCheney [25] and the stochastic model of Roughgarden [26]. The Godoy model is,

$$\begin{cases} N_{1,t+1} = \dfrac{(1-m_{12})}{2} F_1 S_1 e^{-(f+s)N_{1,t}} N_{1,t} + \dfrac{m_{21}}{2} F_2 S_2 e^{-(f+s)N_{2,t}} N_{2,t} \\ N_{2,t+1} = \dfrac{m_{12}}{2} F_1 S_1 e^{-(f+s)N_{1,t}} N_{1,t} + \dfrac{(1-m_{21})}{2} F_2 S_2 e^{-(f+s)N_{2,t}} N_{2,t} \end{cases} . \quad (10.23)$$

This model relates the dynamics of a population of blow flies with a process of migration between two colonies of blow flies. The variables and parameters are:

1. $N_{i,t}$: the population of blow flies of colony i at time t;
2. F_i: maximal fecundity of the blow flies when these are encountered in colony i;
3. S_i: maximal survival of the blow flies in colony i;

4. m_{ij}: rate of migration from colony i to colony j;
5. f and s represent the variation in fecundity and the survival respectively.

The parameters m_{ij}, F_i and S_i are dependent on a series of factors usually hard to evaluate quantitatively. In this case, it seems that the approach of fuzzy set theory can be useful. So, to obtain the solution of our model, we get the parameters via fuzzy method and substituting them on the deterministic equation (10.23).

Let's consider that the parameters m_{ij}, F_i and S_i are uncertainty and modeled by linguitic variable. Also, consider that these parameters are dependent on two input variables, the *Population* ($N_{i,t}$) and its *Environment* (E_i) which is the habitat of each colony. So, we have based rule fuzzy system (if - then) with two input and three output, according to Frame 10.1. For the input variable *Population*, using the experimental data found in Godoy [24], the linguistic terms adolted were, *Small, Medium* and *Large* according to Fig. 10.14. For the input variable *Environment* the linguistic terms considered were *Hostile, Slightly Unfavourable and Favorable* whose membership functions are given in Fig. 10.15. To model the fuzzy parameter *rate of Migration*, m, as an output variable, dependent on *Population* and on *Environment*, we adopt a rule base given by Frame 10.1. The linguistic terms *Small, Medium* and *Large* representing the rate of migration are given by Fig. 10.16. The memberships values of the output linguistic variables *Fecundity F* (Fig. 10.17) and fuzzy *Survival S* (Fig. 10.18) are intuitively derived considering an interpolation between the experimental values for maxima and minima of these variables.

The result of the equation of Godoy (10.23) with the parameters obtained from fuzzy controller with inference of Mamdani (see Chap. 5) are showed in the Figs. 10.19 and 10.20.

A study of metapopulations of blow flies using a fuzzy dynamic population model was developed in [23, 27].

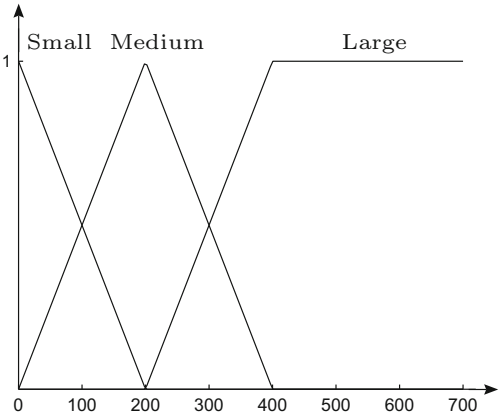

Fig. 10.14 Fuzzy values of the populations [23]

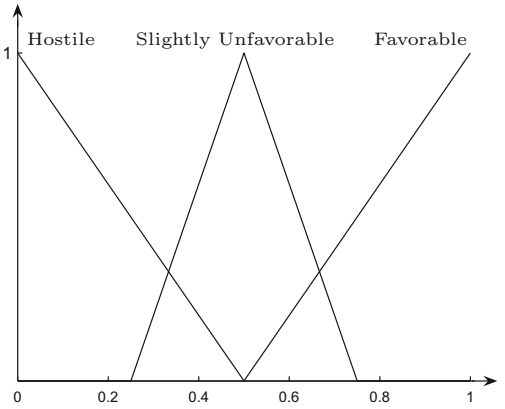

Fig. 10.15 Fuzzy values of the environment [23]

1. **If** Population is Small **and** the Environment is Favorable **then** the Fecundity and Survival are High and Migration is Low;
2. **If** Population is Small **and** the Environment is Slightly Unfavorable **then** the Fecundity is High, the Survival is Medium and Migration is Low;
3. **If** Population is Small **and** the Environment is Hostile **then** the Fecundity is Medium, the Survival is Low and Migration is High;
4. **If** Population is Medium **and** the Environment is Favorable **then** the Fecundity is High, the Survival is Medium and Migration is Low;
5. **If** Population is Medium **and** the Environment is Slightly Unfavorable **then** the Fecundity is Medium, Survival is Low and Migration is High;
6. **If** Population is Medium **and** the Environment is Hostile **then** the Fecundity and Survival are Low and Migration is High;
7. **If** Population is Large **and** the Environment is Favorable **then** the Fecundity is Medium, the Survival is Low and Migration is Moderate;
8. **If** Population is Large **and** the Environment is Slightly Unfavorable **then** the Fecundity and Survival are Low and Migration is High;
9. **If** Population is Large **and** the Environment is Hostile **then** the Fecundity and Survival are Low and Migration is High;

Frame 10.1: Rule base for Blow flies [23].

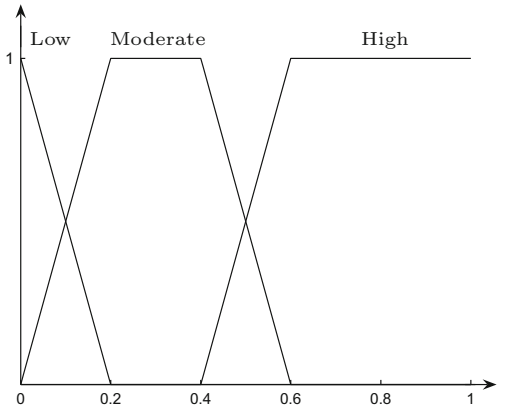

Fig. 10.16 Fuzzy values of migration [23]

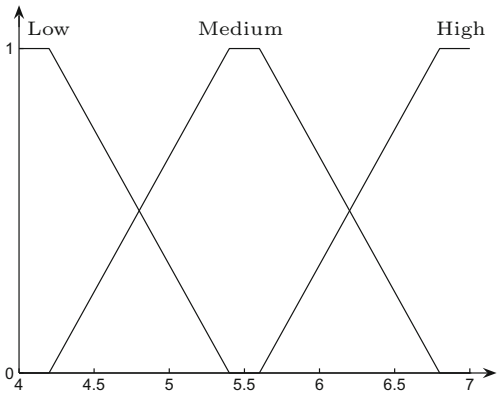

Fig. 10.17 Fuzzy values of fecundity [23]

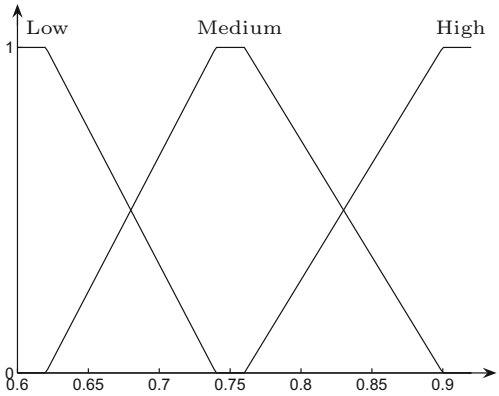

Fig. 10.18 Fuzzy values of survaival [23]

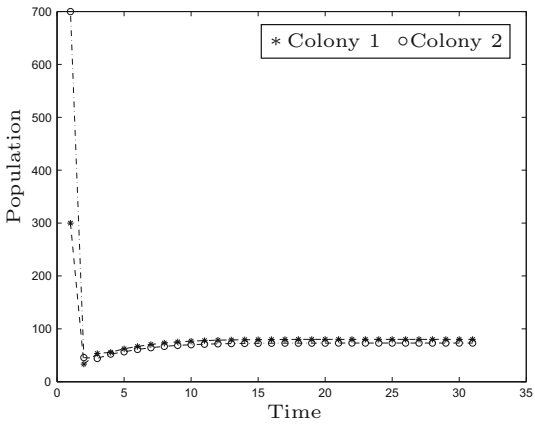

Fig. 10.19 Stability solution of the colonies for $N_{1,0} = 300$, $N_{2,0} = 700$, $E_{1,0} = 0.01$, and $E_{2,0} = 0.3$ [23]

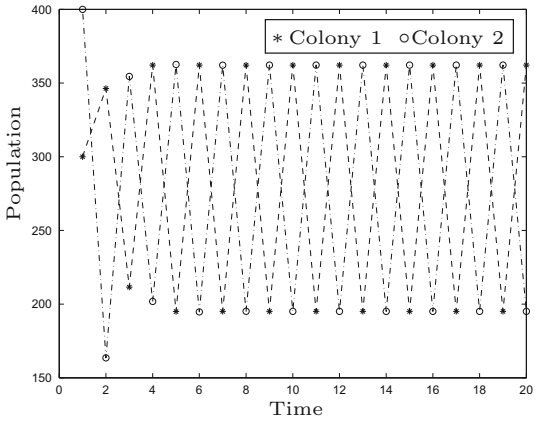

Fig. 10.20 Periodic variations of the populations for $N_{1,0} = 300$, $N_{2,0} = 400$, $E_{1,0} = 1$, and $E_{2,0} = 0.9$ [23]

References

1. K.B. Athreya, S. Karlin, On branching processes with random environments: I: extinction probabilities. Ann. Math. Stat. **42**(5), 1499–1520 (1971)
2. R. McCredie May, *Stability and Complexity in Model Ecosystems*, vol. 6 (Princeton University Press, Princeton, 1973)
3. M. Turelli, Stochastic community theory: a partially guided tour. Biomathematics **17**, 321–339 (1986)
4. L.C. Barros, M.B.F. Leite, R.C. Bassanezi, The SI epidemiological models with a fuzzy transmission parameter. Int. J. Comput. Math. Appl. **45**, 1619–1628 (2003)
5. R.C. Bassanezi, L.C. Barros, A simple model of life expectancy with subjective parameters. Kybernets **7**, 91–98 (1995)
6. L. Arnold, *Random Dynamical Systems*, 2nd edn. (Springer, Berlin, 2003)
7. W.O. Bussab, P.A. Morettin, *Estatística básica*, 5th edn. (Editora Saraiva, São Paulo, 2002)
8. R.G. Bartle, *The Elements of Real Analysis* (Wiley, New York, 1964)
9. W. Rudin, *Principles of Mathematical Analysis* (McGraw-Hill Book Co., Tokyo, 1953)
10. L. Edelstein-Keshet, *Mathematical Models in Biology* (McGraw-Hill, México, 1988)
11. E. Massad, N.R.S. Ortega, L.C. Barros, C.J. Struchiner, *Fuzzy Logic in Action: Applications in Epidemiology and Beyond* (Springer, Berlin, 2008)
12. K. Sadegh-Zadeh, Fundamentals of clinical methodology: 3. nosology. Artif. Intell. Med. **17**, 87–108 (1999)
13. T.M. Apostol, *Calculus*, vol. 2, 2nd edn. (Editorial Reverté, Mexico, 1975)
14. H.L. Guidorizzi, *Um curso de cálculo*, vol. 1, 5th edn. (Livros Técnicos e Científicos Editora S. A, Rio de Janeiro, 2001)
15. B. James, *Probabilidade: um curso de nível intermediário*, Instituto de Matemática Pura e Aplicada, Rio de Janeiro (1981)
16. L.C. Barros, R.Z. Oliveira, R.C. Bassanezi, The influence of heterogeneity in the control of deseases. Front. Artif. intell. Appl. **85**, 88–95 (2002)
17. E. Massad, R. Menezes, P. Silveira, N. Ortega, *Métodos quantitativos em medicina* (Manole, São Paulo, 2004)
18. M.B.F. Leite, R.C. Bassanezi, H.M. Yang, The basic reproduction ratio for a model of directly transmitted infections considering the virus charge and the immunological response, IMA. J. Math. Appl. Med. Biol. **17**, 15–31 (2000)
19. L.C. Barros, R.Z. Oliveira, R.C. Bassanezi, M.B.F. Leite, A desease evolution model with uncertain parameters, in *Proceedings of Joint 9th IFSA World Congress and 20th NAFIPS International Conference (Vancouver, Canada), IFSA, NAFIPS* pp. 1626–1630 (2001)

20. R.M. Jafelice, *Um estudo da dinâmica de transferência de soropositivos para aidéticos via modelagem fuzzy*, Tese de Doutorado, FEEC-UNICAMP, Campinas (2003)
21. R.M. Jafelice, L.C. Barros, R.C. Bassanezi, F. Gomide, Fuzzy modeling in symptomatic HIV virus infected population. Bull. Math. Biol. **66**, 1597–1620 (2004)
22. R.M. Anderson, G.F. Medley, R.M. May, A.M. Johnson, A preliminaire study of the transmission dynamics of the human immunodeficiency virus (HIV), the causitive agent of AIDS. IMA J. Math. Med. Biol. **3**, 229–263 (1986)
23. M.J.P. Castanho, K.F. Magnago, R.C. Bassanezi, W. Godoy, Fuzzy subset approach in coupled population dynamics of blowflies. Biol. Res. **39**(2), 341–352 (2006)
24. W.A.C. Godoy, *Dinâmica determinística e estocástica em populações de dípteros califorídeos: acoplamento por migração, extinção local e global*, Tese de livre docência, UNESP, Botucatu (2002)
25. T. Prout, F. McChesney, Competition among immatures affects their adult fertility: population dynamics. Am. Nat. **126**, 521–558 (1985)
26. J. Roughgarden, *Primer on Ecological Theory* (Prentice-Hall, Upper Saddle River, 1998)
27. K.F. Magnago, *Abordagem fuzzy em modelos populacionais discretos*, Tese de Doutorado, IMECC-UNICAMP, Campinas (2005)