

**A STOCHASTIC AGE-STRUCTURED
POPULATION MODEL**

by

MARUFUL CHOWDHURY, B.S.

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ABSTRACT

Age-structured models for biological species have received much study. In this thesis the age-structured population model is extended to a stochastic age-structured model. The model is solved numerically for two age-structured population examples. The calculational results are compared with Monte Carlo calculations. The results indicate that the two calculational methods are in agreement. Persistence times for two age-structured populations are then studied computationally. It is shown that persistence times increase as the number of age groups increases. Also, persistence times are higher for a stochastic age-structured population than for a nonstochastic (or deterministic) age-structured population.

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CHAPTER I

INTRODUCTION

1.1 Introduction

Mathematical methods have been used to model population dynamics since the twelfth century. Fibonacci proposed his famous sequence to model the growth of a rabbit population. Later, Malthus developed a mathematical model hypothesizing that human populations have a constant natural growth rate. His model was subsequently modified by other researchers taking into account several self-limiting features of populations.

Age-dependent population models are basic in population dynamics. The human population as well as plant and animal populations are age-structured. The analysis of an age-structured population model is of great mathematical and biological interest. An age-structured population at a given time reveals a set of individuals who were born over a range of past times, and whose fertility and probability of survival depend on their age. Age-structured models for biological species were traditionally ignored with the assumption that the populations can be treated as homogeneous with respect to age. This assumption is not valid for many biological species. For example, in the human population, the fertility and probability of survival does depend on age. Accordingly, the age-structure is taken into account in a more realistic model. Recently, this area of mathematical biology has been investigated by Webb [6] and Charlesworth [5].

A stochastic model takes into account the randomness in the birth and death phenomenon where a deterministic model does not. Accordingly, a stochastic age-

structured model is worth developing and investigating. In this thesis we develop a discrete stochastic age-structured population model for the population dynamics.

The stochastic version of the discrete age structured population model is then solved numerically. The numerical results obtained using this model agree with Monte Carlo calculations. The derived stochastic model also extends the deterministic model. We then compare the persistence times of the age-structured model with those calculated for a population with average birth and death rates. Our goal is to find out whether persistence time is greater for age-structured populations, and how stochasticity affects persistence time. We investigate several population examples with different birth and death rates and examine the calculated persistence times.

In the second chapter, we define the continuous age-structured model which is then solved along the characteristics. In the third chapter, the stochastic age-structured population model is derived, and in Chapter III, the results of some numerical examples are considered. The results obtained are then compared with Monte-Carlo calculations. In Chapter IV, a description is presented of the techniques used to calculate the results obtained by the stochastic age-structured model and the Monte-Carlo procedures. Calculations of persistence times for two different age-structured population examples are described and compared in Chapter IV. In the last chapter, we summarize and conclude our results and suggest future research work.

CHAPTER II

STANDARD AGE-STRUCTURED MODEL

2.1 Continuous Age-Structured Model

It is useful to first describe the age-independent version of the population growth model, where the birth and death rates are independent of age. If $u(t)$ is the population at time t , the total population size at time t is given by

$$u(t) = \int_0^{\infty} u(t, a) da.$$

Then,

$$\begin{aligned} \frac{du(t)}{dt} &= [b(t) - \mu(t)]u(t) \\ u(0) &= \int_0^{\infty} u_0(a) da, \end{aligned} \tag{2.1}$$

and the solution to this differential equation is

$$u(t) = u(0)e^{\int_0^t (b(t') - \mu(t')) dt'}, \tag{2.2}$$

where $b(t)$ and $\mu(t)$ are the birth and death rates, respectively. Note that the population increases if birth rate is greater than death rate and decreases if birth rate is less than death rate. The mathematical model proposed by Malthus is one where $(b(t) - \mu(t))$ is considered to be constant.

Now let us describe the population growth model with continuous age distribution. We let $u(t, a)$ be an age distribution function which specifies the age structure

of the population at time t and age a . The McKendrick-Von Foerster equation for the dynamics of an age-structured population is given by

$$\begin{aligned}\frac{\partial u}{\partial t} + \frac{\partial u}{\partial a} &= -\mu(a)u(t, a) \\ u(t, 0) &= \int_0^{\infty} b(a)u(t, a)da \\ u(0, a) &= f(a),\end{aligned}\tag{2.3}$$

where

$u(t, a)$ = population at time t and age a ,

$b(a)$ = age-specific birth rate of the population at age a ,

$\mu(a)$ = age-specific death rate, $\mu \geq 0$,

$u(t, 0) = \int_0^{\infty} b(a)u(t, a)da$ is the birth rate at time t , and

$u(0, a) = f(a)$ initial age distribution, assumed to be known, and

$\int_0^{\infty} u(t, a)da$ = total population at time t .

The first equation in (2.3) is based on the assumption that the changes occurring in the population at time t and age a in a short time interval of length h is proportional to the size of the population and h . Thus

$$u(t+h, a+h) - u(t, a+h) + u(t, a+h) - u(t, a) = -\mu(a)u(t, a)h.$$

Dividing both sides by h and taking the limit as $h \rightarrow 0$ we obtain the first equation in (2.3). It should be noted that the birth rate $b(a)$ and the death rate $\mu(a)$ could also depend on time t . The initial age distribution $f(a)$ is usually a smooth function and is zero for large a .

Equation (2.3) is a linear hyperbolic first-degree partial differential equation. Solving this equation for $u(t, a)$ will allow us to predict the population dynamics at age a and time t . The characteristics of this equation are the straight lines parallel to the line $t = a$. In the next section the method of characteristics is used to reduce this partial differential equation to a first-order differential equation which is then solved along the characteristics.

2.2 Age-Structured Model Along the Characteristics

The continuous age-structured model can be solved by the method of characteristics which reduces a partial differential equation to an ordinary differential equation along the characteristic curves. We note that in our model the domain in a does not extend from $-\infty$ to ∞ . Thus the system is an initial-boundary value problem rather than an initial value problem. In the method of characteristics, we change the coordinates (t, a) to characteristic coordinates (s, τ) , where $t \equiv t(s)$, $a \equiv a(s)$, and $u(t(s), a(s)) \equiv u(s)$, and τ is constant along the characteristic curves. If we let

$$\frac{dt}{ds} = 1 \quad \text{and} \quad \frac{da}{ds} = 1.$$

then

$$\frac{du}{ds} = \frac{\partial u}{\partial a} \frac{da}{ds} + \frac{\partial u}{\partial t} \frac{dt}{ds}$$

and our partial differential equation reduces to an ordinary differential equation

$$\frac{du(s)}{ds} = -\mu(a)u(s). \quad (2.4)$$

The characteristic curves are found by integrating

$$\frac{dt}{ds} = 1 \quad \text{and} \quad \frac{da}{ds} = 1.$$

which gives

$$t = s + t_0$$

$$a = s + a_0.$$

In addition, $s = 0$, $t_0 = 0$ for $a > t$ and $a_0 = 0$ for $a < t$. Thus, eliminating s , the characteristic curves are obtained. In our case these are the straight lines

$$a = \begin{cases} t + a_0 & \text{if } a > t \\ t - t_0 & \text{if } a < t. \end{cases}$$

We solve equation (2.4) for the following two cases:

Case I: $a > t$

We have,

$$\frac{du(s)}{ds} = -\mu(s + a_0)u(s),$$

or,

$$u(s) = u(0)e^{-\int_0^s \mu(s'+a_0)ds'}$$

but since $u(0) = u(s)|_{s=0} = u(t(s), a(s))|_{s=0} = u(0, a_0) = f(a_0) = f(a - t)$, the solution in this case is

$$\begin{aligned} u(t, a) &= u(0, a_0)e^{-\int_0^s \mu(s'+a_0)ds'} \\ &= f(a - t)e^{-\int_0^t \mu(s'+a-t)ds'} \\ &= f(a - t)e^{-\int_{a-t}^a \mu(s'')ds''}. \end{aligned}$$

Case II: $a < t$

$$\begin{aligned} u(s) &= u(0)e^{-\int_0^s \mu(s'+a_0)ds'} \\ u(t, a) &= u(t_0, 0)e^{-\int_0^s \mu(s')ds'} \\ &= u(t - a, 0)e^{-\int_0^a \mu(s')ds'}. \end{aligned}$$

However, the last equation involves u which is unknown and we cannot obtain an explicit solution. Instead, using the boundary condition $u(t, 0) = \int_0^\infty b(a)u(t, a)da$ for zero age, we can write an integral equation for $u(t - a, 0)$ which can be solved iteratively, for example, by Piccard's method of iteration. Thus, the solution in case II can be solved explicitly for the following Volterra integral equation:

$$u(t, 0) = \int_0^\infty b(a)u(t, a)da$$

$$\begin{aligned}
&= \int_0^t b(a)u(t, a)da + \int_t^\infty b(a)u(t, a)da \\
&= \int_0^t b(a)u(t - a, 0)e^{-\int_0^a \mu(s)ds} da + \int_t^\infty f(a - t)e^{-\int_{a-t}^a \mu(s)ds} da,
\end{aligned}$$

or, letting $z = t - a$,

$$u(t, 0) = \int_0^t b(t - z)u(z, 0)e^{-\int_0^{t-z} \mu(s)ds} dz + \int_0^\infty f(z)e^{-\int_z^{z+t} \mu(s)ds} dz.$$

CHAPTER III

DERIVATION OF STOCHASTIC AGE-STRUCTURED MODEL

Along the characteristics, the standard McKendrick-Von Foerster age-structured population equation has the form

$$\begin{aligned}\frac{du(s)}{ds} &= -\mu(a)u(s) \\ u(0) &= f(a_0), \quad \text{for } a > t \\ u(0) &= \int_0^\infty b(a)u(t_0, a)da \quad \text{for } a < t,\end{aligned}\tag{3.1}$$

where $t = s$ and $a = s + a_0$ for $a > t$, and $a = s$ and $t = s + t_0$ for $a < t$.

To numerically solve the above differential equation, we define mesh points for age and time. A discretized form of equation (3.1) assuming discrete ages $a_0, a_1, a_2, \dots, a_I$, where $a_i = i\Delta a$, for $i = 0, 1, 2, \dots, I$, has the form

$$\begin{aligned}u_{i+1, j+1} &= u_{i, j} - d_i u_{i, j} \Delta s \quad \text{for } i = 0, 1, 2, \dots, I-1, j = 0, 1, 2, \dots \\ u_{i, 0} &= \Delta s f(a_i) \quad \text{for } i = 0, 1, 2, \dots, I \\ u_{0, j+1} &= \sum_{i=0}^{I-1} \frac{(b_i u_{i, j} + b_{i+1} u_{i+1, j}) \Delta s}{2} \quad \text{for } j = 0, 1, 2, \dots\end{aligned}\tag{3.2}$$

where $\Delta s = \Delta a = \Delta t$, $t_j = j\Delta t$ for $j = 0, 1, 2, \dots$, and $u_{i, j} \approx u(t_j, a_i)\Delta a$. Note that in equation (3.2), $u_{i, j}$ is the population at age a_i and time t_j , where in equation (3.1) $u(s) = u(t, a)$ is the population per unit age at time t , also $d_i = \mu(a_i)$ and $b_i = b(a_i)$. Thus, for example, the population at time t_j is

$$\begin{aligned}
\int_0^{\infty} u(t_j, a) da &\approx \sum_{i=0}^I u_{i,j} \\
&\approx \sum_{i=0}^{I-1} (u_{i,j} + u_{i-1,j})/2.
\end{aligned} \tag{3.3}$$

We shall develop a stochastic age-structured model using the notion of a Leslie matrix. The simplest model with an age structure is a linear model referred to as the Leslie model [2]. This can be used to model the changes in the age structure of a population, as well as the changes in population size. The Leslie matrix which is sometimes referred to as the projection matrix has the following form:

$$X(n+1) = LX(n),$$

where

$$X(n) = [x_1(n), x_2(n), x_3(n), \dots, x_m(n)]^T,$$

$$X(n+1) = [x_1(n+1), x_2(n+1), x_3(n+1), \dots, x_m(n+1)]^T, \text{ and}$$

$$\mathbf{L} = \begin{pmatrix} b_1 & b_2 & \dots & b_{m-1} & b_m \\ s_1 & 0 & \dots & 0 & 0 \\ 0 & s_2 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & \dots & s_{m-1} & 0 \end{pmatrix}$$

where,

$x_i(n)$ = population in the i th age class in generation n

b_i = age specific birth rate for the i th age class

s_i = fraction of the i th age group surviving to the $(i + 1)$ st age. $0 < s_i \leq 1$, and the first age group x_1 consists of births from all age groups:

$$x_1(n + 1) = b_1x_1(n) + b_2x_2(n) + b_3x_3(n) + \dots + b_mx_m(n) = \sum_{i=1}^m b_ix_i(n).$$

The number in the i th age group that survive to age $i + 1$ is:

$$x_{i+1}(n + 1) = s_ix_i(n).$$

Equations (3.2) that approximate (3.1) are a form of Leslie matrix. These equations can be transformed into a stochastic system. We note that as births and deaths occur in a random manner, equations (3.1) and (3.2) model the average time-dependent behavior of the populations. We need to find the mean and variance of births and deaths in order to transform (3.2) to an appropriate and accurate stochastic system. Note that for a short time interval Δs , the mean and variance of deaths in population $u_{i,j}$ is $d_i\Delta s u_{i,j}$ neglecting terms of order $(\Delta s)^2$. The mean and variance for births is

$$\sum_{i=0}^{I-1} (b_i u_{i,j} + b_{i+1} u_{i+1,j+1}) \frac{\Delta s}{2}.$$

Assuming that changes in births and deaths over a small interval of time Δs are approximately normally distributed, then a stochastic version of (3.2) is

$$u_{i+1,j+1} = u_{i,j} - d_i u_{i,j} \Delta s + \sqrt{d_i u_{i,j} \Delta s} \eta_{ij}$$

for $i = 0, 1, 2, \dots, I - 1, j = 0, 1, 2, \dots$

$$\begin{aligned}
u_{i,0} &= \Delta s f(a_i) \quad \text{for } i = 0, 1, 2, \dots, I \\
u_{0,j+1} &= \sum_{i=0}^{I-1} \frac{(b_i u_{i,j} + b_{i+1} u_{i+1,j}) \Delta s}{2} + \sqrt{\sum_{i=0}^{I-1} \frac{b_i u_{i,j} + b_{i+1} u_{i+1,j} \Delta s}{2}} \hat{\eta}_j \\
&\text{for } j = 0, 1, 2, \dots
\end{aligned} \tag{3.4}$$

where $\eta_{i,j} \in N(0, 1)$ and $\hat{\eta}_j \in N(0, 1)$ [1]. Equation (3.4) is a stochastic version of the discrete age-structured population model.

Notice that as $\Delta s \rightarrow 0$, the first equation in (3.4) becomes

$$\frac{du(s)}{ds} = -d(s)u(s) + \sqrt{d(s)u(s)} \frac{dW(s)}{ds}$$

This is a stochastic version of equation (3.2), where $u(s)$ = population at position s along a characteristic and $W(s)$ is the Wiener process [10].

CHAPTER IV

NUMERICAL SOLUTION FOR STOCHASTIC MODEL

In this chapter we describe the computational methods for the numerical solution of the stochastic and Monte-Carlo age-structured models. We compare the results of both models. Also, mean persistence times for age-structured populations are compared for different age-structured models.

4.1 Description of Computational Methods

In this section, we shall describe the computer algorithm that numerically solves the stochastic age-structured model assuming discrete ages. Also, the Monte Carlo procedure is described. Monte Carlo calculations are used to verify and test the results of the stochastic discrete-age model.

4.1.1 Stochastic Discrete Age-Structured Computer Model

To test the computer model, the initial age distribution and the birth and death rates are based on the equilibrium age-structure solution or, time-independent solution, $u_e(a) \equiv u(t, a)$.

$$\begin{aligned}\frac{du_e(a)}{da} &= -\mu(a)u_e(a) \\ u(0) &= \int_0^\infty b(a)u(a)da\end{aligned}\tag{4.1}$$

$$u_e(a) = u(0)e^{-\int_0^a \mu(z)dz} = u(t, a)\tag{4.2}$$

where, $u(t, a)$ is the population at time t and age a . The initial age distribution $f(a)$ is set equal to $u_e(a)$.

To find the average birth and death rates from the equilibrium age distribution, consider a similarity solution [3] of the following form where $r(a) = u_e(a)$

$$u(t, a) = e^{\gamma t} r(a). \quad (4.3)$$

Thus, the age distribution is changed only by a factor which either grows or decays with time according to whether $\gamma > 0$ or $\gamma < 0$. When $\gamma = 0$, then we have the equilibrium age-structure solution.

Substitution of (4.3) in the first equation of (2.3) gives

$$\frac{dr}{da} = -[\mu(a) + \gamma]r. \quad (4.4)$$

Thus, the solution for $r(a)$ is

$$r(a) = r(0)e^{-\gamma a} e^{-\int_0^a \mu(z) dz}.$$

Note that, $u(0, a) = f(a) = r(a)$.

Therefore,

$$u(t, a) = e^{\gamma t} [r(0)e^{-\gamma a} e^{-\int_0^a \mu(z) dz}].$$

However,

$$\begin{aligned} u(t, 0) &= \int_0^\infty b(a)u(t, a)da \\ &= e^{\gamma t} r(0). \end{aligned}$$

This gives

$$\int_0^{\infty} b(a)e^{\gamma t}[r(0)e^{-\gamma a}e^{-\int_0^a \mu(z)dz}]da = e^{\gamma t}r(0).$$

The above equation gives a condition on the birth and death rates. Specifically,

$$\int_0^{\infty} b(a)e^{-\gamma a}e^{-\int_0^a \mu(z)dz} da = 1.$$

Hence, γ must satisfy

$$1 = \phi(\gamma) = \int_0^{\infty} b(a)e^{-\gamma a}e^{-\int_0^a \mu(z)dz} da. \quad (4.5)$$

Note that $\phi(\gamma)$ monotonically decreases with γ .

For the equilibrium solution, that is for $\gamma = 0$, we need,

$$\int_0^{\infty} b(a)e^{-\int_0^a \mu(z)dz} da = 1. \quad (4.6)$$

Provided that (4.6) is satisfied, the equilibrium solution is obtained which satisfies (4.2). Finally, if \bar{b} and $\bar{\mu}$ are the average birth and death rates, respectively, then

$$\bar{b} = \frac{\int_0^{\infty} b(a)u(t, a)da}{\int_0^{\infty} u(t, a)da} \quad (4.7)$$

$$\bar{\mu} = \frac{\int_0^{\infty} \mu(a)u(t, a)da}{\int_0^{\infty} u(t, a)da}. \quad (4.8)$$

To test computationally our stochastic age-structured model, we consider the following age-specific birth and death rates,

$$b(a) = b_c \chi(a) \quad (4.9)$$

$$\mu(a) = r(a - a_d)^2 + s \quad (4.10)$$

where $\chi(a) = 1$ for $a \in [1, 4]$ and zero otherwise, and r , a_d , and s are constants.

We can adjust b_c so that $\gamma = 0$ in equation (4.5). In the first example, $\chi = 1$ for $a \in [1, 4]$ and zero otherwise and $\mu(a) = .4(a - 2)^2 + .1$. In the second example also $\chi = 1$ for $a \in [1, 4]$, and $\mu(a) = 1$. Thus, for the first example, in order that (4.6) is satisfied, we have

$$b_c = \frac{1}{\int_1^4 e^{-\int_0^a \mu(z) dz} da} = \frac{1}{0.720154}.$$

The initial age distribution $f(a)$ is obtained from equilibrium equation as

$$f(a) = u(0)e^{-\int_0^a \mu(z) dz}.$$

We choose $u(0)$ to fix the total initial population. The equilibrium population is constant with time but it is assumed to be a continuous function with respect to age. However, as the number of discrete ages increases, we would expect that the discrete age-structured population would also be approximately constant as well.

In the computer program, birth and death rates and the initial equilibrium age distribution are calculated for all ages. These are then used as the values in the stochastic discrete age-structured model.

In the computational algorithm of the stochastic discrete age-structured model, the age and time steps are taken to be equal. Using a random number generator, the populations are calculated at each time and age group using (3.4). The new

population is obtained from the previous population after calculating deaths in each age group at each time step. The new births are obtained from the old population for each age group. This is performed for many different populations from which estimates for average birth and death rates and total population sizes as well as variances are obtained. We compare these results with those obtained by the Monte Carlo method.

4.1.2 Monte-Carlo Age-Structured Model

Monte Carlo methods are stochastic techniques and are based on the use of random numbers and probability statistics to investigate population processes. In this section, we describe the Monte Carlo method used to model an age-structured population to check the results of our stochastic age-structured model.

In the Monte Carlo method, we follow the random behavior of each individual of the total population at each time step. The births and deaths are determined for each time step following known probability distributions and the populations are always considered to be whole numbers. Since we have an age-structured model, the probability of births and deaths at each age group is considered.

Some specific details of the Monte Carlo calculational procedure are given in this paragraph. First, a total population size n is specified. Next, n discrete ages are calculated. The j^{th} age $a_j = \frac{\hat{a}_{j+1} + \hat{a}_j}{2}$ where

$$\frac{1}{n} = \frac{\int_{\hat{a}_j}^{\hat{a}_{j+1}} f(a) da}{\int_0^{\infty} f(a) da}.$$

Each individual in the initial population thus has a unique age. Now, the population is followed for a specified length of time t . For each small time step h , each individual in the population is tested to see whether that individual has given birth

or has died. The births are summed into a new age group with zero age. All ages of individuals are increased by time h . This process repeats, although now several individuals may have the same age, until the final time t has been reached. A new population is then followed. This continues until several hundred or thousand populations have been computationally investigated. The calculational results of all these populations is then analyzed for later comparison with the discrete stochastic age-structured population model.

4.2 Numerical Examples

4.2.1 Comparison of Two Computational Methods

In this section we compare the numerical results of two different stochastic age-structured population examples obtained using (3.4) and with Monte Carlo calculations. The two age-structured population examples described in Section (4.1.1). For 200 age groups and a total initial population size of 160, that is, $\int_0^\infty b(a)u_e(a)da = 160$, calculational results were obtained for Example One using Monte Carlo calculations and the stochastic age-structured model (3.4). The populations were simulated up to time 5.0. Recall that in this first example, $b(a) = \frac{1}{0.720154}$, $a \in [1, 4]$, and $b(a) = 0$ otherwise. Also, $\mu(a) = .4(a - 2)^2 + .1$.

From Table 4.1 we see that the average births, deaths and the total population of the first example for Monte Carlo calculations and (3.4) are consistent. Table 4.2 exhibits the second stochastic age-structured example where $\mu(a) = 1$. The calculational results agree for this example as well. Note that the averages are obtained from 500 individual populations for each example.

As an additional check on the stochastic age-structured model, we set $\hat{\eta}_j$ equal

Table 4.1: Comparison of Monte Carlo Calculations and (3.4) for Example 1

Monte Carlo Calculations			Example One	
	Average	Variance	Average	Variance
Births	577.2	3592.5	594.2	3356.0
Deaths	566.9	1585.1	614.7	1619.0
Population	154.0	651.4	148.0	554.1

Table 4.2: Comparison of Monte Carlo Calculations and (3.4) for Example 2

Monte Carlo Calculations			Example Two	
	Average	Variance	Average	Variance
Births	669.2	8290.7	611.5	7250.0
Deaths	677.5	4371.2	617.6	4061.0
Population	132.4	902.2	119.1	727.1

to zero in the computer program. The estimated variance in the births for the first example is 1929.0 which does not agree with the Monte Carlo calculations.

4.2.2 Calculation of Mean Persistence Time

The mean persistence time for several age-structured population can be estimated using (3.4). In the previous section we have seen that the numerical approach used to solve (3.4) compares well with the Monte Carlo calculations. Individual populations are simulated using (3.4) and followed until the total population fails to persist. Averaging many such calculated persistence times yields an estimate for the mean persistence time. In Section 4.1.1 we have computationally

solved (3.4). To compute the persistence time, we set the number of births equal to zero when the total population reaches the maximum size which is 40. Then we follow the total population until it falls below $\frac{1}{2}$. The value $\frac{1}{2}$ is selected in this investigation as a compromise between the values 0 and 1 as theoretically the population persists until the size reaches zero but practically the population persists until the size falls below unity. Thus, after the population size meets this exit criterion, the persistence time of that population is saved and another population trajectory is simulated. This is done for a large time (maximum time = 50000.0), so that we are guaranteed that the population goes extinct before it reaches the final time step. After many individual population trajectories are computed, the mean persistence time is estimated by averaging the individual persistence times.

In computing the mean persistence times, it is assumed that the maximum total population size is 40 for both stochastic age-structured examples. We can find the non-stochastic persistence time considering the similarity solution of the form (4.3) of the equilibrium age-structure (4.2). We note that $\gamma = 0$ gives $\bar{b} = \bar{\mu}$. In the persistence time calculations we increase the age-specific death rate by 50 percent which gives $\bar{\mu} = 1.5\bar{b}$. We then numerically solve equation (4.5) for γ . For the first example $\gamma = -.302$ and for the second example $\gamma = -.5$. With these birth and death rates the non-stochastic persistence time for the continuous age model can be obtained from equation (4.3) by integrating over all the ages. This yields $u(t) = u(0)e^{\gamma t_p}$. Thus the persistence times for the continuous non-stochastic age-structured models are found by solving $\frac{1}{2} = 40e^{\gamma t_p}$. They are, $t_{p_1} = 14.5$ and $t_{p_2} = 8.8$ for the first and second examples, respectively. For comparison between the age-structured and non-age-structured population models, we further compute

Table 4.3: Mean Persistence Times for Examples 1 and 2

Number of Age Groups	Mean Persistence Time	
	Example 1	Example 2
80	10.13	8.50
140	13.67	8.90
200	16.72	9.35
260	18.57	9.74
320	23.07	10.72

the persistence time using the MacArthur-Wilson difference equation [1] which has no age-structure, with $\bar{b} = 1.0$ and $\bar{\mu} = 1.5$ for a total population size 40. The MacArthur-Wilson difference equation yield a persistence time of 6.36.

In Table 4.3 we give the results of calculated persistence times for the stochastic age-structured model for several number of discrete age groups for each example. The maximum population size is 40 and the mean persistence times are estimated from 500 populations with $\bar{b} = 1.0$ and $\bar{\mu} = 1.5$. The table shows that the persistence time increases with the number of age groups. This indicates that the persistence time increases with the number of age groups. This is a new result as the MacArthur-Wilson difference equation does not model persistence of an age-structured population.

CHAPTER V

SUMMARY AND CONCLUSIONS

Stochastic age-structured population models had never been studied before the present investigation. In this thesis we developed a new discrete stochastic age-structured model for the population dynamics. We numerically solved the model and made comparisons with Monte Carlo calculations. The numerical results are consistent. Using the stochastic age-structured model, we computed persistence times for age-structured population examples and compared the results with a stochastic non-age-structured model. The comparisons indicate that persistence times are greater for age-structured models. Two different age-structured population examples have been considered to investigate how the persistence time is affected for different birth and death rates. It is seen that the second example has a lower persistence time as compared with the first example.

Age-structured models have been used to model infectious diseases in humans since age-structure is very important in immunization programs [11]. Our stochastic age-structured model can be used to further improve the application of such non-stochastic age-structured models. The persistence time calculations are of great importance in understanding biological populations and determining, for example sizes of wildlife preserves.

Future research work may possibly be done to modify our discrete model to continuous time, discrete age-structured stochastic model. Also, the model developed in the present investigation may possibly be generalized to a two-sex stochastic age-structured model.

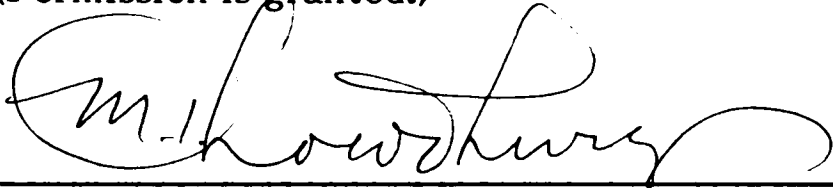
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