Lotka-Volterra Population Model of Genetic Evolution

Mirosław R. Dudek*

Institute of Physics, Zielona Góra University, 65-069 Zielona Góra, Poland.

Abstract. A deterministic model of an age-structured population with genetics analogous to the discrete time Penna model [1, 2] of genetic evolution is constructed on the basis of the Lotka-Volterra scheme. It is shown that if, as in the Penna model, genetic information is represented by the fraction of defective genes in the population, the population numbers for each specific individual's age are represented by exactly the same functions of age in both models. This gives us a new possibility to consider multi-species evolution without using detailed microscopic Penna model. We discuss a particular case of the predator-prey system representing an ecosystem consisting of a limited amount of energy resources consumed by the age-structured species living in this ecosystem. Then, the increase in number of the individuals in the population under consideration depends on the available energy resources, the shape of the distribution function of defective genes in the population and the fertility age. We show that these parameters determine the trend toward equilibrium of the whole ecosystem.

AMS subject classifications: 92D15, 92D25, 92D40, 34C23

PACS: 87.23.-n, 87.53.Wz,02.30.Hq

Key words: Lotka-Volterra equations, Penna model, evolution.

1 Introduction

Thousands of papers have been published on the Lotka-Volterra equations [3,4] describing population growth, competition or speciation. In real populations the reproduction rate of individuals depends on their age and therefore it is necessary to include age structure into these equations. One example of how this can be achieved can be found in [5]. It is also possible to introduce a time delay between cause and effect (see, e.g., [6]). However, the majority of the Lotka-Volterra equations do not usually include genetic information and the question arises how to include it directly into the Lotka-Volterra equations.

---

*Corresponding author. *Email address:* `mdudek@proton.if.uz.zgora.pl` (M. R. Dudek)

The age-specific equations for population growth seem to be a good candidate to represent genetic information because the age structure introduces some analogy to the Penna model [1, 2] of genetic evolution. It is a model of genetic evolution although all details concerning the genes are skipped except of the state of their functionality - is the gene under consideration correct or it is mutated. This simple model has turned out to be very successful in interpreting the demographers data of real populations even as complex as human populations [2, 7–9].

In the original asexual version of the Penna model [1], the population under consideration consists of individuals represented by genomes defined as a string of n bits. The bits represent states of genes where 0 denotes its functional allele and 1 its bad allele. It is assumed that if an individual possesses T bad alleles switched on, it dies. In the model all genes are switched on chronologically - each bit corresponds to one "year" - and maximum life span of an individual is a_D "years". After reaching the fertility age a_F an individual gives birth to B offsprings whose genomes are mutated versions of the parental genome. The mutation rate M is constant. After the mutation the affected gene is represented by a bit with a value opposite to the value before the mutation. The results of the Monte Carlo simulations of three different haploid populations for the Penna model in the case when back mutations from 1 to zero are not allowed have been shown in Fig. 1. In the figure, there have been plotted fraction of defective chronological genes in each population and age distribution of individuals.

In the diploid version of the Penna model the individual's genome is represented by two bitstrings and then each locus possesses two alleles. The diploid individuals can reproduce sexually [2]. Both the haploid model of the equilibrium population and its diploid version are uniquely described by the fraction of defective genes in the population specific for each individual's age. A short review of Monte Carlo simulation results for the Penna model with some additional details, like the presence of the housekeeping genes or the recombination frequency, can be found in [9].

Although the age distribution curves obtained in the Penna model coincide very well with demographers data for real populations, the model is not so "interdisciplinary" as the Lotka-Volterra population model. The reason could be that it is very difficult to obtain analytical results for the general Penna model and therefore one has to use the Monte Carlo method. However Monte Carlo simulations of the Penna model need large populations and the simulation time is very long. Hence, the typical multi-species problem exceeds the computing capability of a single PC-computer. Another problem is how to avoid the correlations arising from parallel computing if one tries to distribute the simulations to many processors. On the other side hand, it is relatively easy to solve numerically even a large set of the differential equations describing the Lotka-Volterra populations. Below we show how to include the fraction of defective genes into the equation for population growth so that the age distribution curves for these two models coincide.

In the following sections we discuss the behavior of the Lotka-Volterra ecosystem in which the age-specific species has been determined by the form of the fraction of defective genes.