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Survivability of Verhulst-free Populations under Mutation Accumulation

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***Abstract*—**Stable nonzero populations without random deaths caused by the Verhulst factor (Verhulst-free) are a rarity. Majority either grow without bounds or die of excessive harmful mutations. To delay the accumulation of bad genes or diseases, a new environmental parameter **Γ** is introduced in the simulation. Current results demonstrate that stability may be achieved by setting **Γ = 0.1**. These steady states approach a maximum size that scales inversely with reproduction age.

***Keywords*—**Aging, mutation accumulation, population dynamics.

I. Introduction

A PREVIOUS WORK [1] demonstrates the possibility of obtaining finite populations without imposing the concept of a carrying capacity (or the Verhulst factor). The model utilizes the bit-string technique presented in [2]. Each individual in a population is described by a 32-bit string of binary numbers - a chronological genome. The string is read in sequence, one bit for each iteration. Whenever a new bit is read, a genetic characteristic is expressed and the individual's age is increased by one unit. A **1** on the i^{th} bit indicates a harmful mutation or disease whose effects are felt beginning at age *i* until death. The bit-string is set at birth and is held constant throughout the individual's lifetime. For simplicity, the population is considered asexual. An offspring copies the genes of its parent and acquires additional mutations that are set at randomly chosen bit locations.

Without the concept of a carrying capacity, a slight increase in birth rate can cause populations to tend towards infinity, as in the Malthusian growth model [3]. Existing Verhulst-free steady states are thus limited to a highly specialized case - individuals that breed once at a fixed age (semelparous) and produce only one offspring. About half of these cases, however, exhibit mutational meltdown. When very few births fail to balance the effects of harmful genetic mutations, populations approximate an exponential decay and die [4], [5].

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Our primary goal is to explore further cases of non-zero Verhulst-free steady states. In population modeling, the Verhulst factor acts as a "catch all" parameter that accounts for all possible environmental interactions. Without the concept of a carrying capacity, population evolution is governed only by genetic mechanisms. To incorporate back environmental effects into the simulation, we introduce a new parameter, **Γ**. At each time of reproduction, a randomly chosen good gene mutates with probability $p=\exp(-1/\Gamma)$. Here, we investigate whether the delay in mutation accumulation, as introduced through the parameter **Γ** and its associated probability, is enough prevent population extinction via mutational meltdown.

II. Methodology

We implement the 32-bit model described in [1] using a Fortran code. The evolutionary process for an initial population, N_0, of 1000 perfect newborns (no bad mutations) is summarized in Fig. 1.

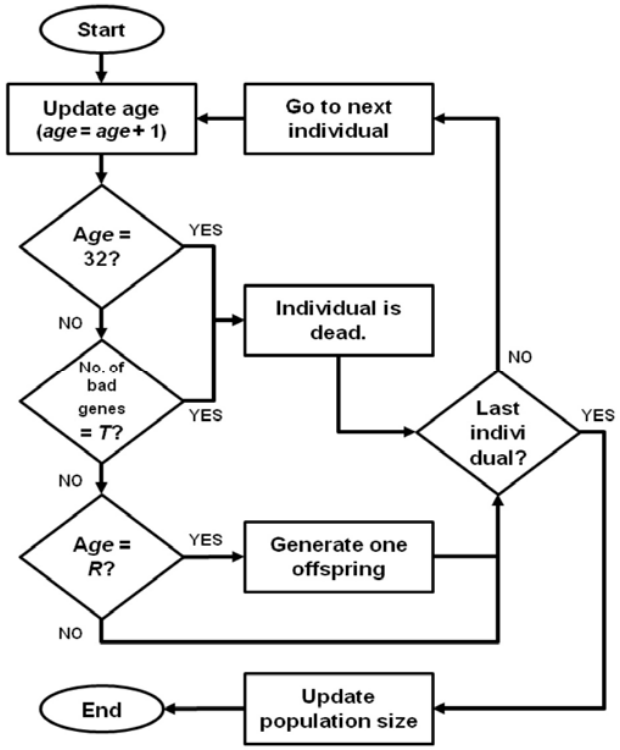

Fig. 1 Flowchart of the evolutionary process

In the Verhulst-free case, deaths are due only to genetic reasons. An individual dies when the total number of active diseases equals the mutations threshold, ***T***, or upon reaching the maximum age, which is equivalent to the bit-string length. In this case, **32**. Surviving adults are allowed one offspring each. As in semelparous species, reproduction is restricted to a fixed age, ***R***.

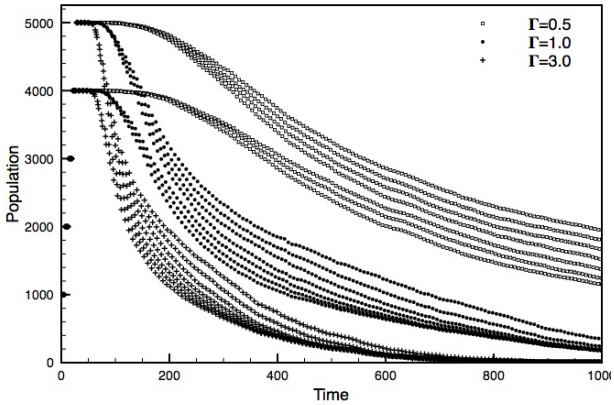

Fig. 2 Extinct populations associated with ***T*=5, *R*=7**

During the birth process, the newborn copies the genes of its parent. A random bit position is then selected. If the chosen bit contains a good gene, it is mutated according to the probability,

$$p = e^{-1/\Gamma}. \quad (1)$$

We consider only deleterious mutations. This is because bad mutations are several times more frequent in nature than good ones [6]. Thus, if the selected bit already contains a bad gene or disease, its value (or state) is retained. Furthermore, we focus on the $T \le R$ case and observe the effect of varying Γ on the resulting populations.

III. Results And Discussion

Fig. 2 presents extinction cases associated with $T \le R$. Simulated populations are observed to increase at the onset. But as harmful genetic mutations accumulate, they tend to die out. Extinction happens at an earlier time when Γ is larger. As expected, smaller Γ values (lower mutation probabilities) result in more persistent populations. This scenario may be related to the accumulation of somatic mutations in *Drosophila melanogaster* (or fruit fly) [7]. Somatic mutations occur more frequently at higher temperatures, thereby decreasing significantly the lifespan of the fruit flies. The parameter Γ may thus be associated to the temperature of the environment.

The latter part of these curves (Fig. 2) may be fitted with an exponential function of the form,

$$N(t) \propto e^{-\alpha t} \quad (2)$$

where α is the decay rate. In Fig. 3, we plot the α-values against the mutation probability given by Eq. 2. Best-fit yields a line with a positive slope. The line becomes less steep at higher mutation thresholds, ***T***. The effect, therefore, of the parameter Γ on the simulated populations diminishes at higher threshold values, when individuals are more tolerant of harmful mutations or are more resilient to diseases.

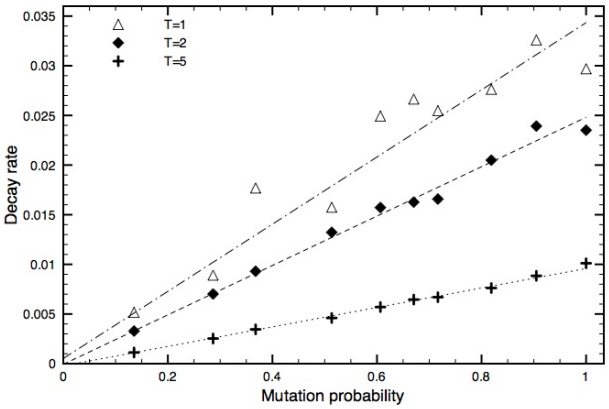

Fig. 3 Decay rate, α, versus the mutation probability, $p=e^{-1/\Gamma}$

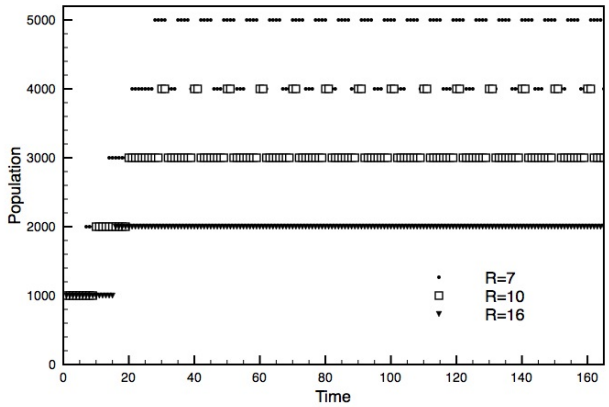

Fig. 4 Steady states associated with $T \le R$ and $\Gamma = 0.1$

Nonzero steady states are found by setting Γ to 0.1. Fig. 4 illustrates stable populations associated with different reproduction ages. Note that a stable population may be single-valued (as with ***R*=16**) or may cycle between two or more values (as with ***R*=7** and **10**). Simulation results also show that for a given R value, populations approach a maximum size that is independent of the mutation threshold. The maximum steady state value, N_{max}, obtained using different reproduction ages are presented in Fig. 5. Reproductive delays (higher ***R***), in general, cause smaller populations. From the best fit, we can deduce

$$N_{\max} = \left(\frac{L}{R}\right) N_0 \quad (3)$$

where ***L*** is the bit-string length and N_0 is the size of the initial population. In our simulation, ***L*** and N_0 have values equivalent to **32** and **1000**, respectively.

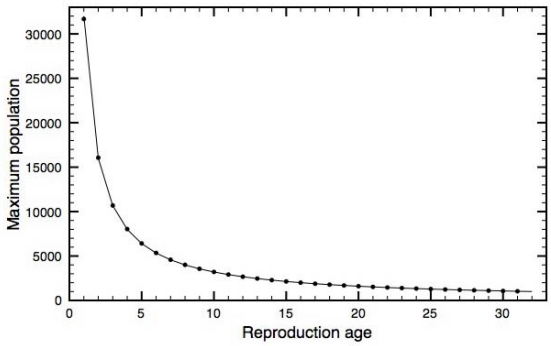

Fig. 5 Variation of the maximum population size with reproduction age, $\boldsymbol{R}$

IV. Summary And Conclusion

The model presented in [1] was modified to include a new parameter $\boldsymbol{\Gamma}$, in the hope of finding more nonzero steady states without imposing a carrying capacity (or random deaths by the Verhulst factor). The parameter $\boldsymbol{\Gamma}$ may be treated as an environmental factor that affects the accumulation of harmful genetic mutations in the genome.

In Verhulst-free simulations, the $\boldsymbol{T \leq R}$ case is generally associated with mutational meltdown. The rate of extinction is slow down with decreasing $\boldsymbol{\Gamma}$. Nonzero steady states are obtained by setting $\boldsymbol{\Gamma = 0.1}$. Simulated populations approach a maximum value that scales is inversely proportional to the value of the reproduction age.

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