Bit-string models for parasex

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Abstract

We present different bit-string models of haploid asexual populations in which individuals may exchange part of their genome with other individuals (parasex) according to a given probability. We study the advantages of this parasex concerning population sizes, genetic fitness and diversity. We find that the exchange of genomes always improves these features.
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1. Introduction

Since a long time the question on why sex evolved has been studied through different models. Some of them justify the sexual reproduction from intrinsic genetic reasons, and others from extrinsic or social reasons like child protection, changing environment or parasites [1].

The Redfield model [2] is an example of an elegant model that requires little computer time. It is not a population dynamics model following the lifetime of each individual, but only simulates their probabilities to survive up to reproduction. The mortality increases exponentially with the number of mutations in the individual. For

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the sexual variant the number of mutations in the child is determined by a binomial distribution such that on average the child has as its own number of mutations half the number of the father, plus half the number from the mother. At birth, new mutations are added following a Poisson distribution, for both asexual and sexual reproduction. Because of the lack of an explicit genome, intermediate forms of reproduction as meiotic parthenogenesis and hermaphroditism were not simulated.

A more realistic model, involving an explicit genome in the form of bit-strings, was more recently used by Örçal et al. [3] to investigate intermediate reproductive regimes. It makes use of a parameter μ, introduced before by Jan et al. [4], defined such that only individuals with μ and more mutations exchange genome. Healthy individuals without many mutations reproduce asexually, that is, by cloning plus deleterious random mutations. In contrast to our purely haploid models described below, these models [3] use also diploid life forms.

The models we present here are of this second type, that is, the genomes of the individuals are represented by bit-strings, and our purpose is to investigate an intermediate strategy (between asexual-haploid and sexual-diploid reproduction) which is called parasex. Parasexuality is any process in which participates more than one parent, without meiosis and fertilisation, which gives as a result a new cell [5]. There are three phenomena leading to the parasexual recombination in bacteria: conjugation, transduction and transformation; and bacteria cannot live without at least one of these mechanisms [6,7]. Since bacteria do not age (at least according to our present knowledge), most of our simulations presented below use models without ageing, similar to the well-known Eigen quasispecies model [8]. Parasex then happens between two bacterial reproduction events, i.e., between two cell divisions. However, we start with an ageing model to have a bridge to earlier comparisons [9,10] of asexual versus sexual reproduction for ageing individuals.

2. Penna-type models

2.1. General

For biological ageing, the Penna model [11] presently is the most widespread computer simulation method. The genome of each individual is given by a string of 32 bits, representing dangerous inherited diseases (detrimental mutations) for the at most 32 intervals of life of this individual. A 0-bit means health, a 1-bit on position a of the bit-string means a mutation affecting the health from that age a on. Three such diseases kill the individual at that age a at which the third disease becomes active. At each time step, i.e., one iteration of the whole population, each living individual above a minimum reproduction age of 8 gives birth to three children with the same genome as the mother except for one mutation: One bit position is randomly selected and its bit is set to one independently of its previous value. Besides these deaths from genetic reasons, individuals also die at each time step with the Verhulst probability N/N_{max} where N is the total population and N_{max} a constant parameter, often called