Testing a hypothesis for the evolution of sex

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An asexual set of primitive bacteria is simulated with a bit-string Penna model with a Fermi function for survival. A recent hypothesis by Jan, Stauffer and Moseley on the evolution of sex from asexual cells as a strategy for trying to escape the effects of deleterious mutations is checked. This strategy is found to provide a successful scenario for the evolution of a stable macroscopic sexual population.

Keywords: Evolution, random walks, self-organized systems.

I. INTRODUCTION

Asexual reproduction is the complete and faithful expression of all the genes of the mother cell in the daughter cells. It is efficient and straightforward. Why then did sex evolve? [1,2] Jan, Stauffer and Moseley have proposed [3] a small environment (small population) with asexual one-celled organisms, (which we will denote as “bacteria” from now on) in which deleterious mutations are driving some into extinction. It is postulated that these soon to be extinct bacteria may indulge in sexual reproduction as a last resort, to give rise to offspring that are better suited to the environment.

The purpose of this paper to provide a partial test of whether this strategy will increase their chances of propagation in the immediate evolutionary game.

The genome of each bacterium is represented by a double bit-string [4]. We use the term wildtype to represent the bit-string that is best adapted (ideal) to the environment. Asexual bacteria have two identical bit-strings (they are “haploid”) whereas sexual types are “diploid,” i.e., they evolve a pair of bitstrings that may be quite distinct. In this very rudimentary model, each bacterium may be regarded as having only one chromosome - so that the “law of independent assortment” [5] does not hold here - all the genes are linked.

The salutary effect of sexual reproduction comes from the important assumption that we make, namely, that deleterious mutations are recessive.

In this paper “sexual reproduction” will mean a process whereby i) a number $n$ of germ cells are formed from each parent cell (meiosis). These germ cells contain half the amount of genetic material present in the parent cell, i.e., only one bit-string. ii) New individuals are formed by pairing germ cells (i.e., single bit-strings) from two parent cells. In this way, the parents are replaced by $n$ offspring. We have confined ourselves to $n = 1$ or $n = 2$. There is no differentiation between the sexes.

We investigate several alternative scenarios for the reproductive rules. In the first, (called Model I below) individuals undergo a mutation which enables them to engage in sex as an extreme survival measure. Their offspring subsequently reproduce asexually (by mitosis or “simple fission”) under less harsh conditions. In this scenario, we find that the asexual population becomes extinct, and the “sexual types” eventually win over the population.

In the second scenario, the descendants of sexual types always reproduce sexually. To safeguard against the number of sexuals dropping too drastically, we first took $n$, the number of offspring, to be two, but the recent converts were still only allowed to mate amongst each other. This is called Model II below, and gave rise to a macroscopic sexual population. Then, we investigated what happens if the recent converts (all of which are in the danger zone, facing extinction) did not just mate amongst each other, but were allowed to pick mates from the better adapted sexual population at large. This was tried both for the case of $n = 2$ (Model III) and $n = 1$ (Model IV). Finally, getting bolder, we tried the case where $n = 1$, and moreover the recent converts are only allowed to mate amongst each other (Model V). We found that in all of these cases, the steady state population comprised a finite fraction of sexual types, with the fraction being dependent on the number $n$ of offspring, and on the rules according to which the individuals may choose their mates. Thus in these models with varying degree of bias against the sexual population, we have found that the survival of the sexual population is rather robust.

In all the models we have adopted the convention [6] that the total population is kept fixed. This is accomplished by duplicating a sufficient number of asexual bacteria in each cycle to make up for the attrition due to deaths or to sexual reproduction with $n = 1$. The efficacy of a particular mode of reproduction is measured by the long term representation in the population of the types engaging in that particular mode of reproduction, i.e., sexual v.s. asexual.

The paper is organized as follows. In section 2 we define our models. We give enough details to enable further simulations and encourage independent checks of our re-
sults. In section 3 we present our findings from the simulations. In section 4 we state our conclusions.

II. MODELS FOR THE EVOLUTION OF SEX IN ONE CELLED INDIVIDUALS

We represent the genetic code of each one-celled individual with a bit-string of "0"'s and "1"'s, after the Penna model [4]. For asexual, haploid, cells, we have two 16-bit strings that are identical copies of each other. For the sexual cells, we have two 16-bit strings("gametes") which are allowed to be different, i.e., the individuals are now diploid. We use the bit defining the "sign", to specify whether the individual is sexual or asexual - negative (1) indicating sexual and positive (0) indicating asexual.

A. Asexual steady state

We start with a set of $N$ initially identical asexual individuals, all identical to the wildtype, i.e., all 0's. The probability of a mutation hitting any individual is $\Gamma = 1/N$ at any step, and it is implemented by scanning all the individuals in the population, and mutating each individual with a probability of 1/$N$. Clearly there may be any number of mutated individuals at any one time step, the number fluctuating around unity. Mutations are defined as the operation of addition modulo 2, applied to a randomly chosen bit in the string, except the sign bit. Alteration of the sex gene takes place only under special conditions, namely the threat of extinction due to too many deleterious mutations. For the asexual individuals, mutation of any one of the bits affects both strings.

The probability of survival, for individuals who have experienced $m$ mutations, is given by a Fermi-like distribution [7], $P(m)$,

$$P(m) = \frac{1}{\exp[\beta(m - \mu)] + 1}, \quad (1)$$

where $m = 0, 1, \ldots, L$, for a bit string of length $L$. For large $\beta$ (or "low temperatures," in the language of statistical mechanics), $P(m)$ behaves like a step function. Individuals with $m > \mu$ die, those with $m < \mu$ survive, and those with $m = \mu$ survive with a probability of 1/2.

At each time step, all individuals are subjected to the fitness criterion represented by this function - i.e., each survives with probability $P(m)$, depending on the number of mutations it has at the moment. (In the simulations we report below, we set $\beta = 10$ and $\mu = 4$.)

The model defined so far clearly describes a random walk in one dimension (the number of mutations), with a sink at $m \geq \mu$ for large $\beta$. With $n_a(m, t) = 0$ for $m < 0$ and $m > L$, $n_a(m, t)$ obeys the set of equations

$$\frac{\partial n_a(m, t)}{\partial t} = \sum_{\delta = \pm 1} [T_{m+\delta,m}n_a(m + \delta, t) - T_{m,m+\delta}n_a(m, t)] - [1 - P(m)]n_a(m, t). \quad (2)$$

There is a drift towards larger values of $m$, since the stepping rates $T_{m,m+1} = \Gamma(L - m)/L$ and $T_{m,m-1} = \Gamma m/L$. For $L > 2\mu$, as is the case here, $T_{m,m-1} < T_{m,m+1}$. The population would decay exponentially to zero, if it were not replenished by reproduction. We keep the total population constant, as in the Redfield model [6], by making up for the deficit in the population after all the bacteria have been either found fit for survival or killed off according to the survival probability in Eq. (1).

An early stage of evolution, (before "sex is introduced") can be modeled by purely asexual reproduction. We make up for the decrease $\delta N$ in the population by randomly selecting $\delta N$ surviving bacteria and replicating them once. This corresponds to adding a source term proportional to $[N - \sum_m n_a(m, t)]n_a(m, t)$ to the RHS of the master equation (2) for the distribution of our asexual population, $n_a(m, t)$. Running through many such cycles, one finds that the population settles down to a steady state distribution $n_a(m)$.

It should be noted that in our model, sexual reproduction at best keeps the population constant, as outlined below, and therefore it is always asexual reproduction that augments the population to make up for the deficit, even after sex has been turned on.

B. Sexual types and sexual reproduction

In this paper, sexual types will be distinguished from asexuals by two features: i) they are diploids and ii) they may reproduce sexually. We now specify what these mean. i) Once the “sex gene” is turned on, we allow the two bit-strings of sexual types to be different. This makes room for greater genetic variety. Moreover, since we take each gene to have an equal and independent probability to be mutated, for diploids, the probability of any gene to be mutated is halved in comparison to the haploid types. All this gives the sexual individuals a greater chance of survival than the haploid asexuals [9].

ii) Sexuals may engage in “sexual reproduction.” We have considered two variants of sexual reproduction (see Fig. 1), depending upon the number of germ cells and subsequent number of offspring.

S1 Two sexual bacteria mate to give rise to one sexual offspring. In this case, each parent cell undergoes meiosis to produce one germ cell, which possesses one of the bit strings (randomly chosen) of the parent cell. The germ cells coming from the two parents merge to form a "daughter." Thus, the "daughter" has a pair of bit-strings ("gametes") each coming from one of the parents, randomly selected from...
the four such pairs that one may form out of the gametes of the parents. In this definition, the population is reduced by one each time an act of sexual reproduction (“mating”) takes place.

S2 Two sexual bacteria mate to give rise to a pair of offspring. In this case, each parent gives rise to two germ cells, which combine to form two daughters. The gametes of the parents (say $Aa$ and $Bb$) can be shared between the offspring in two different ways, i.e., $(AB, ab)$ or $(Ab, aB)$. The population stays constant.

C. The Dominant String

Since the sexual individual has two different gametes, or bit-strings, we have used the concept of the “expressed” or “dominant” string, to compute the survival probability.

We assume at the outset that deleterious mutations are recessive. The way we have implemented this in practice is as follows. Once a sexual offspring comes into being, we form the “dominant” or “expressed” string, by comparing each bit with the wildtype and actually exchanging bits between the strings to make the “expressed” string as close to the wildtype as possible. Clearly, this “expressed” string has fewer deleterious mutations than either of the two strings coming from the germ cells making up this individual, and similarly, the other string is now worse off (has more deleterious mutations). Once this reshuffling has taken place and the “dominant string” has been formed, any further mutations that happen to hit this string are considered dominant, and $m$ is always computed by counting the deleterious mutations on this “expressed” string. The germ cells of this parent will now pass on these reshuffled gametes, possibly further modified by subsequent mutations, to their offspring.

It should be strongly noted that in exchanging bits between the bit-strings in this deterministic way we have incorporated a feature into our model which is called a “meiotic drive” [2], occurring rarely in nature. Although in neglecting to bring into play dominance/recessiveness in subsequent mutations, i.e., after the “dominant string” has been formed, we have an element which counteracts the meiotic drive to a certain extent, the way in which dominance is handled here is not very realistic. This will be further discussed in the last section.

D. Conversion to sex

Faced with a crisis situation, i.e., the number of deleterious mutations $m$ becoming too large and threatening survival, we assume that the bacteria engage in sexual reproduction. For all the different models that we have considered, once the asexual steady state is achieved, we allow the sex gene to be “turned on” for the least fit members of the population. In any pass through the population, if those individuals that are in the tail of the distribution (i.e. those with $m \geq \mu$ mutations) survive, then they are turned sexual by deterministically and irreversibly switching their sign bits to one.

The next two steps make up the reproductive cycle: Once their sex bit is turned on, these individuals will be “sexually active” and mate with another sexual individual. In the last step of the reproductive cycle, the population is allowed to grow back to its fixed value.

We have considered several Models (I-V) which differ from each other in the details of the reproductive cycle: whether and when the sexual types reproduce sexually or asexually, the number of offspring and the choice of mate. We define these models in detail below. We then go on to give a synopsis of all the steps involved in one complete pass, indicating how each step differs from model to model.

Model I Here sex is only used by sexuals in time of crisis. Sexually active individuals ($m \geq \mu$) mate amongst each other according to rule S1 and beget one offspring. Once out of the “danger zone” (i.e., for $m < \mu$), bacteria reproduce asexually, regardless of whether they are sexual or asexual types. Thus, in the last step of the reproductive cycle, if a sexual type is picked at random as a candidate for reproduction, it simply undergoes mitosis, as would an asexual type.

In Models II-V, sexual individuals are only allowed to reproduce sexually. To preserve the symmetry with Model I, however, we have allowed all individuals to be sampled in the last step of the reproductive cycle. If the random sampling yields a sexual individual, it has to reproduce sexually according to the procedure specified below for that model. If the random choice yields an asexual type, then it undergoes mitosis.

Model II Sexually active individuals ($m \geq \mu$) mate amongst each other according to rule S2, begetting two offspring. In the last step of the reproductive cycle, if a randomly picked candidate for reproduction happens to be sexual, it is mated with another randomly picked sexual and reproduces according to S2, leaving the population constant.

Model III Sexually active individuals ($m \geq \mu$) pick a mate from the sexual population at large, and mate with it according to rule S2, begetting two offspring. In the last step of the reproductive cycle, if a randomly picked candidate for reproduction happens to be sexual, it is mated with another randomly picked sexual and reproduces according to S2, leaving the population constant.
Model IV Sexually active individuals \((m \geq \mu)\) pick a mate from the sexual population at large, and mate with it according to rule \(S_1\), begetting one offspring. In the last step of the reproductive cycle, if a randomly picked candidate for reproduction happens to be sexual, it is mated with another randomly picked sexual and begets one offspring according to \(S_1\), thereby reducing the population by one.

Model V Sexually active individuals \((m \geq \mu)\) mate amongst each other according to rule \(S_1\) and beget one offspring, as in Model I. However, unlike Model I, in the last step of the reproductive cycle, if a sexual type is picked at random as a candidate for reproduction, it mates with another randomly picked sexual and begets one offspring according to rule \(S_1\), thereby reducing the population by one.

In summary, in Models I, II and V, individuals turned sexually active in the face of extinction, with \(m \geq \mu\), mate among each other, while in Models III and IV, they are allowed to pick their mates from among the sexual population at large, thus having a chance to mate with \(m < \mu\) individuals closer to the wildtype. On the other hand, while in Models II and III, sexual reproduction does not reduce the number of sexual types (rule \(S_2\)), in Models I, IV and V, it reduces it by one (rule \(S_1\)) everytime it occurs.

As we will see in the next section, these choices lead to different results. In Model I, the asexual population grows extinct and the sexuals completely win over. For Models II-V, we find that the steady state comprises a finite fraction of sexuals.

E. The kinetics including sex

A complete pass now consists of the following steps:

1. **Mutation and Decimation** Each individual is subjected to the possibility of a mutation at the rate of \(\Gamma\), independently of whether it is sexual or asexual.

   For an asexual individual, one proceeds as described in subsection II.A, and the individual either survives with a probability \(P(m)\) or is killed off with probability \(1 - P(m)\).

   If a sexual individual is hit by a mutation, one of the two bit strings is chosen with probability \(1/2\); then one bit on this string is chosen randomly (with probability \(1/L\)) and mutated. The number of mutations \(m\), and subsequently the survival probability \(P(m)\), are computed with respect to the “dominant” string, as described in Section II.C.

2. **Conversion** Of the surviving asexuals those with \(m \geq \mu\) are turned into sexuals, and tagged “sexually active.” If a sexual individual with \(m \geq \mu\) survives in a given pass, then it is also tagged “sexually active.”

3. **Reproduction** 1 At the end of one complete cycle of mutations, decimation or conversion, all the “sexually active” bacteria are made to reproduce according to the following rules:

   - **Model I** We randomly form pairs of all “sexually active” bacteria \((m \geq \mu)\). They reproduce according to \(S_1\), each pair begetting one offspring.

   - **Model II** All “sexually active” bacteria are paired as above, and reproduce according to \(S_2\), each pair begetting two offspring.

   - **Model III** Each “sexually active” bacterium \((m \geq \mu)\) picks a mate at random, from the sexual population at large. They mate according to rule \(S_2\).

   - **Model IV** Each “sexually active” bacterium \((m \geq \mu)\) picks a mate at random, from among the sexual population at large. They mate according to rule \(S_1\).

   - **Model V** All “sexually active” bacteria are randomly paired among each other and reproduce according to rule \(S_1\), as for Model I above.

   The offspring are tagged “sexually inactive,” so that they are not to be mated in this reproductive step. In Models I, II, IV and V, if the number of sexually active bacteria is odd, so that there is an odd guy out after the random pairing, it is still “active” but will have to await the next cycle to see if it gets a mate.

4. **Reproduction** 2 At this (second) step of the reproductive cycle we allow the population to grow back to \(N\) by means of the following rules:

   - **Model I** Out of the surviving population, we randomly pick \(\delta N\) individuals and make them reproduce asexually (i.e., simply replicate them), regardless of whether they are sexual or asexual.

   - **Models II, III** Out of the surviving population, we start to pick out individuals at random. If the chosen individual is asexual, then it reproduces asexually by replication, thereby augmenting the (asexual) population by one. If the individual is sexual, then another individual is picked out of the sexual population at large, and they reproduce sexually according to rule \(S_2\), which leaves the population unchanged.
**Models IV, V** Out of the surviving population, we start to pick out individuals at random. If the chosen individual is asexual, then it reproduces asexually by replication. If the individual is sexual, then it mates with another individual out of the sexual population at large, and they reproduce sexually according to rule S1, which means that the (sexual) population is diminished by one.

We proceed in this manner until sufficiently many individuals have been added to the population so that the total has been restored to \( N \).

It can be seen that in those cases (Models II-V) where the sexual bacteria are not allowed to regress and reproduce asexually, the sexuals have a disadvantage in the number of offspring per parent, and they will owe their survival to their strategic advantage of being able to improve their fitness due to sexual reproduction. To recapitulate, in Models II and III, a pair is allowed to have two offspring, a feature which gives the sexuals less of a disadvantage than in Models IV and V. The feature which distinguishes Model II from III (and Model V from IV) is that in the former, those bacteria turning to sex at the edge of extinction are only allowed to mate among themselves, whereas in the latter, they are allowed to pick their mates from among the sexual population at large. One would naively expect that the conditions are more stringent for Model II (and Model V) than they are for Model III and IV, since the former have a larger variety of fitter individuals to mate with. A surprise awaits us in the next section.

**III. SEX SUCCEEDS**

We performed the simulations for the above models on a fixed population of \( N = 256 \), for 16-bit strings. The equations for the evolution of the sexual and asexual populations, \( n_a(m) \) and \( n_s(m) \), are nonlinear in these quantities. Therefore we checked in every case that there was, at least typically, no ergodicity breaking, and no periodic or strange attractors for the dynamics, by performing 100 different runs for each set of rules. The results which we quote in the tables are averaged over 100 runs. The fluctuations are still relatively large, with a relative error estimate based on one standard deviation typically being 6% for the bar graphs shown in Figs. (2-7).

Before sex is turned on, we find that the asexual population reaches a steady state distribution with respect to the number of mutations. The average distribution for the asexual steady state is given in Table I and Fig. 2. (In this and the subsequent bar graphs, for each \( m \) we report percentages of the total population, to make it easier to grasp the figures.) We see a population that is fixed at \( N = 256 \) but there are almost no ‘wildtype’ bit-strings; on the other hand the graph is peaked at \( m = 3 \), which is the “minimally stable” value of \( m \). Note that this distribution is similar to that seen for the self-organized critical state of the sandpile [8], where \( m \) plays the same role as the units of sand at a particular site.

Once sex is turned on in Model I, it takes a time roughly proportional to the size of the population for asexual individuals to become extinct. Our results for the relaxation time, averaged over 100 runs, still show quite a bit of fluctuation, but are approximately \( 10^3 \), \( 2 \times 10^3 \), \( 2^3 \times 10^3 \), for \( N = 32, 64, 128 \) and \( 256 \).

The distribution over \( m \), of the asexual and sexual types, have been computed as ensemble averages over 100 copies of the system, with the population fixed at \( N = 256 \) in each case. The initial state is always taken with all individuals identical to the wildtype. Each system evolves for 5000 generations and therefore surely reaches the asexual steady state. Then sex is turned on, and each system now evolves for another thirty thousand generations. Then the averages are taken over the independent systems.

Within Model I, the sexual population reaches a steady state (see Fig. 3) still exhibiting a peak at \( m = 3 \); however, this peak is slightly suppressed in comparison to its value in the asexual steady state, whereas the population at \( m = 1 \) is slightly augmented and there is a nonvanishing population of wildtypes. This demonstrates that the sexual individuals are better capable of eliminating deleterious mutations from their expressed genes.

The results for Model II are drastically different. After sex is turned on, one reaches a state of coexistence between the asexual and sexual populations. The asexual population has a distribution with respect to the number of mutations which is the same as in Fig. 2, whereas the distribution of sexual individuals has shifted markedly towards lower values of \( m \) as can be seen in Fig. 4. For the sexuals, there is a rather broad peak around \( m = 1 \), with an appreciable population of wildtypes. The numbers for the steady state populations of Models II-V are given in Table II, and the total fraction of sexual and asexual populations are shown in the pie charts in Fig. 8.

We see from Fig. 5 that the results for Model III are only marginally different from those of Model II, but the difference is in a direction we did not initially expect: in all the \( m \) values, the percentages of the sexual population is slightly higher in Model II than in Model III, and the total sexual population is also a few percentage points higher in Model II (see Fig. 8). This rather small difference, which could be ascribed to a fluctuation, gets amplified when one allows only one offspring per parent, as we do in Models IV and V.

Turning to Models IV and V (Figs. 6, 7) we see that the feature of producing relatively much better fit offspring
(compared to both parents), which we get when sex-out-of-desperation is constrained to take place exclusively between \( m \geq \mu \) individuals (Model V) again outweighs the advantage of being able, as in Model IV, for an \( m \geq \mu \) individual to be able to mate with a better fit partner chosen from among the sexual population at large. The total sexual population in Model V is 5% larger than in Model IV.

IV. CONCLUSIONS

Our findings are consistent with the hypothesis by Jan et al. [3] that sex, practiced as a last resort between individuals on the verge of extinction, might give rise to a stable sexual population. It remains to be investigated whether a finite rate of conversion of the asexual population to sexual for arbitrary \( m \), also leads to a steady state sexual population, as found here.

It should also be noted, that “meiotic parthenogenesis” (MP) is an alternative strategem whereby bacteria may escape the mortal effects of deleterious mutations, without sexual reproduction [2,10]. This refers to the random exchange of sub-sequences of genes between the two bit-strings (paired chromosomes) of a diploid individual. In testing the Jan et al. hypothesis [3] we have not taken into account this rival strategy.

It is interesting to remark that in an alternative scenario [11] a genetical catastrophe can eliminate an asexual, parthenogenetic population, while a sexual population can survive. We have checked the mortality rates for Model I (the most catastrophic for the asexual population), and found that the model does not harbour any genetic catastrophes. One might have thought that its similarity to a “sandpile model” [8] might give rise to intermittently occuring mass deaths (avalanches), with a power law distribution of casualties for large time scales, but this does not turn out to be the case. The number of deaths is typically small, never exceeding five for our population of \( N = 256 \).

We would like to caution that, in the way we have implemented the formation of the “expressed genotype,” an element of “meiotic drive” has actually crept into the model. In forming the “expressed string,” genes (bits) are being exchanged between the two bit-strings in a way that is not even random, but highly purposeful. In the subsequent meiotic stage, this gives rise to two gametes one of which is much closer and the other much farther from the wildtype than either of the gametes of the parent as it was first formed. This mechanism provides a much stronger “mixing” of the gene pool in this model than afforded by sexual reproduction plus the recessiveness of the deleterious mutations, and does not typically occur in nature [2]. Further work is in progress to remove this spurious effect.

We may finally conclude that our model incorporates a delicate balance between the possibility to escape the consequences of deleterious mutations, greater genetic variety, and the number of offspring. Our findings indicate that the tenet “better offspring are more important than the number offspring” might be further refined; the relative improvement of the offspring with respect to the parents turns out to be a factor in determining the ratio of sexuals to asexuals in the steady state, and this dependence is the stronger, the fewer the offspring.

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| m | n(m) (Model I) | n(m) (Model II) | n(m) (Model III) | n(m) (Model IV) | n(m) (Model V) |
|---|---|---|---|---|---|
|   | Asexual | Sexual | Asexual | Sexual | Asexual | Sexual | Asexual | Sexual | Asexual | Sexual |
| 0 | 0.00 | 1.76 | 0.54 | 17.78 | 0.51 | 17.81 | 1.15 | 2.97 | 1.04 | 4.10 |
| 1 | 0.00 | 12.04 | 3.90 | 19.97 | 4.17 | 17.98 | 8.75 | 4.63 | 8.29 | 6.35 |
| 2 | 0.00 | 35.62 | 13.36 | 14.99 | 14.41 | 14.29 | 30.43 | 4.54 | 28.20 | 5.76 |
| 3 | 0.00 | 50.53 | 20.03 | 9.39 | 22.05 | 8.74 | 44.69 | 2.75 | 42.56 | 3.64 |
| 4 | 0.00 | 0.06 | 0.00 | 0.04 | 0.00 | 0.04 | 0.00 | 0.10 | 0.00 | 0.07 |
| Σ | 0.00 | 100.00 | 37.83 | 62.17 | 41.14 | 58.86 | 84.93 | 15.07 | 80.09 | 19.91 |

TABLE I. Distribution with respect to the number of mutations m in the purely asexual steady state population in Model I.

TABLE II. Distribution of the coexisting asexual and sexual steady state populations with respect to the number of mutations m, for Models I-V, after sex has been turned on. Σ indicates the total percentages of asexual and sexual individuals.
FIG. 1. We illustrate how the two bit strings are shared between two sexual individuals as they beget one (two) offspring, according to the rules $S_1$ ($S_2$) of sexual reproduction. See text.

FIG. 2. The steady state distribution (in percentages) of the asexual population after 5000 generations, with respect to the number of mutations $m$, before sex is introduced.

FIG. 3. The distribution of the steady state sexual population in Model I; $m$ is the number of mutations.

FIG. 4. When sexual individuals are only allowed to reproduce sexually, one finds that they reach a finite fraction of the total population, and coexist with the asexuals. Here we show the steady state distribution (in percentages) of the sexual and asexual populations in this coexisting state for Model II.
FIG. 5. Steady state distribution of the asexual and sexual populations (in percentages) for Model III.

FIG. 6. Steady state distribution of the asexual and sexual populations (in percentages) for Model IV.

FIG. 7. Steady state distribution of the asexual and sexual populations (in percentages) for Model V.

FIG. 8. Pie chart showing the relative weight of the sexual and asexual populations in Models II-V.