



A Stochastic Model of Evolution

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Abstract. We propose a stochastic model for evolution. Births and deaths of species occur with constant probabilities. Each new species is associated with a fitness sampled from the uniform distribution on $[0, 1]$. Every time there is a death event, the type that is killed is the one with the smallest fitness. We show that there is a sharp phase transition when the birth probability is larger than the death probability. The set of species with fitness higher than a certain critical value approach a uniform distribution. On the other hand all the species with fitness less than the critical disappear after a finite (random) time.

KEYWORDS: Bak–Sneppen model, evolution, stochastic model, cut-off phenomenon

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1. Introduction

Consider a discrete time model that starts from the empty set. At each time $n \geq 1$ with probability p there is a birth of a new species and with probability $q = 1 - p$ there is a death of a species (if the system is not empty). Hence, the total number of species at time n is a random walk on the positive integers which jumps to the right with probability p and to the left with probability q . When the random walk is at 0 it jumps to 1 with probability p or stays at 0 with probability $1 - p$. Each new species is associated with a random number. This random number is sampled from the uniform distribution on $[0, 1]$. We think of the random number associated with a given species as being the fitness of the species. These random numbers are independent of each other and of everything else. Every time there is a death event, the type that is killed is the one with the smallest fitness. This is similar to a model introduced by Liggett and Schinazi [5] for a different question.

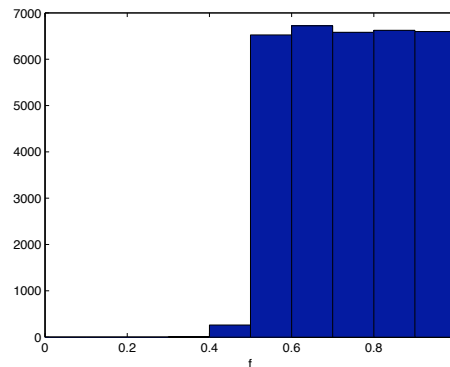


Figure 1. This is the histogram of the fitnesses after 100,000 births and deaths for $p = 2/3$. We have $f_c = 1/2$ and as predicted by the theorem the distribution on $(f_c, 1)$ approaches a uniform.

Take p in $(1/2, 1)$ and let

$$f_c = \frac{1-p}{p}.$$

Note that f_c is in $(0, 1)$. Let L_n and R_n be the set of species alive at time n whose fitness is lower and higher than f_c , respectively. Since each fitness appears at most once almost surely we can identify each species to its fitness and think of L_n and R_n as sets of points in $(0, f_c)$ and $(f_c, 1)$, respectively. Let $|A|$ denote the cardinal of set A . We are now ready to state our main result.

Theorem 1.1. Assume that $p > 1/2$. Let $f_c = (1-p)/p$.

- (a) The number $|L_n|$ of species whose fitness is below f_c is a null recurrent birth and death chain. In particular, the set L_n is empty infinitely often with probability one.
- (b) Let $f_c < a < b < 1$. Then

$$\lim_{n \rightarrow \infty} \frac{1}{n} |R_n \cap (a, b)| = p(b-a) \text{ a.s.}$$

In words, there is a sharp transition at fitness f_c . No species with fitness below f_c can survive forever. On the other hand species are asymptotically uniformly distributed on $(f_c, 1)$.

Observe that the larger p is the more welcoming the environment is to new species. If p is only slightly larger than $1/2$, then f_c is close to 1 and only species

with high fitness will survive. On the other hand if p is close to 1 then f_c is close to 0 and even species with relatively low fitness will survive.

The 'kill the least fit' rule was introduced in the Bak–Sneppen model, see [1]. In that model there is a fixed number N of species arranged in a circular graph. At each discrete time the site on the circle with the lowest fitness and its two nearest neighbors have their fitness replaced by a random number independently sampled from the uniform distribution on $[0, 1]$. Compared to our model there are two important differences: the number of species is fixed in the Bak–Sneppen model (in our model it is random) and there is some local interaction (kill the neighbors of the least fit). However, the same type of uniform behavior on some $(f_c, 1)$ is expected for the Bak–Sneppen model but this is still unproved, see [6, 7].

In fact our result is more general than stated. The reader can easily check in our proof that there is nothing special about the uniform distribution. If fitnesses are sampled independently from the same fixed distribution then the limit in Theorem 1.1, (b) is a.s. $pP(a < X < b)$ where X is a random variable with the fixed fitness distribution. Based on computer simulations we conjecture that the same is true for the Bak–Sneppen model. There too the uniform distribution appears only because fitnesses are sampled from it.

2. Proof of the theorem

Part (a) is a well-known result for birth and death chains. Recall that L_n is the set of species whose fitness is lower than f_c at time n . Observe that $|L_n|$ (the cardinal of L_n) increases by 1 with probability pf_c , decreases by 1 with probability q (if it is not already at 0) and stays put with probability $p(1 - f_c)$. Since $pf_c = q$, it is easy to check that $|L_n|$ is null recurrent. See for instance Proposition II.2.4 in [8].

We now turn to the proof of (b). Let t_n be the number times $k \leq n$ for which L_k is empty. That is,

$$t_n = |\{1 \leq k \leq n : L_k = \emptyset\}|.$$

We will show that, for any $\varepsilon > 0$, t_n is almost surely less than $n^{1/2+\varepsilon}$ for n large enough. The main step in the proof is the following lemma.

Lemma 2.1. *There are positive constants γ and D such that for every $\varepsilon > 0$ we have*

$$P\left(t_n > \frac{2}{pf_c} n^{1/2+\varepsilon}\right) \leq D \exp(-\gamma n^\varepsilon).$$

Proof. Recall that we start from the empty set. After a geometric random time with mean $1/(pf_c)$, denoted by G_0 , the first species appears in $(0, f_c)$. That is,

$$G_0 = \min\{k \geq 1 : L_k \neq \emptyset\}.$$

Let

$$E_1 = \min\{k \geq G_0 : L_k = \emptyset\}.$$

Hence, E_1 is the time it takes starting at time G_0 for $|L_\cdot|$ to return to 0. More generally, we define for $i \geq 1$

$$G_i = \min\{k \geq G_0 + E_1 + \dots + G_{i-1} + E_i : L_k \neq \emptyset\},$$

and

$$E_{i+1} = \min\{k \geq G_0 + E_1 + \dots + E_i + G_i : L_k = \emptyset\}.$$

Note that the $(G_i)_{i \geq 0}$ and the $(E_i)_{i \geq 1}$ are two i.i.d. sequences. Moreover, the G_i follow a geometric distribution with mean $1/(pf_c)$.

Let k_n be the number of times that L_k hits the empty set by time n :

$$k_n = |\{2 \leq k \leq n : |L_{k-1}| = 1 \text{ and } |L_k| = 0\}|.$$

That is, k_n counts the number of times L_k goes from 1 to 0 species for $k \leq n$. Note that if $k_n = 0$ then $t_n \leq G_0$. Let $C = 2/(pf_c)$. We now compute

$$P(t_n > Cn^{1/2+\varepsilon}) \leq P(t_n > Cn^{1/2+\varepsilon}; k_n < n^{1/2+\varepsilon}) + P(k_n \geq n^{1/2+\varepsilon}). \quad (2.1)$$

For $k_n \geq 1$ we have

$$G_0 + G_1 + \dots + G_{k_n-1} < t_n \leq G_0 + G_1 + \dots + G_{k_n},$$

and for $k_n = 0$ we have $t_n \leq G_0$. Hence,

$$P(t_n > Cn^{1/2+\varepsilon}; k_n < n^{1/2+\varepsilon}) \leq P(G_0 + G_1 + \dots + G_{m_n} > Cn^{1/2+\varepsilon}),$$

where m_n is the integer part of $n^{1/2+\varepsilon}$. Now, the expected value of $G_0 + G_1 + \dots + G_{m_n}$ is $(m_n + 1)/(pf_c)$. By a large deviations inequality (see for instance Lemma (9.4) in Chapter 1 of [3]), there exists $\gamma > 0$ such that

$$P(G_0 + G_1 + \dots + G_{m_n} > Cn^{1/2+\varepsilon}) \leq \exp(-\gamma m_n) \leq \exp(-\gamma(n^{1/2+\varepsilon} - 1)). \quad (2.2)$$

We now take care of the second term in the r.h.s. of (2.1). Using that the E_i are i.i.d. and that for $1 \leq i \leq k_n - 1$ they all must be less than n ,

$$P(k_n \geq n^{1/2+\varepsilon}) \leq P(E_1 < n)^{m_n-1}.$$

In order to estimate $P(E_1 < n)$ we will compare $|L_n|$ to a simple symmetric random walk W_n (one that jumps $+1$ or -1 with probability $1/2$ at each step). We construct W_n from $|L_n|$ by erasing the steps where $|L_n|$ stays put. If for instance we have $|L_1| = |L_2| = 0$, $|L_3| = |L_4| = 1$ and $|L_5| = 2$, then we define $W_1 = 0$, $W_2 = 1$ and $W_3 = 2$. By doing so we get a simple symmetric random walk that visits the same sites (in the same order) as $|L_n|$ but in less time.

Hence, $|L_n|$ takes more time to go from 1 to 0 than W_n does. Let T_0 be the time for W_n to hit 0. We have

$$P(k_n \geq n^{1/2+\varepsilon}) \leq P(E_1 < n)^{m_n-1} \leq P_1(T_0 < n)^{m_n-1}.$$

It is well known that $P_1(T_0 \geq n)$ is asymptotically $1/\sqrt{\pi n/2}$, see for instance Chapter III in [4]. Hence, there are constants $\gamma' > 0$ and D such that

$$P(k_n \geq n^{1/2+\varepsilon}) \leq \exp\left(-\gamma' \frac{m_n - 1}{n^{1/2}}\right) \leq D \exp(-\gamma' n^\varepsilon). \tag{2.3}$$

Using (2.2) and (2.3) in (2.1) completes the proof of the lemma. □

We are now ready to complete the proof of part (b) of Theorem 1.1. Let N_n be the total number of births in the model up to time n . Clearly, N_n has a binomial distribution with parameters n and p . Let $f_c < a < b < 1$. We have

$$|R_n \cap (a, b)| \leq \sum_{i=1}^{N_n} 1_{(a,b)}(U_i),$$

where $1_{(a,b)}$ is the indicator function of the set (a, b) and $(U_i)_{i \geq 1}$ is the sequence of fitnesses associated with births. Recall that the U_i are i.i.d. and uniformly distributed on $(0, 1)$. All this inequality is saying is that the number of points in the set (a, b) at time n is less than the number of births that occurred up to time n in the same set.

We now bound the number of deaths. We claim that the number of deaths in $(f_c, 1)$ is at most t_n . This is so because there can be a death in $(f_c, 1)$ only when $(0, f_c)$ is empty and t_n counts the number of times this happens up to time n . Hence,

$$\sum_{i=1}^{N_n} 1_{(a,b)}(U_i) - t_n \leq |R_n \cap (a, b)| \leq \sum_{i=1}^{N_n} 1_{(a,b)}(U_i). \tag{2.4}$$

By the Law of Large Numbers,

$$\frac{1}{n} \sum_{i=1}^{N_n} 1_{(a,b)}(U_i) = \frac{N_n}{n} \frac{1}{N_n} \sum_{i=1}^{N_n} 1_{(a,b)}(U_i)$$

converges a.s. to $pE(1_{(a,b)}(U)) = p(b - a)$.

On the other hand, by our Lemma 2.1 and the Borel–Cantelli Lemma there is almost surely a natural N such that $t_n \leq (2/(pf_c))n^{1/2+\varepsilon}$ for $n \geq N$. In particular, t_n/n converges to 0 a.s. We use the two preceding limits in (2.4) to conclude that a.s.

$$\lim_{n \rightarrow \infty} \frac{1}{n} |R_n \cap (a, b)| = p(b - a).$$

This completes the proof of Theorem 1.1. □

Note We have just learned that Ben-Ari, Matzavinos and Roitershtein [2] proved a central limit theorem and a law of the iterated logarithm for our model, by developing further some ideas presented in this paper.

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