

# Survival of the Unfittest? – The Seceder Model and its Fitness Landscape

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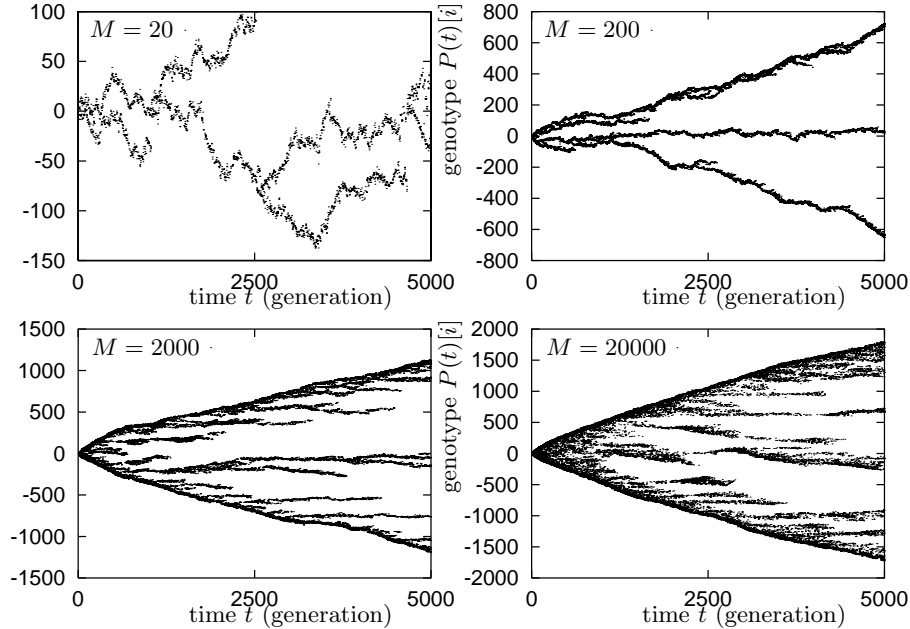
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**Abstract.** The seceder model is an extremely simple individual based model which shows how the local tendency to be different gives rise to the formation of hierarchically structured groups, called the seceder effect. The model consists of a population of simple entities which reproduce and die. In a single reproduction event three individuals are chosen randomly and the individual which possesses the largest distance to their mean is reproduced by creating a mutated copy (offspring). The offspring replaces a randomly chosen individual of the population. In this contribution we investigate the effective fitness landscape of the seceder model. Fitness is measured as reproductive success. The investigation of the fitness landscape revealed an on the first view counterintuitive phenomena: The individuals of the basic seceder model are always located in the worst regions of the fitness landscape where the replication rate is relatively low.

## 1 Introduction

The question of how groups emerge spontaneously from local interactions of individuals is investigated in many different disciplines such as biology, physics, sociology, or computer science. In evolutionary biology the question how evolutionary branching and speciation take place is approached by developing formal models which demonstrate the formation of groups [3, 6, 11, 14, 19]. These models are individual-based in contrast to macro-evolution models which assume a species or group as a given elementary unit [2, 16]. There has also been an increasing interest from statistical physics to deal with simple evolutionary models [2, 3, 6].

The diffusion and separation of individuals in genotype or trait space is either achieved by drift in a neutral fitness landscape [11] or by introducing an explicit fitness function [3, 6, 7, 13] which causes disruptive selection. Sometimes additional explicit functions are introduced to model strength of competition between individuals and ecological interactions [3]. Such functions are also needed to model the benefit of communication among groups on several levels [6].



**Fig. 1.** Typical evolution of the population structure of the seceder model for population size  $M = 20, 200, 2000, 20000$  and  $\sigma = 1$ . The population is initialized at  $t = 0$  with  $P(0)[i] = 0$ . A small dot represents an individual  $i$  where its genotype  $P(t)[i]$  specifies its ordinate value (vertical position).

The seceder model [5] is a microscopic model of an evolving population where the fitness landscape depends on the current population structure, like in [3, 11, 8]. The proposed mechanism is simple compared to other individual-based models [1, 6] for the formation of species or hierarchical organizations. But despite of its simplicity it shows comparably complex behavior. The seceder model does not require global energy functions [3, 6], spatially separated populations [12, 14], or sexual recombination [3, 11, 13].

The question of how microlevel actions explain macro-level regularities is also a central question in sociology [17]. Here, the seceder model may be a contribution as a social mechanism [10] for explaining how individual imitative behavior for the purpose of being different counter-intuitively can lead to the formation of groups on the macro-level. It should also be noted that the mechanism of the seceder model can be used to build practical applications in computer science. For example, it can be applied as a diversity maintenance method for evolutionary optimization algorithms where the reduction of diversity often causes a premature convergence and thus a bad performance of the optimization algorithm [18].

## 2 The Seceder Model

In following the basic seceder model is defined. In the seceder model an *individual* is represented by a real number. The *population* of size  $M$  is represented by an array  $P = \{P[1], \dots, P[M]\}$  of individuals  $P[i] \in \mathcal{R}$ . The population evolves over time according to the following algorithm:

**Algorithm 1 (basic seceder model)**

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while  $\neg terminate()$  do
     $s_1 := P[randomInt(1, M)]$            choose three individuals randomly
     $s_2 := P[randomInt(1, M)]$ 
     $s_3 := P[randomInt(1, M)]$ 
     $\mu := f_{sel}(s_1, s_2, s_3)$          select individual with largest distance to others
     $\lambda := \mu + N(0, \sigma)$          create offspring by adding a random number
     $P[randomInt(1, M)] := \lambda$        replace randomly chosen individual
     $t := t + 1/M$                        increment time counter
od

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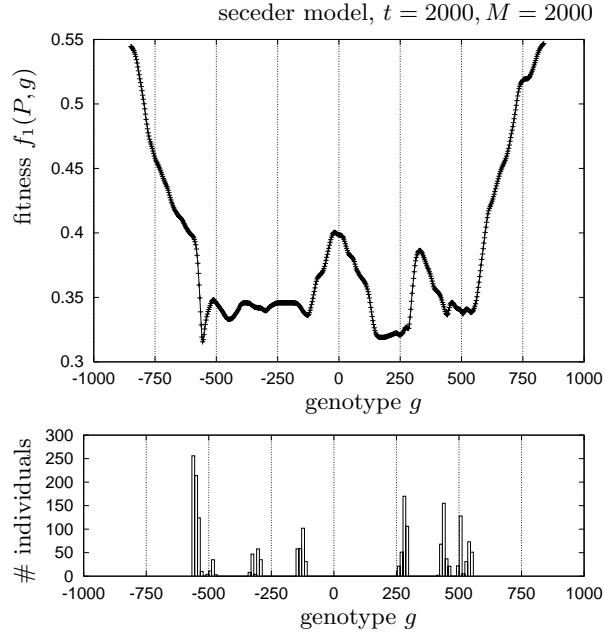
The selection function

$$f_{sel}(g_1, g_2, g_3) = \begin{cases} g_1 & \text{if } F_1 \geq F_2 \wedge F_1 \geq F_3, \\ g_2 & \text{if } F_2 \geq F_1 \wedge F_2 \geq F_3, \\ g_3 & \text{otherwise,} \end{cases} \quad \text{where } F_i = |g_i - \frac{1}{3}(g_1 + g_2 + g_3)|, \quad (1)$$

returns the argument which possesses the largest distance to the mean of the three arguments. One iteration of the above algorithm is called a *step* and  $M$  iterations are called a *generation* which is used to measure time. The *distance* between two individuals is measured by the Euclidean distance (see definition of  $F_i$  in Eq. 1). *Mutation* is performed by adding a normally distributed random number with mean 0 and variance  $\sigma = 1$  denoted by  $N(0, \sigma)$ . The population is usually initialized with one genotype,  $P[i] = 0$  at  $t = 0$ . The procedure  $randomInt(a, b)$  returns a uniformly distributed random number out of  $\{a, a + 1, \dots, b\}$ . The algorithm implies that the population size is constant and that an individual may have an arbitrary number of offsprings or may have no offspring at all. We write  $P(t)$  for the population at time  $t$ , and  $P(t)[i]$  for the  $i$ -th individual of population  $P(t)$ . Figure 1 shows how the population evolves over time in typical simulations for four different population sizes.

## 3 The Effective Fitness Landscape of the Basic Seceder Model

There are many ways to measure fitness [15]. Here we measure fitness as reproductive success ([9], Chapter 13, p. 366). Formally: Given a population



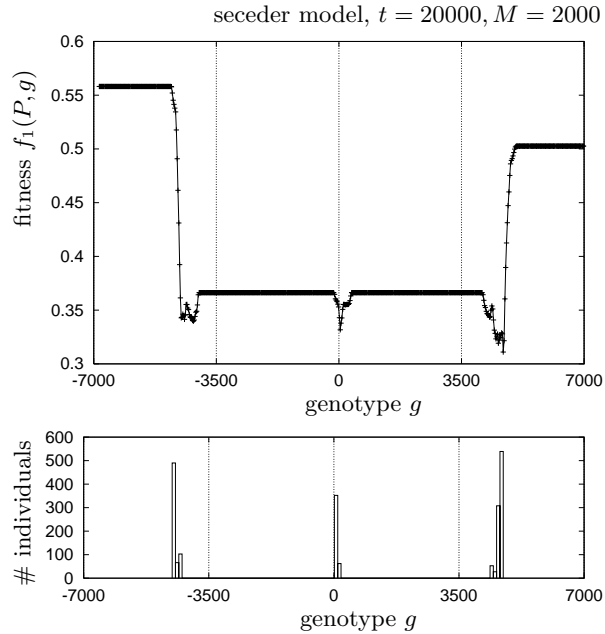
**Fig. 2.** Typical fitness landscape of the seceder model with population size  $M = 2000$  after  $t = 2000$  generations. High fitness value correspond to high replication rate. The lower graph shows the distribution of genotypes in the population.

$P = \{P[1], \dots, P[M]\}$ , the fitness of genotype  $g \in \mathcal{R}$  is defined as:

$$f_1(P, g) = \frac{1}{M^2} \sum_{i,j=1}^M \begin{cases} 1 & \text{if } g = f_{sel}(g, P[i], P[j]), \\ 0 & \text{otherwise.} \end{cases} \quad (2)$$

This fitness  $f_1(P, g)$  measures the probability that a genotype  $g$  would be reproduced if it is chosen as the first individual  $s_1$  in Alg. 1.

Figure 2 and 3 show typical fitness landscapes appearing in the seceder model for population size  $M = 2000$  and an initial population with  $P(0)[i] = 0$ . The distribution of the population in genotype space is also plotted. We can see that (maybe surprisingly) the population is located in regions of low fitness (equal to low replication rate). In Fig. 2 the system is shown at an early stage ( $t = 2000$ ) where the population diameter is still relatively small. The effective fitness landscape is more rugged than at a later point in time shown in Fig. 3. There, at  $t = 20000$ , three main arms coexist. Their individuals reside in the lowest regions of the fitness landscape. Some individuals of the outer arms are located on the increasing steep outer slope of the fitness landscape. Thus they tend to reproduce more likely and cause the two outer arms to depart from each



**Fig. 3.** Typical fitness landscape of the seceder model with population size  $M = 2000$  after  $t = 20000$  generations. The lower graph shows the distribution of genotypes in the population.

other. This effect will become more clear in the following when we investigate the seceder model with additional selection pressure.

## 4 The Seceder Model with Additional Selection Pressure

We will now extend the seceder model by an additional selection pressure by introducing an explicit “fitness” function  $f : \mathcal{R} \rightarrow \mathcal{R}$  [4]. The additional selection pressure is added by modifying the death rate of a genotype  $g$  according to  $f$ . A high value  $f(g)$  corresponds to high death rate and thus to low fitness<sup>1</sup>. This is achieved by the following algorithm:

**Algorithm 2 (seceder model with additional selection pressure)**

Same as Alg. 1, but we replace the insertion of the offspring (namely the line “ $P[\text{randomInt}(1, M)] := \lambda$ ”) by the following algorithm which is in fact a tournament:

<sup>1</sup> Note that in general in biological populations high death rate does not necessarily imply low fitness.

$i := \text{randomInt}(1, M)$	choose two candidates for replacement
$j := \text{randomInt}(1, M)$	
$k := \text{selectProportional}(f(P[i]), f(P[j]))$	select one of them based on $f$
$P[k] := \lambda$	replace it by the offspring

The non-deterministic function  $\text{selectProportional}(F_1, \dots, F_n)$  returns an index  $i \in \{1, \dots, n\}$  where the probability that  $i$  is returned is  $F_i / \sum_{j=1}^n F_j$ . We will investigate the behavior of the model for the following function:

$$f(x) = |x|^\alpha. \quad (3)$$

With  $\alpha = 0$  we obtain the basic seceder model. For  $\alpha > 0$  the death rate increases with distance to the origin in genotype space. There is one global minimum of the death rate. Note that even  $f(g)$  can be zero (here, for  $g = 0$ ), the death rate never becomes zero when Alg. 15 is applied. Furthermore note that the death rate is not only a function of genotype. The actual (absolute) death rate of a genotype depends on the other genotypes present in the population because tournament selection is applied.

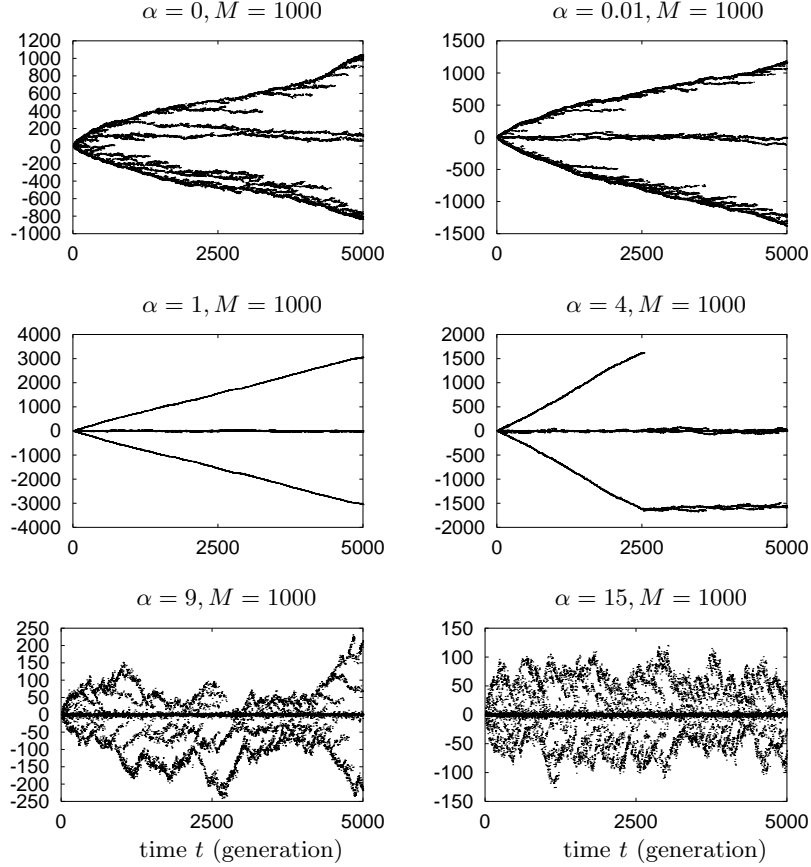
Figure 4 shows how the additional selection pressure influences the time evolution of the population structure. Typical simulations are shown for population size  $M = 1000$  and selection pressure  $\alpha = 0, 0.01, 2, 4, 9, 15$ . If the selection pressure is strong ( $\alpha > 9$  for  $M = 1000$ ) the time evolution is quite complex. New groups [5] emerge, move through genotype space, split up, and die. There is an ongoing change of the population structure. A simple stationary state never appears.

## 5 The Effective Fitness Landscape of Seceder Model with Additional Selection Pressure

In order to derive the effective fitness landscape for the seceder model with additional selection pressure we assume that the population size  $M$  is large. This allows to separately handle the ‘‘seceder’’ reproduction part (part A) and the additional selection part (part B) because if the population size is large it is unlikely that an individual is chosen in part A and part B during one step of Alg. 15. So in principal we can take the fitness landscape  $f_1$  from the basic seceder model and subtract the effect of additional selection part, denoted by the function  $h$ :

$$f_2(P, g) = 3 \underbrace{\frac{1}{M^2} \sum_{i,j=1}^M \begin{cases} 1 & \text{if } g = f_{sel}(g, P[i], P[j]) \\ 0 & \text{otherwise} \end{cases}}_{f_1(P,g)} - 2 \underbrace{\frac{1}{M} \sum_{i=1}^M \frac{f(g)}{f(g) + f(P[i])}}_{h(P,g)}. \quad (4)$$

Figure 6 shows three plots of fitness landscapes for three different situations that appear in simulations with Alg. 15,  $M = 1000$ ,  $\alpha = 9$ . These situations are

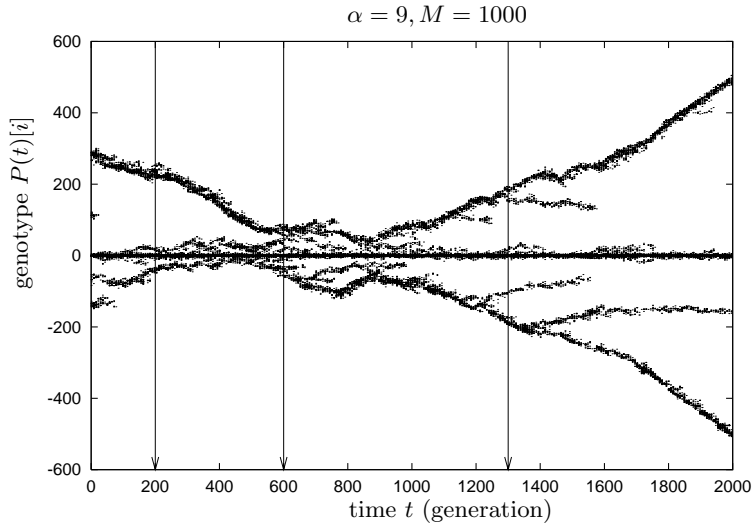


**Fig. 4.** Typical simulations of the secoder model with additional selection pressure. The strength of the additional selection pressure (death rate) increases with  $\alpha$ . Initialization:  $P(0)[i] = 0$ . Parameters:  $f(x) = |x|$ ,  $M = 1000$ ,  $\sigma = 1$ . High value of  $f(x)$  corresponds to high death rate of an individual with genotype  $x \in S$ .

take from a run shown in Fig. 5. They are typical for a (a) shrinking, (b) steady, and (c) increasing population diameter.

Many individuals reside in regions of low fitness. But some groups are not in local minima of the fitness landscape. Some groups are even completely located on a slope of the landscape. These are the groups that are moving through genotype space (compare Fig. 6 with Fig. 5). By looking at the gradient of the fitness landscape we can also predict the movement of a group. But this prediction is only possible for a short amount of time in the future because change in the population causes also change of the fitness landscape.

Looking at the rightmost group of individuals in Fig. 6 (c). This group moves away from the origin. We may imagine for a short while that the group moves up the hill of the fitness landscape. But the change of the population causes



**Fig. 5.** The fitness landscape of the plotted run is displayed for  $t = 200$ ,  $t = 600$ , and  $t = 13000$  in Fig. 6.

this fitness hill to flatten and finally to get a shape similar to the big rightmost fitness hill in Fig. 6 (a). If that happens the group will move back towards the origin or even may die out if its effective fitness becomes too low, as can be seen in Fig. 4 for  $\alpha = 9$ .

## 6 Summary and Conclusion

We have defined an effective fitness landscape for the seceder model and its variant, the seceder model with additional selection pressure. The fitness landscape has been found to be useful to get a deeper insight into the dynamic behavior of the model. The effective fitness allows short time prediction of the movement of a main arm (group of similar individuals). But should neither be regarded as a *cause* for the long-term dynamics, nor as a *cause* for the population structure.

A naive model of evolution draws a picture of “species” or entities moving in a fitness landscape. During this movement (caused by reproduction and mutation) entities increase their fitness, climb up the hills of the fitness landscape, and get “caught” in local optima. Surprisingly, in the seceder model it is exactly the other way round. The entities reside in regions of low fitness, mostly in local *minima* of the fitness landscape.

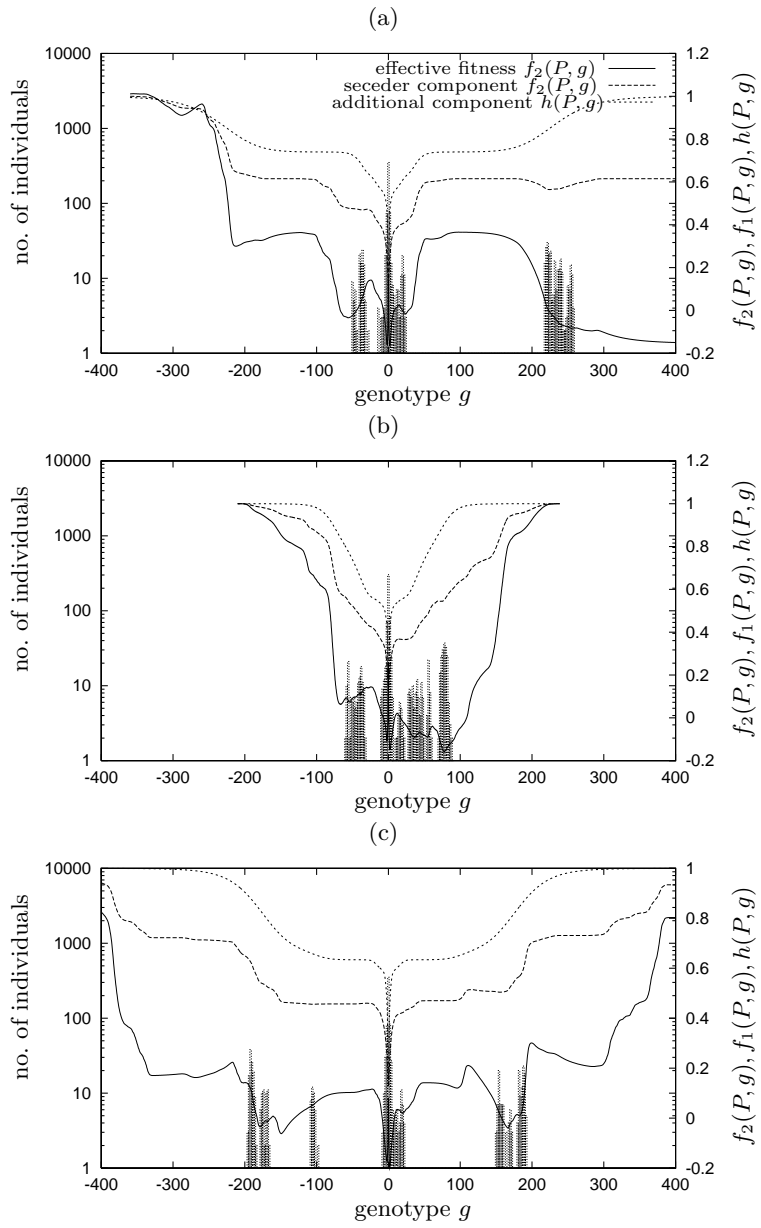
Obviously the seceder model alone is also a naive model of evolution. Real biological evolution is a process which can only be understood as an interplay of many mechanisms. One such mechanism is probably the seceder effect investigated in that contribution.



How can we transfer our findings to the real-world? Can we expect the seceder effect to occur in natural, technical or social systems? Probably not in its pure form as exhibited by the basic seceder model. But the effect could very likely be observed overlaid by other fitness influencing components as modeled by the extended seceder model (Alg. 15). Applying the model to real-world systems in different domains like those mentioned above, would be an interesting prospect for future research.

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**Fig. 6.** Typical fitness landscape of the seceder model with additional fitness pressure. Population size  $M = 1000$  after  $t = 5000$  generations. The distribution of genotypes in the population is now plotted inside the graph.  $f(x) = |x|^\alpha$ ,  $\alpha = 9$ .