Chapter 1

The Seceder Effect in Bounded Space

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The seceder model consists of a population of simple entities which reproduce and die. A reproduction event consists of the following steps: Three individuals are chosen randomly. The most different individual is allowed to have an offspring. The offspring replaces a randomly selected individual of the population. The seceder model shows how the local tendency to be different gives rise to the formation and stable coexistence of groups. But in unbounded space these groups disperse. This contribution investigates the group formation in two variants of bounded space: periodic boundary condition and additional selection pressure. In the rather artificial case of periodic boundary condition the system converges to a simple stable state where only three main groups are present. The second more realistic variant introduces an additional static selection pressure as a unimodal function on the genotype. In this case quite complex patterns of group formation and group disintegration appear depending on the strength of the selection pressure.

1.1 Introduction

The seceder model [6] shows how the local tendency to be different gives rise to the formation and stable coexistence of groups. The mechanism is simple compared to other individual-based models [1, 5, 7] for the formation of species or hierarchical organizations. Despite of its simplicity it shows comparably complex

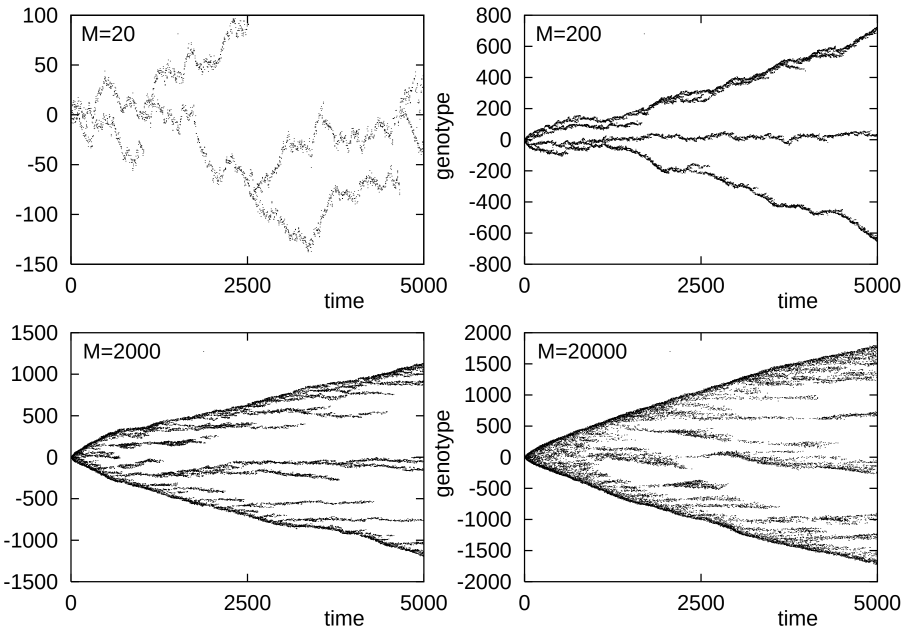

Figure 1.1: Typical evolution of the population structure of the seceder model for population size $M = 20, 200, 2000, 20000$ and $\sigma = 1$. The population is initialized at $t = 0$ with $p_i(0) = 0$. A small dot represents an individual i where its genotype $p_i(t)$ specifies its ordinate value (vertical position).

behavior. The seceder model does not require global energy functions [4, 7, 8], spatially separated populations [11, 14], or sexual recombination [4, 10, 12].

The model consists of a population of simple entities which reproduce and die. Each individual is represented by a real number called **genotype**. The population of size M is represented by an array (or multi set) $P = \{p_1, \ldots, p_M\}$ of individuals $p_i \in \mathcal{R}$. $p_i(t)$ refers to the i-th individual of P at time t. The population evolves over time according to the following simple algorithm: (1) Three individuals s_1, s_2, s_3 are chosen randomly from the population without removing them. (2) The individual $\mu = f_{sel}(s_1, s_2, s_3)$ which is most different (the *seceder*) is selected as a parent according to the selection function

$$f_{sel}(s_1, s_2, s_3) = \begin{cases} s_1 & : \quad F_1 \geq F_2 \wedge F_1 \geq F_3, \\ s_2 & : \quad F_2 \geq F_1 \wedge F_2 \geq F_3, \\ s_3 & : \quad \text{otherwise}, \end{cases} \tag{1.1}$$

with $F_i = |s_i - \frac{1}{3}(s_1 + s_2 + s_3)|$. (3) The offspring $\lambda = \mu + N(0, \sigma)$ is created by adding a normally distributed random number with mean 0 and variance σ to the parent μ. (4) The offspring λ replaces a randomly chosen individual of the population. M iterations of the algorithm are called a **generation**. The unit "generation" is used to measure time.

In [6] the behavior of the model has been analyzed for an unbounded genotype space namely $\mathcal{R}$ (s. Fig. 1.1). This is somehow unrealistic because there is no trait which can increase or decrease infinitely. Imagine, e.g., the weight of the body. It can be changed by evolution in a reasonable interval, but its range is bounded "smoothly" by an upper and lower bound. Therefore this contribution explores the behavior of the seceder model in bounded genotype space. Two methods are investigated that impose a boundary: (a) cyclic genotype space with periodic boundary condition, and (b) additional external fitness pressure such that the death rate of a genotype increases with its distance to the origin (equal to its absolute value).

In this paper the term **group** refers to a set of similar individuals which is a subset of P and which is separated from other individuals by an empty "gap" in genotype space. The **number of groups** (denoted by # groups) is then computed by partitioning the population P so that (1) each element in P is assigned to exactly one partition, (2) the distance between two object belonging to different partitions is at least $gapSize$, and (3) a partition or group can not be subdivided into two subgroups which are separated by at least a gap size $gapSize$. To reduce noise, a group is only counted if the number of individuals inside exceeds $minGrpSize$.

1.2 Periodic Boundary Condition

The first boundary condition we investigate is rather unrealistic, but is commonly used in computer science and cellular automaton like models. We simply fold up the genotype space so that is becomes cyclic. In doing so we get two properties which are also present in natural fixed-length genotypes: Mutation can only operate in a finite range and the maximal distance between two arbitrary genotypes is bounded.

To modify the seceder model such that the genotype space becomes cyclic we just have to redefine the mutation and the distance d between two genotypes. Now, each individual is represented by a real number p. $p \in S$. $S = [-r, r]$. r is called **world radius**. The distance between two genotypes $s_1, s_2 \in S$ is defined as

$$d(s_1, s_2) = \begin{cases} 2r - |s_1 - s_2| & \text{if } |s_1 - s_2| > r, \\ |s_1 - s_2| & \text{otherwise.} \end{cases} \tag{1.2}$$

A mutation by addition of a normally distributed number may lead to an offspring whose distance to its parent can become arbitrarily large. To "fold back" the offspring to the valid genotype space S the following function is applied:

$$foldback(s) = \begin{cases} foldback(s - 2r) & \text{if } s > r, \\ foldback(s + 2r) & \text{if } s < -r, \\ s & \text{otherwise.} \end{cases} \tag{1.3}$$

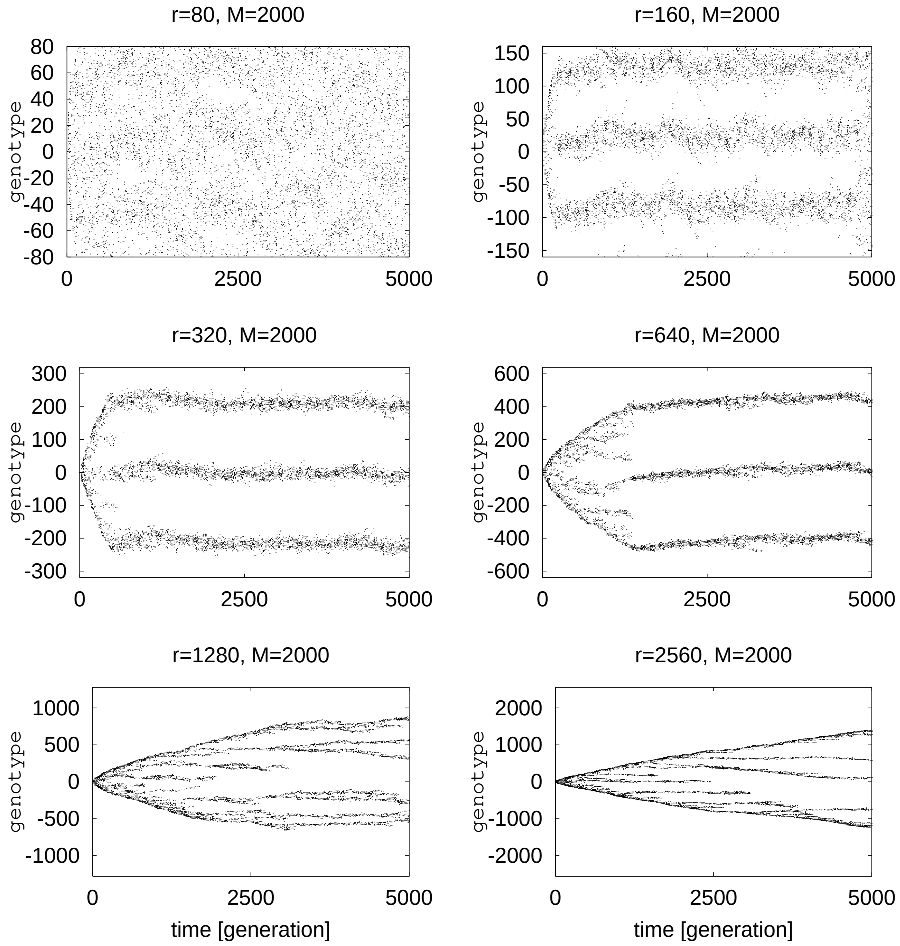

Figure 1.2: Seceder model with periodic boundary conditions (cyclic genotype space). Simulation performed for population size $M = 2000$ and world radius $r = 80, 160, 320, 640, 1280, 2560$. $\sigma = 1$.

We can now redefine the functions for the periodic boundary conditions: $F_1 = d(s_1, s_2) + d(s_1, s_3), F_2 = d(s_2, s_1) + d(s_2, s_3), F_3 = d(s_3, s_1) + d(s_3, s_1)$ and the offspring $\lambda = mutate(\mu) = foldback(\mu + N(0, \sigma))$.

1.2.1 Results

Figure 1.2 shows how the world radius r influences the time evolution of the population. For all simulations the population is initialized with $M = 2000$ instances of the genotype 0 ($p_i(0) = 0$) and simulated for 5000 generations. If the radius is small ($r < 100$) group formation can not been observed. For

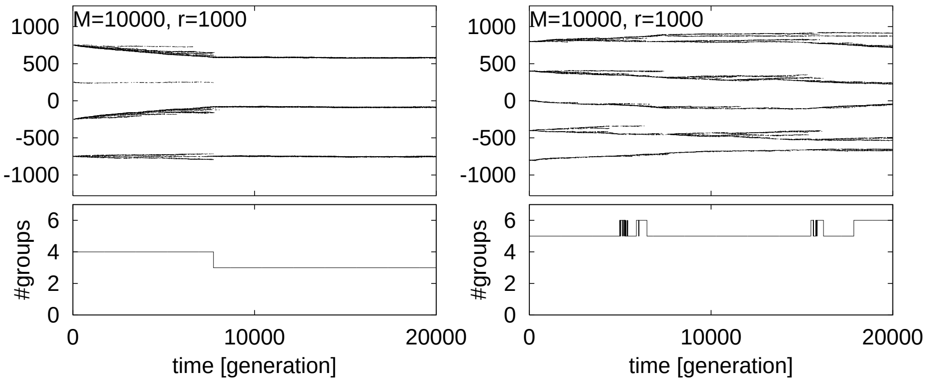

Figure 1.3: **Left:** Typical simulation of a population initialized with four groups ("equidistant" genotypes). $M = 1000, r = 1000, \sigma = 1$. **Right:** Population initialized with five groups ("equidistant" genotypes). $M = 1000, r = 1000, \sigma = 1$. In three out of 15 runs the length of the transient phase exceeded 20000 generations. Number of groups measured in both cases with $gapSize = 50, minGrpSize = 50$.

$r = 160$ three groups emerge and coexist in a stable way. For larger r the time evolution of the population structure becomes more complex. We can identify a complex transient phase where the population expands. The length of the transient phase increases with r. The stationary phase is characterized by three very stable[1] groups. All 50 simulations that have been performed with different settings of $r < 3000, M \leq 20000$ and the initial condition $p_i(0) = 0$ have entered the stationary phase where only three main groups are present.

If we initialize the population with four groups as shown in Fig. 1.3 we could expect that they are able to coexist because the theoretical ODE model of [6] predicts stable coexistence. But that is only the case for mutation rate $\sigma = 0$. If mutation is activated ($\sigma = 1$) the groups expand and move in genotype space such that one group is pushed out. If the population is initialized with five groups the transient phase is longer compared to the case where the population is initialized with four groups. Surprisingly the transient phase is also shorter when the population is initialized with random individuals drawn from the whole genotype space $S = [-r, r]$ (not shown here).

Figure 1.4 shows an interesting behavior which might be described as spontaneous *mass extinction* and by which the transient phase comes to an end. Without external influence "suddenly" more than 60% of the groups die out. Mass extinction occurs when the expansion of the population reaches a critical diameter d_{crit} which depends on the world radius r. All performed simulations confirm that $d_{crit} \approx 2r/3$.

[1] Note that the concept of stability is not well defined for constructive non-deterministic systems with finite number of components. For this paper it should be sufficient to consider a system to be in a stable state if for all small disturbances the system will go back into that state.

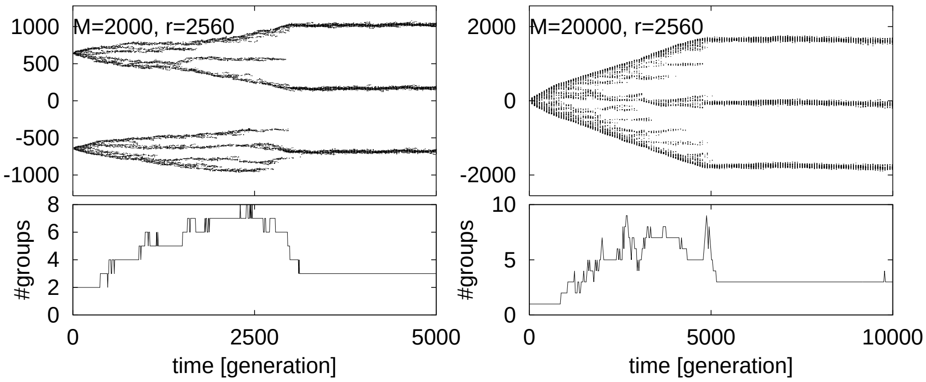

Figure 1.4: **Left:** Population initialized with two different genotypes $g_1 = -2r/3$ and $g_2 = 2r/3$ such that each genotype $M/2$ individuals are present at $t = 0$. $M = 2000, r = 2560, \sigma = 1$. **Right:** Typical simulation of a large population initialized with one genotype. $M = 20000, r = 2560, \sigma = 1$. Number of groups measured in both cases with $gapSize = 50, minGrpSize = 50$.

1.3 Boundary by Explicit Selection Pressure

Now, instead of the periodic boundary condition, a "smooth" boundary is introduced by an additional external selection pressure such that the death rate of an individual depends on its genotype. For this we define a "fitness" function

$$f(x) = |x|^\alpha, x \in S, S = \mathcal{R}. \tag{1.4}$$

The parameter α allows to tune the selection pressure. High α corresponds to high selection pressure. For $\alpha = 2$ the function f becomes the *sphere model* [17] and for $\alpha = 0$ we get the basic (unbounded) seceder model [6]. To include the external selection pressure, Step (4) of the algorithm (Sec. 1.1) is modified. Instead of choosing an individual randomly which is replaced by the offspring we choose *two* individuals x_1, x_2 randomly and select one individual to be replaced. The probability that x_i is selected is $f(x_i)/(f(x_1) + f(x_2)), i \in \{1, 2\}$.

1.3.1 Results

Figure 1.5 shows how the 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 emerge, move through genotype space, split up, and die. There is an ongoing change of the population structure. A simple stationary state, like the three stable groups in simulations with periodic boundary conditions, does not appear.

For intermediate selection pressure ($0.01 < \alpha > 9$ for $M = 1000$) a rather surprising phenomena appears. The expansion of the populations diameter is

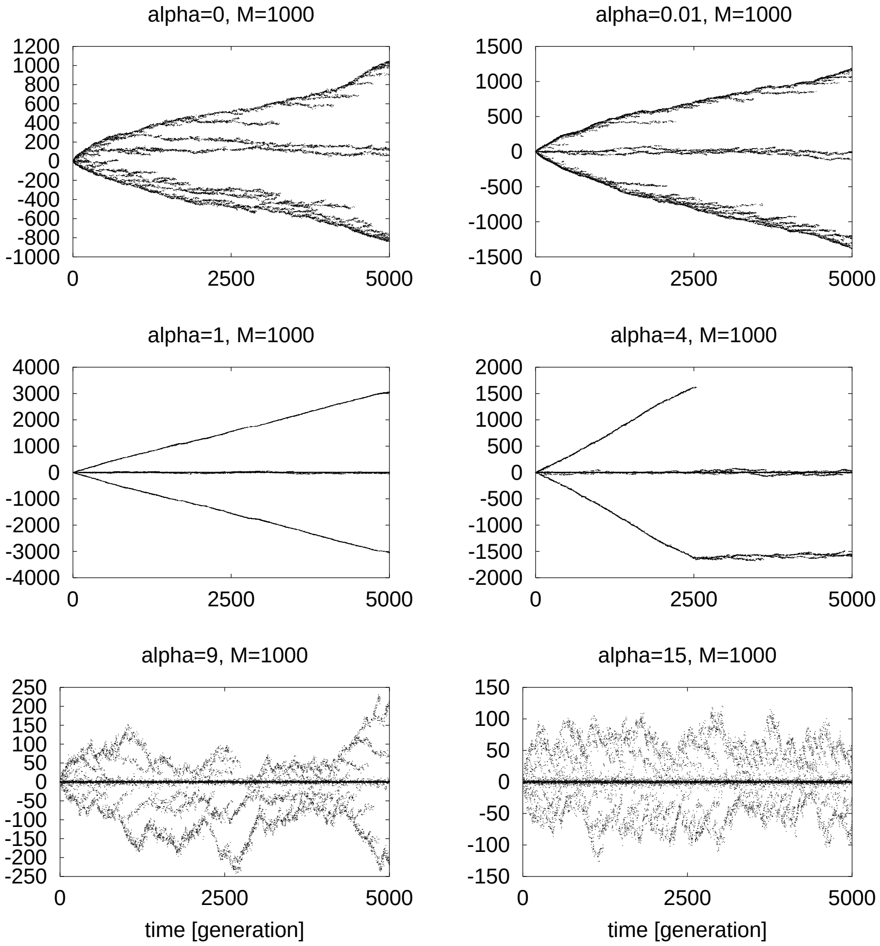

Figure 1.5: Seceder model with additional external selection pressure. The strength of the external selection pressure increases with α. Initialization: $p_i(0) = 0$. Parameter: $f(x) = |x|^\alpha, M = 1000, \sigma = 1$. High value of $f(x)$ corresponds to high death rate of an individual with genotype $x \in S$.

faster than without selection pressure. The expansion is limited because one side-arm finally dies out (s. Fig 1.5 middle right, $\alpha = 4$). After that, the other side-arm returns to the origin of the genotype space (not shown here). It can also been observed in Fig. 1.5 that (a) the diameter of the two main groups that move away from the origin in genotype space is smaller than in simulations without selection pressure, and (b) the formation of side-arms which appear spontaneously for $\alpha = 0$ is drastically reduced. This may provide an explanation, but it seems too early to speculate about the reason.

1.4 Discussion and Outlook

The experiments show that both methods prevent an unlimited growth of the population diameter. But the resulting pattern is quite different. The external selection pressure (Method 2) can cause a complex temporal structure. whereas the cyclic genotype space (Method 1) results in three stably coexisting groups. The cyclic genotype space is a rather artificial method for introducing a boundary. Thus we can hardly imagine a natural system where the phenomena depicted in Fig. 1.2 become visible. Nevertheless they may appear in an artificial system, such as an evolutionary algorithm where the genotype space is periodic and a diversity maintenance method is used similar to the seceder model (e.g., a certain variant of fitness sharing).

The second variant of the seceder model, where an additional external selection pressure is added, is much more realistic. Thus we can expect to observe the phenomena shown in Fig. 1.5 in nature, too. The model predicts that an evolutionary system where the seceder effect and an additional simple selection pressure (e.g., Eq. 1.4) determines the effective fitness of a genotype may be in at least two modes: (1) In the "simple mode" only a few (two or three) main groups are present. An initial population of individuals with identical genotypes will increase its diameter quickly by forming distinct groups with relatively small diameter. (2) The "complex mode" appears when the additional selection pressure is increased, here by increasing α. In that mode complex spontaneous branching of the population structure appears nearly all the time. This mode (or behavior) may be interpreted as an instance of *open-ended evolution* [2, 13]. Discussing the problem of open-ended evolution in detail goes beyond the scope of this paper. But one aspect should be addressed: Open-ended evolution demands that new species or components appear permanently. In the presented model after a while "new" groups (originating through branching) consist of genotypes which have been already present before (e.g., Fig. 1.5). This may argue against open-ended evolution. But we can avoid this artifact easily by replacing the one-dimensional genotype by a high-dimensional – and thus more realistic – genotype, e.g., a long binary string. In that case new groups of genotypes ("quasi-species") would appear over and over again.

Future investigations should explore whether the phenomena observed here are typical for systems where being different is an advantage, or whether they are artefacts caused by certain components of the model, e.g., the function f. Finally the application of the seceder model to explain phenomena of molecular evolution[15], sympatric species formation [9, 12], or the emergence of groups in social systems [3, 16] should be examined.

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