

A Cellular Automata Model of Population Infected by Periodic Plague

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Abstract. Evolution of a population consisting of individuals, each holding a unique “genetic code”, is modeled on the 2D cellular automata lattice. The “genetic code” represents three episodes of life: the “youth”, the “maturity” and the “old age”. Only the “mature” individuals can procreate. Durations of the life-episodes are variable and are modified due to evolution. We show that the “genetic codes” of individuals self-adapt to environmental conditions in such a way that the entire ensemble has the greatest chance to survive. For a stable environment, the “youth” and the “mature” periods extend extremely during evolution, while the “old age” remains short and insignificant. The unstable environment is modeled by periodic plagues, which attacks the colony. For strong plagues the “young” individuals vanishes while the length of the “old age” period extends. We concluded that while the “maturity” period decides about the reproductive power of the population, the idle life-episodes set up the control mechanisms allowing for self-adaptation of the population to hostile environment. The “youth” accumulates reproductive resources while the “old age” accumulates the space required for reproduction.

1 Introduction

The cellular automata paradigm is a perfect computational platform for modeling evolving population. It defines both the communication medium for the agents and the living space. Assuming the lack of individual features, which diversify the population, the modeled system adapts to the unstable environment, developing variety of spatially correlated patterns (see e.g. [1-3]). Formation of patterns of well-defined multi-resolutional structures can be viewed as the result of a complex exchange of information between individuals and the whole population.

Another type of correlations - correlations in the feature space - emerges for the models of populations in which each individual holds a unique feature vector evolving along with the entire system [4]. The aging is one of the most interesting puzzles of evolution, which can be investigated using this kind of models.

It is widely known that the aging process is mainly determined by the genetic and environmental features. The most of computational models of aging involving genetic factor are based on the famous Penna paradigm [5,6]. This model uses the theory of accumulation, which says that destructive mutations - which consequences depend on the age of individual - can be inherited by the following generations and are accumu

lated in their genomes. The Penna model suffers from the following important limitations.

1. The location of the individuals in space is neglected, thus the system evolves in spatially uncorrelated environment with unbounded resources.
2. Only two episodes of life are considered, i.e., the “youth” and the “maturity”. The durations of the two are the same for each individual. The “old age” is neglected.

In this paper we propose a new model, complementary to the Penna paradigm. It does not consider genetic mutations. Instead, it allows for studying the influence of environmental factors on the aging process.

The paper is constructed as follows. First, we describe our algorithm, its principal assumptions and implementation details. In the following section we discuss the results of evolution and self-adaptation of population to the hostile environment represented by periodic plaques. Finally, our findings are summarized.

2 CA Model of Evolution

Let us assume that an ensemble of $S(t)$ individuals is spread on 2D $N \times N$ mesh of cellular automata (CA). The mesh is periodic. Each individual, residing in (i, j) node, is equipped with a binary chain – the “genetic code” – of length L . The length and the number of “1”s in the chain correspond to the maximal and actual life-time of individual, respectively. Only “1”s from “genetic codes” of each individual are read one by one along with the evolution while “0”s are skipped. Afterwards the last “1” has been read, the individual is deleted from the lattice. The individuals are treated as independent agents, which can move and reproduce according to recombination (*cross-over*) operator from the genetic algorithms. The code chain consists of three sub-chains corresponding to three episodes of life: the “youth” \mathbf{y} , the “maturity” \mathbf{m} and the “old age” \mathbf{o} . They do not represent biological age of individuals, but reflect their reproduction ability. Only the “mature” individuals from the Moore neighborhood [7] of an *unoccupied* node of CA lattice are able to reproduce. Every individual can move randomly on CA lattice if there is a free space in its closest neighborhood.

Let $\mathbf{A} = \{a_{ij}\}_{N \times N}$ is the array of possible locations of individuals on the 2D $N \times N$ lattice of the cellular automata. The value of $a_{ij} \in \mathcal{R}$, $\mathcal{R} = \{0, 1\}$, where “0” means that the node is “*unoccupied*” and “1” that it is “*occupied*”. An individual is defined by corresponding “genetic code” $\alpha_{ij} \in \mathcal{R}^L$ such that:

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if ( $a_{ij} = 1$ ) then  $(i, j) \rightarrow$  ‘is occupied’;
 $\alpha_{ij} \rightarrow [y_{ij}^1, m_{ij}^1, o_{ij}^1];$ 
 $y_{ij} \rightarrow [y_{ij}^1, y_{ij}^2, \dots, y_{ij}^l], m_{ij} \rightarrow [m_{ij}^1, m_{ij}^2, \dots, m_{ij}^m], o_{ij} \rightarrow [o_{ij}^1, o_{ij}^2, \dots, o_{ij}^n],$ 
 $\wedge y_{ij}^k, m_{ij}^k, o_{ij}^k \in \{0, 1\}, L = n + m + l$ 

else
 $(i, j) \rightarrow$  ‘is unoccupied’ and  $\alpha_{ij} \rightarrow \mathbf{0}$ 

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In Fig.1 we show the sequence of instructions describing the process of evolution. The binary vectors \mathbf{y}_{ij} , \mathbf{m}_{ij} , \mathbf{o}_{ij} represent the subsequent episodes of individual life: the

“youth”, the “maturity” and the “old age”, respectively. The values of l, m, n are the maximum lengths of each of the episodes while their actual durations are equal to the number of “1”s in the corresponding vectors \mathbf{y}_{ij} , \mathbf{m}_{ij} , \mathbf{o}_{ij} . The symbol Ω denotes the classical recombination operator from the genetic algorithms, t is the number of generation cycle (time), $p(\alpha_{ij})$ is the unitation operator, (i.e., it returns the number of “1”s in α_{ij} chain) and the function $p_k()$ is the “counter” operator defined as follows:

$$\forall (a_{ij} = 1 \wedge p(\alpha_{ij}) \geq k); p_k(\alpha_{ij}) = k.$$

while $t < \text{MAX}$ do begin	// Initialize the following generation g.
for $i = 1$ to N do begin	// Go through every lattice site.
for $j = 1$ to N do begin	
if $a_{ij} = 0$ then	// If lattice site (i,j) is unoccupied
$m = \text{find_two_mature_neighbors}(i,j, \alpha_1, \alpha_2)$	// find two different “mature” individuals
/	// in the Moor neighborhood of a_{ij}
if $(m=1)$ then	// If they do not exist $m=0$, otherwise $m=1$
$a_{ij}^{s+1} \rightarrow 1,$	
$(\beta_1, \beta_2) \rightarrow \Omega(\alpha_1, \alpha_2)$	// Reproduce them.
$\alpha_{ij} \rightarrow (\beta_1, \beta_2)_{pr},$	// pr - a probability for selection of
	// one out of two offspring (β_1, β_2)
$k_{ij} \rightarrow 1$	
else	// If a site (i,j) is occupied
if $p_{kill}(\alpha_{ij}) = p(\alpha_{ij})$ then	// delete it if its life-time passed
$k_{ij} \rightarrow 0, a_{ij}^{s+1} \rightarrow 0$	
else	
$k_{ij} \rightarrow p_{kill}(\alpha_{ij}); k_{ij} \rightarrow k_{ij} + 1$	// or make it older
end	
end	
end.	

Fig. 1. The pseudo-code describing evolution rules.

We assume that, the population can be attacked by a plaque represented by “seeds”. The “seeds”, which are generated periodically in time, are scattered randomly on the CA lattice. The strength of the plaque is defined by ϵ_0 - the ratio between the number of “seeds” and the total number of individuals. If a “seed” is located at the same place as the population member, both are removed from the lattice. Otherwise, the “seed” moves randomly on the CA lattice until it “annihilates” with the first encountered individual. The “seeds” cannot reproduce.

Our system consisting of elements with “genetic codes” evolves not only on CA lattice but also in the abstract multi-dimensional feature space \mathfrak{R}^L represented by the coordinates of binary chains α_{ij} . As shown, e.g., in [4], the clusters of similar individuals are created both on the mesh and in the feature space \mathfrak{R}^L due to the genetic drift. These clusters can be extracted using clustering algorithms [8,9] and then visualized in 3-D space by employing multidimensional scaling (MDS) algorithms [8,9].

3 Results of Modeling

The parameters assumed for a typical run are shown in Tab.1. The periodic lattice of cellular automata 200x200 and 100x100 were considered as optimal ones balancing well adequate representation and computational requirements. These parameters are also sufficient to obtain stable populations and partly eliminate boundary effects.

Table 1. The parameters for typical simulation.

<i>Lattice size (N×N)</i>	100×100, 200×200	<i>Mobility factor $\epsilon(0,1)$</i>	1
<i>Initial density (P0)</i>	0.2 – 0.5	<i>Probabability of reproduction</i>	1
<i>“Youth” - length</i>	32	<i>Probabability of mutation</i>	0
<i>“Mature” - length</i>	32	<i>Plague period</i>	50
<i>“Old age” - length</i>	32	<i>Dose (ϵ_n)</i>	0.4

At the start of evolution, the population is generated randomly with P0 density ($P0 \in (0,1)$, see Tab.1). Because all individuals are initially “young”, the evolution scenario depends strongly on P0 (see Fig.2). For both too large and too small P0 values, after some time, the number of offspring can become marginal in contrast to massive extermination of “old” individuals from the initial population. This may lead to fast extinction of the whole population. This effect can be considerably reduced by increasing mobility factor of individuals, their life-time and initial diversity of population.

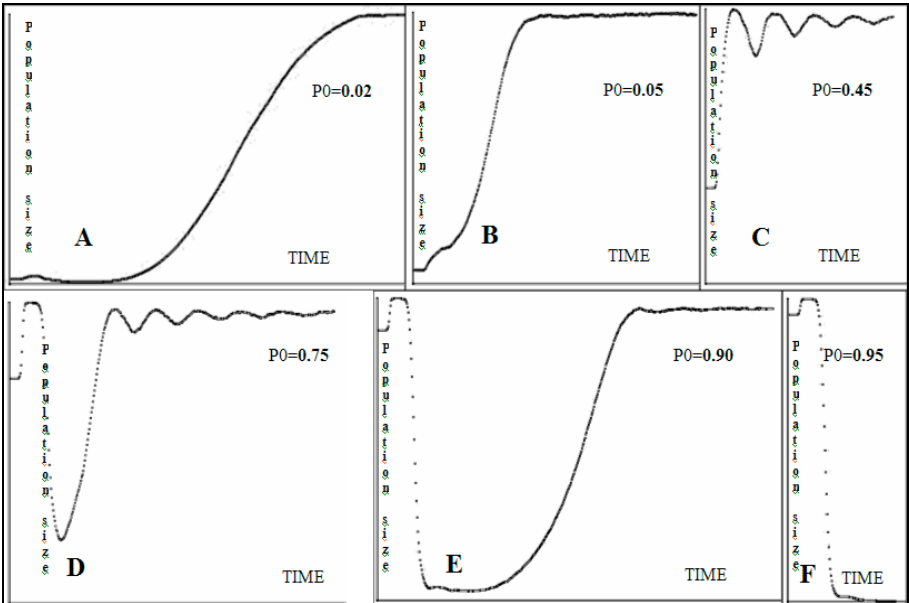


Fig. 2. Various scenario of the growth of population size in time for increasing P0 (initial population size). The simulation was started assuming that all the individuals are “young”. The CA lattice of size 100x100 was simulated.

We have assumed additionally that:

- the length L of the vector representing the “genetic code” is equal to 96,
 - the lengths of vectors \mathbf{y} , \mathbf{m} , \mathbf{o} are identical, i.e., $l=m=n=32$ (see Definition 1).
- The value of L was selected intentionally to have more compact representation (thus more efficient code) of individual, whose “genetic code” can be implemented then as three *float* values. The value of L cannot be too small due to statistical validity (the number of “1”s in various episodes of individual’s life has initially the Gaussian distribution) and due to high sensitivity of the system on various simulation conditions. Other configurations and vector lengths were also examined. The first conclusion is that, the individuals, even those with the same life-time lengths L , can behave in various ways depending on the lengths of subsequent life-episodes \mathbf{y} , \mathbf{m} , \mathbf{o} . On the one extreme, the population with too short “maturity” period will die quickly. On the other, the populations with greater reproduction potential (defined by the length of \mathbf{m} vector) will tend to fill the \mathbf{m} part of vector α with “1”s. This is due to the population members who are “mature” for a longer time, have a greater chance to reproduce and pass their “genetic code” to other generations. One can expect that the similar behavior will be observed for “idle” episodes of individual’s life i.e., the “youth” and the “old age”, i.e., the individual’s life-time will increase due to the evolution to the maximum length L . However, the situation is completely different.

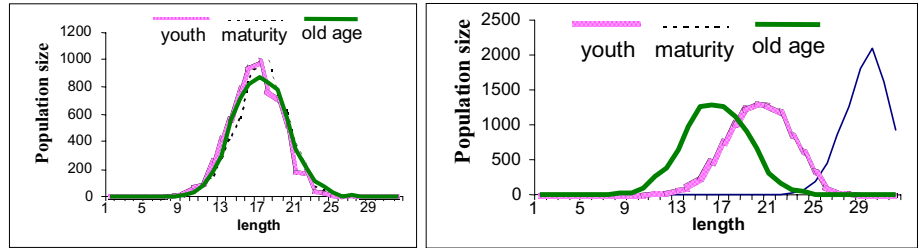


Fig. 3. The histograms representing the number of individuals with various lengths of \mathbf{y} , \mathbf{m} , \mathbf{o} life-episodes. For initial generation of individuals the distributions are similar (the plot on the left), but after $g=2000$ steps they diversifies considerably (the plot on the right).

Let us assume that initially the distribution of “1”s in each of the three episodes of life is Gaussian and there are in average 16 “1”s in each of \mathbf{y} , \mathbf{m} and \mathbf{o} vectors. These initial conditions are shown in Fig.3a. After $t=2000$ time-steps, the situation considerably changed. The distributions of “1”s for each period of life undergo strong diversification (Fig.4b).

As displayed in Fig.4, the distribution of individuals both on the CA lattice and in the feature space, changed also dramatically. Instead of initially chaotic configuration of individuals populating 2D lattice, they form distinct clusters. The individuals belonging to the same cluster are similar according to the Hamming distance in the L-D feature space. As shown in Fig.4b there exist four distinct “families” of individuals in the feature space. In Fig.4a we show them projected onto the CA lattice.

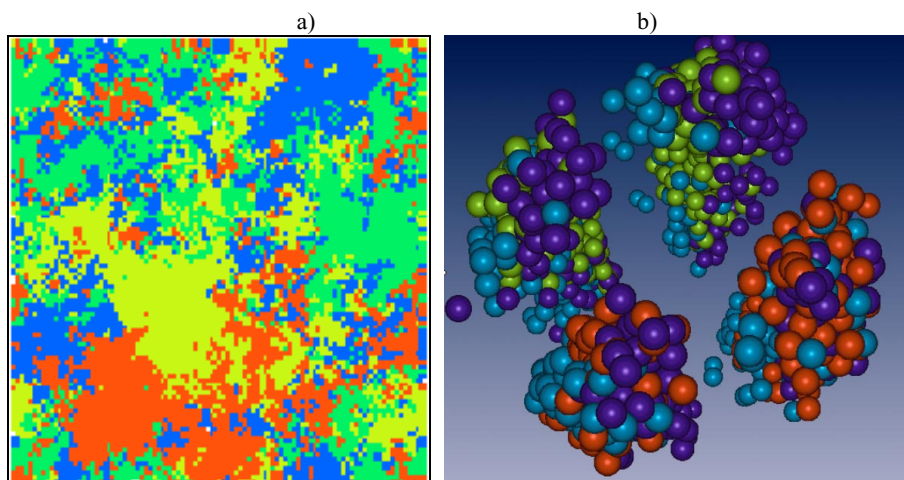


Fig. 4. Clusters of individuals on 2D lattice (a) and in the feature space (b). Single plate in Figs.4b corresponds to a group of individuals with identical “genetic codes”. Fig.4b shows the result of *k-mean* clustering in the L-D feature space transformed by using multi-dimensional scaling to 3-D space. Various colors in b) indicate the spurious clusters obtained using *k-means* clustering scheme. While colored 2-D clusters on the CA lattice in Fig.4a represent the four clusters recognized visually from Fig.4b.

The continuation of the evolution from Fig.4 produces a stable attractor, which consists of four “families” of individuals, which have exactly the same “genetic codes”. The codes differ between clusters only on two bits positions. Therefore, the offspring generated due to recombination belong to one of the existing clusters. We did not obtain any global solution with only one large cluster of individuals having the same genetic code. It means that the fitness factor for the populations of individuals with the three life periods is not a trivial, increasing function of the length of life. This is unlike for populations, which are “mature” and ready for reproduction during the whole life-time ($L=m$, $l,n=0$). In this case the attractor of the evolution process would consist of individuals with “genetic codes” filled exclusively by “1”s.

The most basic features of attractors resulting from modeling are collected in Tab.2. As shown in Tab.2, where apart from the “natural” elimination - resulting from the limited life-time inscribed in the “genetic code” - there are not any other lethal factors, the “maturity” period fills with “1”s after relatively small number of evolution cycles t . This is obvious because longer ability of reproduction gives a greater chance for passing the genetic code to the offspring. By extending the evolution time about threefold, also the “youth” vector will be filled with ‘1’ s. Surprisingly, even much longer simulation does not affect the “old age” vector. It remains the mixture of “1”s and “0”s. This observation confirms also for:

- variable lengths of $\mathbf{y}, \mathbf{m}, \mathbf{o}$ ($l \neq m \neq n$),
- long “old age” period ($n=64$),
- much shorter remaining episodes ($l=16$, $m=24$, respectively).

Table 2. Number of “1”s in the average “genetic chains” of different lengths for corresponding episodes of individual’s life after 50,000 time-steps. “*mix*” - the mixture of “0”s and “1”s, “*perished*” - the population decreases quickly.

		YOUNG	MATURE	OLD
1	<u>No plague</u>			
	(32,32,32)	32	32	<i>mix</i>
	(16,16,16)	16	16	<i>mix</i>
	(8,8,8)	8	8	<i>mix</i>
2	<u>No plague</u>			
	(16,24,64)	3	24	<i>mix</i>
	(8,32,64)	1	30	<i>mix</i>
	(0,40,64)	0	<i>perished</i>	<i>perished</i>
3	<u>Plague period < L</u>			
	(32,32,32)	0	32	<i>mix</i>
	(32,32,0)	0	32	0
	(0,32,32)	0	32	<i>mix</i>
4	<u>Plague period > L</u>			
	(32,32,32)	0	32	0
5	<u>Plague period < L</u>			
	(8,8,8)	0	8	<i>mix</i>
6	<u>Plague period > L</u>			
	(8,8,8)	<i>mix</i>	8	0

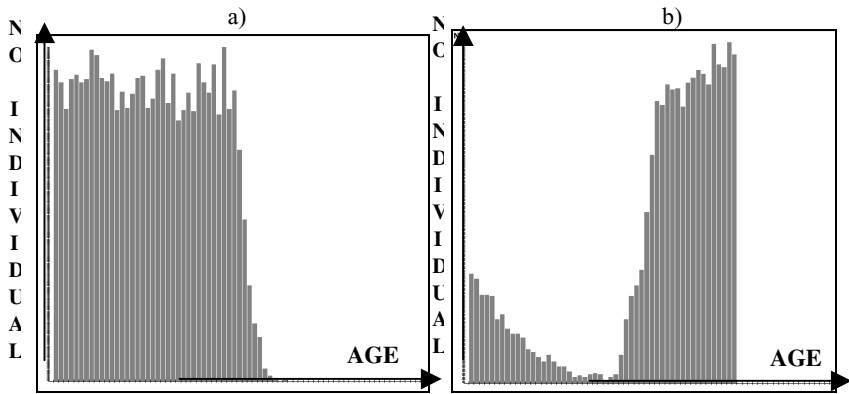


Fig. 5. The histograms of individuals vs. their age for a) stable ($l=32$, $m=32$, $n=32$), and b) unstable ($l=0$, $m=40$, $n=64$) populations.

Surprisingly, further decrease of the “youth” episode ($l=8$, $m=32$, $n=64$) with respective extension of the “maturity” episode weakens considerably the population. For ($l=0$, $m=40$, $n=64$) it dies eventually. This behavior shows that the “youth” period accumulates reproductive ability of the population. If released too fast it will cause non-uniform aging (see Fig.5b), which may result in fast extinction of the whole population.

As depicted in Fig.6, the population attacked by the periodic plague dies if the strength (“Dose” in Tab.1) of the plague ϵ_0 , defined as the ratio of the number of “seeds” to the number of individuals, and/or its period exceeds a certain threshold.

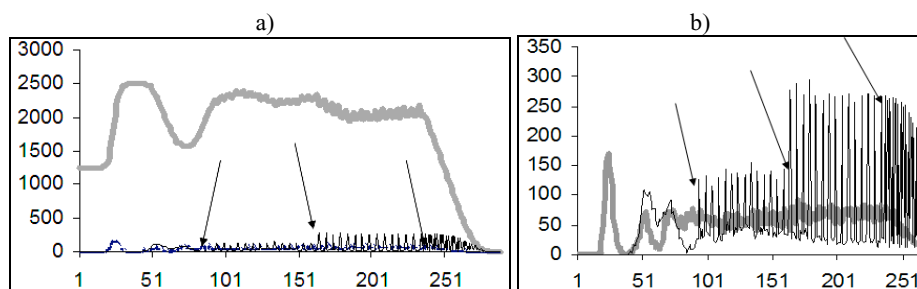


Fig. 6. a) The influence of periodic plague (thin line) on the number of individuals (thick line). b) The number of individuals (thick line) eliminated by the periodic plague (thin line) in time.

The attractors (i.e., the non-evolving populations of individuals with similar “genetic codes” obtained due to the long evolution) in a stable environment die very quickly due to the lack of adaptation ability represented by diversification in the “genetic codes” of individuals. For example, a uniform population (e.g., see Tab.2 for $l=m=n=32$) obtained after long evolution ($t=50,000$ time-steps) and attacked then by the plague extinctions during the following 100 steps. The same population, but this time infected at the early stage of evolution (after $t=200$ steps) survives. The “genetic codes” of individuals self-adapt to the unstable environment. As shown in Tab.2, the “genetic codes” of attractors of attacked population are different than those obtained for the stable environment. Moreover, they differentiate depending on the period of the plague.

For the outbreak with a period shorter than the average life-time of individuals, the “youth” episode, as the obstacle for fast reproduction, is eliminated completely (all “0”s in vector y). Surprisingly, the “old age” period remains relatively long. Because the population can have not enough time for reproduction between subsequent plaques, it has to elaborate sophisticated control mechanism of growth. Let us assume that:

1. the “old age” is inhibited ($n=0$) and the population consists of only “mature” individuals,
2. the majority of individuals are eliminated by the plague from the lattice in a very short time.

At the very moment when the plague ceases, all survivors will produce many new-borns due to plenty of free space on the lattice. Therefore, after some time, the individuals of a similar age and approximately the same life-time will dominate in the population. Their simultaneous death will weaken the population (see Fig.5b). Thus, the number of “mature” individuals, which survive after the following disasters, may be too small to initiate new generations and the population may extinct eventually.

Assuming that the “old age” episode is greater than 0 ($n>0$), post-plague demographic eruption (resulting in demographic catastrophe after some time) can be

much smaller than for $n=0$. It is easy to remark that the demographic eruption will be monotonically decreasing function of n because only the “mature” survivors have reproductive ability. Moreover, the existence of “old” individuals will decrease the probability of reproduction. The replacement of “old” individuals with newborns will be also postponed and possible only after their death. All of these demographic inhibitors cause that the post-plague reconstruction of the population takes more time than in the previous ($n=0$) case. Instead, the age distribution in the population is more stable (see Fig. 5a). Thus the population allowing the “old age” episode is stronger and has a greater chance to survive in unstable environment than that consisting of only “mature” individuals. We can conclude that the “old” individuals accumulate the environmental resources (free space) for stable growth eliminating dangerous post-plague effects such as demographic eruptions.

When the plague period is greater than the average life-time of individuals and simultaneously the “strength” of the plague increases, the “old age” is also eliminated due to evolution. This is because the population has enough time for reproduction and demographic minimum does not coincide with the plague.

4 Concluding Remarks

We have discussed the influence of the lengths of three life-episodes: the “youth”, the “maturity” and the “old age” on population evolution. Of course, their duration of depends on the biological construction of individuals. The organism requires a minimum time to grow-up and be ready for reproduction. However, the terms “youth”, “maturity” and “old age” used in this paper have not only biological meaning. Environmental factors influence both reproduction ability and the life-time. They may cause that the same organism can be treated as “young”, “mature” or “old” independently on his age.

Summarizing our findings, we can conclude that “maturity” period decides about the reproductive power of the population and its survival ability. Thus the population increases its length to a maximum value allowed. The idle episodes of life, i.e., the “youth” and the “old age” play the role of accumulators of the population resources and control their growth. The “youth” accumulates reproductive resources while the “old age” accumulates the space required for reproduction. The idle life-episodes develop the control mechanisms, which allow for self-adaptation of the population to unstable environment.

1. In the case of a stable growth the reproductive resources are accumulated in the “youth” episode of life. The “old age” remains the secondary control mechanism.
2. For periodically infected populations with the period longer than the average length of the life-time L the population is biased only for reproduction, eliminating idle episodes of life.
3. For strong enough and frequent pests the „old age” remains non-zero accumulating additional space required for burst-out of population just after the plague vanishes.

Many aspects of the model have not been explored yet. For example, the influence of lethal mutations and other hostile environmental factors on the survival ability of the population. However, our model can be an interesting complementary constituent to the Penna paradigm of aging.

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