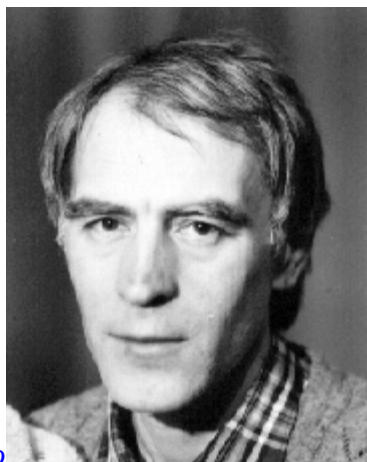


Macrophylon: simulation model of an evolutionary process

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What are the factors which lead and drive the process of biological evolution? The *Macrophylon* simulation program was created in order to clear up at least several of them by looking at evolutionary trees on a computer screen. The known point of view on any simulation which is distributed broadly is that we have to get along the process of simulation just the such results which may be predicted in advance. This point is too simple to be absolutely truth and isn't true in this case in particular. We define here some *rules of the game* as well as some properties of individuals (populations) which participate in this game called *evolution*; but we attempt here to understand just a general picture of history of their *landscape* after many steps. In fact, we have in this case some evolutionary version of the well-known *game of life* or, more broadly, a realization of an approach called *cellular automata*; when defining several features of micro-objects a investigator tries to see an evolution or development of macro-object, i.e. of the whole. Theoretically, the final overall picture could be predicted, because each step of work of computer program is driven by an algorithm but that is not possible in practice, because too many calculations should have to be made, at least as many as the algorithm itself.

Several words about the particularities of this *scientific game*. We base ourselves here on Darwinian approach as a rule. Every population is described by 25 phenotypic traits. Up to twelve types of the model environments may be used by populations in this simulation simultaneously. The maximum number of population is 120. Each population is rated by a *survival* variable, which represents the fitness of such population under the specific condition of the environment; this parameter is used in the model in order to simulate different types of evolutionary and ecologic interrelations, and is computed for each population as the sum of values (environmental importance) of all phenotypic traits of this population. The competition results depends on the survival of populations participating in competition; the population which has a bigger survival forces out population with the smaller one. It is possible to change the *level* of competition defining an interval parameter (or *gap*) for the difference between a survival of each of competing populations, within which the competition have not to happen. The high level of competition (*hard* competition) corresponds small value of above difference. The mutation process is provided as accidental changes of phenotypic traits. Each population may also choose ether environment for living *aspiring* to find some the best one and to passing to the right place.

The program interface allows change the model environment and the frequency of mutation as well as the level of competition. It gives also a possibility to observe the *ways of evolution* for separated populations or their group.

This first IBM version of this program, called [Macrophylon](#) works with populations of *Chordata* but we could choose

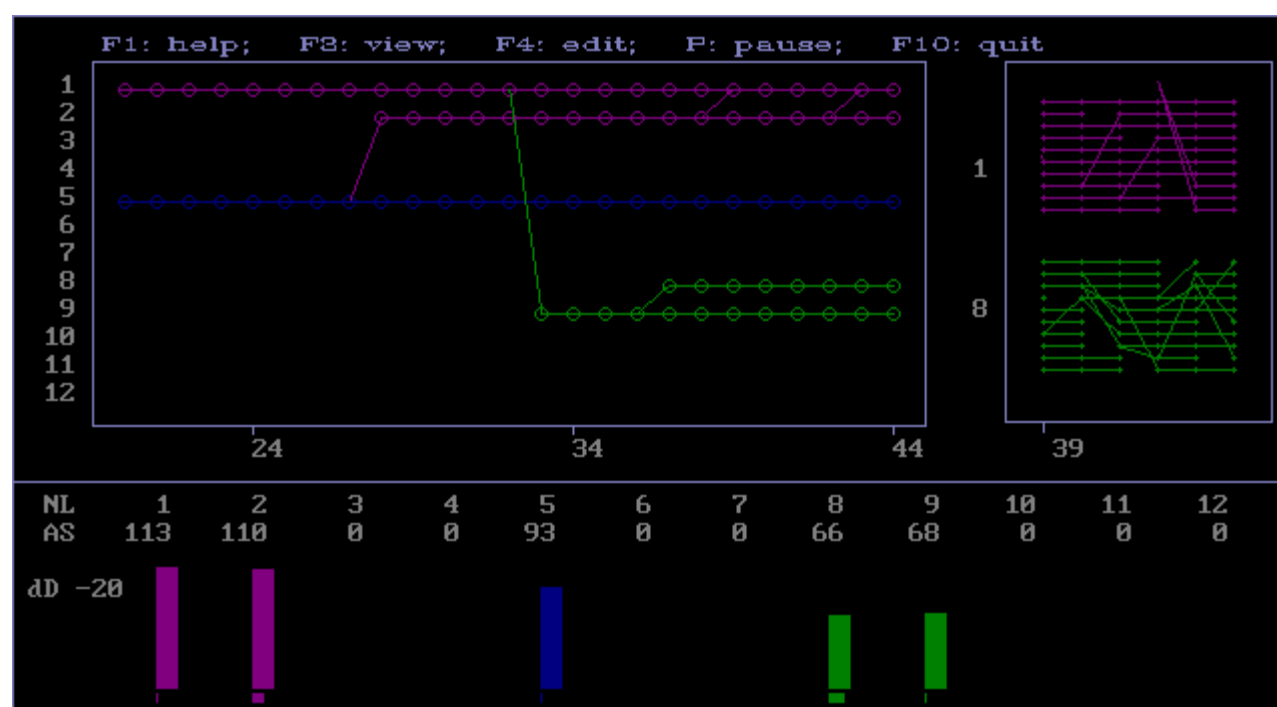
also another taxa in principle by replacement of special tables of phenotypic traits. The *mutations* in our modeling correspond to major changes in adaptive traits: they represent adaptive breakthroughs such as major changes in size, or in the nature of respiration. In nature, of course, the actual time taken for such events is on the order of 0.5-1 million years. It should be noted that these are macro-mutational changes and the model, therefore, deals with the consequences of such major adaptive shifts, rather than their causes.

The simulation of evolutionary patterns studied here demonstrated that certain unexpected effects which may be observed in the patterns produced by evolutionary processes. For example, our results demonstrate that the *reinmigration of near descendants* is a very significant factor in the creation of evolutionary trees.

Other interesting results have been obtained in experiments concerning changes in the parameters governing competitive interactions. We found that hard competition provokes such processes when the ones of specialization predominate processes of filling out of free environment. Both processes appear to be a function of the mutation rate. The increase of frequency of mutations promotes in the intensification of predomination tendency.

The description of model as well as some results of simulation are given in the file `article.txt` enclosed into the `arj` file.

The [program](#) runs in MS-DOS machines. You will need the `arj` decompression program to decompress it.



Screen shot

REFERENCES

Levchenko V.F. and Menshutkin V.V. *Simulation of macroevolutionary process* // Zhur. evol. biokh. i fiziol. (Journ. of Evolut. Biochem. and Physiol.; the English version exists). 1987, Vol. 23, no. 5 (Sep-Oct): 668-673.

Levchenko V.F. *The Models in the Theory of Biological Evolution* (monograph in Russian). St.Petersburg, 1993, 384 pp.

An [extended description of the program](#) is available from the set of [talk.origins](#) FAQs.