

Basic model description

The model is elementary so this description follows a simplified version of the ODD (overview, design concepts and details) protocol for describing individual and agent-based models (Grimm & Railsback 2005; Grimm et al. 2006). The model is implemented in NETLOGO v. 6.0.4 (Wilensky 1999; freely downloadable from <http://ccl.northwestern.edu/netlogo/download.shtml>) and available in the electronic supplementary material (basic model).

Purpose. The purpose of the model is to show the process followed by a genetic algorithm in performing a simple problem-solving process. The problem is to find the greatest natural number composed of a given digits' number.

State variables and scales. The entities of the model are agents carrying a "chromosome" represented as a string and codifying a candidate solution to the problem.

Process overview and scheduling. Every time step, the chromosomes numeric values are compared and the higher transfer a random gene sequence to recipient chromosome according to bacterial genetic shuffling mechanism known as "conjugation". A second genetic process can take place: it is called "mutation" and interest a single gene (codifying for a single digit) along the chromosomal string.

Design concepts. The program follows the typical general flux-diagram of a genetic algorithm and involves three types of operators: selection, crossover, and mutation. Selection doesn't require any fitness function because it is immediately given by the numeric value of the chromosome string: in other words, the genotype is equal to the phenotype. The program will be stopped when a chromosome will reach a numerical value corresponding to the solution of the problem, that is $10^n - 1$.

Initialization. Initialization creates a number of agents (turtles) having a chromosome represented as a string and set equal to the worst answer to the given problem, that is 10^{n-1} , where the n represents the digits composing the searched number: every digit correspond to a "gene" on the chromosome.

Input. The n -value, the number of the agents, and the mutation rate can be set initially by the user through the graphical interface.

Submodels. The model has two submodels: mutation and genetic shuffling.

MUTATION. Generation after generation, mutations happen on a single random gene with the given frequency (corresponding to one digit of the candidate number) that is a digit place on the chromosome.

GENETIC SHUFFLING. It takes place between a randomly chosen turtle (recipient) and the most performing one (donor) that offers a fragment of its chromosome to the first one; the two turtles involved in this process will be highlighted by a link. This process is analogue to crossing-over usually utilized in genetic algorithms; this kind of genetic-shuffling is more similar to bacterial conjugation, in fact, it leads to the formation of just one hybrid chromosome made up by the chromosome of the recipient turtle in which a fragment of genes (digits) included between two randomly chosen positions are replaced by the corresponding genes (digits) of one of the donor turtle's chromosome.

References

- Grimm, V., Railsback, S.F., 2005. Individual-Based Modeling and Ecology. Princeton University Press, Princeton.
- Grimm, V. et al. 2006 A standard protocol for describing individual-based and agent-based models. Ecol. Modell. 198, 115–126. (doi:10.1016/j.ecolmodel.2006.04.023)
- Wilensky, U. 1999 NETLOGO. Center for Connected Learning and Computer-Based Modeling, Northwestern University, Evanston, IL. See <http://ccl.northwestern.edu/netlogo> <http://ccl.northwestern.edu/netlogo>.
- Melanie Mitchell 1996 An Introduction to Genetic Algorithms, Cambridge, MA: MIT Press.