USER MANUAL

What does this Manual do?

This manual explains how to install and use the user interface of the model PanModel33. The purpose of this model is to understand the potential for local adaptation of populations with different life strategies under scenarios of environmental change. The model was designed for hypothesis testing, theory development and for communication and learning.

The model was designed in such a way that there is no need to modify the code for its operation, unless the user feels confident enough as to extend the model to suit his/her particular needs.

More technical details about the model can be found in the ODD protocol that comes along with this manual.

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1 Installation of Netlogo

The first step is to get Netlogo up and running in the computer. Netlogo is a free open source software, very popular for education and research worldwide, that provides a programmable multiagent modeling environment.

To download and install Netlogo visit the following link:
https://ccl.northwestern.edu/netlogo/index.shtml

1.2 Compatibility

Netlogo is compatible with Linux, Windows, and Mac OS, and can run on almost any computer. The link below leads to Netlogo System Requirements
https://ccl.northwestern.edu/netlogo/requirements.html

2 Model versions and description

There are two model versions available to download. The full version takes advantage of the Netlogo *r extension* for the simulation of different scenarios of beneficial mutations. If this feature is not of interest for the user(s), the other simplified version is recommended. The simplified version uses Netlogo resources only (no need of additional programs and complications).

To use the full version of the model, please follow the steps on the link below. This link explains how to set up the Netlogo r extension which is important before using the model (search for “installing r”, and “configuring the r extension”). Otherwise, it will not work properly.
https://ccl.northwestern.edu/netlogo/docs/r.html

2.1 Using the model user interface

If you are using Netlogo for the first time, it is strongly recommended to get familiar with the basics regarding the operation of the user interface of the software. For example, it is important to understand what the different bottoms do (setup, go and forever bottoms), as well as how to change parameter values using sliders, choosers and input boxes. Netlogo provides a friendly tutorial on their webpage for the learning of the user interface and more (link below)

https://ccl.northwestern.edu/netlogo/docs/tutorial1.html

2.2 Plots

The user interface of the model contains the following plots that display output data in real simulation time (Fig 1):

- *Frequency distribution:* display the phenotypic (blue) and genotypic (black) frequency distributions in the population. It also shows the optimum phenotype as given by the environment (red vertical line).
- *Time series:* this plot monitors the population size.
- *Genotypic-phenotypic-variance:* keeps track of the actual genetic and phenotypic variances in the population.
- *Degree of local adaptation:* monitors how fit the population is to the environment (fitness proxy).
- *Environmental optimum vs mean phenotypic response:* display how far is the population mean phenotype from the optimum as given by the environment.

2.3 Bottoms

The bottoms (top left) allow to set up the experiment, and run the model for only one iteration, or until either, the ending condition of time-limit is met, or extinction occurs.

2.4 The Ecology and Evolution modules

The input parameters of the eco-evolutionary model that the user can modify are grouped into two modules: the ecological module (Ecology), and the evolutionary module (Evolution). The Ecology module governs the scenario of environment and the type of organism, while the Evolution module, the underlying genetics, and plasticity. The genetics is further split into explicit or implicit, depending on whether the chromosomes, loci, mutation rates and other genomic properties are explicitly simulated or not.

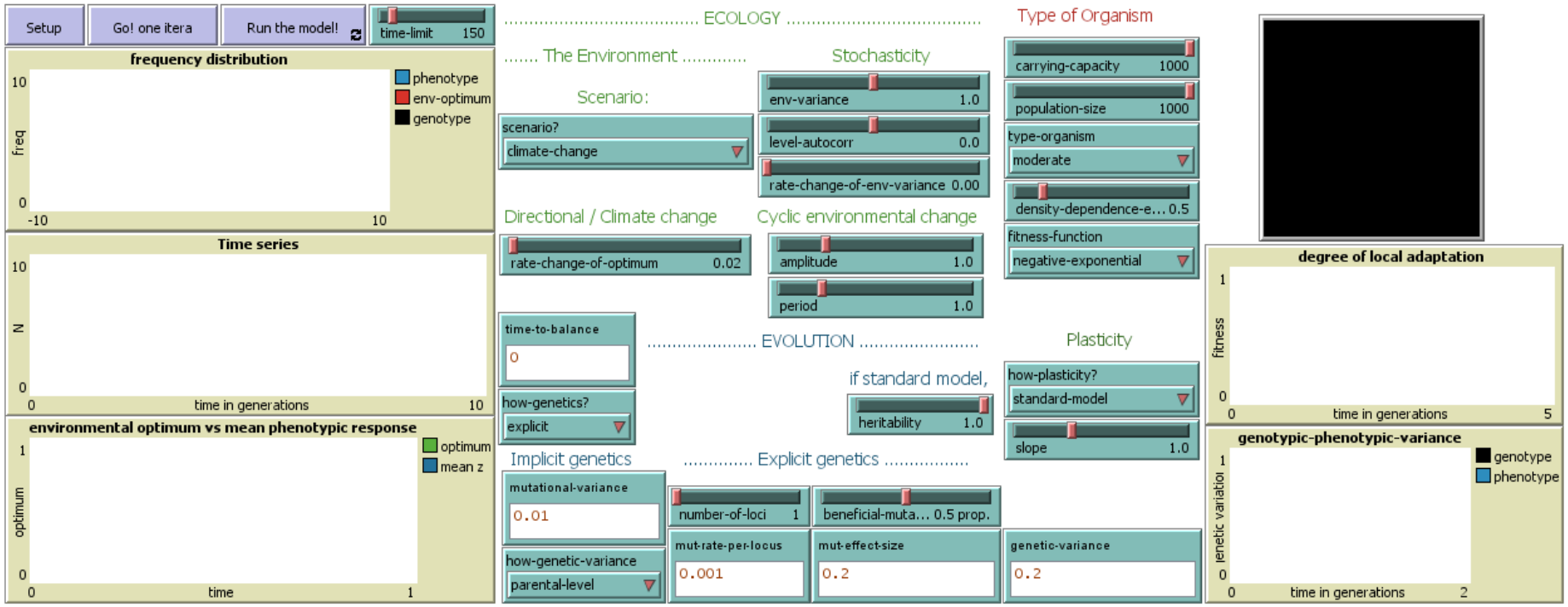

Fig 1 Picture of the graphical user interface (GUI) of the eco-evolutionary model.

3 **Parameters description** List of adjustable parameters of the GUI, their description and range of values.

Module		Parameter name	Description	Range	default
Ecology	Environmental scenario	scenario?	whether climate change or cyclic environment		Climate-change
		rate-change-of-optimum	rate of change of environmental optimum per time step (climate change only)	[0.00; 1.00]	0.02
		amplitude	amplitude of the wave (only for cyclic environmental scenario)	[0.0; 4.0]	1.0
		period	period of the wave (only for cyclic environmental scenario)	[0.0; 4.0]	1.0
		env-variance	the variance of the stochastic environment	[0.0; 2.0]	1.0
		rate-change-of-env-variance	rate at which the environmental variance change per time step	[0.00; 0.10]	0
		level-autocorr	the level of autocorrelation, for simulating colored stochastic noise: white, blue or red noise	(-1.0; 1.0)	0 (white noise)
	Type of organism	carrying capacity	the carrying capacity of the local environment (in number of individuals)	[10; 1000]	1000
		population-size	initial number of individuals in the population	[10; 1000]	1000
		type-organism	level of specialization of the simulated organism	[specialist; moderate; generalist]	moderate
		density-dependence-effect	whether the simulated organism is an *r* or *K* strategist, depending on whether the density dependence effect is strong or weak	[0; 3.0]	0.5 (weak)
		fitness-function	two possible methods, both assuming a bell-shaped fitness function	[Bjoerklund2009; negative-exponential]	negative-exponential
Evolution		time-to-balance	the number of time steps before the actual scenario of environment starts	≥ 0	0
		how-plasticity?	Selection among different methods for phenotypic plasticity. For the method standard-model, its contribution to phenotypic variance depends on the value of heritability	standard-model, random, linear-RN, adaptive-sinusoidal, adaptive-logistic	standard-model
		slope	degree of plasticity	[0.5; 2.0]	1.0
		heritability	the value for trait heritability. A value of one, means that the correlation genotype-phenotype is one (*i.e.*, no plasticity or environmental effect). Only works for standard model (see how-plasticity)	[0.01; 1.00]	1.0
		genetic-variance	initial genetic variance in the population	≥ 0	1
		how-genetic-variance	specifies the method for simulating the dynamics of the genetic variance (works only for the standard model)	[parameter; parental-level; population-level]	parental-level
		how-genetics?	set the method for simulating genetics	[implicit ; explicit]	explicit
	Implicit genetics	mutational-variance	the amount of genetic variance contributed by mutations	≥ 0	0.01
	Explicit genetics	number-of-loci	the number of loci affecting the fitness-related trait (evolving trait)	[1 ; 50]	1
		mut-rate-per-locus	probability of mutation per locus	≥ 0	$1x10^{-3}$
		mut-effect-size	the variance of the fitness effect-size of mutations. The model assumes a Gaussian distribution of effect-size	≥ 0	0.2
		beneficial-mutations	set the percentage of beneficial mutations (affect the distribution of mutation effects accordingly)	[0.1; 0.9]	0.5