

# SimEVO project

## Index of notation

Notation	Definition
$\mathcal{P}$	Population
$p_\delta$	Selected population
$p_\beta$	Population which reproduces
$p_\psi$	Removed population (individuals who die)
$\mathcal{E}$	Environment
$\mathcal{E}_D$	Set of environmental factor(s) $\mathcal{E}_\delta$
$\mathcal{E}_\delta$	Environmental factor
$S_F$	Set of selective function(s) $S_{fun}$
$S_{fun}$	Selective function
$\lambda$	Reproductive coefficient (number of offspring per individual)
$\psi$	Lethality of environmental factor
$O$	Organism
$g_p$	Phenotype
$g_t$	Genotype
$\mathbf{G}$	Abbreviated notation of $(g_t, g_p)$

## Non-dependent binary phenotypic determinance

We consider the set  $\mathcal{P}$ , which consists of individual organisms  $O$  such that  $\mathcal{P} = \{O_1, \dots, O_N\}$ , where  $N$  is the total number of organisms and hence the size of the population (i.e.  $|\mathcal{P}| = N$ ). Per traditional eco-evolutionary biology we assume the population to be located within the environment  $\mathcal{E}$ . The set  $\mathcal{E}_D$  denotes the set of environmental factors  $\mathcal{E}_\delta$

present within the environment such that  $|\mathcal{E}_D| \geq 1$ . The lethality coefficient  $\psi \in [0; 1]$  determines the probability that a selected organism ( $O \in p_\delta$ ) will pass to the removed population  $p_r$  i.e. the selected organism dies.

We estimate the per turn change in population size to be proportional to the number of births into the population and the number of individuals who die as a result of selection. Mathematically, we can denote this as  $\mathcal{P}'$  such that

$$\mathcal{P}' = \lambda(p_\delta - p_\psi) - p_\psi \quad (1)$$

Because each step in time represents a population generation, we assume that most individuals within the population (or all) reproduce. This is where the reproductive coefficient  $\lambda$  comes into play, e.g.  $\lambda = 0.7$  denotes that 70% of organisms within the population to reproduce which results in  $n_b = \lambda(p_\delta - p_\psi) = p_\beta \lambda$  "newborn" individuals. (We are not interested in the particular age of each organism during the time of reproduction as the timeframe we are observing is in generations)

The selective population  $p_\delta$  is determined by passing the  $\mathcal{P}$  set through selective function(s)  $S_{fun} \in S_F$ . The benefit of defining the set  $S_F$  which contain all the selective functions  $S_{fun}$  is that it allows for the instantiation of new selective functions. Assume that the selective functions are a subclass of the function `selFunc`, we can define a new function `selLow` which sorts individual's by trait value and picks the lowest percent percent:

```
import numpy as np

class SelectionMethods:

    # Other selective functions
    # [ ... ]

    def selFunc(population, percent):
        # Sort the list by descending trait value
        np.sort(population, fitness, descending=TRUE)
        select_range = ceil(len(population) * percent)
        return np.select[select_range]
```

```
# This code is trash. Revise this once the actual code is in place
```

```
# EOF
```

In cases where we want to include multiple environmental factors, we can imagine that the population is passed in some arbitrary order through a chain of environmental factors each with a designated selective function (note that this does not mean that environmental factors can not share the same selective function). This is represented by equation (2) below, where  $M$  represents the total number of environmental factors:

$$\text{Input } \mathcal{P}_t \rightarrow \underbrace{\mathcal{E}_\delta(1)}_{S_{fun1}} \rightarrow \dots \rightarrow \underbrace{\mathcal{E}_\delta(M)}_{S_{funN}} \rightarrow \text{Output } \mathcal{P}_{t+1} \quad (2)$$

We view each environmental factor as a binary operation which takes in individual parameters of an organism  $O$  and logically compares them. For example, in cases of binary phenotypic determinance of survival, we can notate the environmental factor as a logical comparison with output  $\omega$ , which is either `1` or `0`, i.e. `True` or false `False`, which we interpret as the boolean statement `survives` :

$$\mathcal{E}_\delta(g_p) : g_p \rightarrow \omega \mid \omega = \begin{cases} 1 & \text{if } g_p > 0 \\ 0 & \text{if } g_p = 0 \end{cases} \quad (3)$$

Notice that in this case, where phenotype is binary and determines survival, the selective function  $S_{fun}$  has the same operation as the environmental factor.

