Exercise sheet 1: Age-structured populations

Sex, Ageing and Foraging Theory

In this exercise sheet, we model the dynamics of a wild boar population (*Sus scrofa*) using data from the literature. For simplicity, we assume boars cannot live for more than six years, such that the population is structured into a newborn age-class (year 0) and six reproducing age-classes (from year 1 to year 6). Age-specific fecundities and survival are given in Table 1.

Age a (in years)	Fecundity m_a	Survival probability p_a
0	-	0.8
1	0.57	0.52
2	2.10	0.60
3	4.25	0.71
4	4.25	0.71
5	4.25	0.71
6	4.25	-

Table 1: *Sus scrofa* life-table.

1 Population dynamics

a. Modify the individual-based simulation program constructed during the R tutorial (the 'DYN()' function) to allow survival probabilities and fecundities to vary with age, as in Table 1 (Hint: you can give vectors containing age-specific survival probabilities and fecundities as arguments to your simulation program).

b. Simulate the stochastic dynamics of the wild boar population for ten years, starting with $n_{1,0} = 1000$ individuals of age 1 (parameter **n0** in the simulation program), and plot the population size as a function of time. What do the observed dynamics imply for the lifetime reproductive success of a wild boar, R_0?

c. Construct the Leslie matrix for the wild-boar population from Table 1 (recall that a Leslie matrix depends on **effective** fecundities, f_a). Using this matrix, compute the dynamics of the population with R (or another programming language) over ten years, starting with $n_{1,0} = 1000$ individuals of age 1 and none in the other age classes (Hint: matrix product is achieved by the **%*%** operator in R). Plot the predicted population size as a function of time along with the simulation results. Do they match?

2 Density regulation

We now turn to a more realistic scenario where the wild boar population is density-regulated. Specifically, we assume that the establishment probability, p_0, decreases with the total population size $N_t = \sum_{a=1}^{6} n_{a,t}$ at time t

(Equation 1):

$$p_0(N_t) = \frac{c}{1 + \gamma N_t}, \tag{1}$$

where $0 < c \leq 1$ and $\gamma > 0$ are positive constants.

a. Modify the individual-based simulation program (from part 1) to incorporate this new assumption. Simulate the population for a hundred years, starting with $n_{1,0} = 1000$ individuals of age 1, with $c = 0.8$ and $\gamma = 0.0005$. How does population size vary over time? Why?

b. Construct the Leslie matrix associated with this new model and use it to compute the dynamics of the population over a hundred years starting with $n_{1,0} = 1000$ individuals of age 1 in R. How is population size predicted to vary? Does it match your simulation results (from 2a)?

3 Selection

Consider a population where individuals reproduce once and live for a single year so that there are just two age classes, class 0 (newborns) and class 1 (adults). Adults express a trait x (e.g. beak length) that affects their fecundity according to

$$m_1(x) = 100 \exp\left[-\omega(x-2)^2\right], \tag{2}$$

where 100 is the maximum possible fecundity and $\omega > 0$ is a parameter.

a. Make a plot of $m_1(x)$ as a function of x. What can you say about the nature of selection acting on trait x? What does $\omega > 0$ correspond to biologically?

We assume that individuals produce newborns and then die. The next generation is formed through density-dependent survival of newborns so that the probability p_0 that a given offspring survives depends on the x expressed in the population at large:

$$p_0 = \frac{1}{m_1(x)}. \tag{3}$$

We wish to characterise the evolution of trait x. To do so, we consider the fate of a rare mutant expressing trait value y in a population otherwise fixed for x.

b. Compute the lifetime reproductive success of the mutant, $R_0(y, x)$, and check the lifetime reproductive success of a resident individual is equal to 1, i.e. that $R_0(x, x) = 1$.

c. Compute the selection gradient acting on trait x, and calculate the singular strategy x^*.