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 Leslie Matrix

a. Construct the Leslie matrix for this wild-boar population (recall that a Leslie matrix depends on **effective** fecundities, f_a).

b. 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). Plot the trajectories of the number of individuals in each class predicted by the matrix and comment it briefly (Hint: matrix product is achieved by the **%*%** operator in R).

c. Using eigen analysis (tip: use the **eigen()** function in R), work out the growth rate λ of the population, and its stable age distribution $\boldsymbol{u}$.

d. Compute R_0. What does it tell you about the fate of the population in the long run?

2 Individual based simulations

We provide an R program that allows to track the birth and fate of each individual in an age-structured population, i.e. that allows to perform individual-based simulations (https://lab-mullon.github.io/SAF). Download and familiarise yourself with this program.

a. Using the provided individual-based simulation program and the information given above, 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).

b. Plot the simulated population's size as a function of time along with the trajectory predicted from the Leslie matrix (from question 1b above). Do they match?

c. Plot the final age distribution of the simulated population and the one predicted by the Leslie matrix on the same graph (from question 1c above). Do they match?

3 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):

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

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

a. Modify the individual-based simulation program (from part 2) to incorporate this new assumption (hint: you have to add an argument to the 'DYN' function). 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 iterate it over a hundred years starting with $n_{1,0} = 1000$ individuals of age 1 to model changes in population size. How is population size predicted to vary? Does it match your simulation results (from 3a)?

c. Calculate lifetime reproductive success R_0 for each time step in the simulation and plot it over time. How does R_0 change with time and why?

4 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

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

$$p_0 = \frac{1/2}{m_1(x)}. \tag{3}$$

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^*.