

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

- Construct the Leslie matrix for this wild-boar population (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). 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).
- Using eigen analysis (tip: use the **eigen()** function in R), work out the growth rate λ of the population, and its stable age distribution u .
- 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.

- 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).
- 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?
- 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):

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

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

- 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?
- 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)?
- 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

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

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

- 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:

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

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^* .