

Population Projection Matrix Models in R

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Analysis with *POPBIO*

Here we will use the `library(popbio)` to analyse population projection models. *popbio* is an package that implements the equations from Caswell (2001), and Morris and Doak (2002) to study matrix populations models.

popbio also contains functions to calculate vital rates and construct projection matrices from raw census datas, as is typical of plant demography studies.

Firs load the library:

```
library(popbio)
```

Building a projection matrix

Once you have calculated the demographic rates of **survival**, **growth or transition rates**, and **fertility**, you can build a projection matrix.

A typical matrix in which there are three stages (e.g., seedling, juvenile, and adult), looks like this:

$$\mathbf{A} = \begin{bmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ a_{31} & a_{32} & a_{33} \end{bmatrix}$$

where the a represent transition probabilities. *The transition rates represent the movement of the **j_th column** stage to the **i_th row** stage P_{ij} .

In an organism where there are three pre-reproductive stages, and one reproductive stage, the projection matrix A may look like this:

$$\mathbf{A} = \begin{bmatrix} P_{11} & 0 & 0 & F_4 \\ P_{21} & P_{22} & P_{23} & 0 \\ 0 & P_{32} & P_{33} & 0 \\ 0 & 0 & P_{43} & P_{44} \end{bmatrix}$$

where P represent the transition probabilities between stages P_{ij} or within a stage P_{ii} . The element F is reserved for *reproduction*. A matrix entry of zero indicates that the transition does not occur.

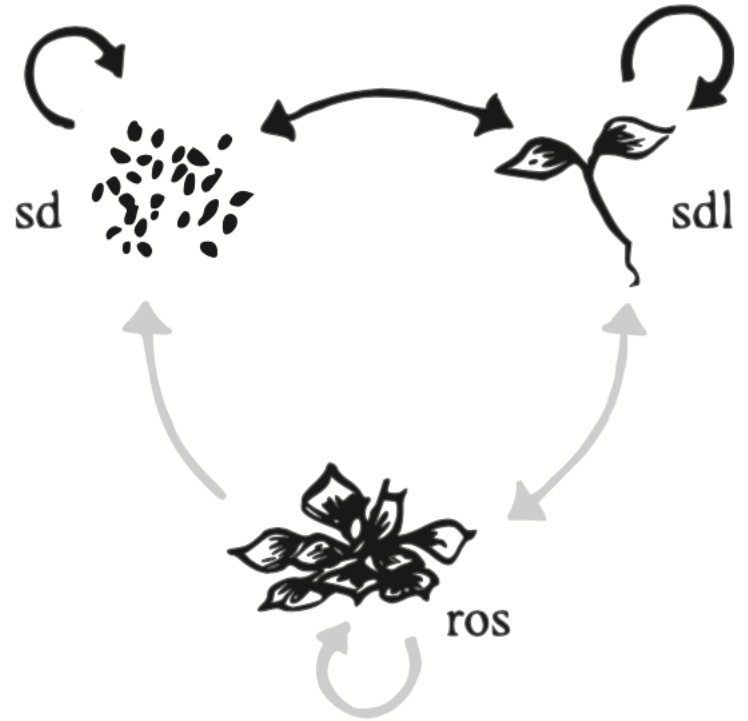
To build the matrix you need to combine the vital rates to generate each matrix element, where:

- s_j is the survival rate of class j
- f_j is the fertility rate for class j
- g_{ij} is the probability that an individual in class j in this census makes the transition to class i

An example with clonal *Mimulus*

Here we will use a recent example of estimating population growth rate in *Mimulus* populations reproducing both sexually and clonally. This study was conducted by Megan Peterson and colleagues:

Peterson ML, Kay KM, Angert AL (2016) The scale of local adaptation in *Mimulus guttatus*: comparing life history races, ecotypes, and populations. *New Phytologist*, 211, 345–356.



The general life cycle of *Mimulus* is shown here:

Figure. Life cycle graph of *Mimulus*. Grey arrows indicate transitions for annuals, and grey+black are transitions for perennials. From Peterson et al. (2016).

The vital rates for the life cycle graph are given below.

	$Seed_t$	$Seedling_t$	$Rosette_t$
$Seed_{t+1}$	$D(1 - G)$	$FOA(1 - G)$	$FOA(1 - G)$
$Seedling_{t+1}$	DG	$FOAG$	$FOAG$
$Rosette_{t+1}$	0	SR	SR

For a definition of the parameters, see Peterson et al. (2016).