**Monday February 10th: Matrix Population Models**

Today you will use existing matrix models for acai (*Euterpe precatoria*, from Beni department in Bolivia) and mahogany (*Swietenia macrophylla*, fromSanta Cruz department in Bolivia) to analyse population dynamics and simulate harvesting. You can use the script MatrixPopulationModels.R

After installing and loading packages, and reading the data, conduct the following steps. You can run the code and try to understand and interpret the output.

**Acai: *Euterpe precatoria***

**Step 1. Explore data**

* Have a look at the transition matrix (typing “A”) identify the three types of transitions: stasis, progression and reproduction.
* We can now get the values for stasis, progression and reproduction
* You can also check and read the Zuidema 2000 chapter with background information on how this matrix model was constructed.

**Step 2. Population projections**

* **Project** the population for 10 years. This is done using the function pop.projection. This function multiplies the matrix by the vector. The resulting object “n” contains population structures, population sizes and population changes during 10 years.
* The population is increasing during the first 10 years. We will now check whether the increase continues if we project over 150 years.
* You can see in the plot that the population is projected to decline. We can also plot the annual changes in the population.
* In this plot you can observe that the growth rate is declining at first, and then becomes stable. Get the population growth rate in the final year of simulation as follows:

**Step 3. Asymptotic pop growth and stable structure**

* When the population growth rate becomes stable, we call this the **asymptotic population growth rate** or **lambda** (****). This is a mathematical property of the transition matrix. It can be calculated lambda(A)
* You can observe that the difference between the final growth rate in the projection and lambda is very small. After 100 years of simulation, the population is growing at a stable growth rate.
* After many iterations, the population has also reached a stable size distribution. This means that the relative population structure does not change. So the % of individuals in each of the classes remains similar. We can show this by making stacked bar graphs of the relative population size for all 150 years.
* You can observe that the proportion of individuals in the categories is gradually becoming stable. The simulated population has reached the ‘**stable stage distribution**’. This is another mathematical property of the transition matrix, which we can get by this command n$stable.stage
* We can also compare the size distributions by looking at bar graphs. We make these for year 0, 10 years, 150 years and stable size distribution. You can see that the distribution of individuals in the stable stage distribution is very similar to that of the final year of the simulation.

**Step 4. Elasticity analysis**

* The asymptotic population growth rate () is a very important metric in population models. It can be used in evolutionary studies (to estimate fitness), in conservation (to know population growth of threatened species), for invasive species (to calculate invasion speed) and in studies on exploitation (to verify the sustainability of exploitation systems).
* So, we are interested to know how sensitive  is to changes in the values in the transition matrix.
* Elasticity analysis is the tool to do this. Calculate the elasticity values for all transitions in the matrix using the function elasticity()
* Check which of the transitions has the highest elasticity? And which one has the lowest? What does this mean?
* The sum of all elasticities is 1. You can check this (sum(E)). This implies that the value of the elasticity for a transition can be considered the contribution of that transition to population growth.
* We can sum elasticities per category to evaluate the contribution of size categories to population growth. Using the following code you can see which is the most important category.
* We can also compare the contributions of different types of transitions: stasis, progression and fecundity. Which of these three is most important?
* Finally, we can use matrix models to estimate the ages of size categories. In this example we calculate the generation time. So the average amount of years it takes an individual to produce offspring.

generation.time(A)

* The generation time depends on the transition values in the matrix and on the size of the matrix

**Mahogany/Mogno-do-Brasil: *Swietenia macrophylla***

**Step 5. Load data and check**

* Mahogany (*Swietenia macrophylla*) is a valuable and overexploited tropical timber species. Mahogany occurs throughout Latin America and is a CITES species. One way to help restoring exploited mahogany populations is by applying ‘silvicultural treatments’. These are activities in the forest that increase survival and growth of desired (so, economically valuable) tree species.
* Verwer et al. (2008) conducted a study on mahogany demography in a Bolivian logging concession where silvicultural treatments are applied. We will work with the Light Silviculture treatment.
* Please read relevant parts of the publication to understand what the authors did. Verwer and colleagues constructed matrices for Control (C; no logging) and for Light Silviculture (LS) treatments. We will implement the activity of felling trees in the LS matrix.
* Load the matrices and starting vector. Check what the matrices look like.
* Also conduct some basic analysis (lambda, elasticity) and compare the transitiona matrices with each other

**Step 6. Do logging projections**

* Remove 80% of trees that can be harvested (>70 cm DBH) from the population structure at year 0 (so before you start simulating the population). Then project the population for 20 years, assuming that LS applies to the first 9 years, and C to the rest of the time.
* To get an overview of the population development, we plot the population development
* Now, answer the question: What is the number of trees that can be logged at the end of the simulation? You can find the number of individuals for the last 11 years of simulation in the object "n10\_20 ".
* The answer is: with 80% harvest intensity and after 20 years, there are 7.8 trees available for logging; which is two third of what was harvested during the first harvest.
* Now reduce the logging intensity to 50% and evaluate whether this has an effect on the number of trees logged after 20 years. What is the number of trees that can be logged after 1 logging cycle of 20 years, with the reduced logging intensity?
* The answer: With 50% harvest intensity and after 20 years, there are 7.2 trees available for logging; which is 10% less than what was felled at the first logging event.

**Step 7. Compare logging scenarios**

* With 80% harvest intensity and after 30 years, there are 10.4 trees available for logging; which is 80% of what was harvested during the first harvest. So, with 50% harvest intensity and after 30 years, there are 8.7 trees available for logging; which is 111% of what was harvested during the first harvest.
* See the table produced with the R script

**Step 8. Search for extract matrix models from the Compadre database**

* A very large number of matrix models is currently available in two databases. The compadre database for plant species and the comadre database for animal species (see here: [www.compadre-db.org](https://www.compadre-db.org/)).
* In this step you can find code to download, search and extract information from these databases. And then conduct analyses on these matrices.

**Step 9. Density dependence for deer populations**

* This code is for a red deer population of red deer (Cervus elaphus) on the island of Rum in Scotland. The red deer population on this island has been monitored for several decades. In the early 1970s, culling (hunting) of red deer ceased, allowing the red deer population to grow. Red deer have a life span of about 13 years; females reproduce from the age of 2 years onwards. Coulson et al. (2005) reported on the development of red deer populations on Rum, and present information that can be used in a Leslie (i.e., age-based) matrix model.
* There are three classes: Y = yearling (so, aged 1); A = prime-aged adult female (aged 2); S = older (senior) adult females.
* You can use the code to implement density dependence of reproduction. Note that the effect of density dependence is estimated!

**Step 10. Stochastic simulations**

* Here is some code to analyse the stochastic dynamics of *Euterpe precatoria* palms using a transition model for a normal (N) and a dry (D) year.
* It calculates the final population size after stochastic simulations and the stochastic population growth rate.