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• Study of population growth and intrinsic growth rate

- We have several processes to find the population growth for a specific year. Some of them are as follows:
 - * Estimates derived by extrapolation of census results.
 - $\ast\,$ Ratio and correlation method.
 - * Geometric or logistic growth rate formula.
 - * Age-structure matrix model.

Now the question which arises is that why we not use any of the first three processes listed above for our cause? For answering this we first go through the first three processes in brief.

- Estimates derived by extrapolation of census results :

In this process extrapolation is used by means of arithmetic rates of increase. The simplest method of extrapolation is to compute the average annual number by which the population has increased from one census to the next. We then add an equal number for every year which has elapsed since the last census.

E.g. in Switzerland, 156,715 persons were enumerated in 1936, and 185,215 in 1946. The increase observed in the census interval of ten years was 28,500 persons, giving an average annual increase of 2,850. The estimate for 1950 was therefore, 185,215 plus four times 2,850, i.e., 196,615. In this process for better results the utilisation of the results of minimum two censuses is important.

- Ratio and correlation method :

In this method the population growth of a smaller area is closely related to that of the region in which the smaller area is situated.

$$\frac{Pf}{Pf'} = \frac{Pi}{Pi'} = k$$

Pf = population forecast for the area under study.

- Pf' = future population for the region.
- Pi = population at the area under study at the last census.
- Pi' = population of the region at the last census.

k = constant

- Geometric or logistic growth rate formula :

In this process we use a very well-known formula.

$$N(t+1) = N(t) + (b-d)N(t)$$

Where,

N(t) = number of individuals λ present in the population and t is a time interval of interest.

b = per capita birth rate and

d = per capita death rate for a population that is growing in discrete time.

- So it is clear that the first three processes are based on some assumptions.

- * They describe a population which does not have any age structure, gender structure
- * All individuals are reproductively active.
- * The growth rate is unaffected by the size of the population.

But, there is no creature in nature which does not violate one of these assumptions. So, the forth process comes handy.

In this process for modelling purposes we divide individuals into groups by either their age or age class.
 Although age is a continuous variable by this convention individuals are grouped or categorized into discrete time intervals.

E.g. the age class of 3 year olds consists of individuals that just had their third birth day plus individuals that are 3.5 years old or 3.8 years old.

Thus whether we are dealing with age classes or ages, individuals are grouped into discrete classes that are of equal duration. We do this for modelling purposes. Survival probabilities P(i) = the probability that an individual in age class (i) will survive to age class (i + 1) is also noted. **E.g.** let us assume the probability the individuals of age class 1 survive to age class 2 is P(1) = 0.3. This means 30% of the individuals in age class 1 will survive to be censured as age class 2.

We can compute the number of individuals of age class 2 at time (t + 1) as the number of individuals of age class 1 at time (t) multiplied by P(1). We can write the more general equation as

$$N_{i+1}(t+1) = P(i)N_i(t)$$

Where,

 $N_i(t)$ =number of individuals in class (i) at time (t)

This equation works for calculating the number of individuals at time (t+1) for each age class in the population except for the first, because individuals in the first age class arrives only through birth.

Here, we will assume a simple **birth pulse model**, in which when individuals give birth they enter a new age class. The birth rate is called **fecundity** or the average number of offspring born per unit time to an individual in female of a particular age. Obviously, individuals that are pre-reproductive or post-reproductive age have fecundities 0. Individuals if reproductive age typically have fecundities greater than 0.

Now, individuals must survive a long period of time (almost a full year until the birth pulse) before they have another opportunity to breed. Thus we have to discount the fecundity b(i) by the probability P(i). These adjusted estimates are called **fertilities** and it is given by

$$F_i = b(i)P(i)$$

Generally, the total number of individuals in age class 1 in year (t + 1) is simply the fertility rate of each age class multiplied by the number of individuals in that age class at time (t).

$$N_1(t+1) = \sum_{i=1}^{k} F_i N_i(t)$$

We assume that our population has four age classes. We can calculate the number of individuals in each age class at time (t + 1) given the number of individuals in each class at time (t):

$$N_1(t+1) = \sum_{i=1}^{4} F_i N_i(t)$$

$$N_i(t+1) = P(i-1)N_{i-1}(t) \text{ for } i=2,3,4$$

This system of linear equations can be written as

 $N_{t+1} = A.N_t$

Where,

$$N_t = \left[\begin{array}{c} N_1(t) \\ N_2(t) \\ N_3(t) \\ N_4(t) \end{array} \right]$$

and,

$$A = \begin{bmatrix} F_1 & F_2 & F_3 & F_4 \\ P(1) & 0 & 0 & 0 \\ 0 & P(2) & 0 & 0 \\ 0 & 0 & P(3) & 0 \end{bmatrix}$$

This matrix A is known as **Leslie matrix** and N_t is our population vector at time t. So, when we multiply these two matrix we get $N_t (t + 1)$.

We can represent the composition of our population as a column vector N(t), which is a matrix that consists of a single column. Our column will consist of the number of individuals in age classes 1,2,3 and 4, since we assumed that our population has 4 distinct age classes.

$$\mathbf{N}(\mathbf{t}) = \begin{bmatrix} \mathbf{w} \\ \mathbf{x} \\ \mathbf{y} \\ \mathbf{z} \end{bmatrix}$$

Now when Leslie matrix A multiplied by the population vector N(t), the result is another population vector which provides how many individuals are in age classes 1,2,3 and 4 in year (t + 1). The multiplication works like this:

$$\begin{pmatrix} a & b & c & d \\ e & f & g & h \\ i & j & k & l \\ m & n & o & p \end{pmatrix} \times \begin{pmatrix} w \\ x \\ y \\ z \end{pmatrix} = \begin{pmatrix} aw+bx+cy+dz \\ ew+fx+gy+hz \\ iw+jx+ky+lz \\ mw+nx+oy+pz \end{pmatrix}$$
(1)

This new population vector is also known as vector of abundance.

* Calculation of time specific growth rate (λ_t) :

The time specific growth rate (λ_t) can be computed as the total population at time (t+1) divided by at total population at time (t). So, it is defined as

$$\lambda_t = \frac{(aw+bx+cy+dz)+(ew+fx+gy+hz)+(iw+jx+ky+lz)+(mw+nx+oy+pz)}{w+x+y+z}$$

* Calculation of asymptotic/intrinsic growth rate (λ):

The Leslie matrix not only allows to calculate time specific growth rate, but also to evaluate how the composition of the population changes over-time. Multiplying the new vector of abundances by Leslie matrix we will get population size for yet another year. Continued multiplication of a vector of abundance by the Leslie matrix eventually produces a population with a **stable age distribution**. Practically, the population of a specific year is higher than previous year and increase with a decreasing rate. So this will form a monotonic decreasing sequence which is bounded below by 1. So, in this case the proportion of individuals in each age class remains constant over time. Time specific growth rate also remains stable. When λ_t converges to a constant value, this constant value is an estimate of λ . Technically, λ is called the **asymptotic growth rate** when the population converges to a stable age distribution.

Perron-Frobenius Theorem

For any Leslie Matrix M, there exists a real positive eigen value λ_1 i.e. a simple root of the characteristic equation. This eigen value which called Dominant eigen value is strictly greater in magnitude than any other eigen value. The associated eigen vector is real.

 λ took care of the asymptotic property. So, $\lambda = 1$ the population is stationary

 $\lambda \leq 1$ the population is increasing

 $\lambda \geq 1$ the population is decreasing The corresponding eigen vector is proportial to stable age distribution. After stable age distribution the population grows exponentially.

$$N(t) \lambda^t = exp(rt)$$

The Intrinsic growth rate defined as $r = ln\lambda$ for, $r \ge 0$ population is increasing $r \le 0$ population is decreasing

An example for demonstrating:

We are supplied the Leslie matrix corresponding to a population and the population vector where age is classified in 4 distinct age classes.

We can assume the age classes to be as follows:

- \cdot 0-14 yrs
- \cdot 15-29 yrs
- \cdot 30-44 yrs
- \cdot 45-59 yrs

We can also scale the given data of the population vector for easier computation. Thus, let after scaling we have the following data.

$$A = \begin{bmatrix} 0 & 1 & 1.5 & 0.2 \\ 0.8 & 0 & 0 & 0 \\ 0 & 0.5 & 0 & 0 \\ 0 & 0 & 0.25 & 0 \end{bmatrix}$$

and,

$$N_t = \begin{bmatrix} 45\\18\\11\\4 \end{bmatrix}$$

Predicting the population:

we use the formula stated to find the population of the next year.

$$N_{t+1} = A.N_t$$

Predicting the growth rate:

From the **Perron-Frobenius Theorem** stated before we will be calculating the absolute dominant eigen value by Power Method to find the asymptotic growth rate.

We will be writing the matrix in Python code as follows:

$$[[0,1,1.5,0.2], [0.8,0,0,0], [0,0.5,0,0], [0,0,0,0.25]]$$

The output gives us the dominant eigen value. Hence, we will be able to find the intrinsic growth rate also.

The python code for calculating the dominant eigen value by power method:

```
class power:
               l1 = [[0]]
         def matmult(self,m1,m2):
               i=j=k=0
               mm = []
         for i in range(0, len(m1)):
                row=[]
        for j in range(0, \text{len}(m2[0])):
                r=0
        for k in range(0, \text{len}(m1[i])):
          r = (m1[i][k]*m2[k][j])
             row.append(r)
            mm.append(row)
              return mm
           def norm2(self,mm):
              l = len(mm)
                 s=0
            for i in range(0,l):
            s = mm[i][0] * 2
             return s^{**}0.5
          def transpose(self,mm):
               mmt=[]
        for i in range(0, len(mm[0])):
                row = []
         for j in range(0, len(mm)):
           row.append(mm[j][i])
            mmt.append(row)
              return mmt
            def main(self,a,x):
           y = self.matmult(a,x)
          for i in range(0, len(y)):
        x[i][0]=y[i][0]/self.norm2(y)
l2=self.matmult(self.matmult(self.transpose(x),a),x)
           e=12[0][0]-self.11[0][0]
               self.l1=l2
           if e \ge 0.000000001:
             self.main(a,x)
                else:
             print(12[0][0])
```

Output: p=power() x = [[1], [1], [1], [1]]a = [[0, 1, 1.5, 0.2], [0.8, 0, 0, 0], [0, 0.5, 0, 0], [0, 0, 0, 0.25]] So, $log(1.0968356161493409) = 0.04 \ge 0$ Hence the population is increasing.

- References:

- $\ast\,$ "Mei-Qin-chen", Xiehang Li
- * "The use of matrices in certain population mathematics" (Biometrica 33:183-212) by P.H.Leslie
- * "Matrix population models", second edition Sinauer Associates, Inc. Sunderland