# INSTRUCTIONS for *Phython*:

1. Download the file **MPM.py** to your computer.
2. You need to have a life table in a .csv file, organized as follows: (see file LT3.csv as an example)
3. **First column**: time units, 1,2,3,…
4. **Next S columns**: number of individuals alive by the end of each interval for each one of the S stages. (Note: add males and females in every stage).
5. **Next column**: newborn production by the end of each interval.
6. **Next S columns**: number of individuals dead by the end of each interval for each one of the S stages.
7. Make sure this .csv file is in the same directory as the file MPM.py
8. Inside the program MPM.py, the first lines are the parameters definitions:

# \*\*\*\*\*\*\*\*\* Parameters \*\*\*\*\*\*\*\*\*\*

fname = "LT3.csv"

nsim = 5000

c=0

# alpha = 0.1; Z=1.6449;

alpha = 0.05; Z=1.96;

# alpha=0.01; Z=2.5758

# \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

1. **fname** is the name of the csv file
2. **nsim** is the number of simulations used in the boostrap method to calculate confidence intervals. 5,000 is OK.
3. **c** defines where individuals are born in each interval: **c** = 0 is at the beginning, **c** = 1 is at the end. A value **c** = 0 is OK. (See Hernandez‐Suarez, C. M. 2011. “A note on the generation time”. Oikos, 120(1), 159., doi: 10.1111/j.1600-0706.2010.18789.x)
4. Use the alpha that you need. Comment the lines you don’t need using a ‘#’ at the beginning of the line.
5. Run the program as:

runfile(‘MPM.py’)