INSTRUCTIONS for *Phython*:

a) Download the file **MPM.py** to your computer.

b) You need to have a life table in a .csv file, organized as follows: (see file LT3.csv as an example)

c) **First column**: time units, 1,2,3,…

d) **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).

e) **Next column**: newborn production by the end of each interval.

f) **Next S columns**: number of individuals dead by the end of each interval for each one of the S stages.

g) Make sure this .csv file is in the same directory as the file MPM.py

h) 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
# ********************************
```

i) **fname** is the name of the csv file

j) **nsim** is the number of simulations used in the boostrap method to calculate confidence intervals. 5,000 is OK.

k) **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)

l) Use the alpha that you need. Comment the lines you don't need using a '#' at the beginning of the line.

m) Run the program as:

```
runfile('MPM.py')
```