

## INSTRUCTIONS for *R*:

- a) Download the file **MPM.R** 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.R
- h) Install package "resample " if necessary.
- i) Inside the program MPM.R, the first lines are the parameters definitions:

```
#### PARAMETERS ####
nsim = 5000
c = 0
#alpha = 0.1
#Z = 1.6449
alpha = 0.05
Z=1.96
#alpha = 0.01
#Z = 2.5758
#####
```

- j) **nsim** is the number of simulations used in the bootstrap 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.

You can practice with the LT3.csv file, the data set provided.