INSTRUCTIONS for *Mathematica*:

a) Download the file **MPM script.wls** 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 script.wls**

h) Open *Mathematica*.

i) Open the file **MPM script.wls**

j) Inside the file **MPM script.wls**, the first lines are the parameters definitions:

```
fname = "LT3.csv"
nsim=5000; (* 5,000 simulations is usually enough *)
c=0;   (* c is usually set to zero *)


(* Select the alpha value for CI (default is 0.05) *)


(* alpha = 0.1; Z=1.6449; *)
alpha = 0.05; Z=1.96;
(* alpha=0.01; Z=2.5758 *)
```

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

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

m) **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)

n) Use the alpha that you need. Comment the lines you don't need using a '(*' at the beginning and '*)' at the end of the line.

o) In the upper right corner of the window, click on "Run All Code"

Note: the program will run for less two minutes. To ensure everything is OK, you may start with *nsim* = 100. If everything works, get back to *nsim* = 5000.