# INSTRUCTIONS for *Matlab*:

1. Download the file **MPM.m** 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.m
8. Inside the program MPM.m, 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

% \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

1. **nsim** is the number of simulations used in the boostrap method to calculate confidence intervals. 5,000 is OK.
2. **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)
3. Use the alpha that you need. Comment the lines you don’t need using a ‘%’ at the beginning of the line.
4. Run the program as:

>>MPM(‘fname.csv’)

You can practice with MPM(‘LT3.csv’), the data set provided.