# INSTRUCTIONS TO USE LHT\_CI.r

The file **LHT\_CI.r** is the R-studio program that performs the calculations.

1. Data should be in a .csv file with only three columns, for instance:

|  |  |  |
| --- | --- | --- |
| **t** | **n** | **h** |
| 1 | 50 | 0 |
| 2 | 50 | 0 |
| 3 | 50 | 0 |
| 4 | 49 | 0 |
| 5 | 49 | 0 |
| 6 | 49 | 0 |
| 7 | 49 | 0 |
| 8 | 48 | 0 |
| 9 | 46 | 0 |
| 10 | 44 | 28 |
| 11 | 44 | 28 |
| 12 | 44 | 10 |
| 13 | 43 | 118 |
| 14 | 41 | 111 |

The **first column** are the units of time. The **second column** contains number of individuals alive at that unit of time. The **third column** contains offspring production in that unit of time.

1. Inside the code, modify the alpha required and change the file name:

*alpha <- 0.05*  # 1-alpha is the confidence level of CI,

*fnam <- "Data.csv"* # Change file name.

1. Use one of these two lines and comment the other:

*dir\_path <- getwd() # use this if data is in current directory.*

*#file <- file.path(dir\_path, fnam). # ....or change directory here.*

1. Run the program, an example output is:

> # Results:

> cat("Initial number of individuals N :", N) ----(Initial number of individuals)

Initial number of individuals N : 50

> cat("Offspring size K :", K) ) ----(Total offspring)

> cat("R0 :", R0)

R0 : 48.6 ----(R0, the basic reproductive number)

Offspring size K : 2430

> cat("Longevity :",CI\_L)

Longevity : 28.34 302.064 23.5226 33.157 ---- (mean variance and CI for longevity)

> cat("Generation time :",CI\_mu)

Generation time : 26.884 151.773 26.394 27.374 ----(mean variance and CI for generation time)

> cat("r :", CI\_r)

r : 0.2020956 0.1988703 0.2055041 -----(mean and CI for r)

> cat("lambda:", CI\_lam)

lambda: 1.223965 1.220024 1.228144 -----(mean and CI for lambda)

New data saved to: test\_data\_added.csv -----(Name of file with table with columns added)