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.

2. 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.

3. 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.

4. 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)
```