

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 <- "test_data.csv" # Change file name.  
                        # (Put data file and R program in same folder)
```

3. 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, the basic reproductive number)
R0 : 48.6
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)
```