

Semente = 191

m = 900

$\lambda = 0.58$

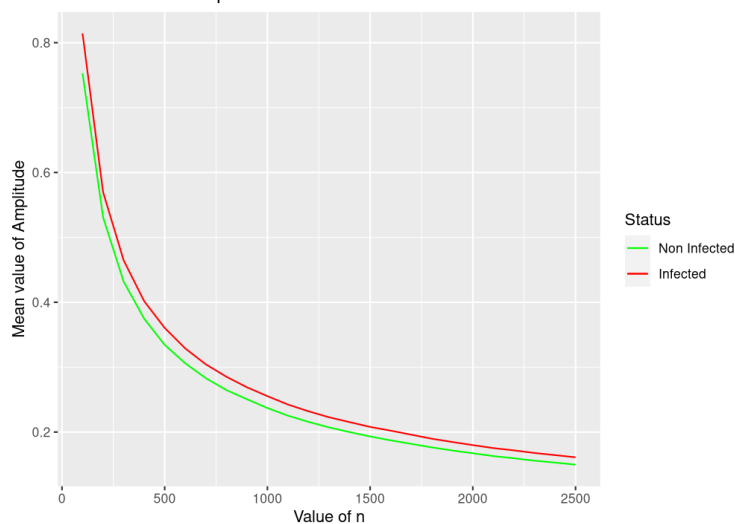
$\lambda_c = 0.38$

$\epsilon = 0.1$

$(1-\alpha) = 0.97$

```
1 library(ggplot2)
2 library("rnorm")
3
4 set.seed(191)
5
6 lambda1 <- 0.58
7 lambda2 <- 0.38
8 confidence <- 0.97
9 m <- 900
10 perc <- 0.1
11 # tamanho de amostra
12 # CI = confidence * (standard deviation/sqrt(n))
13 CIsale <- function(vectore)
14 {
15   len <- length(vectore)
16   sd_vec <- sd(vectore)
17   value <- qt((confidence + 1)/2, df = n - 1)
18   return (value * sd_vec/sqrt(len)*2)
19 }
20
21 index <- numeric()
22 values_non_infected <- numeric()
23 values_infected <- numeric()
24
25 for (n in seq(from = 100 , to = 2500, by =100))
26 {
27   num_inf = n * perc
28   amplit_infected <- 0
29   amplit_non_infected <- 0
30   for (i in 1:n)
31   {
32     non_infected <- rexp(n,lambda1)
33     infected <- rexp(num_inf,lambda2)
34     infected <- c(infected, non_infected[(num_inf+1):n])
35
36     CI_non_infected <- CIsale(non_infected)
37     CI_infected <- CIsale(infected)
38     amplit_infected <- amplit_infected + CI_infected
39     amplit_non_infected <- amplit_non_infected + CI_non_infected
40
41     index <- append(index,n)
42     amplit_non_infected <- amplit_non_infected/n
43     amplit_infected <- amplit_infected/n
44
45     values_non_infected <- append(values_non_infected,amplit_non_infected)
46     values_infected <- append(values_infected,amplit_infected)
47   }
48 }
49
50 table <- cbind(index, values_non_infected, values_infected)
51
52 df <- data.frame(table)
53
54 ggplot(df, aes(x=index)) +
55   geom_line(aes(y = values_non_infected, color = "Non Infected")) +
56   geom_line(aes(y = values_infected, color = "Infected")) +
57   scale_color_manual(name = "Status", values = c("Non Infected" = "green", "Infected" = "red")) +
58   labs(title = "Mean value of Amplitude from n = 100 to n = 2500 of infected and non-infected", x = "Value of n", y = "Mean value of Amplitude")
59
60
61
62
63
64
```

Mean value of Amplitude from n = 100 to n = 2500 of infected and non-infected



Pela a observação do gráfico podemos notar que para qualquer valor de n, a amplitude média de contaminado é sempre superior à de não contaminado. Ambos os valores diminuem para n maiores, isto é a amplitude vai sendo cada vez menor porque existem as amostras a serem criadas têm tamanho maior.