Lab 02

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library(help='datasets')

#Growth of Loblolly pine trees- dataset  
p=Loblolly  
p

## height age Seed  
## 1 4.51 3 301  
## 15 10.89 5 301  
## 29 28.72 10 301  
## 43 41.74 15 301  
## 57 52.70 20 301  
## 71 60.92 25 301  
## 2 4.55 3 303  
## 16 10.92 5 303  
## 30 29.07 10 303  
## 44 42.83 15 303  
## 58 53.88 20 303  
## 72 63.39 25 303  
## 3 4.79 3 305  
## 17 11.37 5 305  
## 31 30.21 10 305  
## 45 44.40 15 305  
## 59 55.82 20 305  
## 73 64.10 25 305  
## 4 3.91 3 307  
## 18 9.48 5 307  
## 32 25.66 10 307  
## 46 39.07 15 307  
## 60 50.78 20 307  
## 74 59.07 25 307  
## 5 4.81 3 309  
## 19 11.20 5 309  
## 33 28.66 10 309  
## 47 41.66 15 309  
## 61 53.31 20 309  
## 75 63.05 25 309  
## 6 3.88 3 311  
## 20 9.40 5 311  
## 34 25.99 10 311  
## 48 39.55 15 311  
## 62 51.46 20 311  
## 76 59.64 25 311  
## 7 4.32 3 315  
## 21 10.43 5 315  
## 35 27.16 10 315  
## 49 40.85 15 315  
## 63 51.33 20 315  
## 77 60.07 25 315  
## 8 4.57 3 319  
## 22 10.57 5 319  
## 36 27.90 10 319  
## 50 41.13 15 319  
## 64 52.43 20 319  
## 78 60.69 25 319  
## 9 3.77 3 321  
## 23 9.03 5 321  
## 37 25.45 10 321  
## 51 38.98 15 321  
## 65 49.76 20 321  
## 79 60.28 25 321  
## 10 4.33 3 323  
## 24 10.79 5 323  
## 38 28.97 10 323  
## 52 42.44 15 323  
## 66 53.17 20 323  
## 80 61.62 25 323  
## 11 4.38 3 325  
## 25 10.48 5 325  
## 39 27.93 10 325  
## 53 40.20 15 325  
## 67 50.06 20 325  
## 81 58.49 25 325  
## 12 4.12 3 327  
## 26 9.92 5 327  
## 40 26.54 10 327  
## 54 37.82 15 327  
## 68 48.43 20 327  
## 82 56.81 25 327  
## 13 3.93 3 329  
## 27 9.34 5 329  
## 41 26.08 10 329  
## 55 37.79 15 329  
## 69 48.31 20 329  
## 83 56.43 25 329  
## 14 3.46 3 331  
## 28 9.05 5 331  
## 42 25.85 10 331  
## 56 39.15 15 331  
## 70 49.12 20 331  
## 84 59.49 25 331

#dimension of the dataset  
dim(p)

## [1] 84 3

#first 6 rows  
head(p)

## height age Seed  
## 1 4.51 3 301  
## 15 10.89 5 301  
## 29 28.72 10 301  
## 43 41.74 15 301  
## 57 52.70 20 301  
## 71 60.92 25 301

#last 6 rows  
tail(p)

## height age Seed  
## 14 3.46 3 331  
## 28 9.05 5 331  
## 42 25.85 10 331  
## 56 39.15 15 331  
## 70 49.12 20 331  
## 84 59.49 25 331

# population- Height of the pine trees  
target\_var=Loblolly$height  
target\_var

## [1] 4.51 10.89 28.72 41.74 52.70 60.92 4.55 10.92 29.07 42.83 53.88 63.39  
## [13] 4.79 11.37 30.21 44.40 55.82 64.10 3.91 9.48 25.66 39.07 50.78 59.07  
## [25] 4.81 11.20 28.66 41.66 53.31 63.05 3.88 9.40 25.99 39.55 51.46 59.64  
## [37] 4.32 10.43 27.16 40.85 51.33 60.07 4.57 10.57 27.90 41.13 52.43 60.69  
## [49] 3.77 9.03 25.45 38.98 49.76 60.28 4.33 10.79 28.97 42.44 53.17 61.62  
## [61] 4.38 10.48 27.93 40.20 50.06 58.49 4.12 9.92 26.54 37.82 48.43 56.81  
## [73] 3.93 9.34 26.08 37.79 48.31 56.43 3.46 9.05 25.85 39.15 49.12 59.49

#Mean of the population  
mean(target\_var)

## [1] 32.3644

#standard deviation of the population  
 sd(target\_var)

## [1] 20.6736

samplesize=10

samp=sample(target\_var,35,replace=FALSE)  
samp

## [1] 63.05 26.54 53.88 25.85 4.38 27.93 44.40 4.51 27.90 10.89 56.81 30.21  
## [13] 3.88 25.45 4.12 52.43 11.37 10.57 40.20 58.49 52.70 28.97 51.33 60.28  
## [25] 40.85 48.43 3.93 41.13 4.32 41.66 55.82 56.43 4.33 25.66 29.07

##TESTING OF HYPOTHESIS

TWO-TAILED H0: mean=40 vs H1:mean!=40

library(BSDA)

## Warning: package 'BSDA' was built under R version 4.2.3

## Loading required package: lattice

##   
## Attaching package: 'BSDA'

## The following object is masked from 'package:datasets':  
##   
##

z.test(x=samp,alternative="two.sided",mu=40,sigma.x=sd(target\_var),conf.level=0.95)

##   
## One-sample z-Test  
##   
## data: samp  
## z = -2.2258, p-value = 0.02603  
## alternative hypothesis: true mean is not equal to 40  
## 95 percent confidence interval:  
## 25.37295 39.07105  
## sample estimates:  
## mean of x   
## 32.222

#INTERPRETATION : The p-value is <0.05 which implies that we reject the null hypothesis,i.e.,that population mean is 40.

## RIGHT TAILED TEST

H0:mean=35 vs H1:mean>35

z.test(x=samp,alternative="greater",mu=35,sigma.x=sd(target\_var),conf.level=0.95)

##   
## One-sample z-Test  
##   
## data: samp  
## z = -0.79497, p-value = 0.7867  
## alternative hypothesis: true mean is greater than 35  
## 95 percent confidence interval:  
## 26.4741 NA  
## sample estimates:  
## mean of x   
## 32.222

#INTERPRETATION : Since the p-value is greater than 0.05 we accept the null hypothesis,that is, the population mean will be 35.Also the p-value states that the value of the test statistic under H0 can be as extreme as the value of the test statistic calculated using the sample.

## LEFT TAILED

H0:mean=22 H1:mean<22

z.test(x=samp,alternative="less",mu=22,sigma.x=sd(target\_var),conf.level=0.95)

##   
## One-sample z-Test  
##   
## data: samp  
## z = 2.9252, p-value = 0.9983  
## alternative hypothesis: true mean is less than 22  
## 95 percent confidence interval:  
## NA 37.9699  
## sample estimates:  
## mean of x   
## 32.222

#INTERPRETATION:Since the p-value is greater than 0.05 we accept the null hypothesis,that is, the population mean will be 22.Also the p-value states that the value of the test statistic under H0 can be as extreme as the value of the test statistic calculated using the sample.