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Lab 7

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Q1: The sample size n = 123.The R code I used is:

gentoos <- subset(penguins, penguins$species == "Gentoo")

gentoos <- subset(gentoos, gentoos$bill\_length\_mm != "NA")

length(gentoos$bill\_length\_mm)

Q2: The sample standard deviation is 3.081857. The code I used is:

sd(gentoos$bill\_length\_mm)

Q3: The critical t-values are 1.657439 and - 1.657439. the R code I used is:

df <-length(gentoos$bill\_length\_mm) - 1

qt(0.05, df, lower.tail = FALSE)

Q4: The sample standard error is 0.2778817. The R code I used is:

sse\_mean(gentoos$bill\_length\_mm)

Q5:The CI is intervals are 48.05497 and 46.95478. The R code I used is:

xbar <- mean(gentoos$bill\_length\_mm)

gen2sse <- sse\_mean(gentoos$bill\_length\_mm)

tcrit <-qt(0.05/2, df, lower.tail = FALSE)

CI

Q6: The CI is 48.05497 and 46.95478

Q7: The code I used to call the boot () function is:

require(boot)

boot\_mean <- function(x,i)

{

return(mean(X[i],na.rm = TRUE))

}

Q8:The R code I used to calculate the quantiles is:

# numeric() creates an vector of length m with all values initialized to zero

result = numeric(m)

head(result)

m = 10000

# numeric() creates an vector of length m with all values initialized to zero

result = numeric(m)

head(result)

mean(result)

quantile(result,c(0.025,0.975))

Q9: arefaction\_sampler = function(input\_dat, n\_iterations)

{

n = nrow(moth\_dat) #number of rows or sample observations

m = 100 #number of bootstrap iterations

moth\_result = matrix(

nrow = m,

ncol = n)

# The outer loop: runs once for each bootstrap iteration. index variable is i

for(i in 1:m)

{

# The inner loop: simulates increasing sampling intensity

# Sampling intensity ranges from 1 site to the complete count of sites (24)

# index variable is j

for(j in 1:n)

{

# sample the input data row indices, with replacement

rows\_j = sample(n, size = j, replace=TRUE)

# Creates a new data matrix

t1 = moth\_dat[rows\_j, ]

# Calculates the column sums

t2 = apply(t1, 2, sum)

# Counts the number of columns in which any moths were observed

moth\_result[i, j] = sum(t2 > 0)

}

Q10:Finding what to define outside and inside the function.

Q11:

matplot(

rare,

type='l',

xlab='Number of sampling plots',

ylab='Species richness',

main='Rarefaction Curve')

legend(

'bottomright',

legend=c('mean','2.5%','97.5%'),

lty=c(1,2,3),col=c(1,2,3), inset=c(.1,.1))

Chart

Description automatically generatedQ12:

Q13: I should visit about 9 sites because that’s where the mean starts to plateau.