BACS-hw4.R

2022-04-12

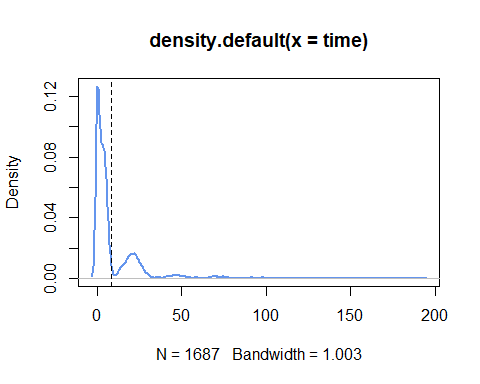
#Question 1  
#a  
pnorm(-3.7)

## [1] 0.0001077997

#b  
pnorm(-3.7)\*2500000

## [1] 269.4993

#Question 2  
#a  
setwd("C:/Users/eason/Desktop/清大 BACS/資料/")  
verizon <- read.csv("verizon.csv")  
time <- verizon$Time  
  
#1  
#Density Plot  
plot(density(time), lwd=2, col="cornflowerblue")  
abline(v=mean(time), lty="dashed")

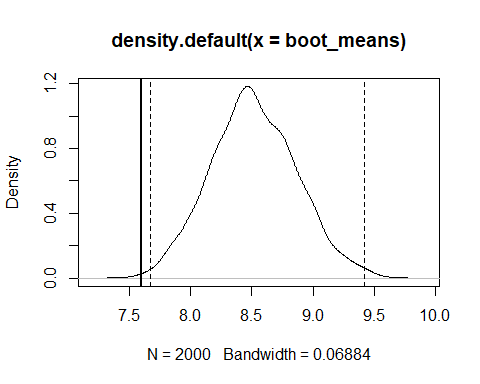


#2  
Hnull: The population mean is 7.6  
Halt: The population mean is significantly greater than or less than 7.6

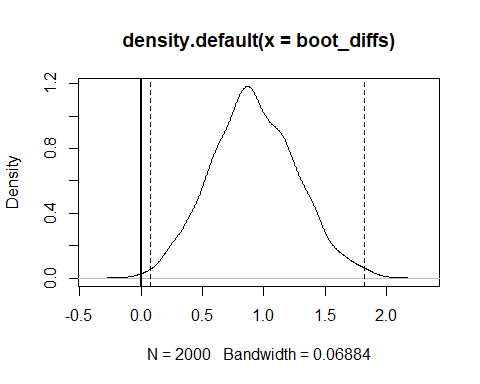
#The hypothesis  
hyp\_mean <- 7.6  
  
#Sample descriptive statistics  
sample\_n <- length(time)  
sample\_mean <- mean(time)  
sample\_sd <- sd(time)  
sample\_se <- sd(time)/sqrt(length(time))  
  
#3 就是這裡會有點不懂(不過就假設有一個t分布)  
#Confidence Interval  
quants\_99\_2sided <- qt(c(0.005, 0.995), sample\_n - 1)  
sample\_mean + quants\_99\_2sided \* sample\_se

## [1] 7.593524 9.450495

#4 想問t分布跟原本hyp\_mean的圖形會長一樣嗎  
t\_value <- (mean(time)-hyp\_mean) / sample\_se  
p\_value <- pt(t\_value, sample\_n - 1, lower.tail = FALSE)  
  
#5  
Classical hypothesis testing(t-value, p-value) seems to relate to the Null t-distribution  
  
#6  
The hypothesis cannot be rejected at 99% CI(two-tailed), but we should probably collect more data  
  
#b 下面這個解把三種合起來 學起來  
sample\_boot <- function(sample0, hyp\_mean) {  
 resample <- sample(sample0, replace = TRUE)  
 resample\_se <- sd(resample) / sqrt(length(resample))  
   
 boot\_mean <- mean(resample)  
 boot\_diff <- mean(resample) - hyp\_mean  
 boot\_t <- (mean(resample) - hyp\_mean) / resample\_se  
 c(boot\_mean, boot\_diff, boot\_t)  
}  
set.seed(42)  
boot\_stats <- replicate(2000, sample\_boot(time, hyp\_mean))  
  
#1 Bootstrapped means  
boot\_means <- boot\_stats[1,]  
q\_means <- quantile(boot\_means, probs = c(0.005, 0.995))  
plot(density(boot\_means))  
abline(v=hyp\_mean, lwd=2)  
abline(v=q\_means, lty="dashed")



#2 Bootstrapped differences  
boot\_diffs <- boot\_stats[2,]  
q\_diffs <- quantile(boot\_diffs, probs = c(0.005, 0.995))  
plot(density(boot\_diffs))  
abline(v=0, lwd=2)  
abline(v=q\_diffs, lty="dashed")



#3 Bootstrapped t-statistics  
boot\_t\_vals <- boot\_stats[3,]  
q\_boots <- quantile(boot\_t\_vals, probs = c(0.005, 0.995))  
plot(density(boot\_t\_vals))  
abline(v=0, lwd=2)  
abline(v=q\_boots, lty="dashed")

