```r
myData <- read.table("Mean20.txt", header=T)

# QUESTION 1

# Programming.  Verify the input data before doing the computation!

secondMax <- function(x) {
 # check the arguments
 if (!is.vector(x)) {
  return("not a vector!")}
 if (length(x) < 1) {
  return("vector length must be > 1!")}
 x <- x[!is.na(x)] # Remove the NAs
 x <- x[- which(x==max(x))]
 return(max(x))
}

secondMax(time)
secondMax(c("aa", "bb", "cc", "dd"))
secondMax(c(1,2,"dog"))

# QUESTION 2

mySummary <- function(x, na.rm = T) {
 if (!is.numeric(x)) {
  return("not a numeric vector!")}
 if (na.rm) {
  insa <- which(is.na(x))
  if (length(insa) > 0) {
   x <- x[-insa]
  }
 }
 return(c(mean=mean(x), median=median(x), sd=sd(x), min=min(x), max=max(x)))
}

mySummary(time)
mySummary(c("aa", "bb", "cc", "dd"))

# QUESTION 3

results <- numeric(20) # Put here 20 p-values from t.test()
biglist <- numeric(0)

for (i in 1:20) {
 val <- rnorm(20, mean = 2, sd = 1.5) # 2 values from a Gaussian with mean = 2, stdev = 1.5
 test <- t.test(val, mu = 1.5, alternative = "two.sided")
 results[i] <- test$p.value
 biglist <- c(biglist,val) # Put all samples in biglist
}

results # the p-values

percentage <- 100*results # maybe it's easier to read the p-value as a percentage
percentage

median(percentage)

percentage[percentage < 5]
sum(percentage < 5)

# Let's perform t.test() over 400 observations
test.biglist <- t.test(biglist, mu = 1.5, alternative = "two.sided")
# The (percentage) evidence supporting the null hyp (mu = 1.5) is:
test.biglist$p.value*100
# So using this big sample we are able to reject the null hypothesis
```