code.R

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question1 <- function(){  
 ##Simple data exploratory  
 library(datasets)  
   
 d<- ToothGrowth  
   
 library(ggplot2)  
   
 g <- qplot(dose,len,data=d, facets=supp~.,geom = c("point","smooth"),color=supp)  
 g + xlab("Tooth length") + ylab("Dose level of Vitamine C")  
   
 g  
   
}  
  
  
  
analyse\_dose <- function(){  
 library(datasets)  
 d<- ToothGrowth  
   
 split\_set <- split(d,as.factor(d$supp))  
   
 oj <- split\_set$OJ  
   
 vc <- split\_set$VC  
   
 oj\_len <- oj$len  
 vc\_len <- vc$len  
   
 n1 <- length(oj\_len)  
 n2 <- length(vc\_len)  
   
 m1 <- mean(oj\_len)  
 m2 <- mean(vc\_len)  
   
 sd1 <- sd(oj\_len)  
 sd2 <- sd(vc\_len)  
   
 df <- (sd1^2/n1 + sd2^2/n2)^2/((sd1^4/n1^2)/(n1-1) + (sd2^4/n2^2)/(n2-1))  
   
 intvall <- (m1-m2) + c(-1,1)\*qt(0.975,df)\*(sd1^2/n1 + sd2^2/n2)^0.5  
 intvall  
   
}  
  
##Project 1  
  
simulation2 <- function(){  
 set.seed(5)  
 lambda <- 0.2  
 n <- 40  
 total <- 1000  
   
 ##Simulate  
 simulated <- replicate(total,rexp(n, lambda))  
   
 ##Calculate the mean of 40  
 simulated\_means <- apply(simulated, 2, mean)  
   
 ##Get the experimental mean  
 experimental\_mean <- mean(simulated\_means)  
 var\_exp <- var(simulated\_means)  
 st1 <- paste('Sample variance =',var\_exp,sep = ' ')  
   
 print(st1)  
   
   
}  
  
simulation3 <- function(){  
 set.seed(5)  
 lambda <- 0.2  
 n <- 40  
 total <- 1000  
   
 ##Simulate  
 simulated <- replicate(total,rexp(n, lambda))  
   
 ##Calculate the mean of 40  
 simulated\_means <- apply(simulated, 2, mean)  
   
 ##Draw the histogram  
 hist(as.numeric(simulated\_means),breaks=50,main="1000 runs of 40 exponential distributions",xlab="mean of exponential distribution")  
 mean\_sim <- mean(simulated\_means)  
   
 ##Add the mean  
 abline(v=mean\_sim, col="red", lwd=4, lty=20)  
   
}