```
set.seed(123)
#problem 1
N = 1000
Xtilde = matrix(rnorm(N*K, 0, 1), N, K)
X1=Xtilde[,1]
X2=Xtilde[,2]+X1
X3=Xtilde[,3]+X2
X4=Xtilde[,4]+X3
X5=Xtilde[,5]+X4
X=matrix(c(X1, X2, X3, X4, X5), N, 5)
E = apply(X, 2, mean)
print(E)
V = var(X)
print(V)
#ii
first funct <-function(N,B, X){
  x=X[1:N,]
  beta 0 = rep(1,5)
  beta_matrix = matrix(0, B, K)
  t1 <- rep(0, B)
  t2 <- rep(0, B)
  hat_s1 <- rep(0, B)
  hat_s2 <- rep(0, B)
  for(b in 1:B) {
     #create error
     e b <- rnorm(N,0, sqrt(2))
     y_b <- x %*% beta_0 + e_b
     #calc beta
     \label{eq:beta_b} \texttt{beta_b} <- \ \texttt{solve} \, (\, (\texttt{t} \, (\texttt{x}) \, \$^* \$ \texttt{x}) \, ) \, \$^* \$ \texttt{t} \, (\texttt{x}) \, \$^* \$ \texttt{y\_b}
     beta_matrix[b,] <- beta_b</pre>
     #calc residuals
     u_b <- y_b - x%*%beta_b
     hat\_s1[b] <- 1/N*sum(u\_b^2)
     hat_s2[b] <- 1/(N-K)*sum(u b^2)
    t1[b] <- (beta_b[1]-beta_0[1])/sqrt(hat_s1[b]*solve(t(x)%*%x)[1,1])
t2[b] <- (beta_b[1]-beta_0[1])/sqrt(hat_s2[b]*solve(t(x)%*%x)[1,1])
  return(list(betas=beta_matrix, hat_s1=hat_s1, hat_s2=hat_s2, t1=t1, t2=t2))
#iii
N = c(10, 20, 100, 1000)
B=1000
#storing results
s1_means <- rep(0,length(N))
s2_means <- rep(0, length(N))
\#runs the function for each N value
for(i in 1:length(N)){
  reg <- first_funct(N[i], B, X)
s1_means[i] <- mean(reg$hat_s1) #stores means
s2_means[i] <- mean(reg$hat_s2)
  #stores t stats
  t1 stats[,i] <- reg$t1
  t2_stats[,i] <- reg$t2
var(reg$betas)
2*solve(t(X)%*%X)
print(s1_means)
print(s2_means)
#generates the norm
Z = rnorm(1000)
m = mean(Z)
for(i in 1:length(N)){
  hist(tl_stats[,i], prob=TRUE,xlab= "tl", main = "tl dist against std normal") #plots vector of tl stats
  curve(dnorm(x,mean=m, sd=sd(Z)), col="blue", lwd=2, add=TRUE, yaxt="n") #puts mean curve
hist(t2_stats[,i], prob=TRUE,xlab= "t2", main = "t2 dist against std normal")
curve(dnorm(x,mean=m, sd=sd(Z)), col="blue", lwd=2, add=TRUE, yaxt="n")
second_funct <-function(N,B, X){
  rejections = 0
  x=X[1:N,]
  beta_0 = rep(1,5)
beta_matrix = matrix(0, B, K)
  t1 <- rep(0, B)
  t2 <- rep(0, B)
hat_s1 <- rep(0, B)
  hat_s2 <- rep(0, B)
  for(b in 1:B) {
     #create error
```

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e_b <- rnorm(N,0, sqrt(2))</pre>
      y_b <- x %*% beta_0 + e_b
      #calc beta
      beta_b <- solve((t(x)%*%x))%*%t(x)%*%y_b
     beta_matrix[b,] <- beta_b</pre>
      #calc residuals
     u_b <- y_b - x%*%beta_b
      #calc var
      hat_s1[b] <- 1/N*sum(u_b^2)
     hat_s2[b] <-1/(N-K)*sum(u_b^2)
      #tstats
     t1[b] \leftarrow (beta_b[1]-0)/sqrt(hat_s1[b]*solve(t(x)%*%x)[1,1])
     t2[b] \leftarrow (beta_b[1]-0)/sqrt(hat_s2[b]*solve(t(x)%*%x)[1,1])
   #calcualtes percentage of rejections if abs of tvalue exceed barrier
  rejections = rejections + length(t1[abs(t1) > 1.96])
rejections = rejections + length(t2[abs(t2) > 1.96])
percent_rejections = rejections/(2*B)
   return(percent_rejections = percent_rejections)
for(i in 1:length(N)){
   reg <- second_funct(N[i], B, X)</pre>
  print (reg)
#problem 2
install.packages('foreign')
library(foreign)
setwd('C:/Users/Ethan/Desktop/Columbia/Senior_Fall/Advanced_Econometrics/pset_1')
data = read.dta('TeachingRatings.dta')
v=data$course eval
X=cbind(1, data$beauty, data$age)
colnames(X) = c('intercept', 'beauty', 'age')
plot(X[,'beauty'], y)
beta_hat <- solve(t(X)%*%X)%*%t(X)%*%y #computes beta_hat using formula
residual <- y - X%*%beta hat
mean(residual)
var(residual)
sd(residual)
\#makes residual maker and finds residuals
 \begin{tabular}{ll} M <- & diag(length(y))-X - $^*$ solve(t(X) - $^*$X) - $^*$ (X) residual_2 <- & M - $^*$ y \\ \end{tabular} 
#reports values of residuals
mean(residual_2)
sd(residual 2)
X1 = rep(1, length(X[,'beauty']))
XI = lep(I, length(X[, beauty ]))
X0 = cbind(X[,'beauty'], X[,'age'])
I = diag(length(y))
M1 = I - X1%*%solve(t(X1)%*%X1)%*%t(X1)
\texttt{beta\_demean} \; = \; \texttt{solve} \; (\texttt{t} \; (\texttt{X0}) \; \$ \, * \; \$\texttt{M1} \; \$ \, * \; \$\texttt{X0}) \; \$ \, * \; \$\texttt{t} \; (\texttt{X0}) \; \$ \, * \; \$ \; (\texttt{M1} \; \$ \, * \; \$\texttt{y})
beta
beauty_x = X[,'beauty']
age_x = X[,'age']
 \texttt{s\_squared} = \texttt{t(residual\_2)} \$ * \$ \texttt{residual\_2/(length(beauty\_x)-3)} \ \# \texttt{computes} \ \texttt{sample} \ \texttt{variance} 
sigma = s_squared[1]*solve(t(X)%*%(X)) #computes var covar matrix
#CIs based on formula
bl_upper_confidence = beta_demean[1,1]+1.96*sqrt(SE[2,2]) #2,2 is the variance entry in cov/var matrix bl_lower_confidence = beta_demean[1,1]-1.96*sqrt(SE[2,2])
b2_upper confidence = beta_demean[2,1]+1.96*sqrt(SE[3,3]) #3,3 is the variance entry in the cov/var matrix
b2_lower_confidence = beta_demean[2,1]-1.96*sqrt(SE[3,3])
#demeans the y_hat y_hat_demean = (M1%*%X0)%*%beta_demean
#computes normal yhat
y_hat = X%*%beta_hat
\#computes centered r squared on demeaned y and demeaned yhat
centered_R_sqrd = t(y_hat_demean) \% \% (y_hat_demean) / (t(M1\% \% y) \% \% (M1\% \% y)) \# computes uncentered r squared on original y and y_hat
uncentered_R_S = t(y_hat)%*%y_hat/(t(y)%*%y)
#vi
#computes mean of residual
m_resid = mean(residual_2)
\pmcomputes correlation b/w residuals and each regressor
cor(residual_2, X[,'beauty'])
cor(residual_2, X[,'age'])
```