# #Load dataset Birthweights <- read.csv("~/Data1204/RData1204/Final Project/Birthweights.csv") View(Birthweights) library(lattice) library(psych) library(gmodels) Birthweights summary(Birthweights\$bwt) sd(Birthweights\$bwt) summary(Birthweights\$gestation) sd(Birthweights\$gestation) summary(Birthweights\$age) sd(Birthweights\$age) summary(Birthweights\$height) sd(Birthweights\$height) summary(Birthweights\$weight) sd(Birthweights\$weight) #Histogram bwt library(ggplot2) x=Birthweights\$bwt h<-hist(x, breaks=10, col="red", xlab="birthweight",main="Frequency Distribution of Birthweights")

```
xfit<-seq(min(x),max(x),length=50)
yfit<-dnorm(xfit,mean=mean(x),sd=sd(x))
yfit<- yfit*diff(h$mids[1:2])*length(x)
lines(xfit, yfit, col="blue", lwd=2)

str(Birthweights)</pre>
```

### #Check the t-test is valid

library(ggplot2)

## #Histogram

```
hist(Birthweights$bwt, freq = FALSE, col = 'yellow', main = "Birthweights Data", xlab = 'Scores')
lines(density(Birthweights$bwt), col = "red")
```

### **#Two Tail test**

mean(Birthweights\$bwt)
sd(Birthweights\$bwt)

### #Calculate z parameters

mu <- 3386.788 mu0 <- 3400 # Given mean alpha <- 0.05 # Specify the significance level sigma <- 519.6163 # population standard deviation n <- nrow(Birthweights) # get the sample size

### #Calculate z

```
z<-(mu-mu0)/(sigma/sqrt(n))
Z
#Calculate p-value
2*pnorm(abs(z),lower.tail=FALSE)
#Linear Regression
#Build Linear Model
simple.fit<-lm(bwt~smoke, data=Birthweights)</pre>
LinearModel<-simple.fit
#Summary of Key Statistics of the Model
summary(LinearModel)
#Load Libraries
library(dplyr)
library(ggplot2)
ggplot(Birthweights,aes(x = factor(smoke), y = bwt)) + geom_point(colour = "green", size = 5, alpha =
0.5)
#Multivariate Regression
#Load Data
data(Birthweights)
Birthweights
#Create Dataset
input <- Birthweights[,c("bwt","gestation","region","age","height","weight", "smoke")]
print(head(input))
```

# # Create the relationship model. model <- Im(bwt~gestation+region+age+height+weight+smoke, data = input) # Show the model. print(model) #Model Summary summary(model) #Predict # Create the relationship model with significant predictors model1 <- Im(bwt~gestation+height+weight+smoke, data = input) # Show the model print(model1)</pre>

newdata = data.frame(gestation=200, height = 200, weight = 100.0, smoke = 1)

predict(model1, newdata)