```
age <- c(20, 30, 40, 50, 60)
data <- c(4, 7, 8, 9, 7, 10, 5, 7, 6, 8)
                                                      buy <- c(0, 1, 0, 1, 1)
mean value <- mean(data)
                                                      model <- glm(buy ~ age, family = binomial)
cat("Mean:", mean value, "\n")
median value <- median(data)
                                                      summary(model)
cat("Median:", median value, "\n")
                                                      predicted probs <- predict(model, newdata =</pre>
mode value <- as.numeric(names(sort(table(data),
                                                      data.frame(age = c(25, 35)), type = "response")
decreasing = TRUE)[1])
                                                      print(predicted probs)
cat("Mode:", mode value, "\n")
                                                      age seq \le seq(min(age), max(age), length.out = 100)
                                                      fitted probs <- predict(model, newdata = data.frame(age =
                                                      age seq), type = "response")
8)b
input <- mtcars[,c("am","mpg","hp")]</pre>
                                                      plot(age, buy, main = "Logistic Regression: Age vs.
                                                      Buying",
print(head(input))
input <- mtcars
                                                         xlab = "Age", ylab = "Buying Probability", pch = 16,
result <- aov(mpg~hp*am,data = input)
                                                      col = "blue", ylim = c(0, 1)
                                                      lines(age seq, fitted probs, col = "red", lwd = 2)
print(summary(result))
result <- aov(mpg~hp+am,data = input)
print(summary(result))
                                                      9)d poisiion regression
result1 <- aov(mpg~hp*am,data = input)
result2 <- aov(mpg~hp+am,data = input)
                                                      input <- warpbreaks
                                                      print(head(input))
print(anova(result1,result2))
                                                      output <-glm(formula = breaks ~ wool+tension, data =
9)a Linear regression
                                                      warpbreaks,
height <- c(150, 160, 170, 180, 190)
                                                        family = poisson)
weight <- c(50, 60, 70, 80, 90)
model <- lm(weight ~ height)
                                                      print(summary(output))
plot(height, weight, main = "Height vs.
Weight",xlab = "Height (cm)", ylab = "Weight
                                                      10)a time series
                                                      snowfall <- c(790,1170.8,860.1,1330.6,630.4,9
(kg)'', pch = 16)
abline(model, col = "red")
                                                                 11.5,683.5,996.6,783.2,982,881.8,1021)
                                                      snowfall timeseries<- ts(snowfall,start =</pre>
9)b Multiple regression
                                                      c(2013,1), frequency = 12
                                                      print(snowfall timeseries)
age <- c(25, 30, 35, 40, 45)
                                                      png(file = "snowfall.png")
height multi <- c(150, 160, 170, 180, 190)
                                                      plot(snowfall timeseries)
weight multi <- c(50, 60, 65, 75, 85)
                                                      dev.off()
multiple model <- lm(weight multi ~ height multi
+ age)
                                                      10)b non linear leat square
summary(multiple model)
                                                      xvalues <- c(1.6, 2.1, 2, 2.23.19, 2.21)
library(ggplot2)
                                                      yvalues <- c(5.19, 7.43, 6.94, 8.11, 18)
ggplot(data = data.frame(weight multi, fitted =
                                                      png(file = "nls.png")
fitted(multiple model)), aes(x = fitted, y =
weight multi)) +geom point()
                                                      plot(xvalues, yvalues)
+geom smooth(method = "lm", color = "blue", se =
                                                      model <- nls(yvalues \sim b1*xvalues^2 + b2, start = list(b1 =
FALSE) +ggtitle("Multiple Regression: Residuals
                                                      1, b2 = 3)
vs Fitted Values") +
                                                      lines(seq(min(xvalues), max(xvalues), length.out = 100),
                                                      predict(model, newdata = data.frame(xvalues =
 theme minimal()
                                                      seq(min(xvalues), max(xvalues), length.out = 100))))
                                                      dev.off()
                                                      print(sum(resid(model)^2))
                                                      print(confint(model))
```

10) Decision tree

```
library("MASS")
data("iris")
install.packages("caret")
                                                              print(str(Cars93))
install.packages("C50")
                                                              car data<-
library(caret)
                                                              data.frame(Cars93$AirBags,
library(C50)
                                                              Cars93$Type)
set.seed(7)
                                                              car data = table(Cars93$AirBags,
inTraininglocal <- createDataPartition(iris$Species, p = .70,
list = FALSE)
                                                              Cars93$Type)
training <- iris[inTraininglocal, ]
                                                              print(car data)
testing <- iris[-inTraininglocal, ]
                                                              print(chisq.test(car data))
model < -C5.0(Species \sim ., data = training)
summary(model)
                                                              12)b t test
pred <- predict(model, testing[, -5]) # use predict() instead of</pre>
                                                              x < c(0.593, 0.142, 0.329, 0.691, 0.231,
predict.C5.0()
                                                              0.793, 0.519, 0.392, 0.418)
a <- table(testing$Species, pred)
                                                              t.test(x, alternative="greater", mu=0.3)
accuracy <- sum(diag(a)) / sum(a)</pre>
print(accuracy)
plot(model)
11) Normal Dist
                                                              12) c t test
dnorm
                                                              install.packages("randomForest")
x \le seq(-10, 10, by = .1)
                                                              library(party)
y < -dnorm(x, mean = 2.5, sd = 0.5)
                                                              print(head(readingSkills))
png(file = "dnorm.png")
                                                              library(party)
plot(x,y)
                                                              library(randomForest)
dev.off()
                                                              output.forest <-
pnorm
                                                              randomForest(nativeSpeaker ~ age +
x \le seq(-10,10,by = .2)
                                                              shoeSize + score,
y < -pnorm(x, mean = 2.5, sd = 2)
                                                                                 data = readingSkills)
png(file = "pnorm.png")
                                                              print(output.forest)
plot(x,y)
                                        x < -seq(0,50,by = 1)
dev.off()
qnorm
                                        dbinom(x,50,0.5)
                                                              Week 2 associate
x \le seq(-10,10,by = .2)
                                                              Step 1: load the data set (open weka and
                                        png(file =
y <- pnorm(x, mean = 2.5, sd = 2)
                                                              click on 'Explore', click open file and load the
                                        "dbinom.png")
png(file = "pnorm.png")
                                                              contact lenses arff dataset)
                                                              Step 2 select the aprori alg (go to 'associate'
plot(x,y)
                                        plot(x,y)
dev.off()
                                        dev.off()
                                                              , clich 'choose 'and click weka association
rnorm
                                                              apriori from the list). step 3 configure and
v <- rnorm(50)
                                        plot(x,y)
                                                              run apriori (click on the 'associator' and set
png(file = "rnorm.png")
                                                              minisupped and minmetric, click start to run
hist(v, main = "Normal DIstribution")
                                                              alg)
dev.off()
```