

```
#Univariate Plot
```

```
x = 2
```

```
print(x)
```

```
?plot
```

```
x = c(5,7,8,7,2,2,9,4,11,12,9,6)
```

```
plot(x)
```

```
plot(x,type = "l",main = "First Graph",
```

```
sub = "first subtitle",xlab = "X-axis",
```

```
ylab = "Y-axis")
```

```
iris
```

```
View(iris)
```

```
plot(iris$Sepal.Length,main = "Graph of Sepal Length of iris data")
```

```
mtcars
```

```
View(mtcars)#Viewing data
```

```
?mtcars#data description
```

```
names(mtcars)#column names
```

```
str(mtcars)#variable types
```

```
dim(mtcars)#dimension of data
```

```
plot(mtcars$mpg)
```

```
#Bivariate Scatter Plot
```

```
x <- c(5,7,8,7,2,2,9,4,11,12,9,6)
```

```
y <- c(99,86,87,88,111,103,87,94,78,77,85,86)
```

```
plot(x, y, main="Observation of Cars", xlab="Car age", ylab="Car speed")
```

```
abline(lm(y~x),col = 'red')
```

```
cor(x,y, method = "pearson")#correlation
```

```
cor(x,y, method = "spearman")#correlation
```

```
#Regression
```

```
#One Variable
```

```
model = lm(y~x)
```

```
summary(model)
```

```
format(1.387e-05,scientific = FALSE)
```

```
#Two Variable
```

```
model1 = lm(Petal.Length~Sepal.Width+Sepal.Length,data = iris)
```

```
model1
```

```

summary(model1)

# load the MASS package
install.packages("MASS")
library(MASS)
print(str(survey))

# Create a data frame from the main data set.
stu_data = data.frame(survey$Smoke,survey$Exer)

# Create a contingency table with the needed variables.
stu_data = table(survey$Smoke,survey$Exer)

print(stu_data)

# applying chisq.test() function
print(chisq.test(stu_data))

##### qqplot #####
# Set seed for reproducibility
set.seed(121)

# Create random normally distributed values
x <- rnorm(1200)

# QQplot of normally distributed values
qqnorm(x)

# Add qqline to plot
qqline(x, col = "darkgreen")

qqnorm(iris$Sepal.Length)

# Add qqline to plot
qqline(iris$Sepal.Length, col = "darkgreen")

?qqnorm

```