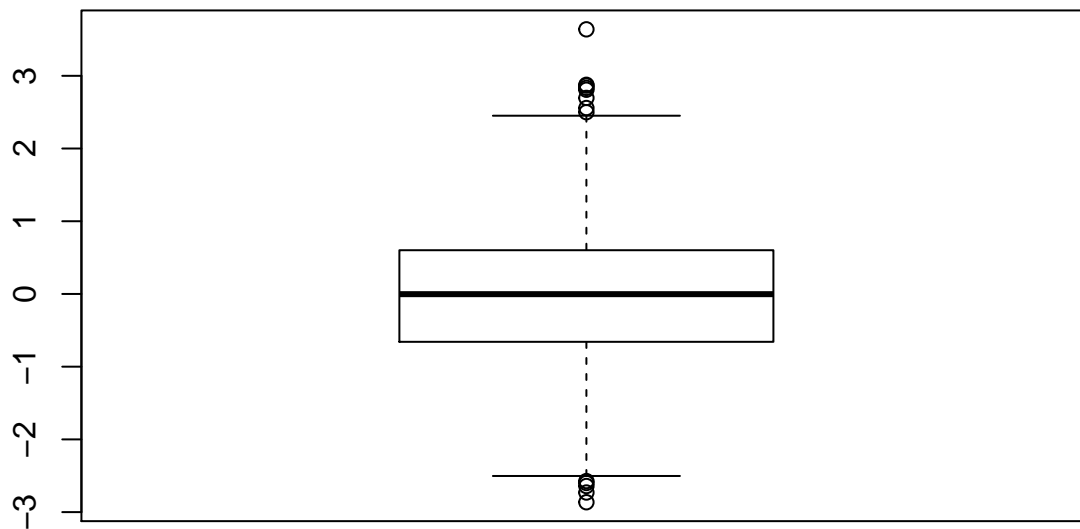# Crop Analysis Q3 2013

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Class 05 R graphics intro This is some test and I can have **bold** and *italic* and `code`
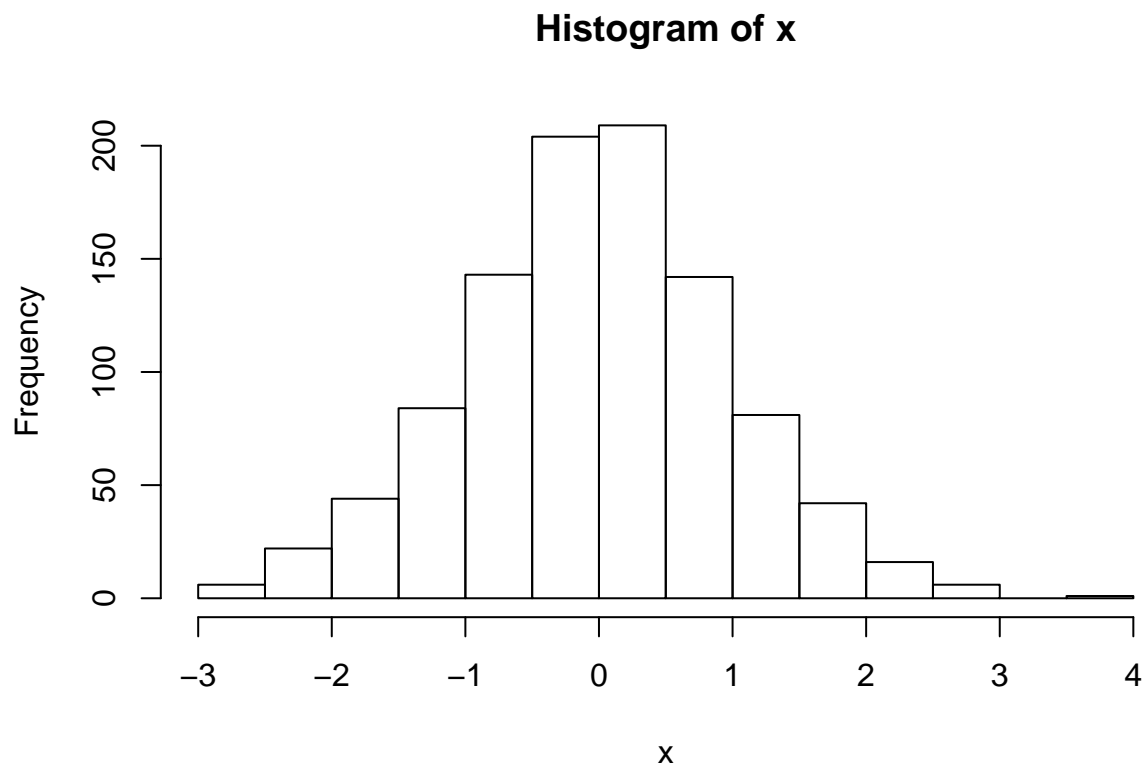
```r
# My first boxplot
x <- rnorm(1000,0)
boxplot(x)
```
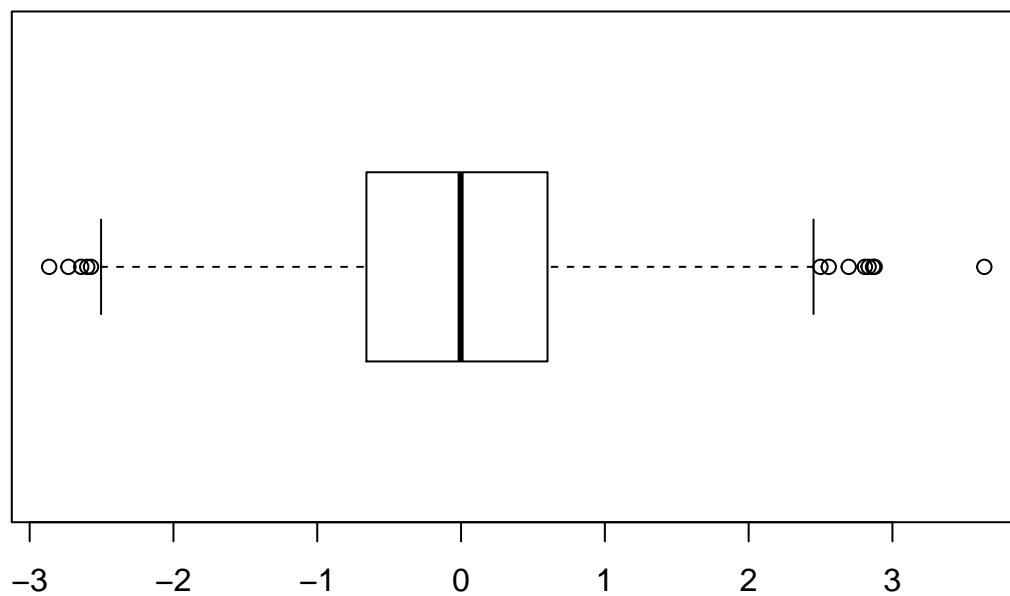


```r
summary(x)
```

```
##      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## -2.864328 -0.656926 -0.003077 -0.011145  0.601342  3.638899
```
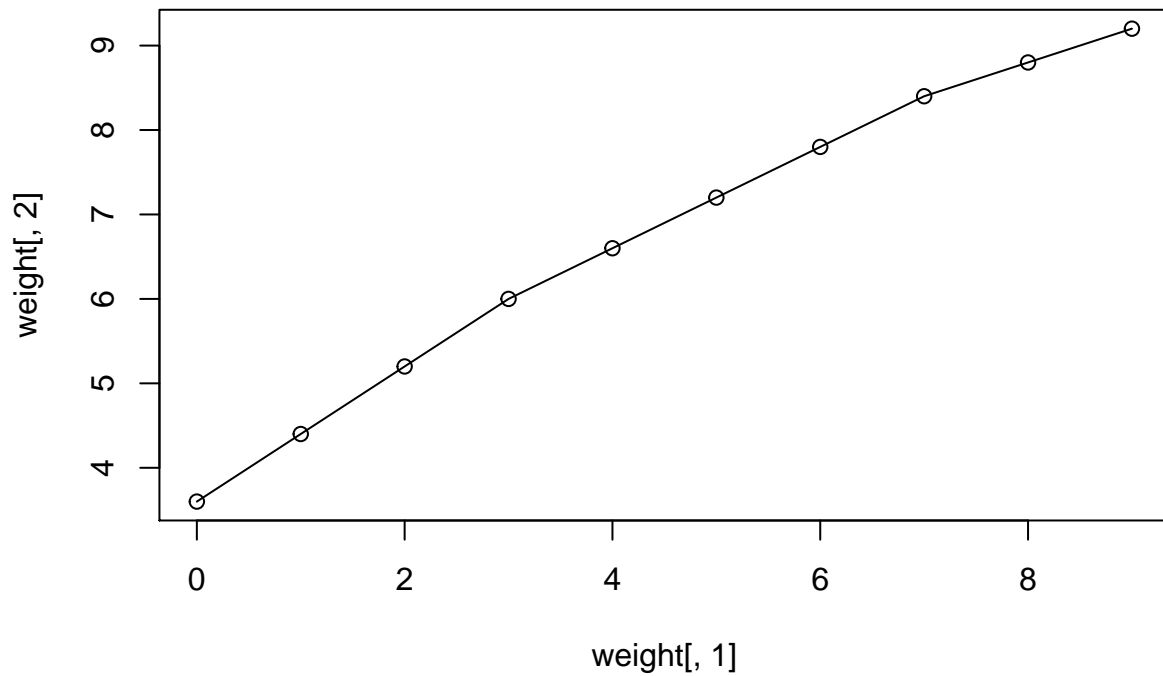
```r
hist(x)
```

Histogram of x


```r
boxplot(x, horizontal = TRUE)
```
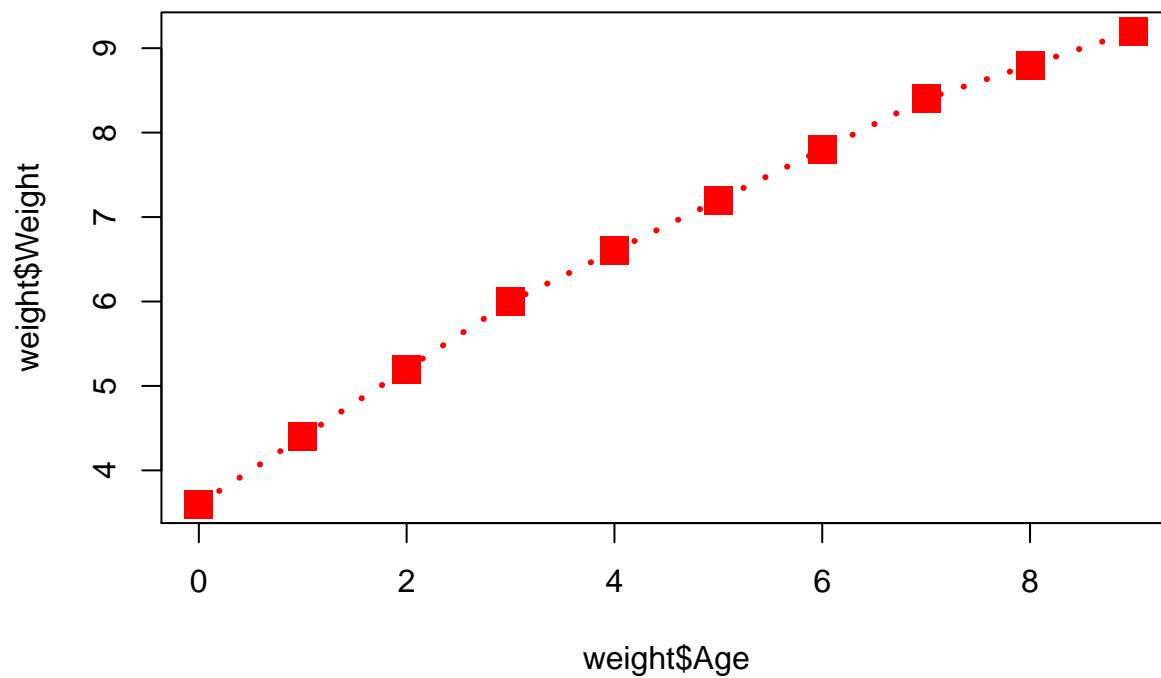

I have generated x and it has 1000

```r
# Hands on session 2

weight <- read.table("bimm143_05_rstats/weight_chart.txt", header = TRUE)

plot(weight[,1], weight[,2], typ="o")
```
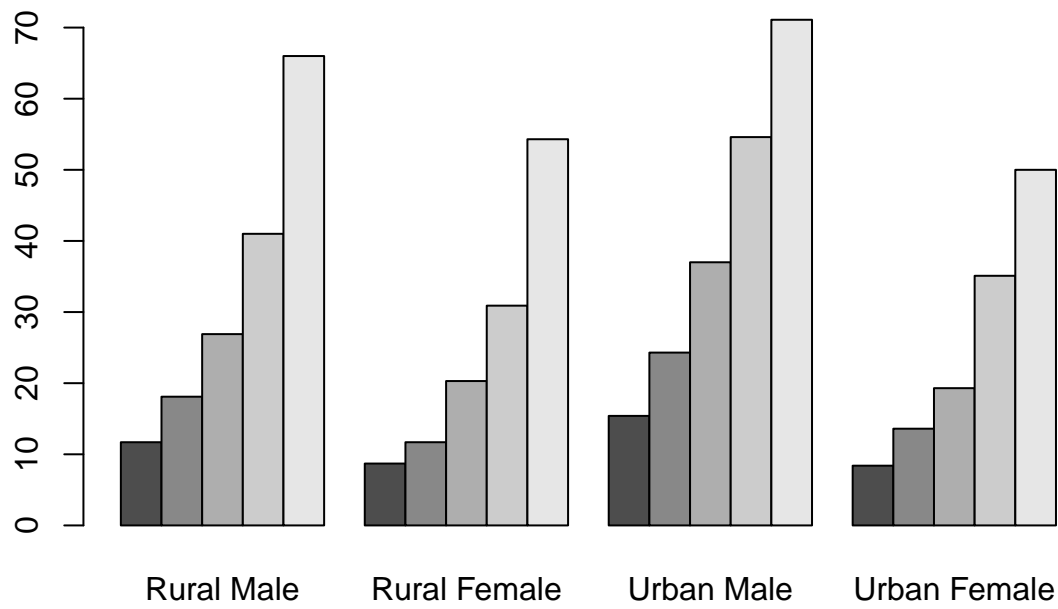
```
plot(weight$Age, weight$Weight, typ="o", main="some main title",
     pch=15, cex=2, col="red",
     lwd=3, lty=3)
```
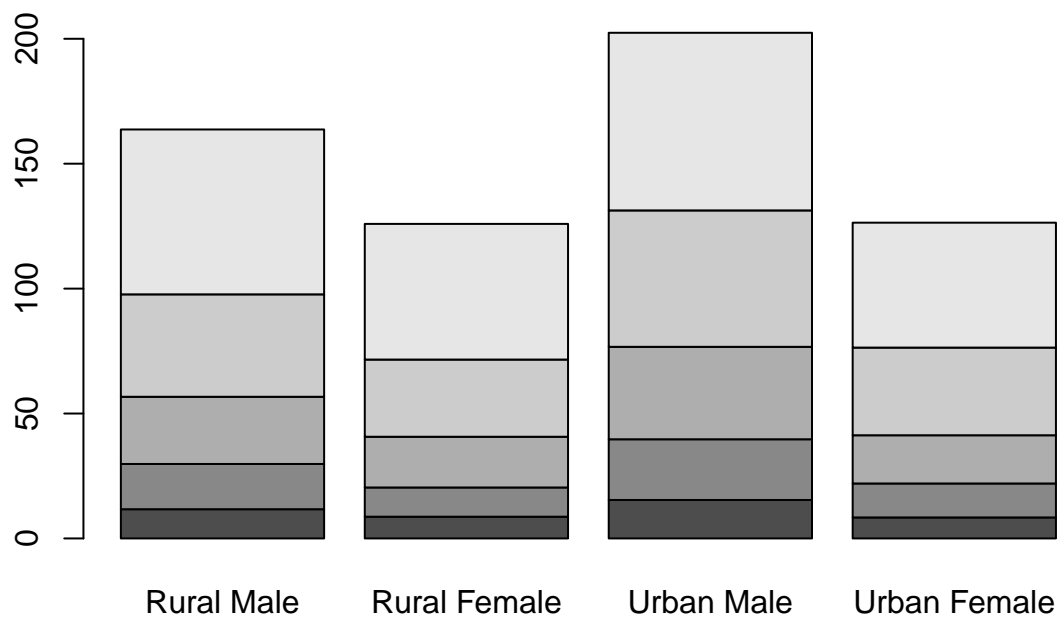
some main title


```
# Try a barplot
barplot(VADeaths, beside = TRUE)
```
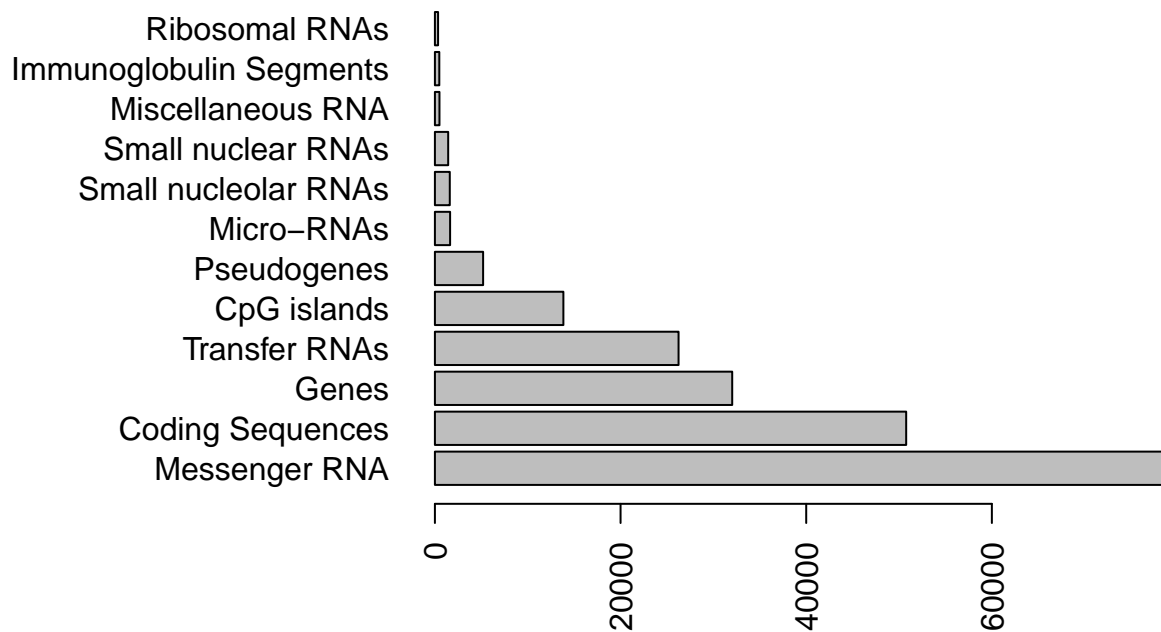
```
barplot(VADeaths, beside = FALSE)
```



```
## Input our feature count data
mouse <- read.table("bimm143_05_rstats/feature_counts.txt", header=TRUE, sep="\t")

barplot(mouse$Count, horiz=TRUE, names.arg = mouse$Feature, las=2)

# Change margin so we can see the labels
par(mar=c(5.1, 11.1, 4.1, 2.1))
barplot(mouse$Count, horiz=TRUE, names.arg = mouse$Feature, las=2)
```
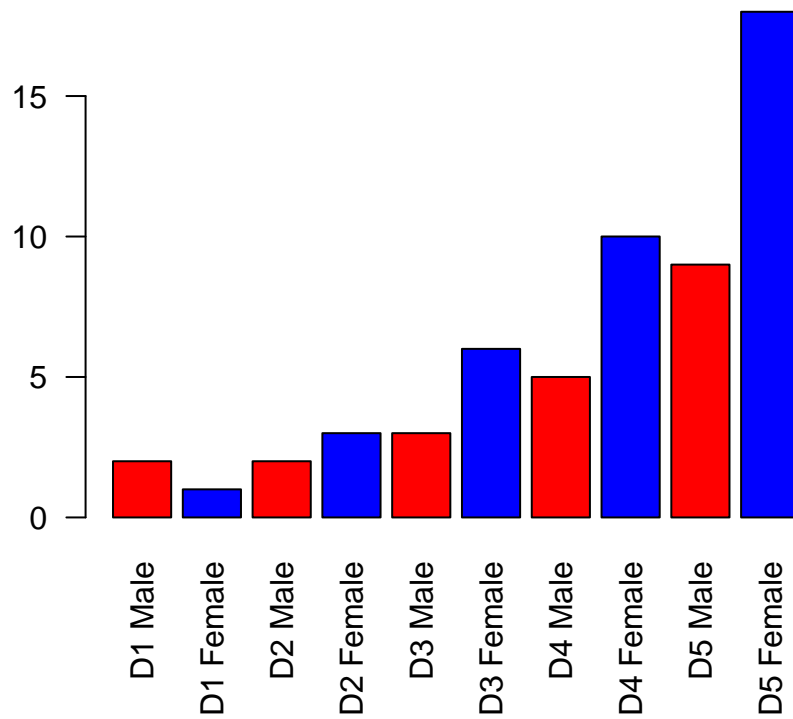
```
# add some color
barplot(mouse$Count, horiz=TRUE, names.arg = mouse$Feature, las=2, col=rainbow(11))
```
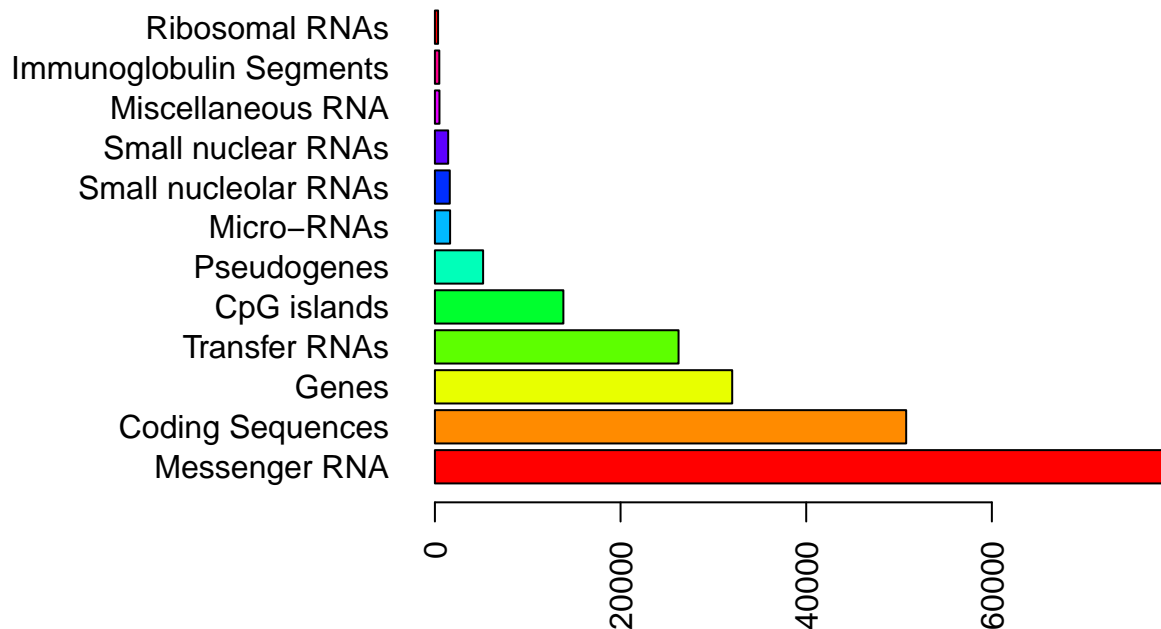


```
# Section 3
# Using color

mf <- read.table("bimm143_05_rstats/male_female_counts.txt", sep="\t", header=TRUE)

barplot(mf$Count, names.arg = mf$Sample, col=c("red","blue"), las=2)
```

```r
# Expresion data
e <- read.table("bimm143_05_rstats/up_down_expression.txt", header=TRUE)

# how many genes
nrow(e)
```

```
## [1] 5196
```

```r
# How many up, down and all around?
table( e$State )
```
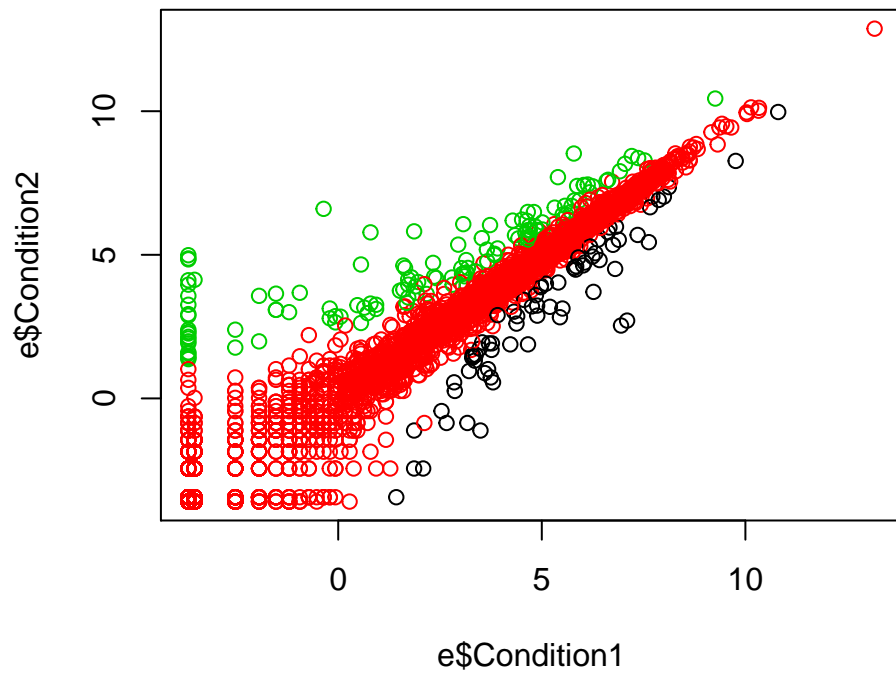
```
##
##      down unchanging          up
##        72       4997         127
```

```r
plot(e$Condition1, e$Condition2, col=e$State)
```

```
# Play
palette(c("red","lightgray","blue"))
plot(e$Condition1, e$Condition2, col=e$State)
```