# Class5 R graphics

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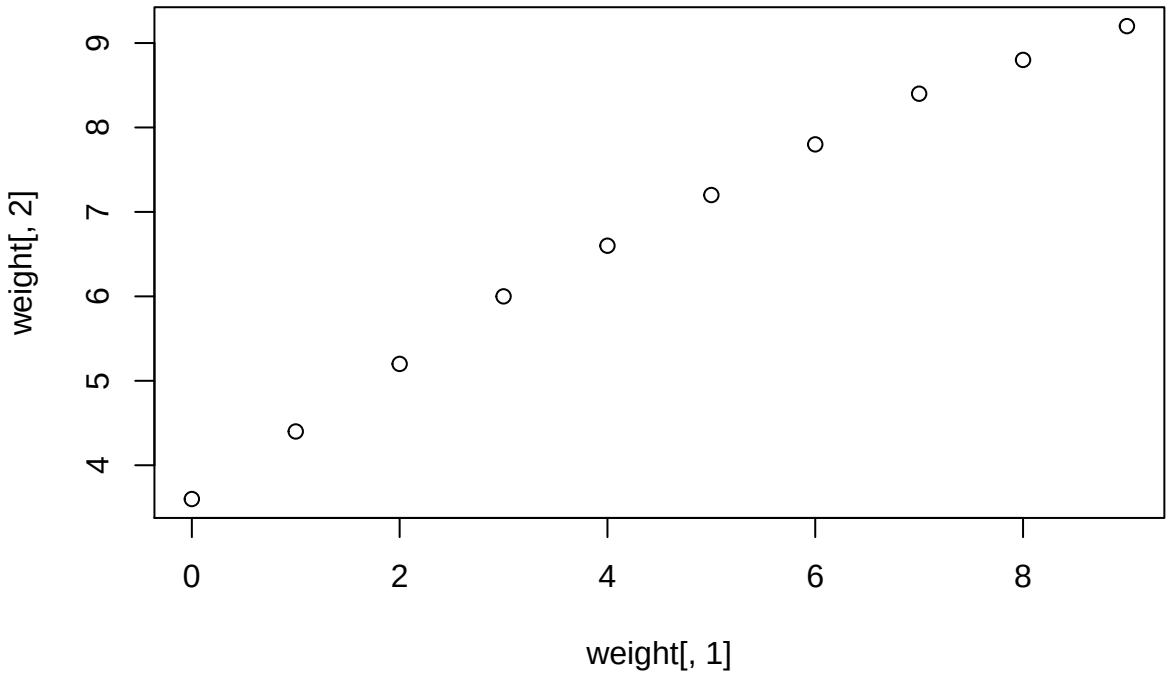
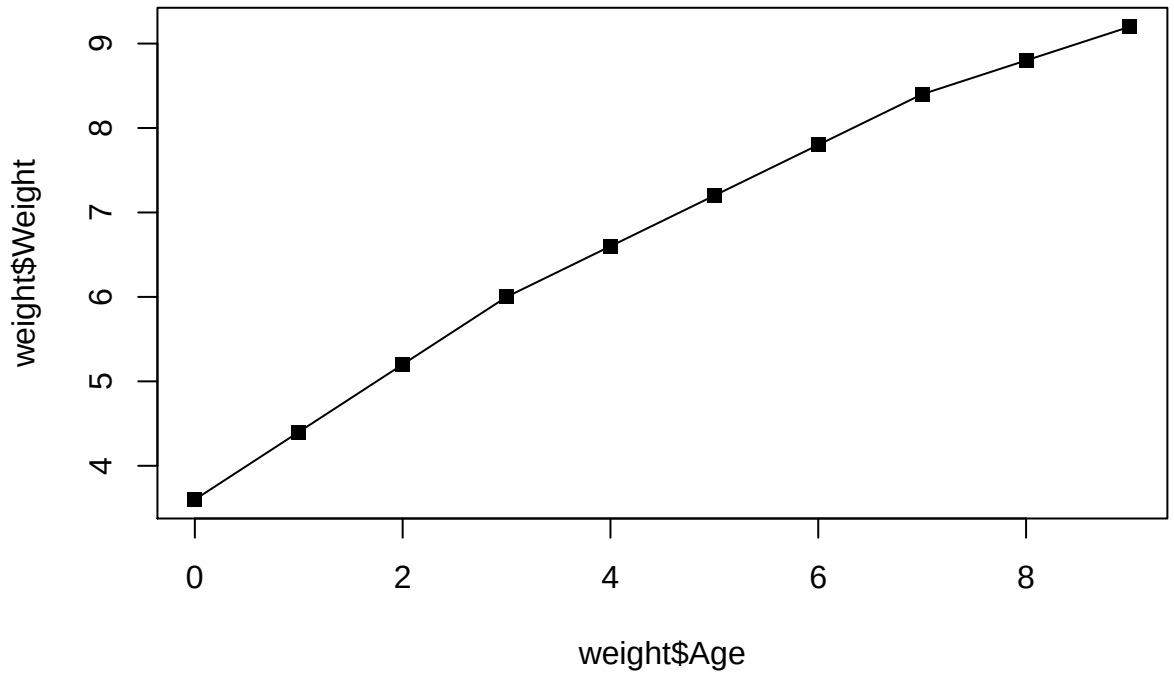
Class 05 Graphics and plots with R This is some narative text that I can style **bold** and *italic* and add links to webpages

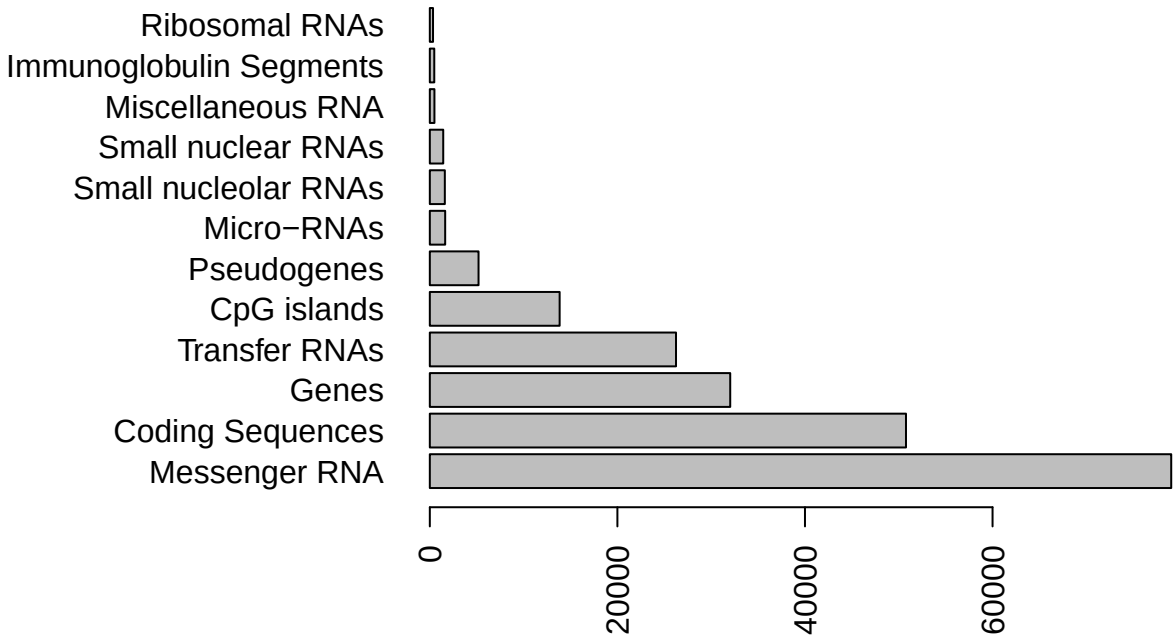
```
# Section 2A: line plot

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

plot(weight[,1], weight[,2])
```



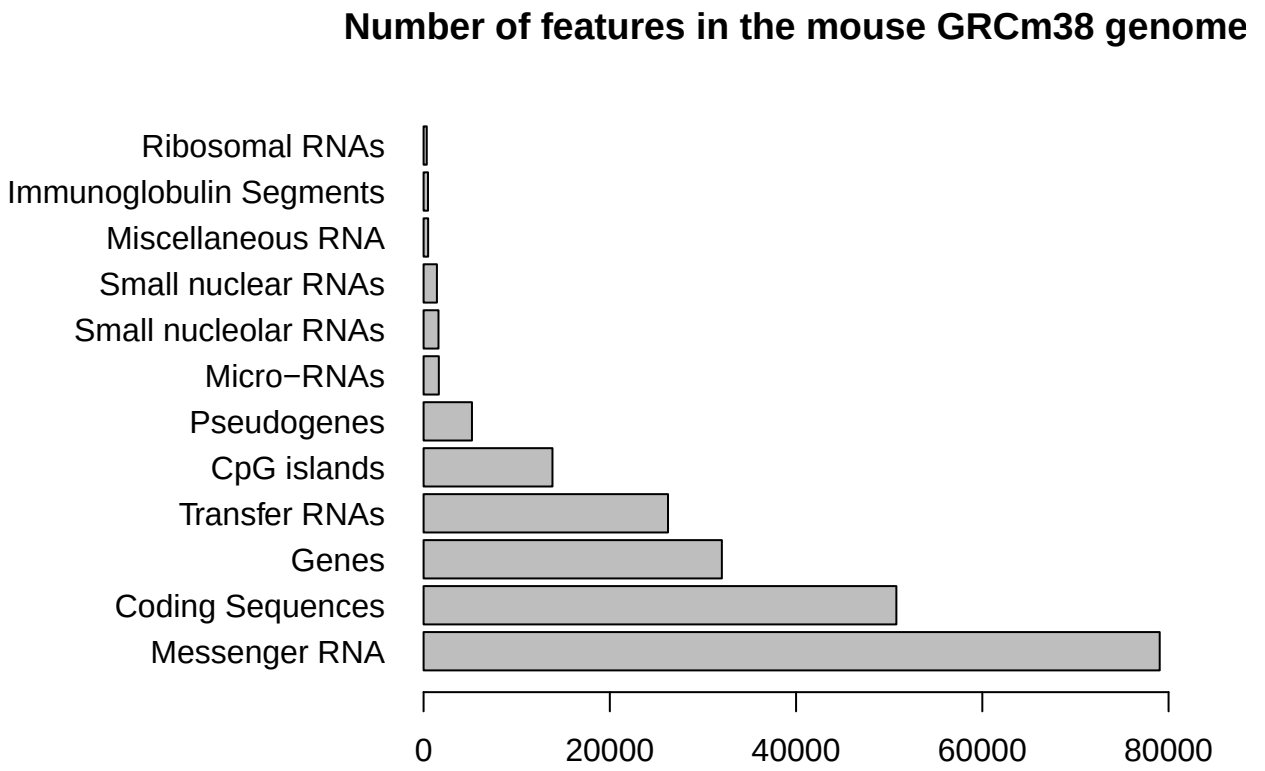

```
plot(weight$Age, weight$Weight, pch=15, type="o" )
```



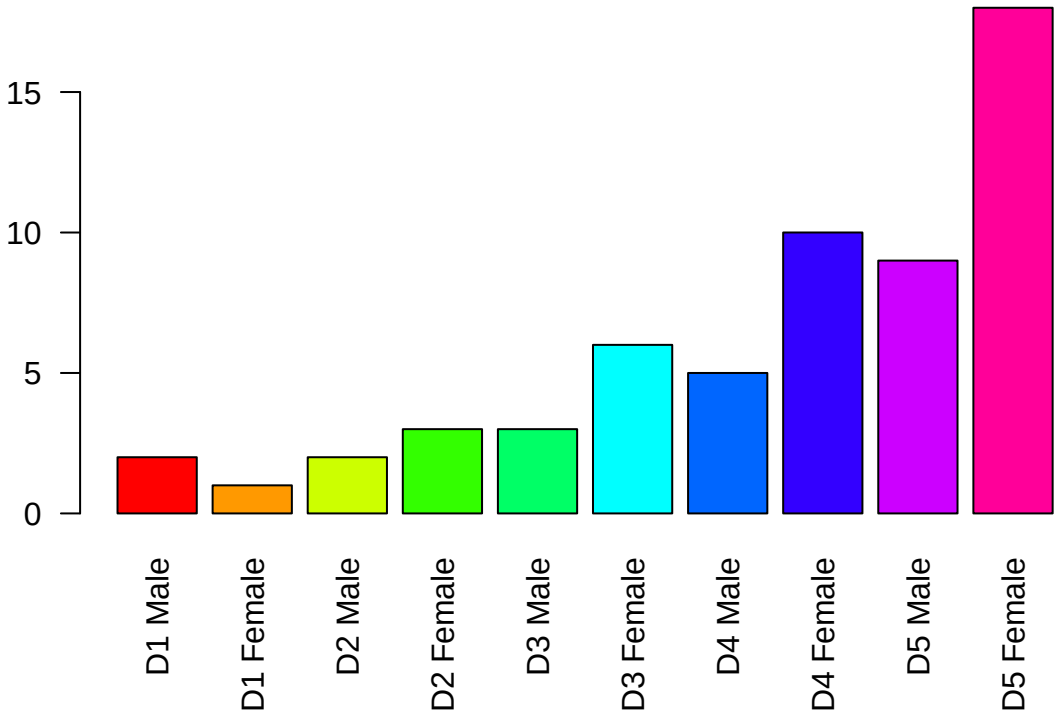

```
# 2B Barplot

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

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

old.mar <- par()$mar

par(mar=c(5, 11, 4, 2))
barplot(feat$Count, names.arg = feat$Feature, las=2, horiz=TRUE)
```



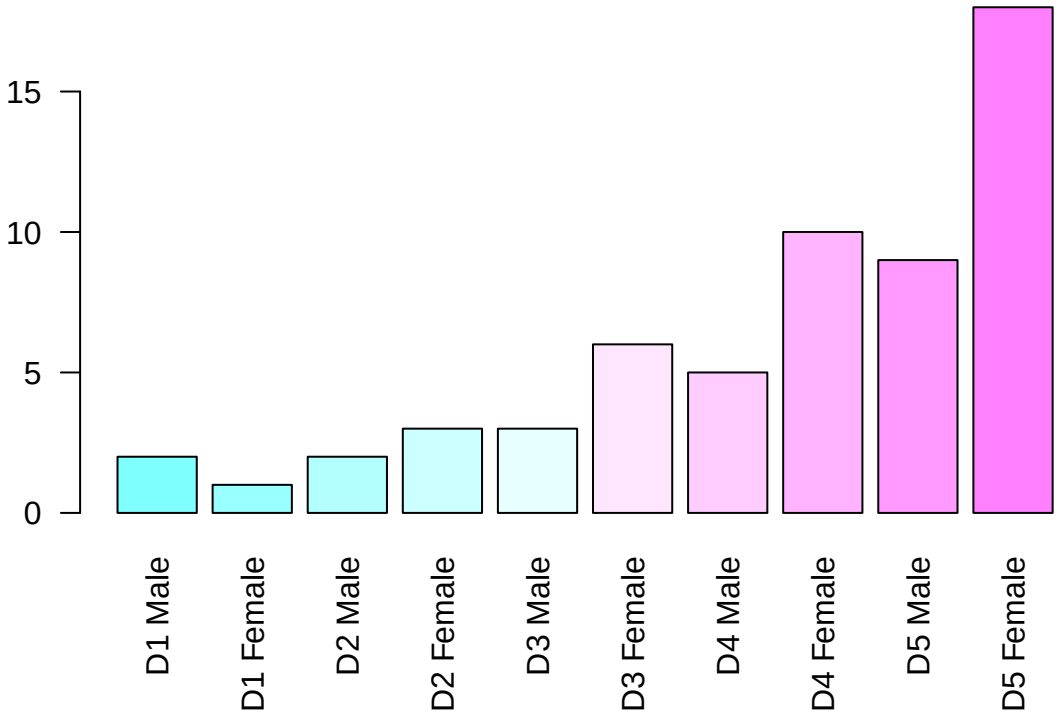
```
# More custom arguments
par(mar=c(3.1, 11.1, 4.1, 2))
barplot(feat$Count, names.arg=feat$Feature,
        horiz=TRUE, ylab="",
        main="Number of features in the mouse GRCm38 genome",
        las=1, xlim=c(0,80000))
```



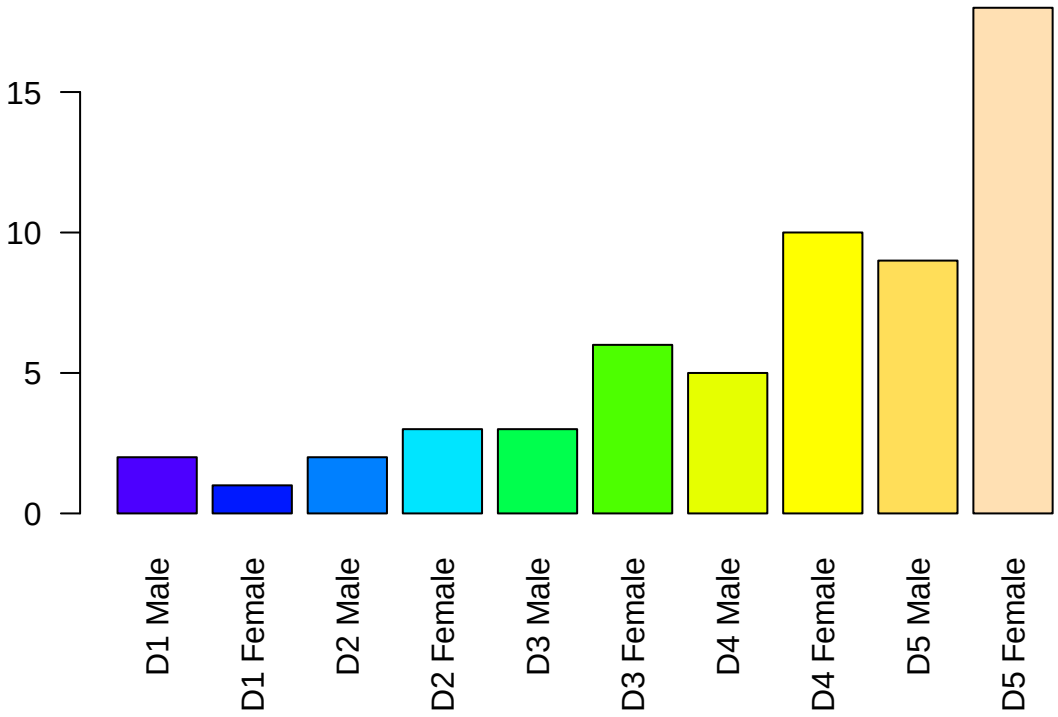

```
par(mar=old.mar)

# Section 3

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

barplot(mf$Count, names.arg = mf$Sample, las=2, col=rainbow( nrow(mf) ))
```




```
barplot(mf$Count, names.arg = mf$Sample, las=2, col=cm.colors( nrow(mf) ))
```




```
barplot(mf$Count, names.arg = mf$Sample, las=2, col=topo.colors( nrow(mf) ))
```



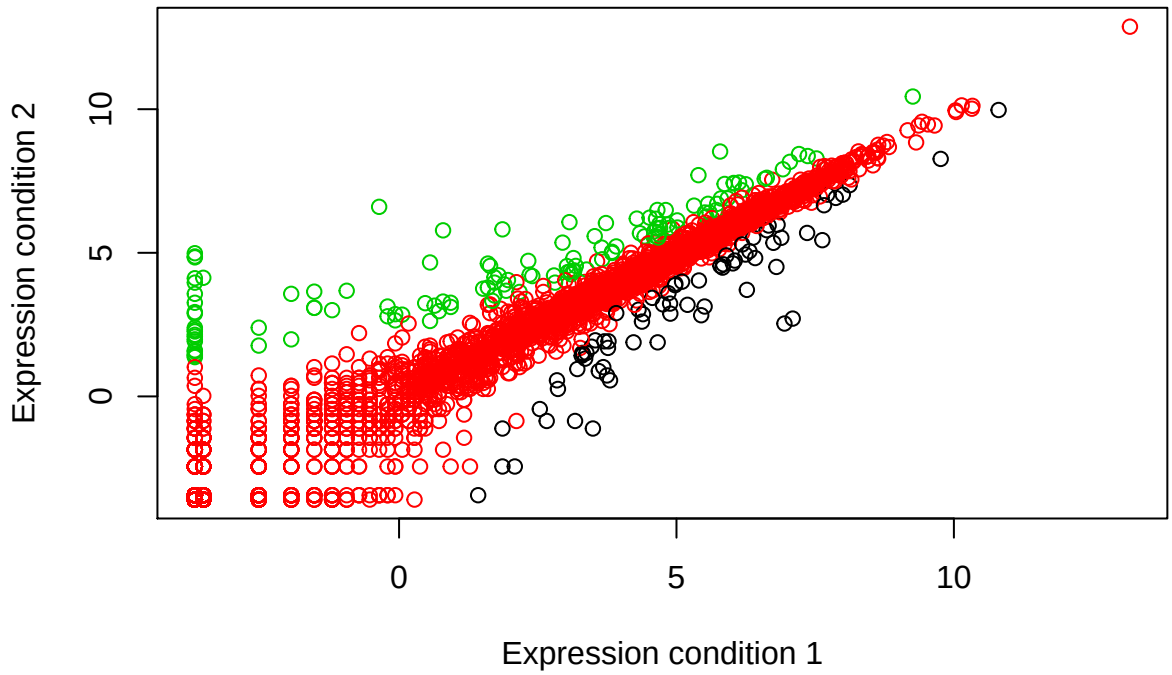

```
# Section 3B RNA-Seq data

exp <- read.delim("bimm143_05_rstats/up_down_expression.txt")

# how many genes
nrow(exp)
```

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

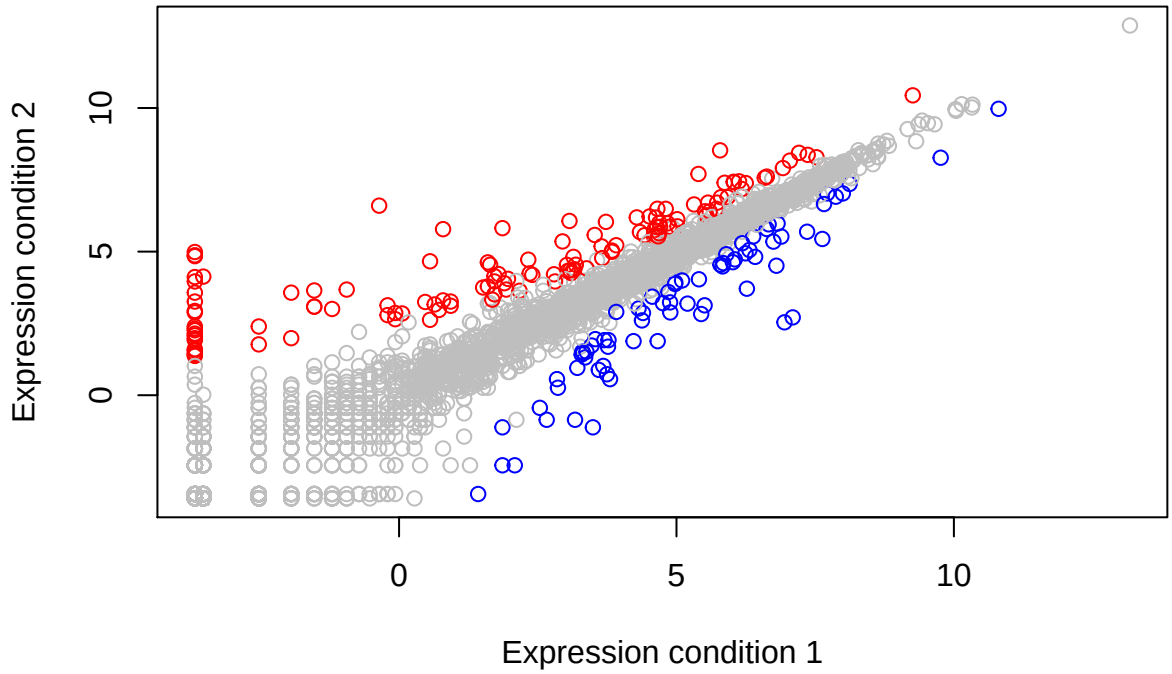
```
table(exp$State)
```

```
##
##       down unchanging         up
##         72       4997        127
```

```
plot(exp$Condition1, exp$Condition2, col=exp$State,
     xlab="Expression condition 1", ylab="Expression condition 2")
```




```
old.pal <- palette()
palette(c("blue","gray","red"))
plot(exp$Condition1, exp$Condition2,
     col=exp$State, xlab="Expression condition 1", ylab="Expression condition 2")
```




```
palette(old.pal)


#View(exp)
```