

# class05.R

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```
# Class 05 Data Visualization
```

```
#This is the "base" R plot
```

```
plot(cars)
```

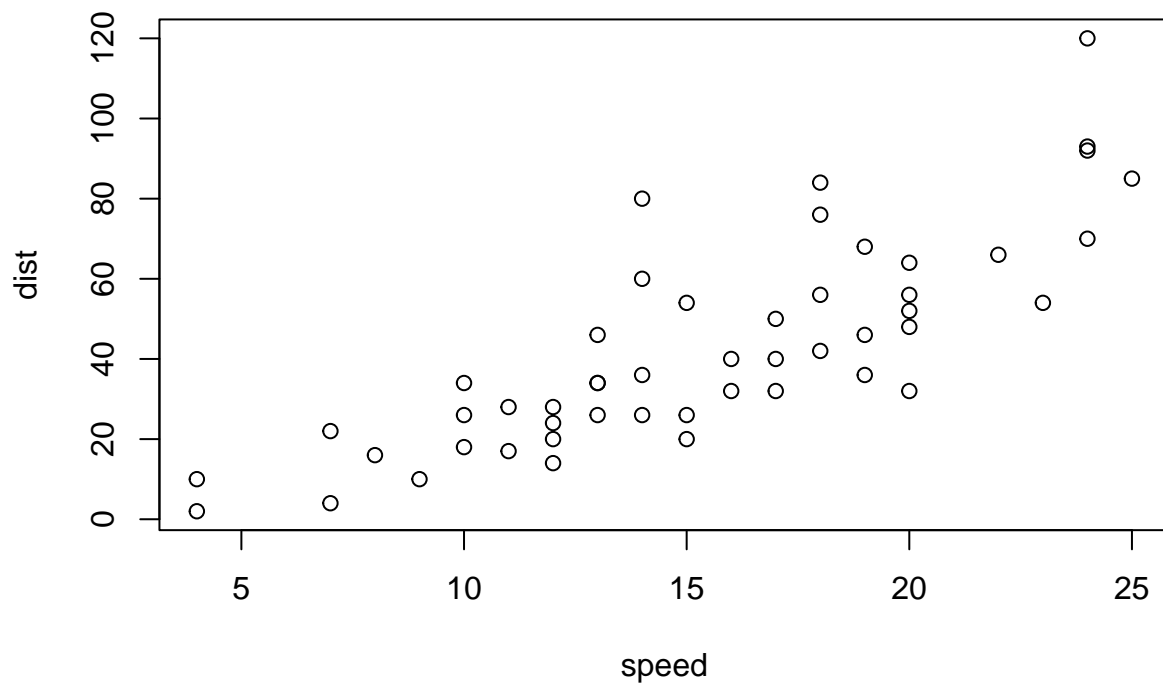
```
#We are going to get a new plotting package called ggplot2
```

```
#install.packages("ggplot2")
```

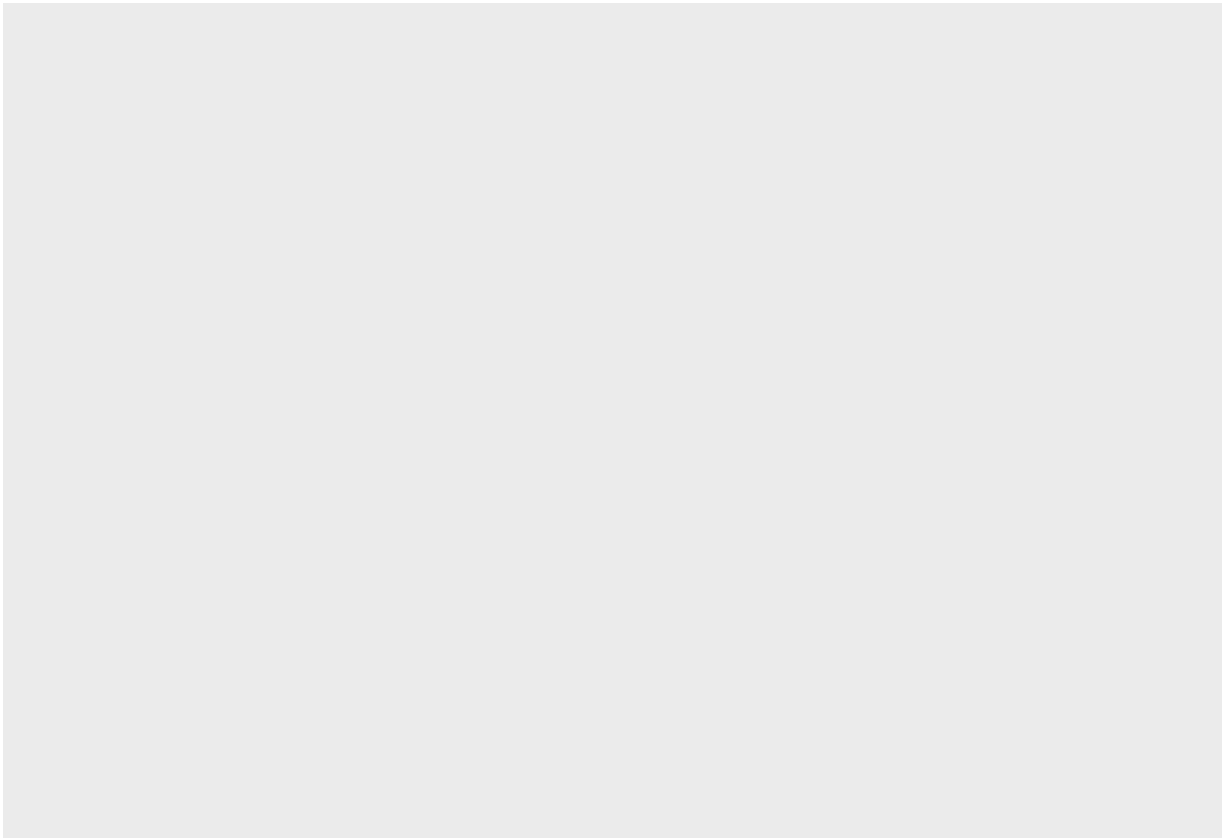
```
#now we need to call/load the package
```

```
library(ggplot2)
```

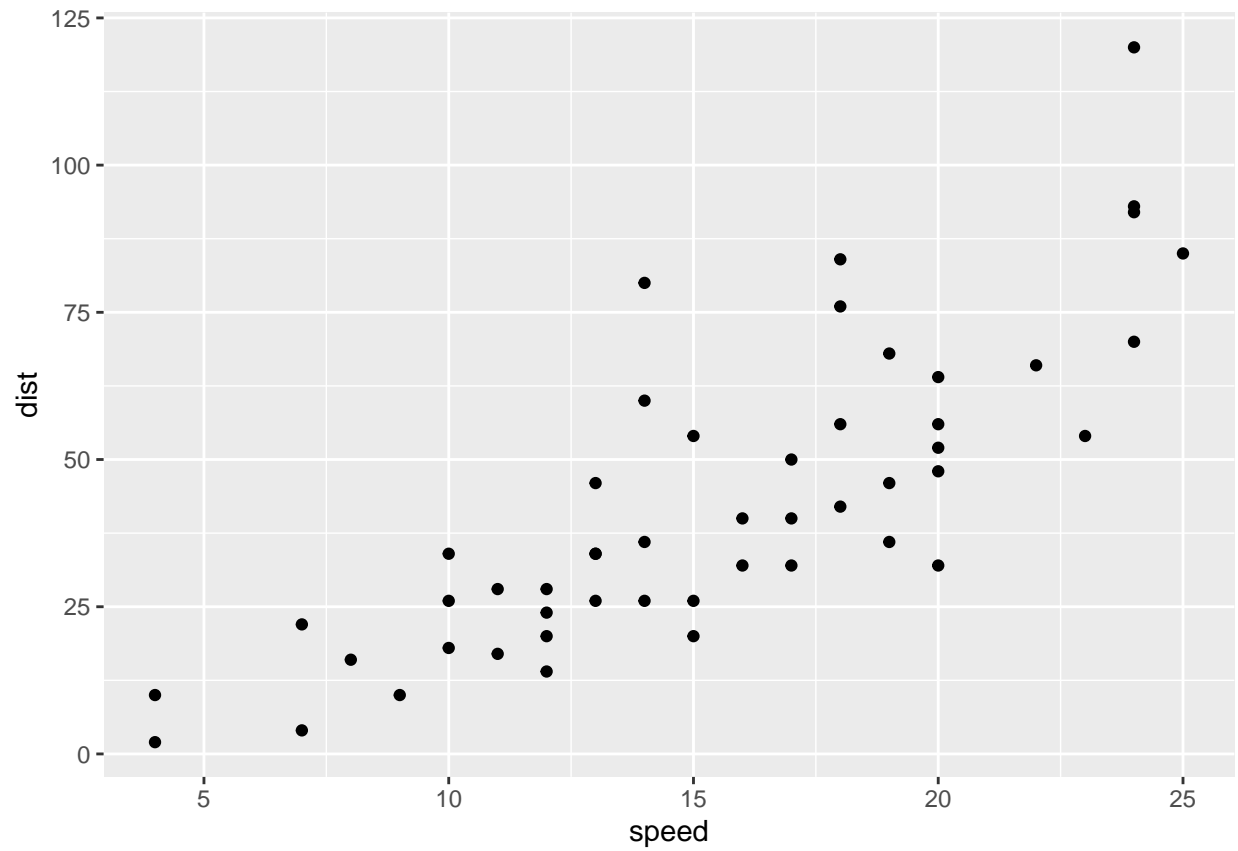
```
## Warning in register(): Can't find generic 'scale_type' in package ggplot2 to  
## register S3 method.
```



```
#This sets up the plot  
ggplot(cars)
```

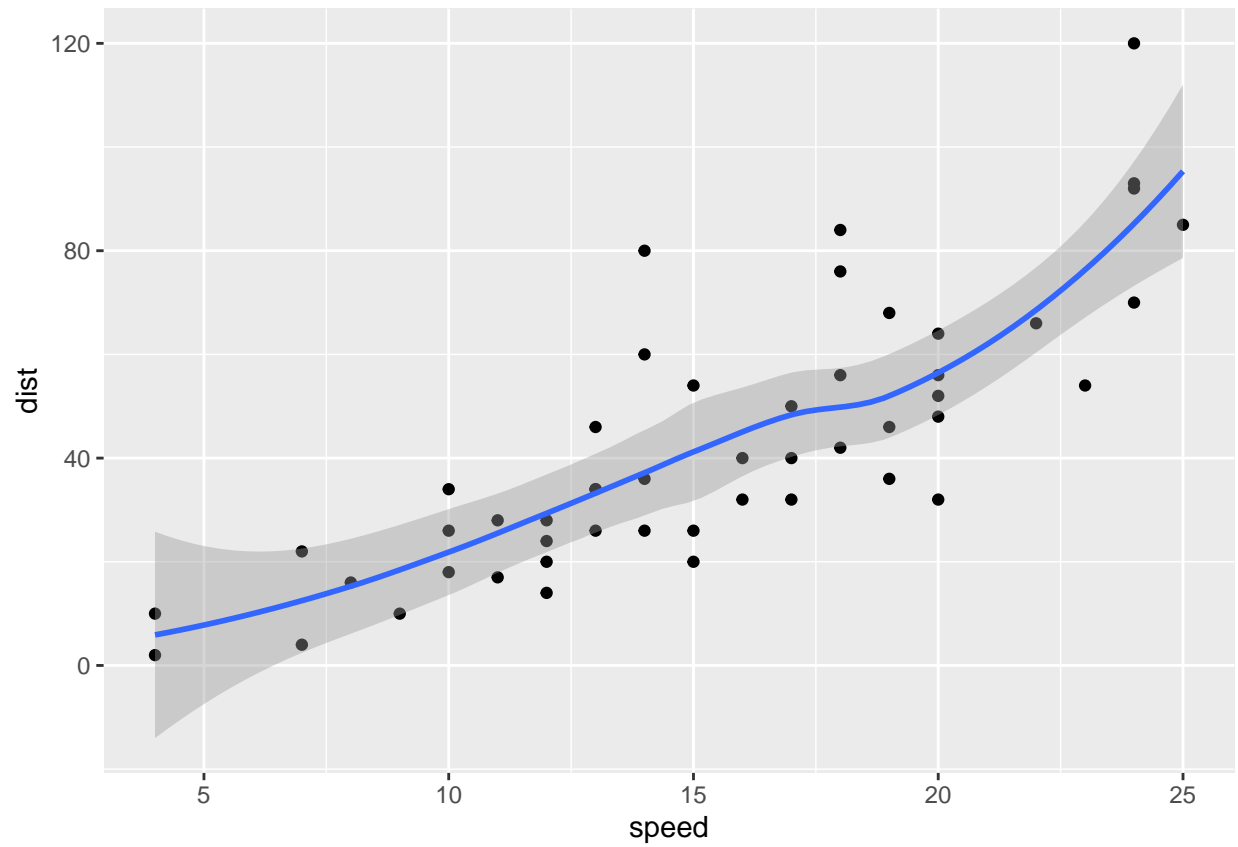


```
gg<- ggplot(data=cars) + aes(x=speed , y=dist) + geom_point()  
gg
```



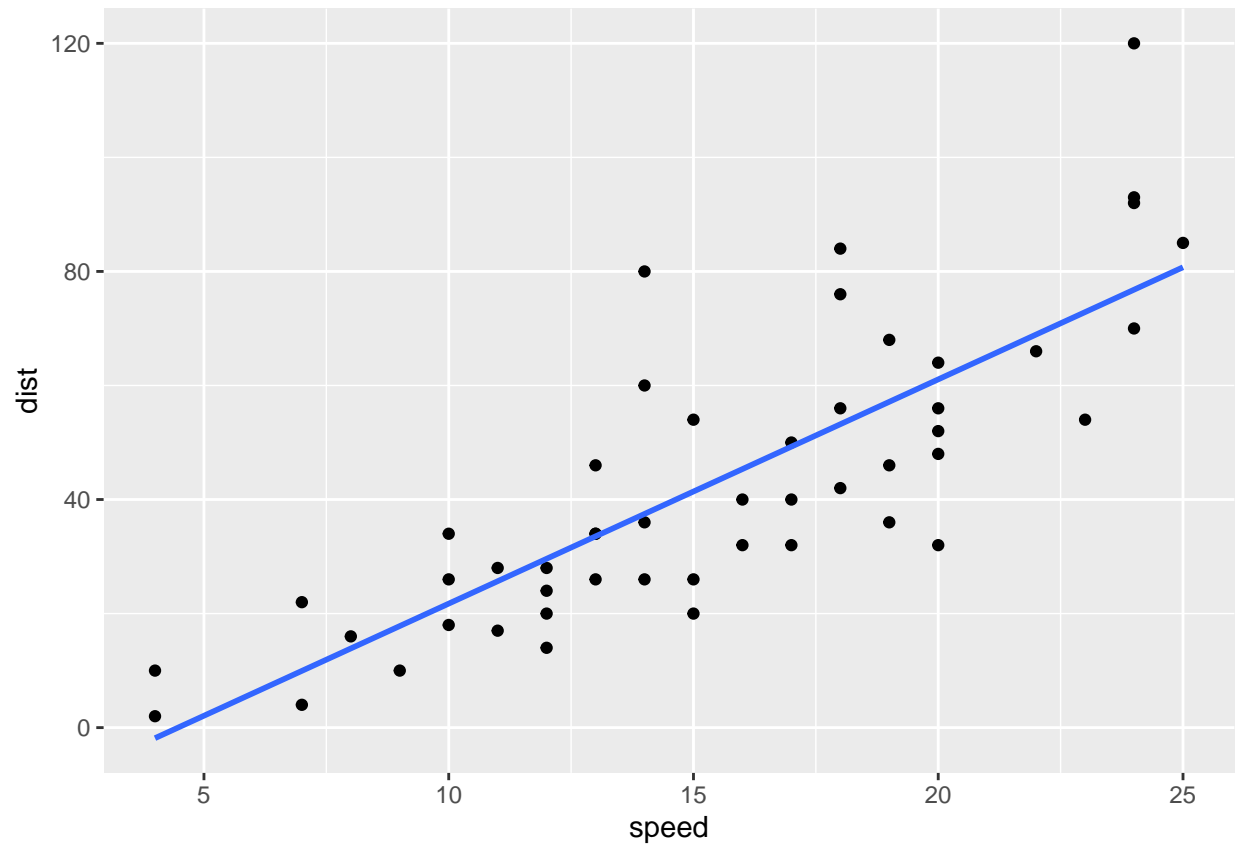
```
#One last thing. Lets add a line to the data  
gg + geom_smooth()
```

```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



```
#I want a linear model  
gg + geom_smooth(method="lm", se=FALSE)
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



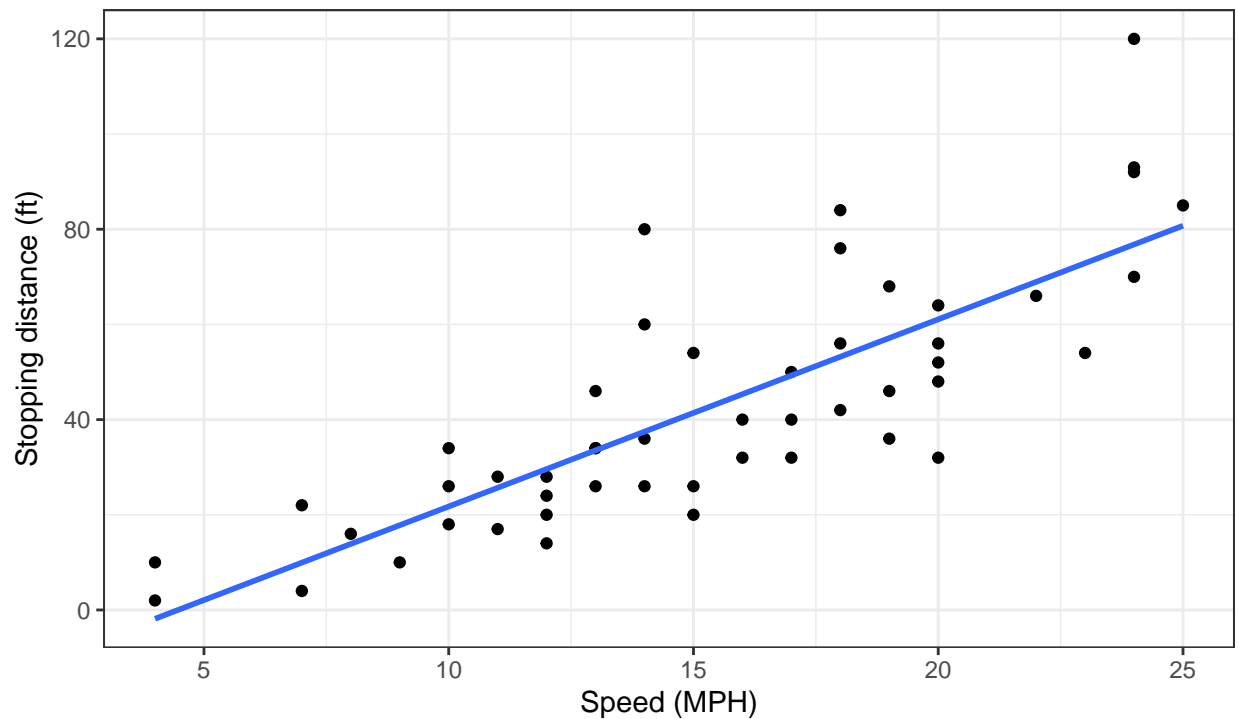
*#my own attempt*

```
gg + geom_smooth(method="lm", se=FALSE) + labs(title= "Speed and Stopping Distances of Cars", x="Speed",
        subtitle= "Your informative subtitle text here", caption="Dataset:'Cars'") +
```

## 'geom\_smooth()' using formula 'y ~ x'

## Speed and Stopping Distances of Cars

Your informative subtitle text here



Dataset: 'Cars'

```
# RNASeq experiment data set
# Read the data into R
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

```
##      Gene Condition1 Condition2      State
## 1    A4GNT -3.6808610 -3.4401355  unchanging
## 2    AAAS  4.5479580  4.3864126  unchanging
## 3    AASDH  3.7190695  3.4787276  unchanging
## 4    AATF  5.0784720  5.0151916  unchanging
## 5    AATK  0.4711421  0.5598642  unchanging
## 6 AB015752.4 -3.6808610 -3.5921390  unchanging
```

```
#How many genes in data set rows?
nrow(genes)
```

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

```
#How many columns and its names?
ncol(genes)
```

```
## [1] 4
```

```
colnames(genes)
```

```
## [1] "Gene"          "Condition1" "Condition2" "State"
```

```
# Using the table() function to find how many up regulated genes  
table(genes$State)
```

```
##  
##      down  unchanged      up  
##      72      4997      127
```

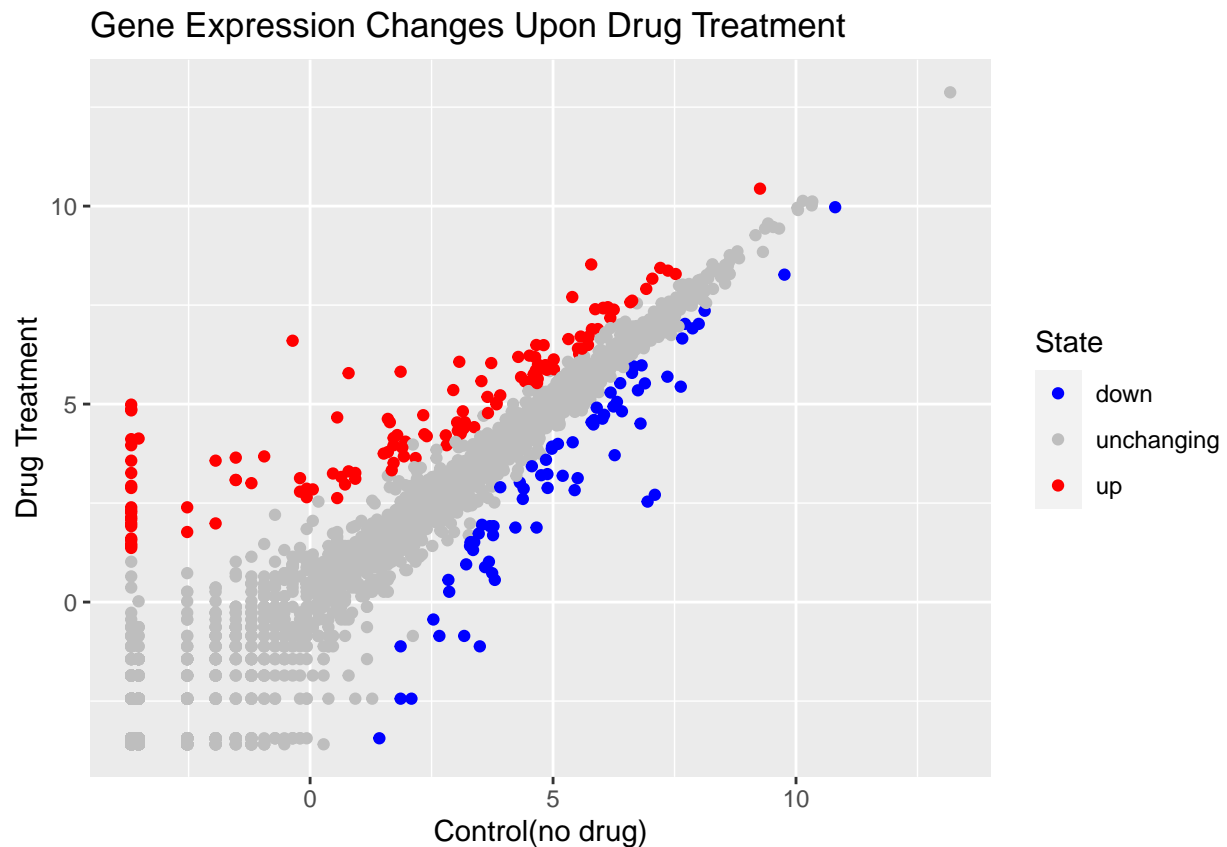
```
# Rounding  
round(table(genes$State)/nrow(genes) *100 , 2)
```

```
##  
##      down  unchanged      up  
##      1.39      96.17      2.44
```

```
#Complete code for plot  
p <- ggplot(genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point()
```

```
#Change color and add labels
```

```
p + scale_colour_manual( values=c("blue","gray","red") ) + labs(title= "Gene Expression Changes Upon Drug Treatment",  
                                                                x= "Control(no drug)" , y= "Drug Treatment")
```



```
#Install package for PDF  
#install.packages("tinytex")
```