

Class

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```
#Class 5: Data Visualization
```

```
#let's start with a scatterplot
```

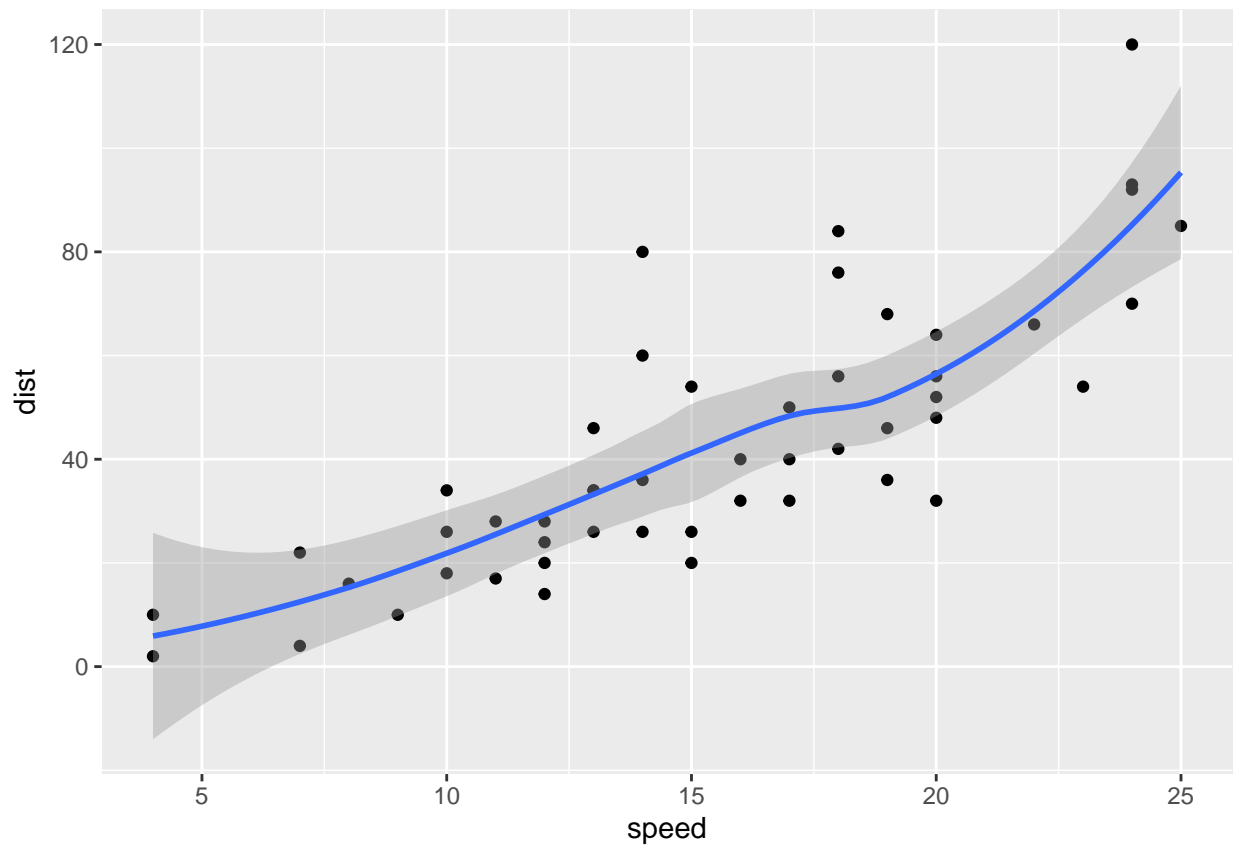
```
#before we use it we need to load it
```

```
library(ggplot2)
```

```
#Every plot has data +aes+ geoms
```

```
ggplot(data=cars)+aes(x=speed, y=dist)+ geom_point()+geom_smooth()
```

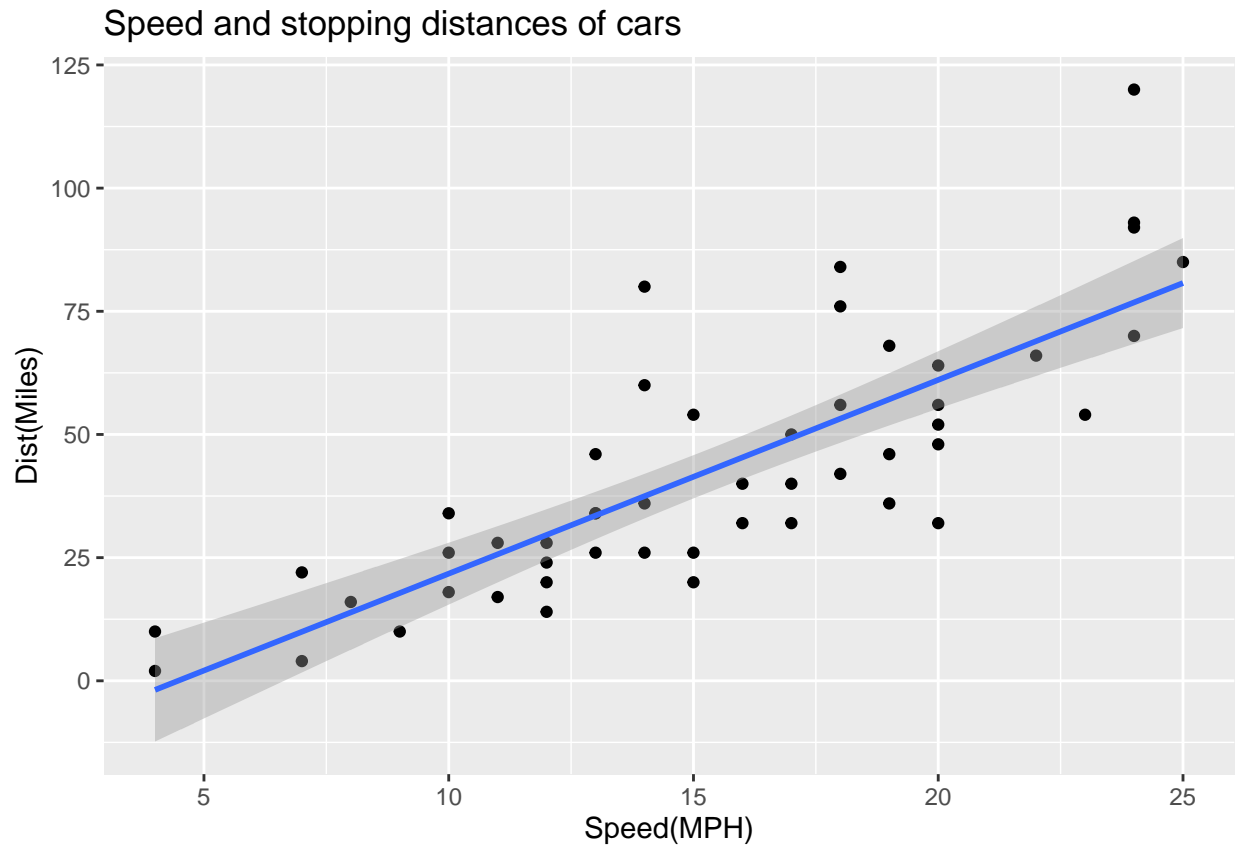
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



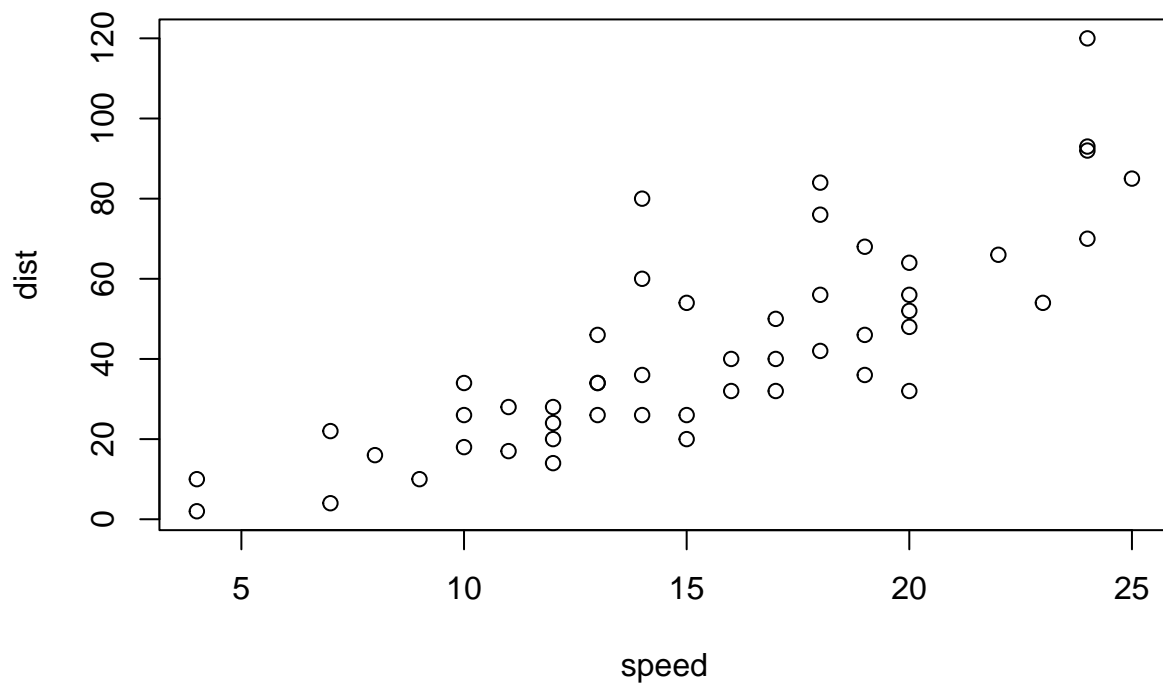
```
#change to a linear model
p <- ggplot(data=cars)+aes(x=speed, y=dist)+
  geom_point()+
  geom_smooth(method="lm")

p+ labs(title="Speed and stopping distances of cars", x="Speed(MPH)", y="Dist(Miles)")

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



```
#Base graphics is shorter
plot(cars)
```



```
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
```

```
#Q) how many genes?
nrow(genes)
```

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

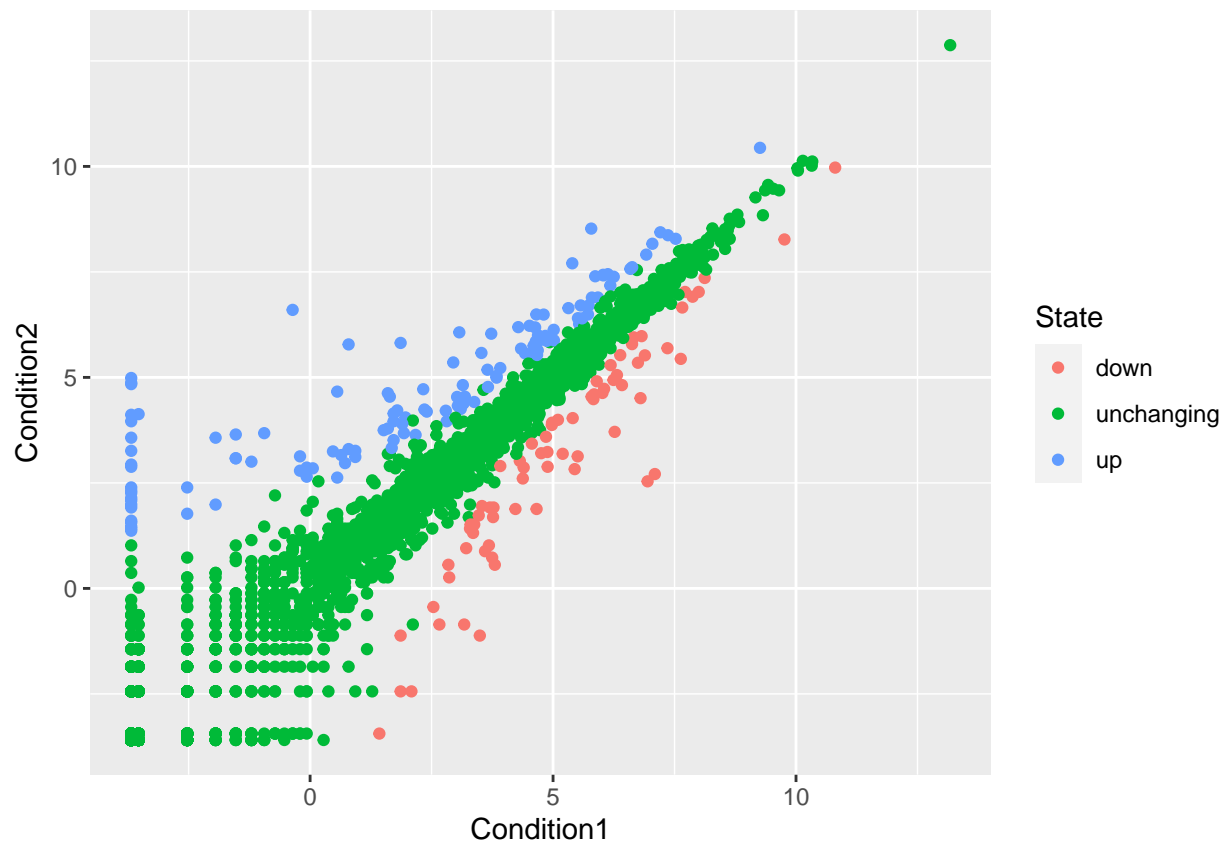
```
#Q) how to access state col
table(genes$State)
```

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

```
#Q) What % up or down
prec <- table(genes$State)/nrow(genes)* 100
round(prec, 2)
```

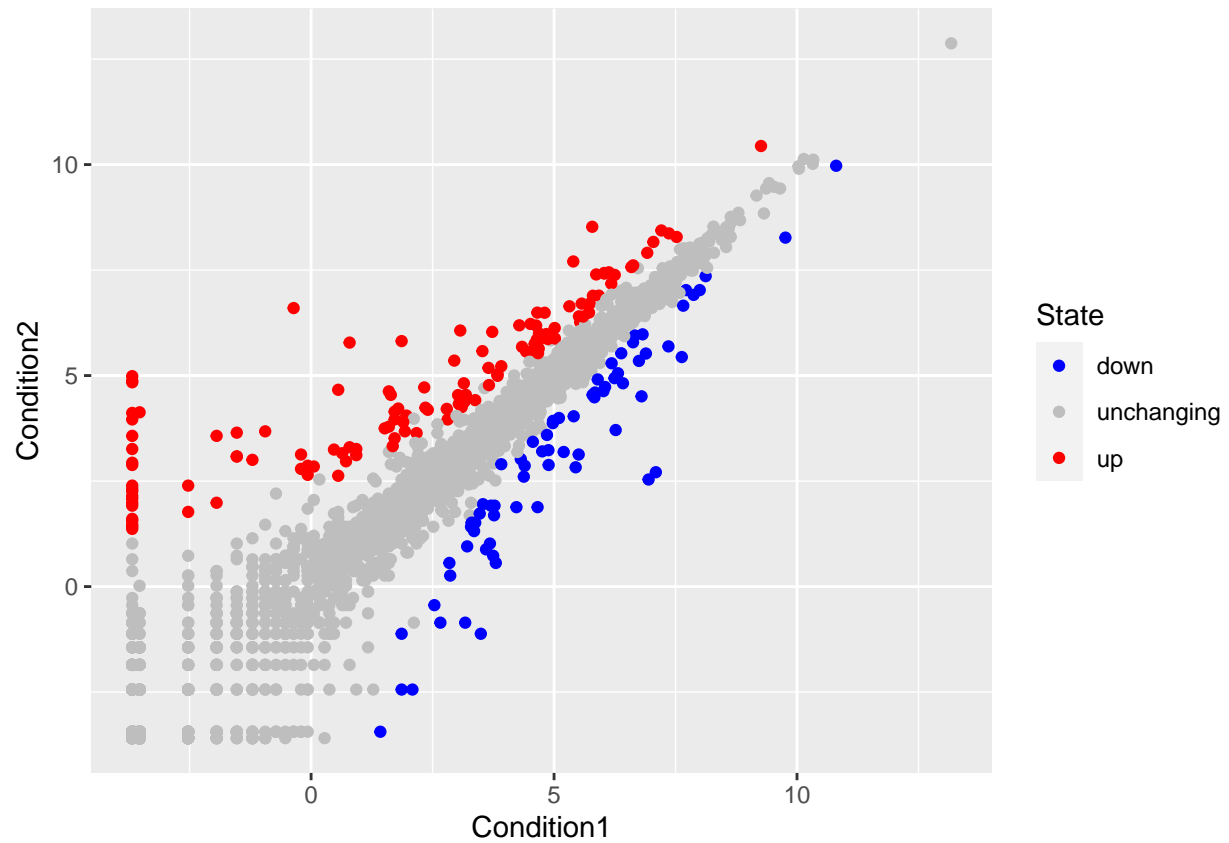
```
##
##      down  unchanged      up
##      1.39    96.17    2.44
```

```
#GGPLOT Genes
ggplot(data=genes)+ aes(x=Condition1, y=Condition2, col=State) + geom_point()
```



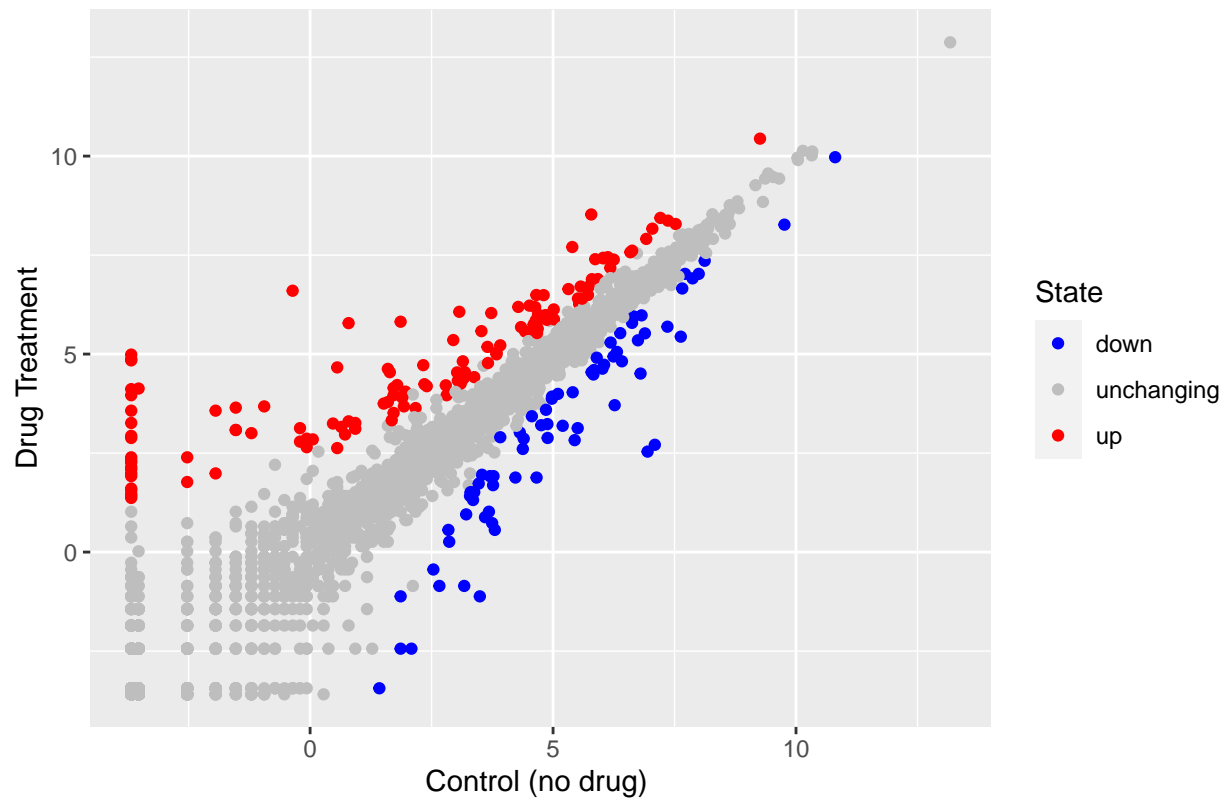
```
#Set p
p<- ggplot(data=genes)+ aes(x=Condition1, y=Condition2, col=State) + geom_point()

#Colors
p + scale_colour_manual( values=c("blue","gray","red") )
```



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

Gene Expression Changes Upon Drug Treatment



```
#Going further  
#gapminder  
library(gapminder)
```