

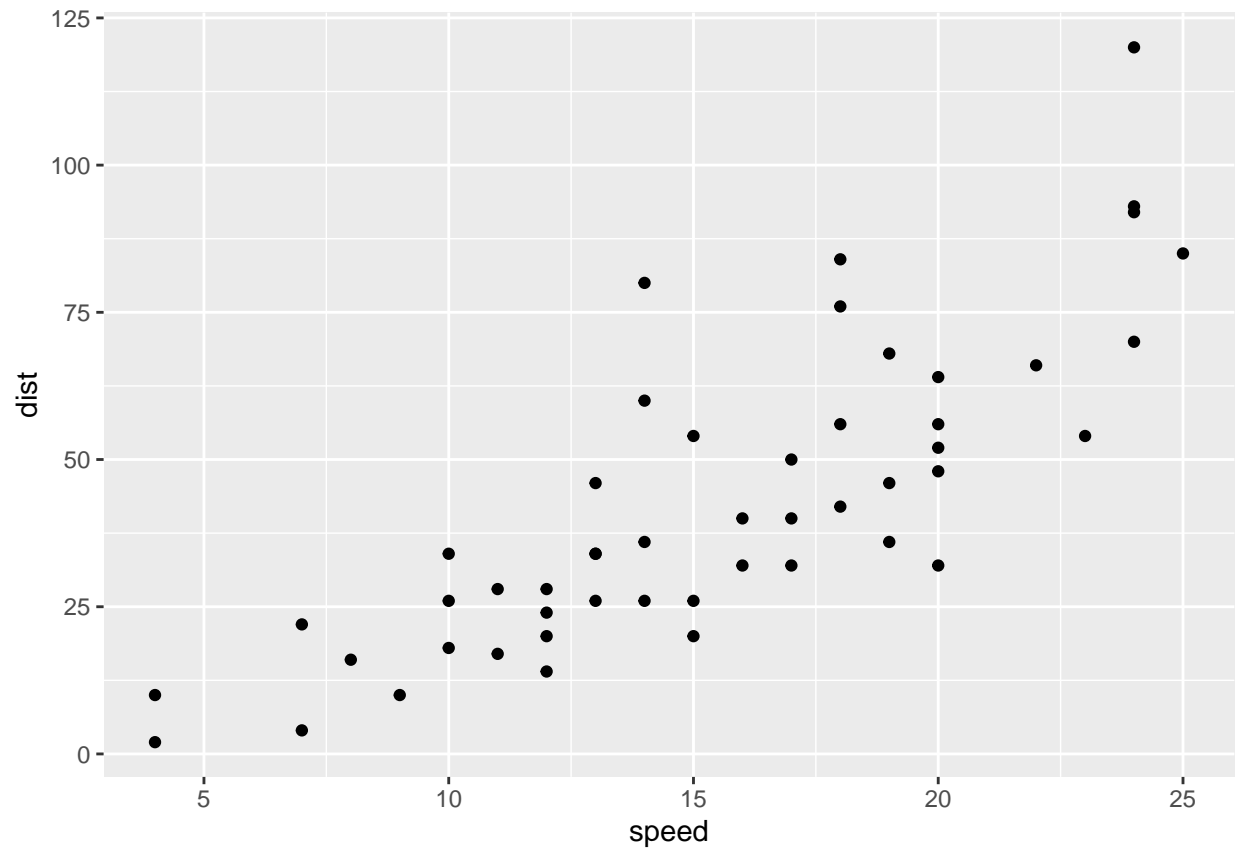
# Lab5.R

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```
#install.packages("ggplot2")  
  
#Lets us use the ggplot2 package  
library(ggplot2)  
  
ggplot(cars)
```

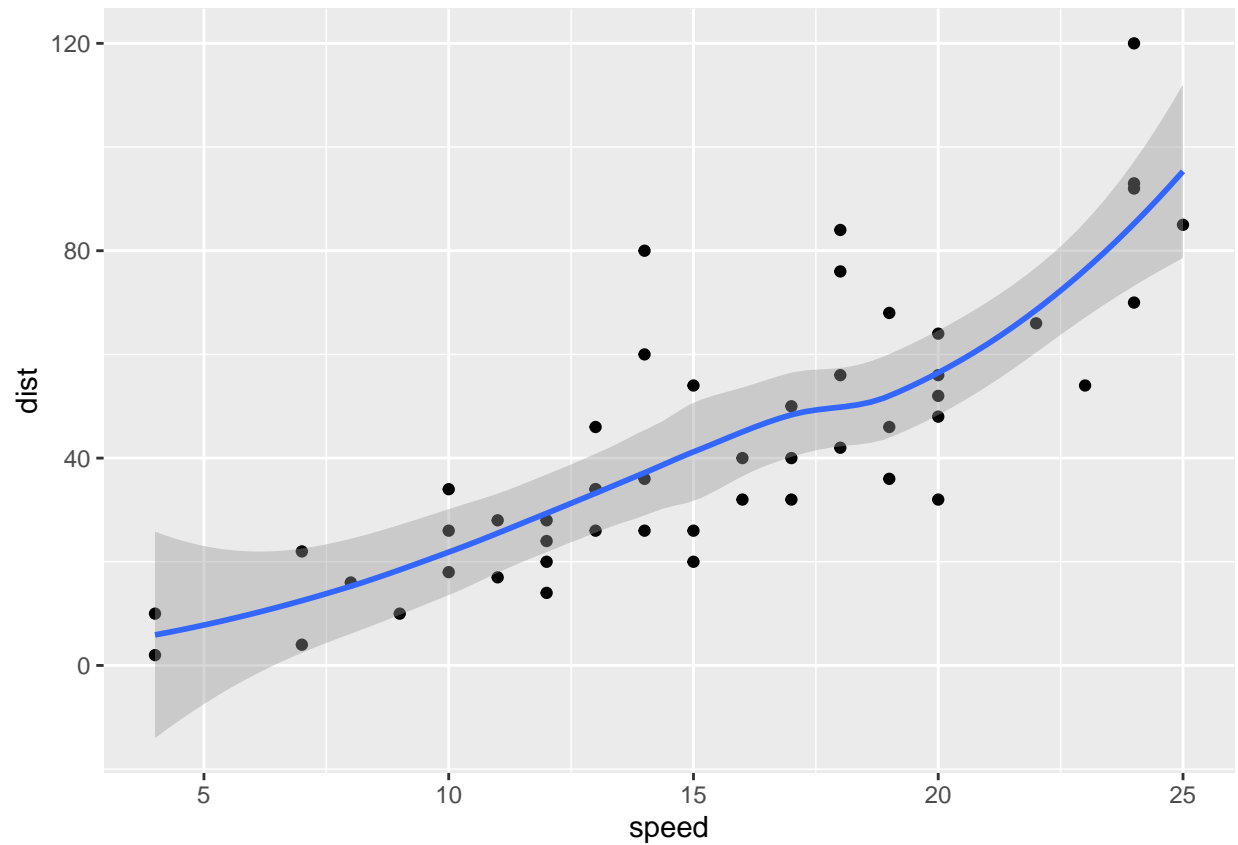
```
#First plot  
ggplot(cars) + aes(x=speed, y=dist) + geom_point()
```



```
#Second plot more geoms
```

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

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

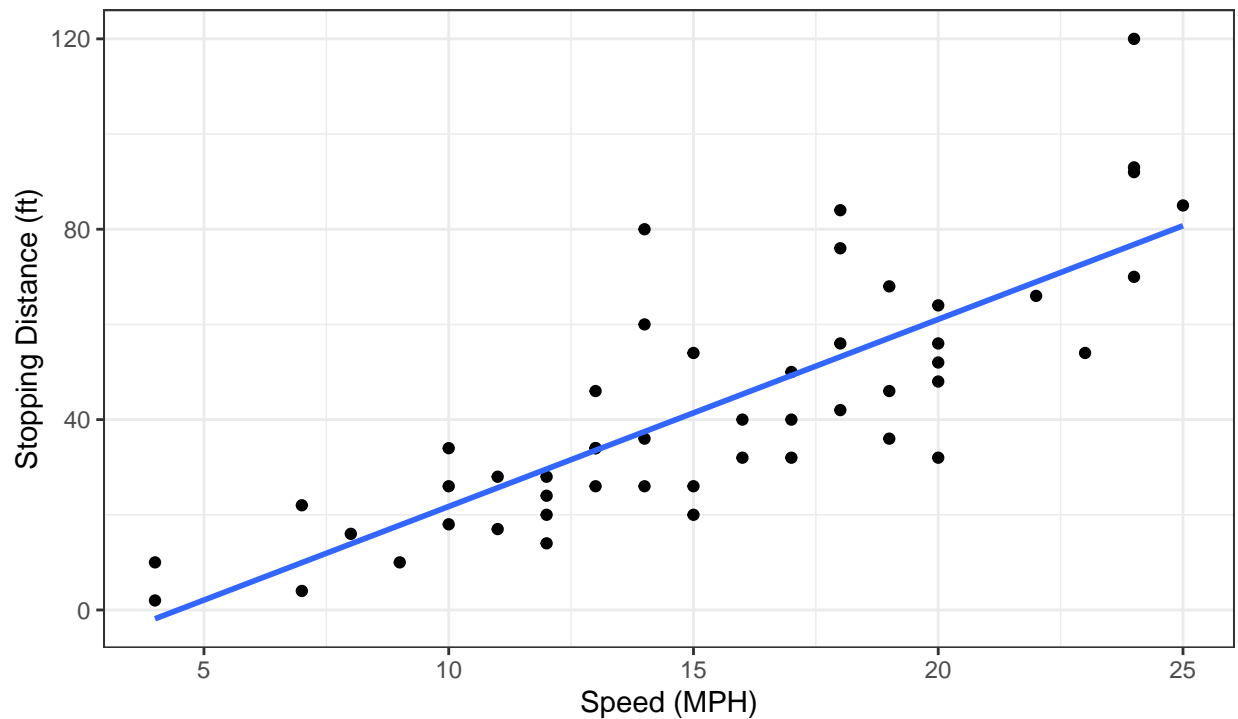


```
#Finished plot
ggplot(cars) + aes(x=speed, y=dist) +geom_point() +
  labs(title="Speed and Stopping Distances of Cars",
        x="Speed (MPH)", y="Stopping Distance (ft)",
        subtitle = "Informative subtitle",
        caption="Dataset: 'cars'") +
  geom_smooth(method="lm", se=FALSE) +
  theme_bw()
```

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

## Speed and Stopping Distances of Cars

Informative subtitle



Dataset: 'cars'

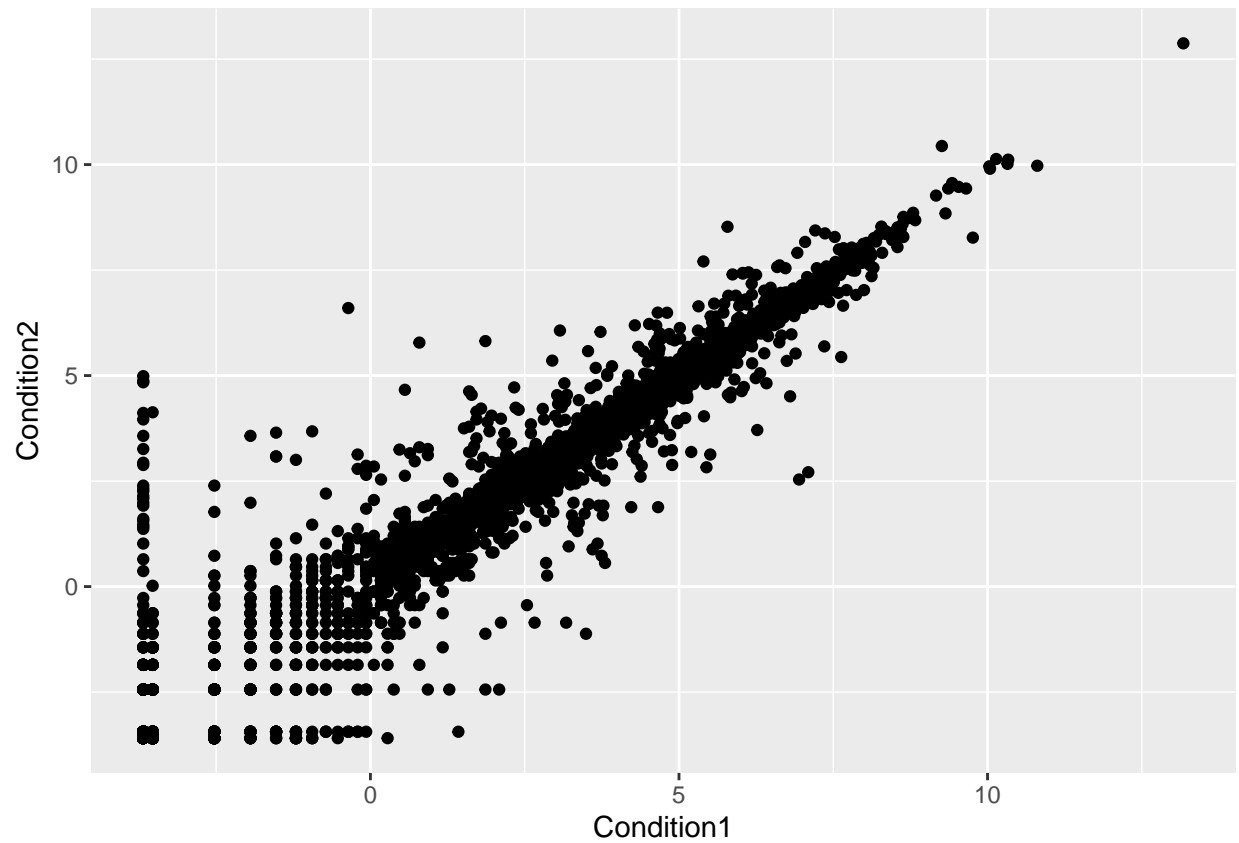
*#Example data set, differential expression analysis*

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

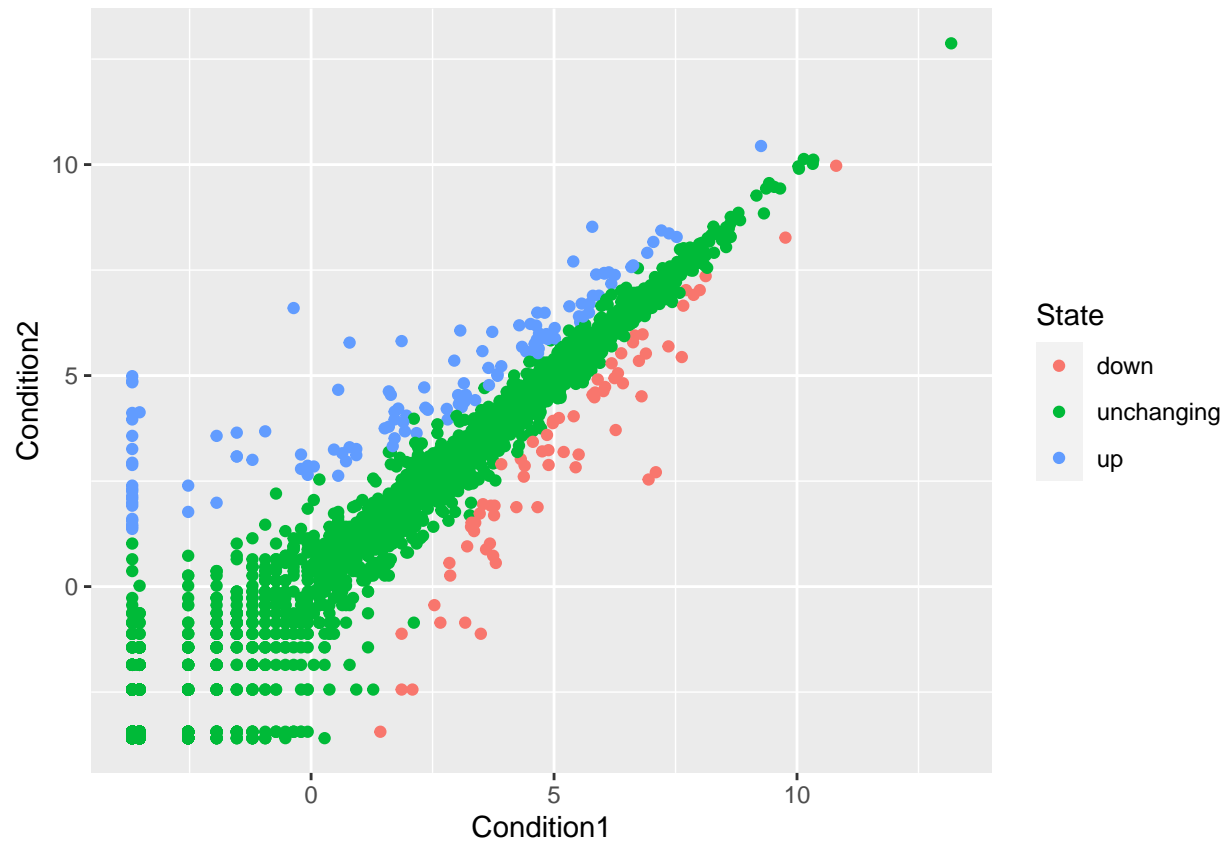
```
##      Gene Condition1 Condition2      State
## 1    A4GNT -3.6808610 -3.4401355  unchanging
## 2    AAAS  4.5479580  4.3864126  unchanging
## 3    AASDH  3.7190695  3.4787276  unchanging
## 4    AATF  5.0784720  5.0151916  unchanging
## 5    AATK  0.4711421  0.5598642  unchanging
## 6 AB015752.4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

*#Genes plot*

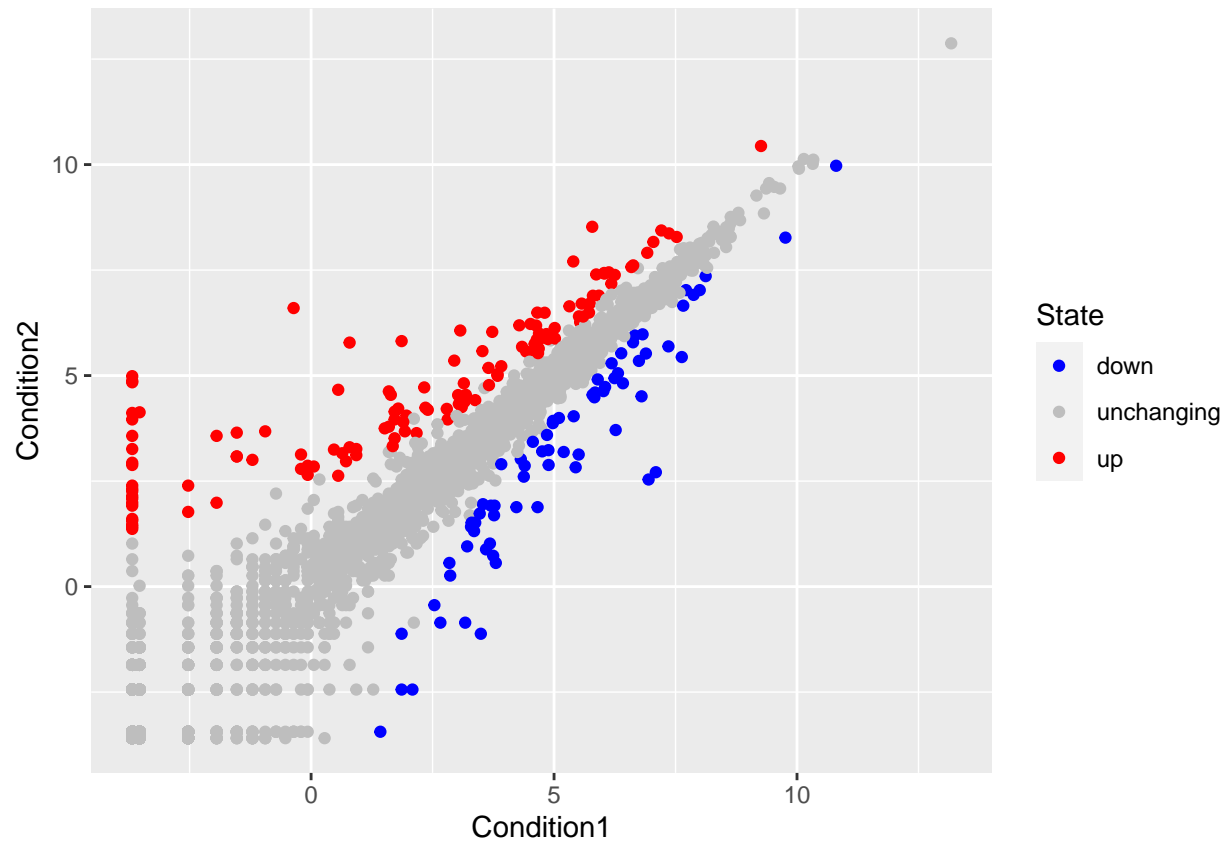
```
ggplot(genes) + aes(x=Condition1, y = Condition2) + geom_point()
```



```
#Genes plot with color  
p <- ggplot(genes) +  
  aes(x=Condition1, y=Condition2, col=State) +  
  geom_point()  
p
```



```
#Specify desired colors  
p + scale_colour_manual( values=c("blue","gray","red") )
```



```
#adding labels
p +
  labs(title="Gene Expression Changes Upon Drug Treatment",
        x="Control (no drug)",
        y="Drug")
```

