

Class05.R

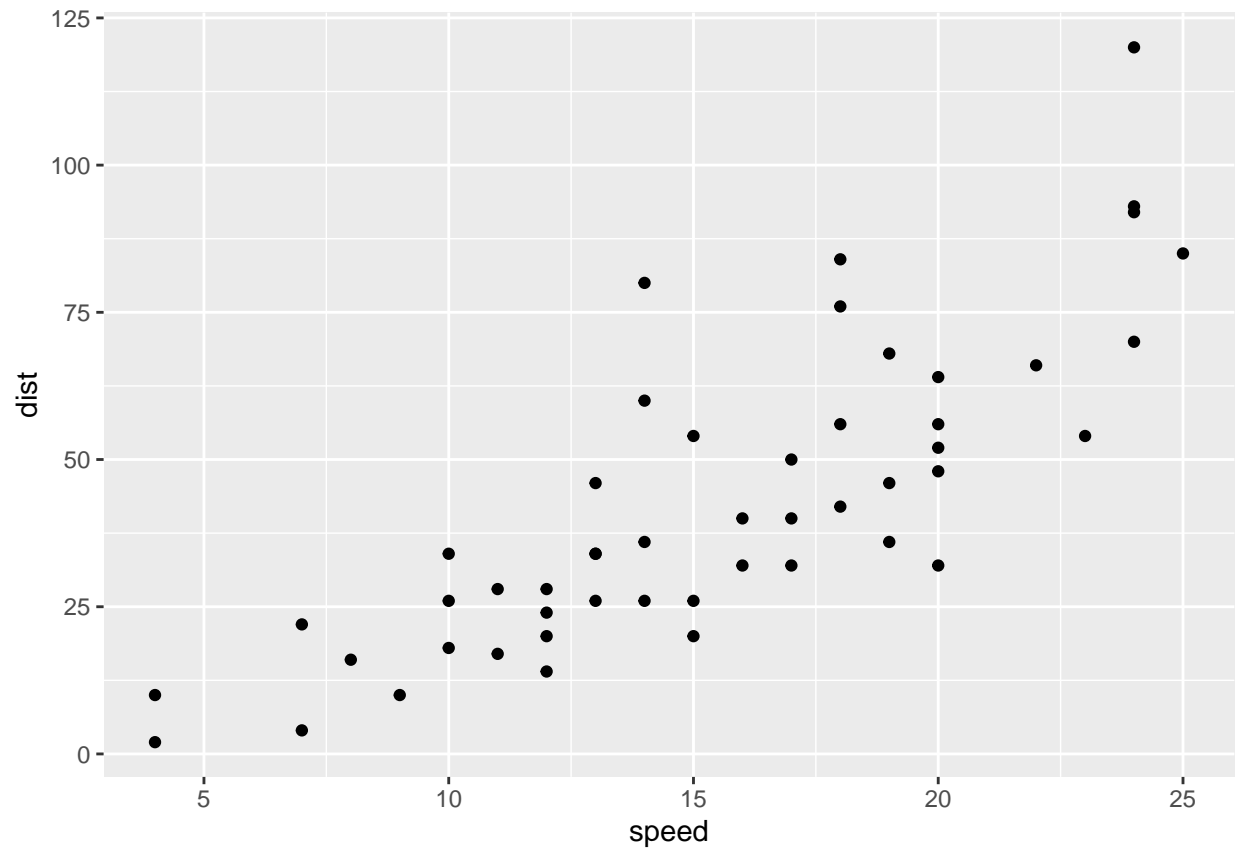
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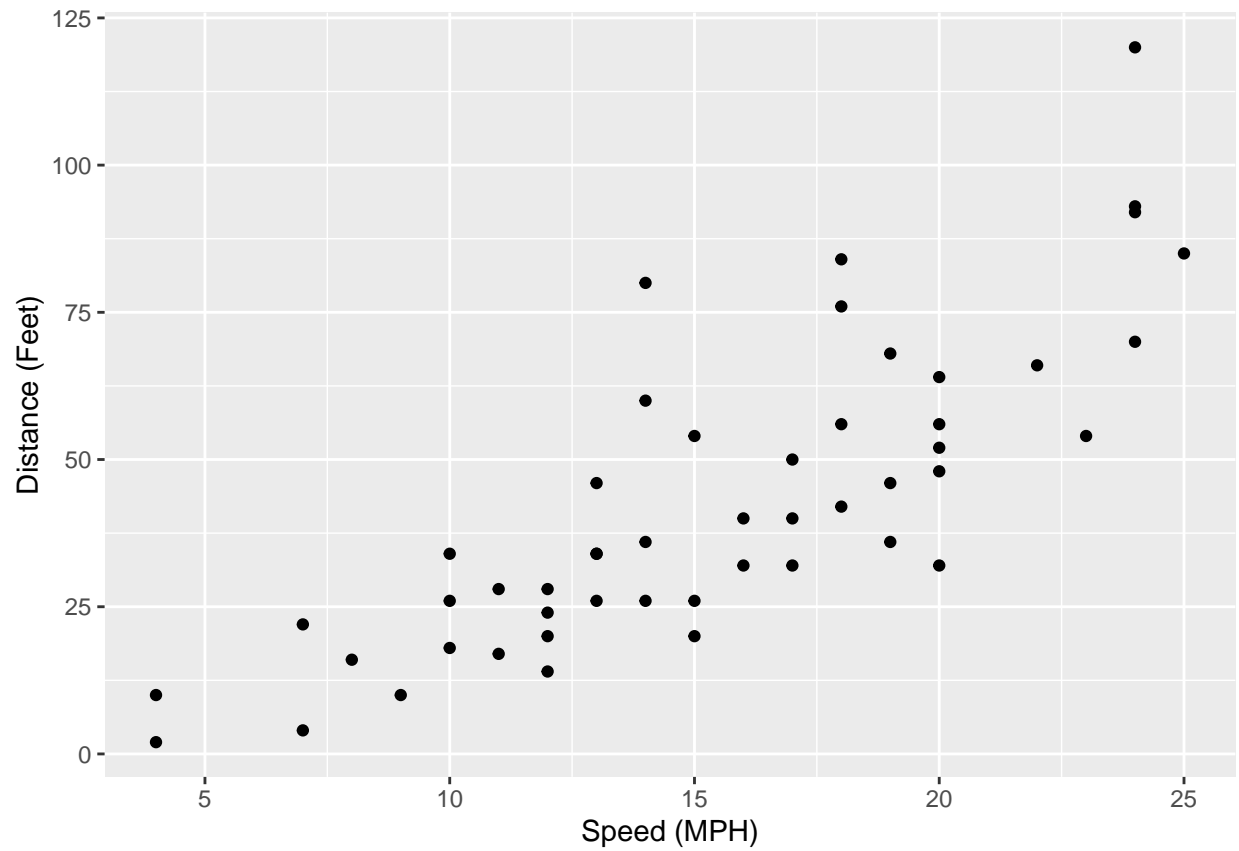
```
# Class 5 data visulaization  
#In thi sclass we are going ot learn and go over ggplot2 dta package  
  
#you have to call ggplot2 everytime you go to use it- go to library and load  
# use library(ggplot2)  
#now builiding a ggplot wiht the cars data that is a fearure of R  
#all ggplots have at least 3 layers  
  #data + aes + geoms  
library(ggplot2)  
head(cars)
```

```
##   speed dist  
## 1     4    2  
## 2     4   10  
## 3     7    4  
## 4     7   22  
## 5     8   16  
## 6     9   10
```

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

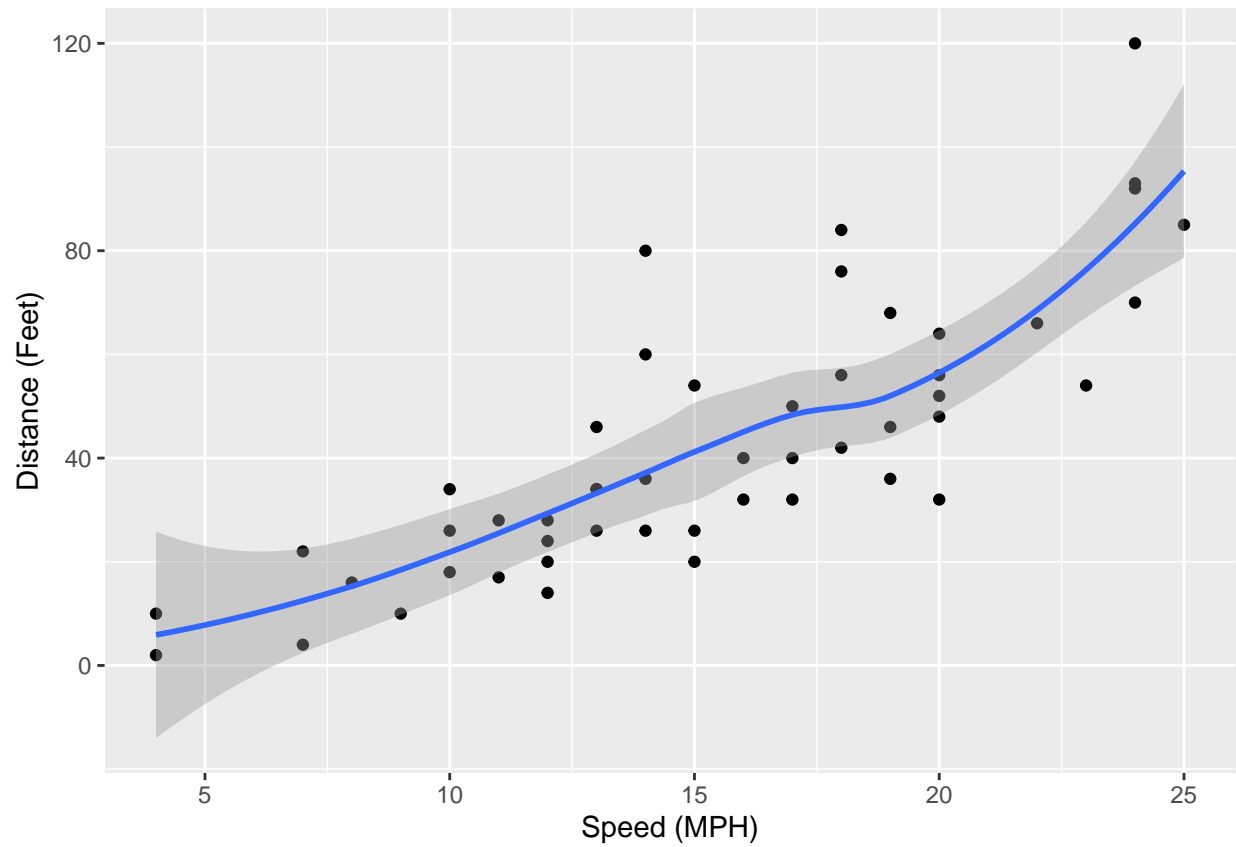


```
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  labs(title="Stopping distance of old cars",  
        x="Speed (MPH)",  
        y="Distance (Feet)")
```

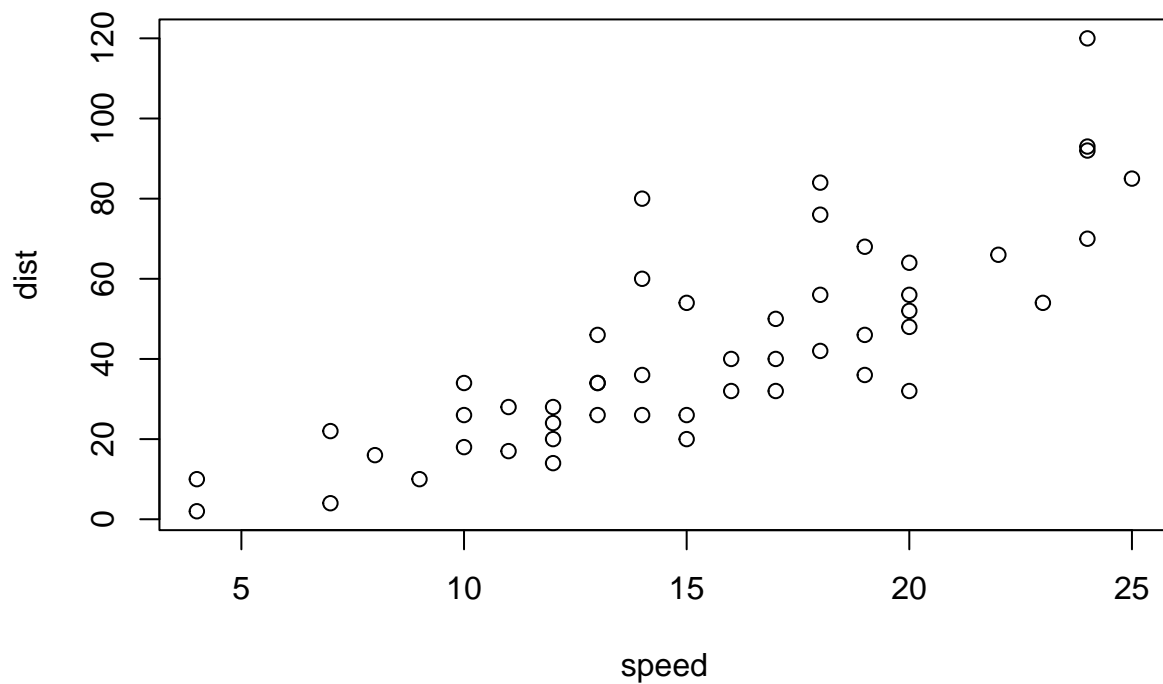


```
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth() +  
  labs(title="Stopping distance of old cars",  
        x="Speed (MPH)",  
        y="Distance (Feet)")
```

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



#ggplot is not the only graphics system, a very popular one is "base" R graphics
`plot(cars)`



#now time for the class lab worksheet stuff

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
#Playing around with this genes dataframe to understand
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
```

```
nrow(genes)
```

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

```
colnames(genes)
```

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

```
ncol(genes)
```

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

```
table("State")
```

```
##  
## State  
##      1
```

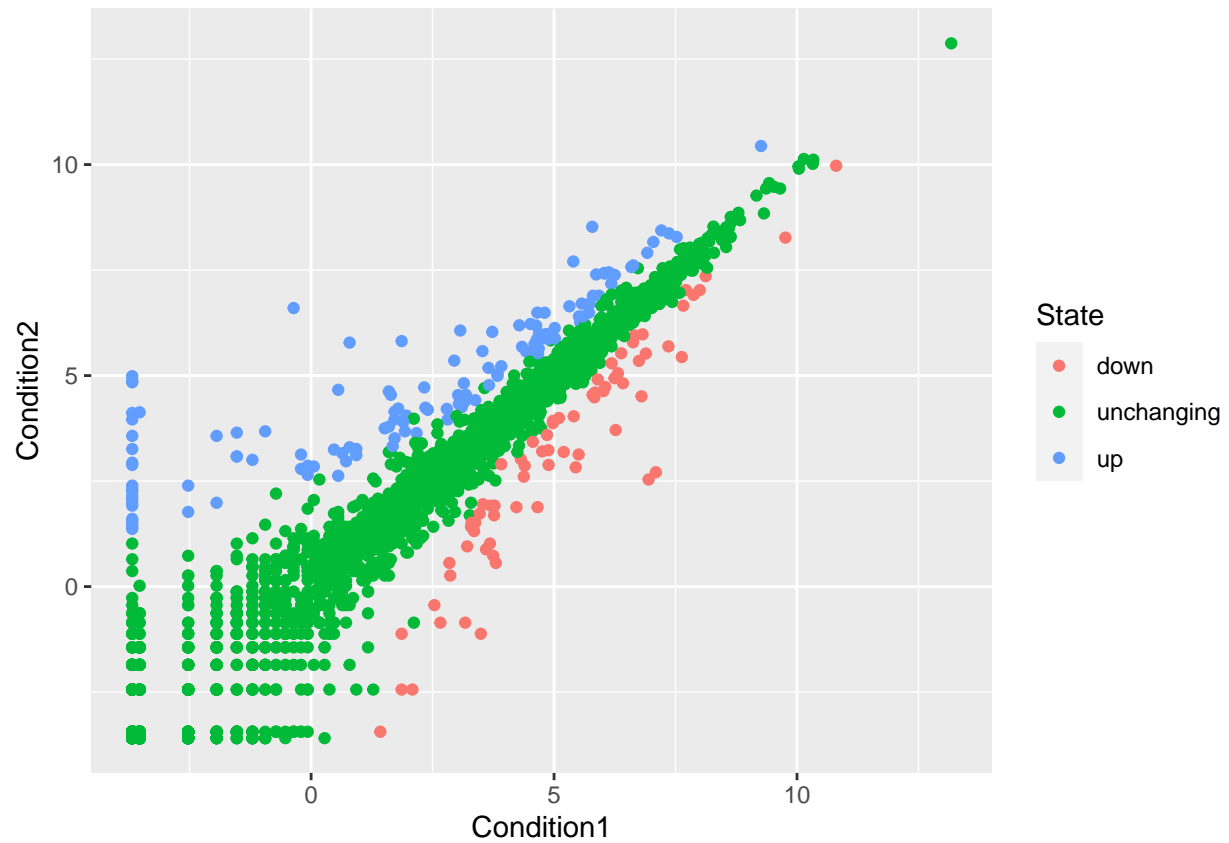
```
table(genes$State)
```

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

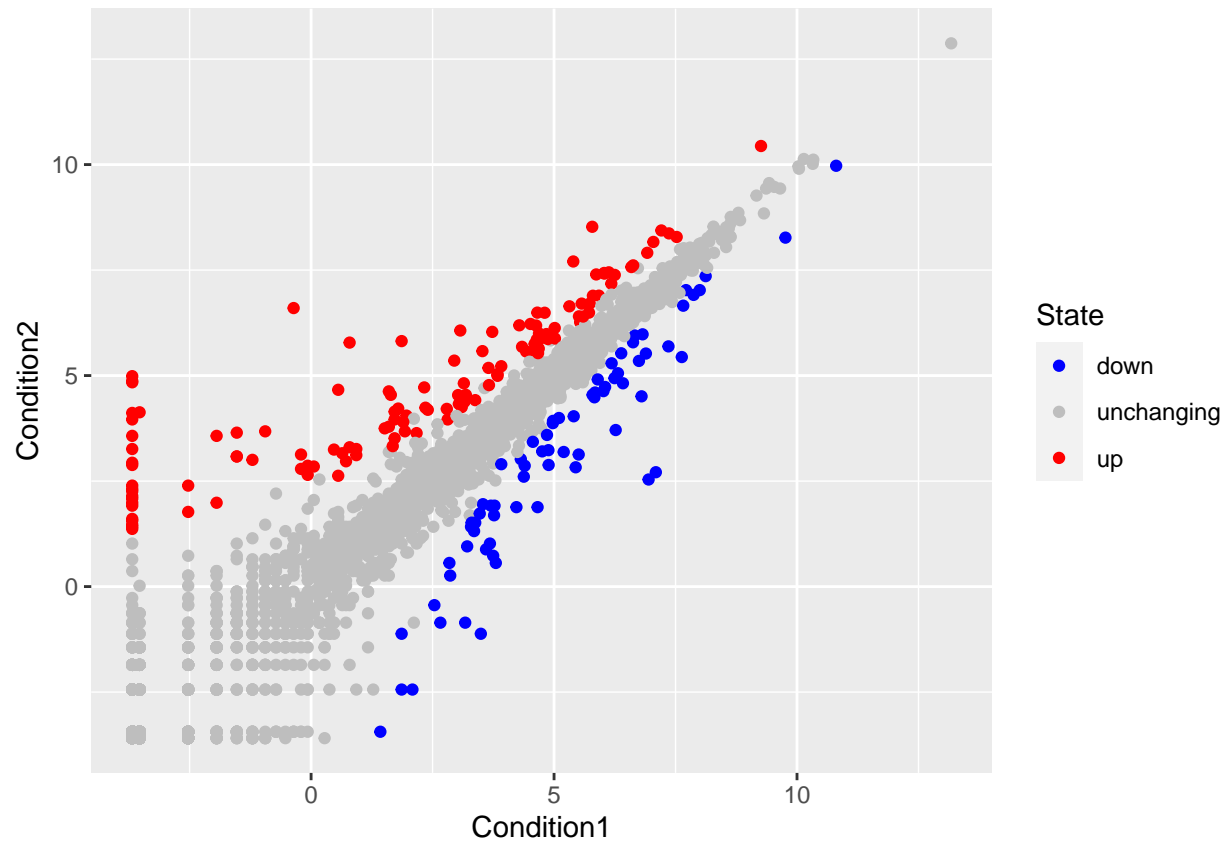
```
#How many genes are upregulated? Rounded to the 2nd sig fig  
round(table(genes$State)/nrow(genes)*100,2)
```

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

```
#taking this dataset for genes and working up in ggplot  
ggplot(data=genes) +  
  aes(x=Condition1, y=Condition2, col= State) +  
  geom_point()
```

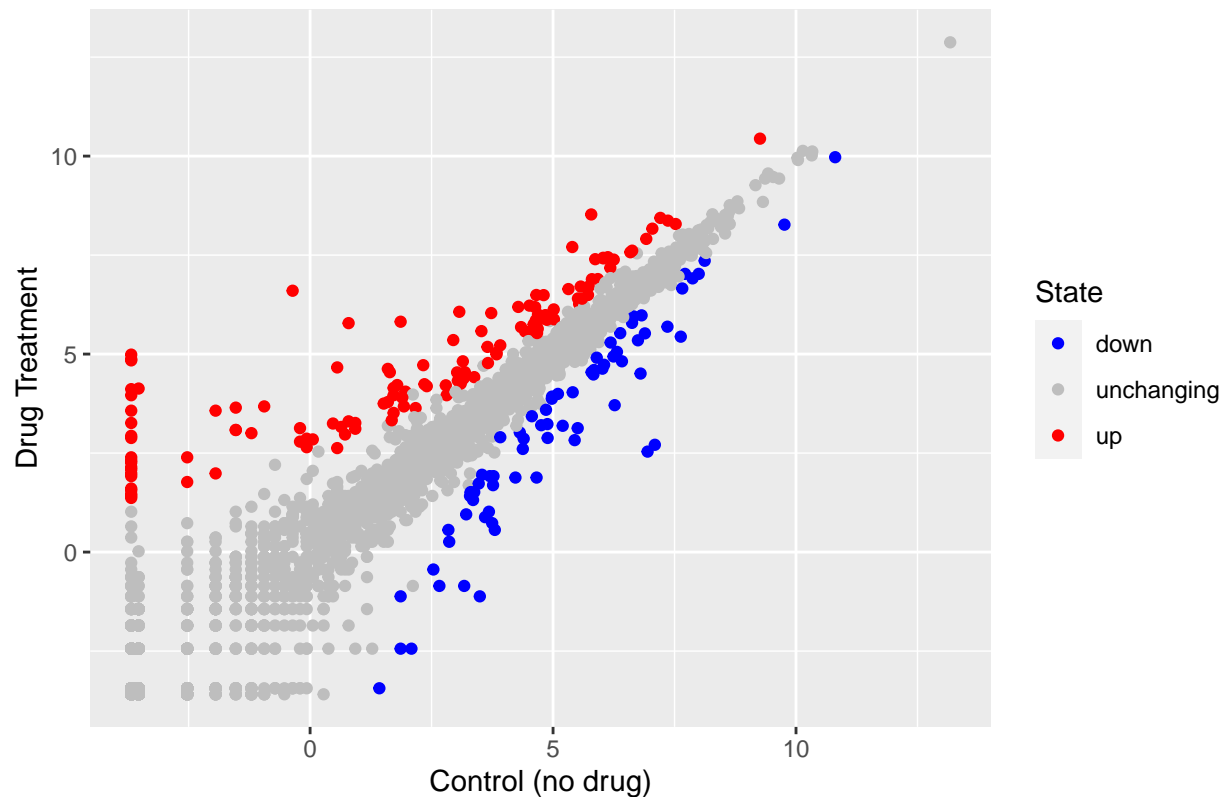


```
#Save the basic pieces as p so it is easier to build and add lines
p <-ggplot(data=genes) +
  aes(x=Condition1, y=Condition2, col= State) +
  geom_point()
p + scale_color_manual(values = c( "blue", "grey","red"))
```



```
p <-ggplot(data=genes) +
  aes(x=Condition1, y=Condition2, col= State) +
  geom_point() +
  scale_color_manual(values = c( "blue", "grey","red"))
p + labs(title= "Gene Expression Changes Upon Drug Treatment",
  x= "Control (no drug)",
  y= "Drug Treatment")
```


Gene Expression Changes Upon Drug Treatment



```
#now doing stuff with the dataset gapminder
#install.packages("gapminder")
```

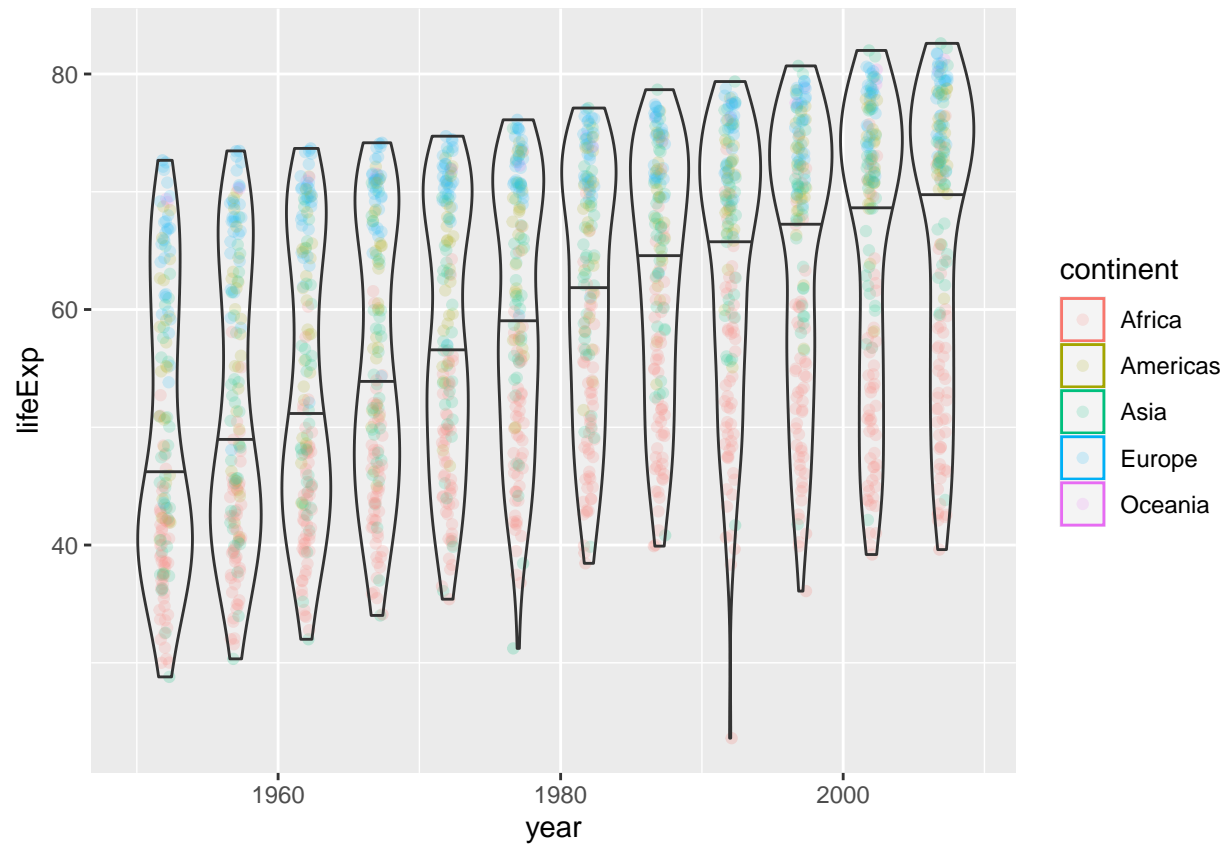
```
library(gapminder)
```

```
head(gapminder)
```

```
## # A tibble: 6 x 6
##   country    continent  year lifeExp    pop gdpPercap
##   <fct>      <fct>    <int> <dbl>    <int>    <dbl>
## 1 Afghanistan Asia      1952   28.8  8425333    779.
## 2 Afghanistan Asia      1957   30.3  9240934    821.
## 3 Afghanistan Asia      1962   32.0 10267083    853.
## 4 Afghanistan Asia      1967   34.0 11537966    836.
## 5 Afghanistan Asia      1972   36.1 13079460    740.
## 6 Afghanistan Asia      1977   38.4 14880372    786.
```

```
# lets make a new plot of life vs. life exp
```

```
ggplot(gapminder) +
  aes(x=year, y=lifeExp, col= continent) +
  geom_jitter(width= 0.4, alpha= 0.2) +
  geom_violin(aes(group=year), alpha=0.2, draw_quantiles = 0.5)
```



```
geom_point()
```

```
## geom_point: na.rm = FALSE
## stat_identity: na.rm = FALSE
## position_identity
```

#this didnt quite work and I got behind on the section^^, look at his page for reference

```
#Install the plotly
#install.packages("plotly")
```