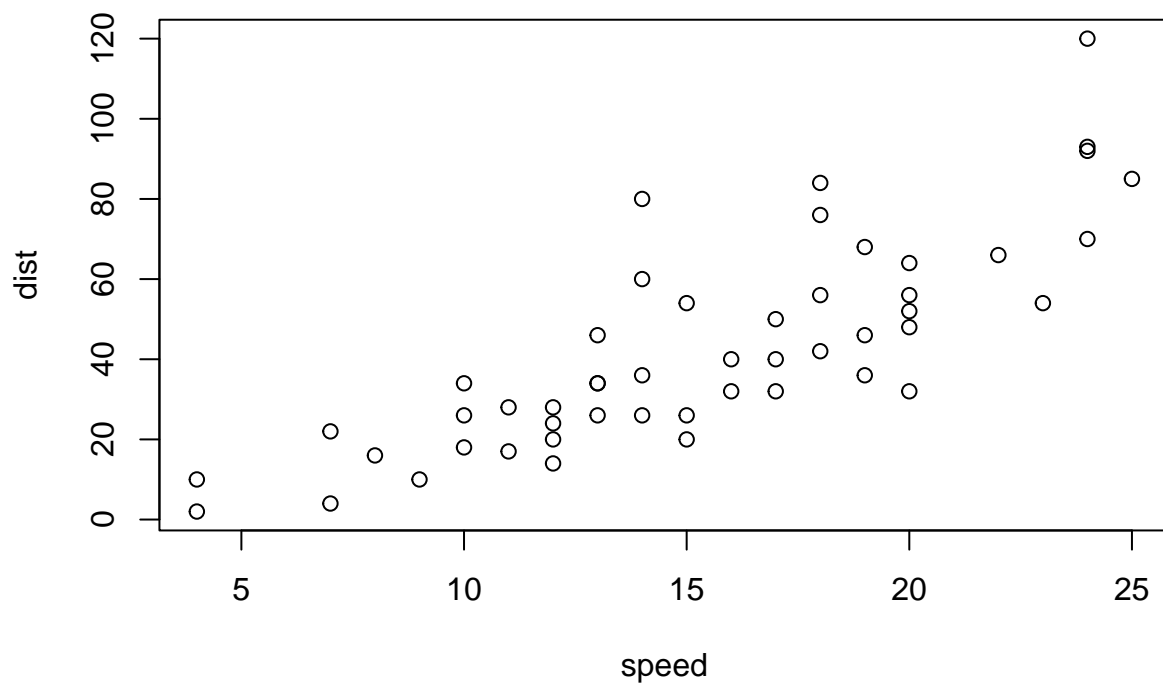


## class05.R

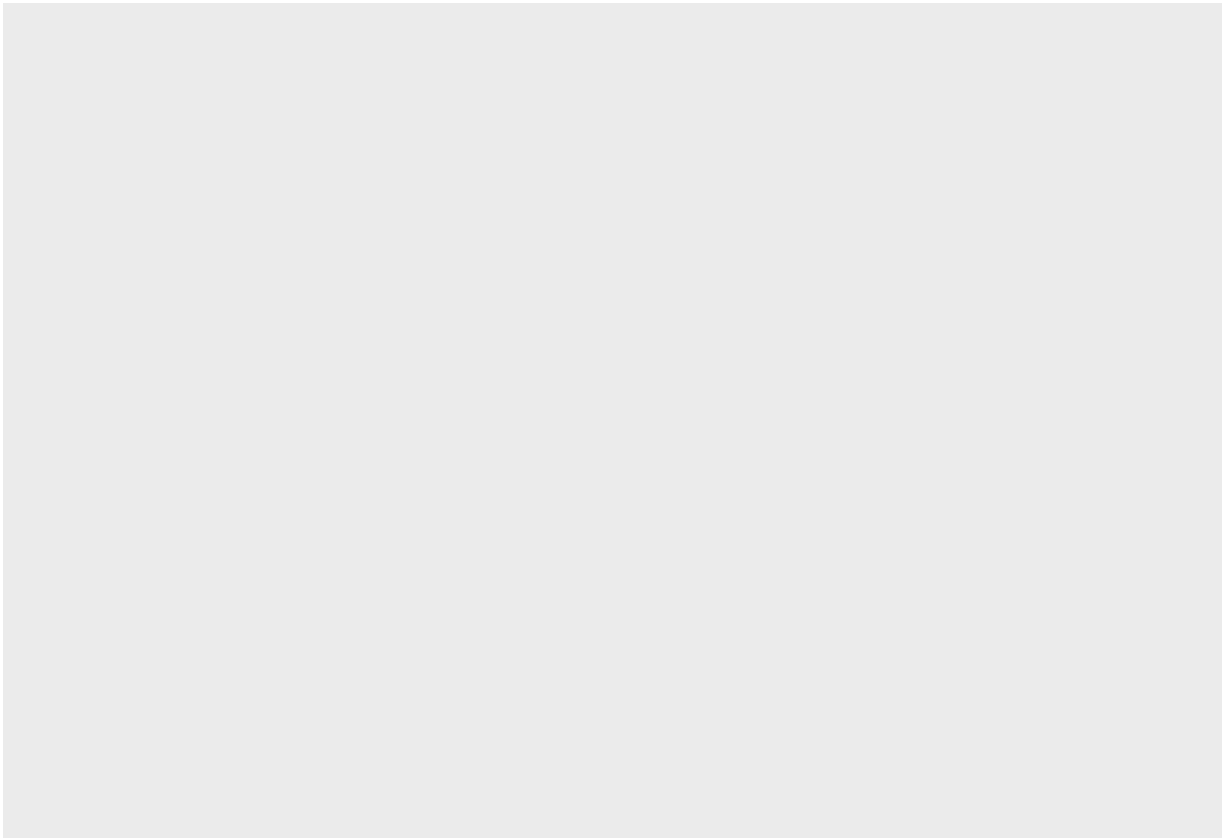
barry

2022-02-01

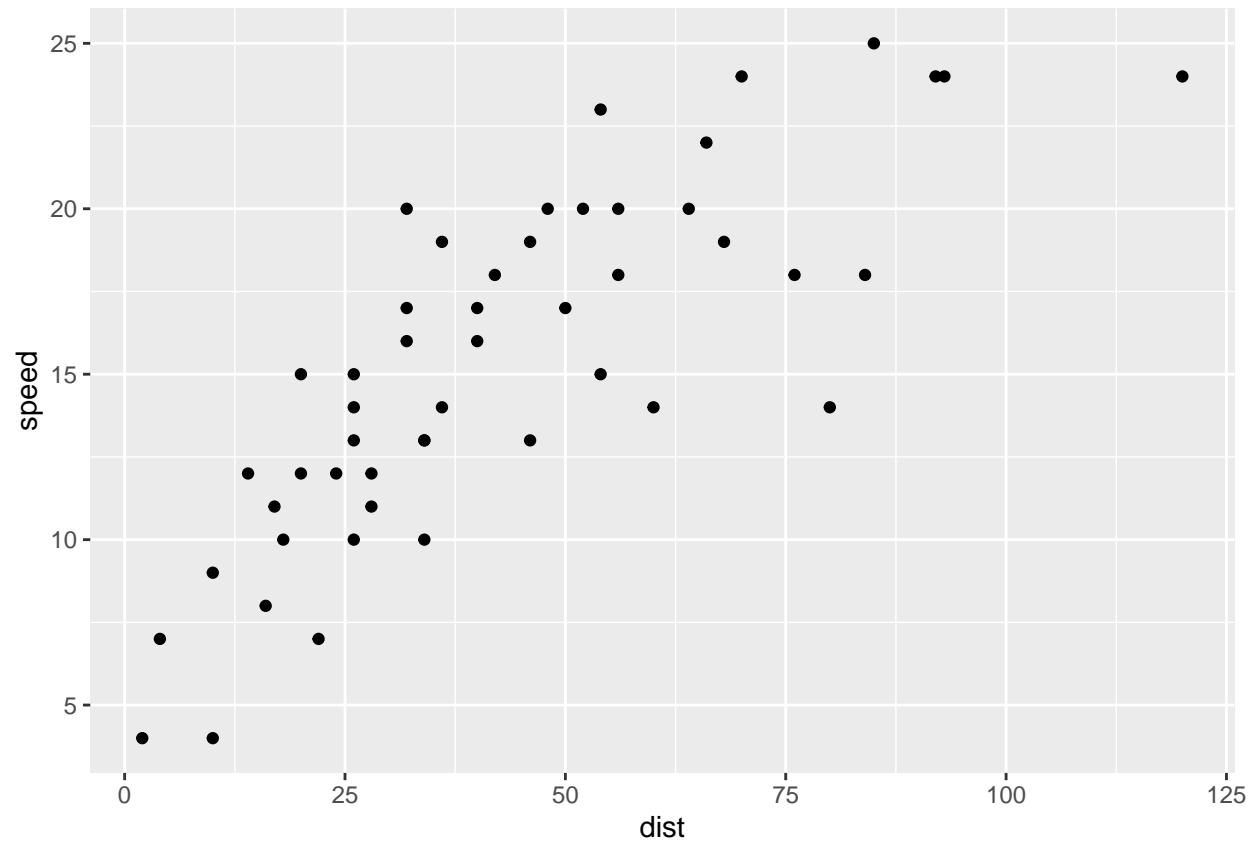
```
# Class 05 Data Visualization  
  
# This is the "base" R plot  
plot(cars)  
  
# We are going to get a new plotting package called ggplot2  
#ggplot(cars)  
  
# install.packages("ggplot2")  
# Now we need to call/load the package  
library(ggplot2)
```



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

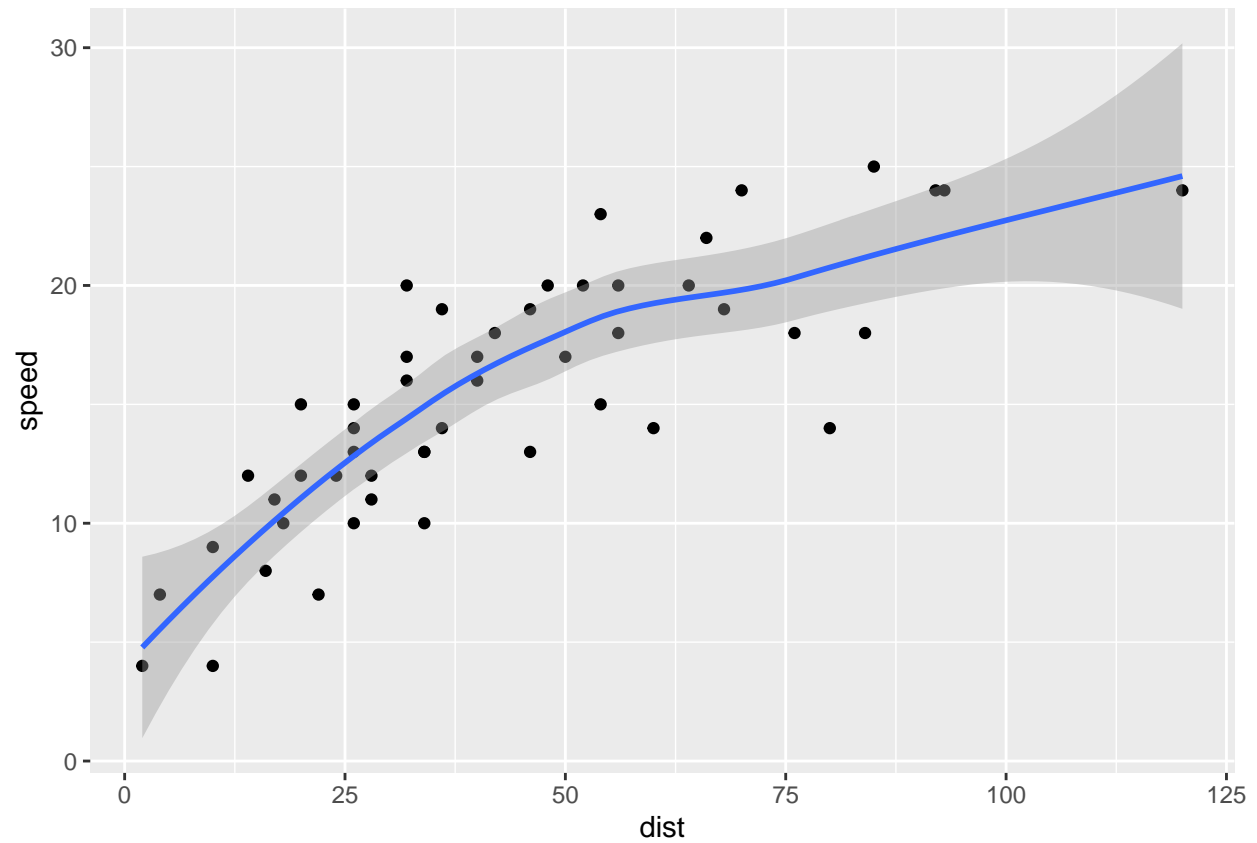


```
gg <- ggplot(data=cars) + aes(x=dist, y=speed) + geom_point()  
gg
```



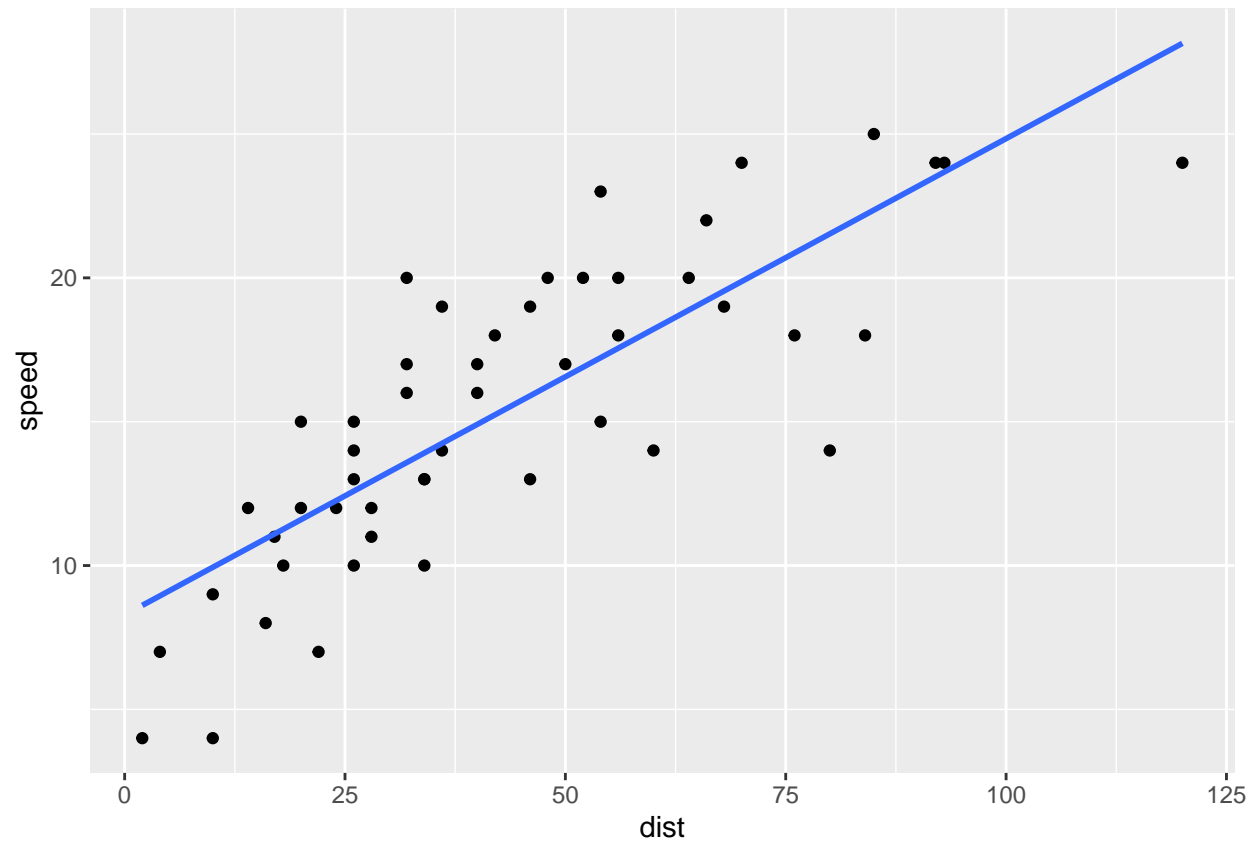
```
# One last thing. lets add a line to the data  
gg + geom_smooth()
```

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



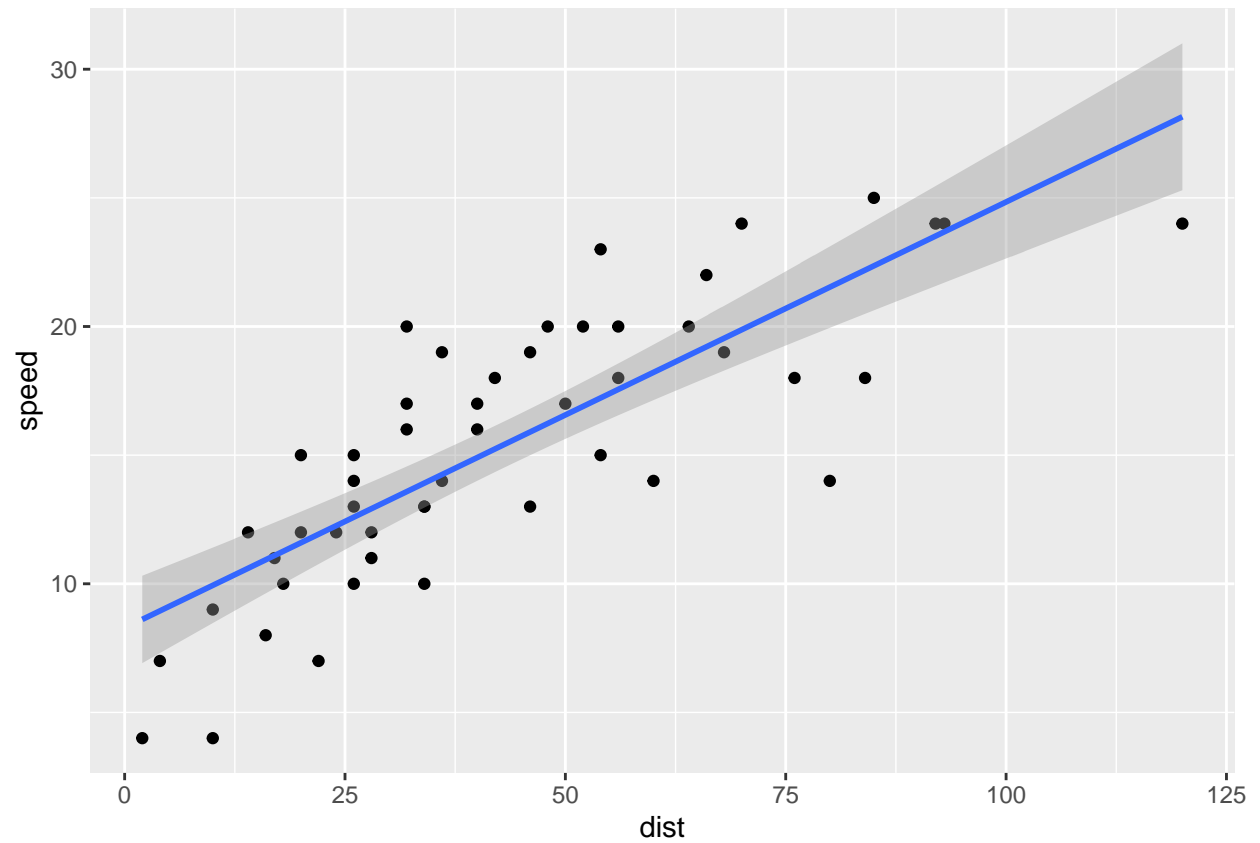
```
# I want a linear model  
gg + geom_smooth(method="lm", se=FALSE)
```

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



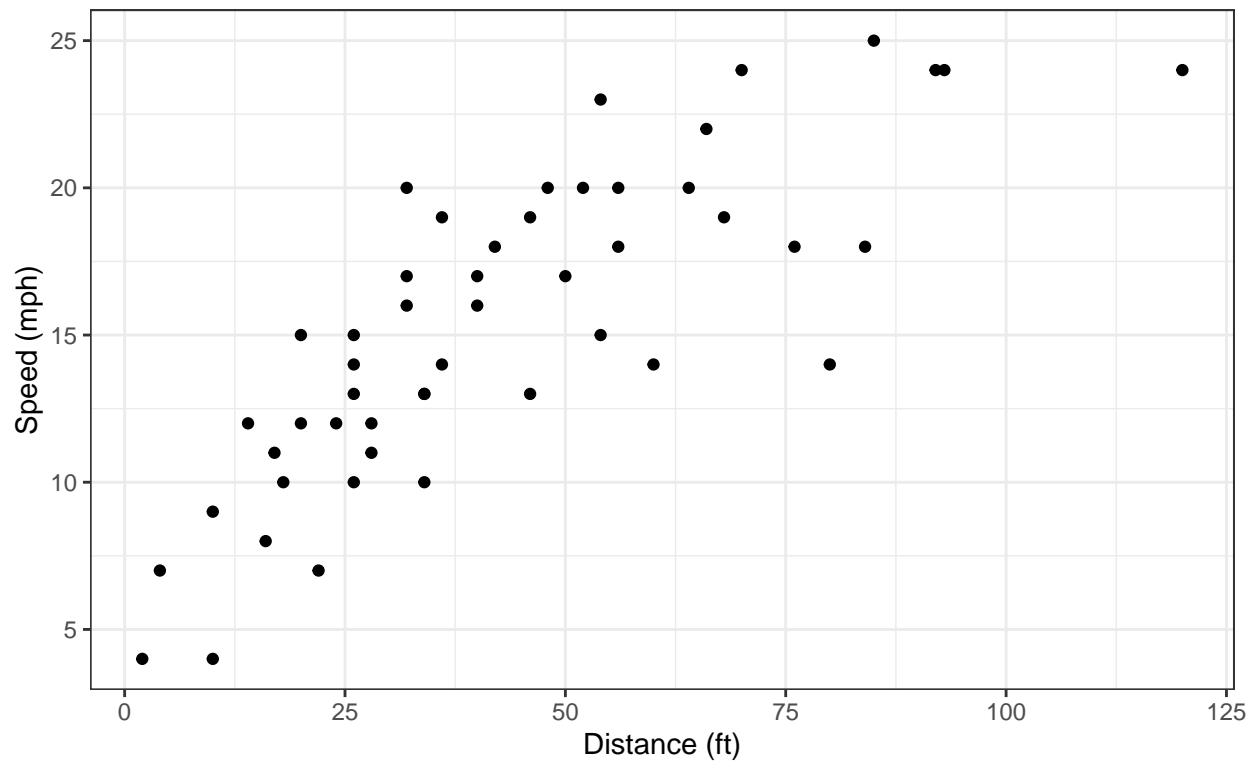
```
ggplot(data=cars) +  
  aes(x=dist, y=speed) +  
  geom_point() +  
  geom_smooth(method="lm")
```

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



```
# Add more layers
gg + labs(title="Some old title",
          caption="What is this?") +
  xlab("Distance (ft)") +
  ylab("Speed (mph)") +
  theme_bw()
```

Some old title



What is this?

```
# RNASeq experiment dataset.
```

```
# 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
```

```
# > Q. How many genes in this dataset?
```

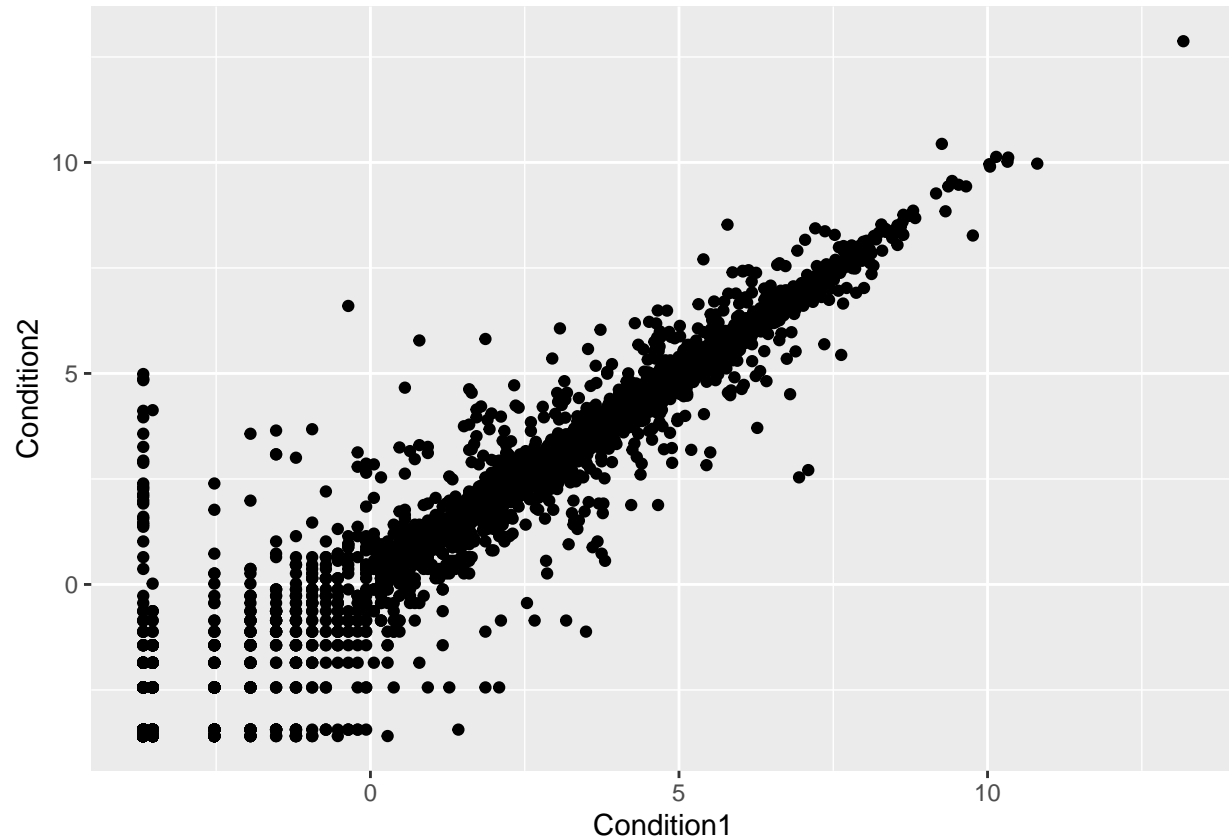
```
nrow(genes)
```

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

```
colnames(genes)
```

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

```
# I want to plot this result
ggplot(genes) +
  aes(x=Condition1, y=Condition2) +
  geom_point()
```



```
#Q. How many genes are "up" regulated in this experiment
table( genes$State )
```

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

```
# Add some color to denote up/down values
ggplot(genes) +
  aes(x=Condition1, y=Condition2, color=State) +
  geom_point() +
  labs(title="Some gene expression data")
```



Some gene expression data

