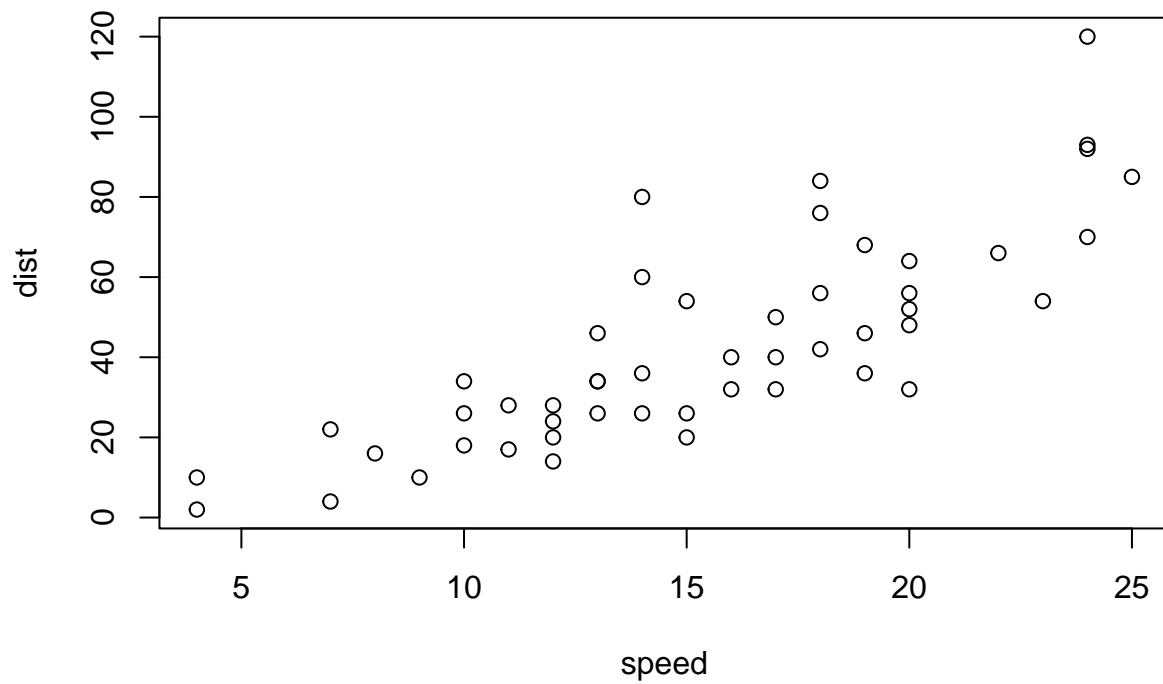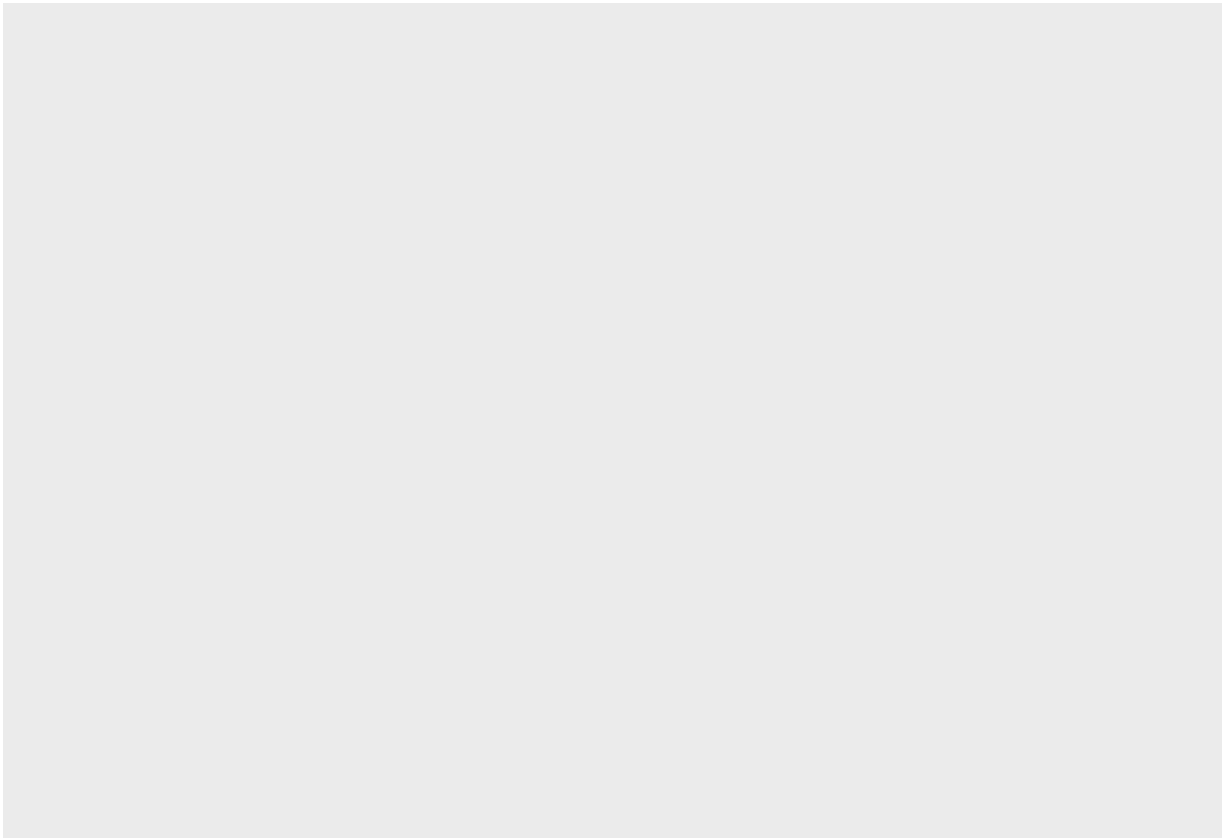# class05.R

kainguyen

2022-02-01
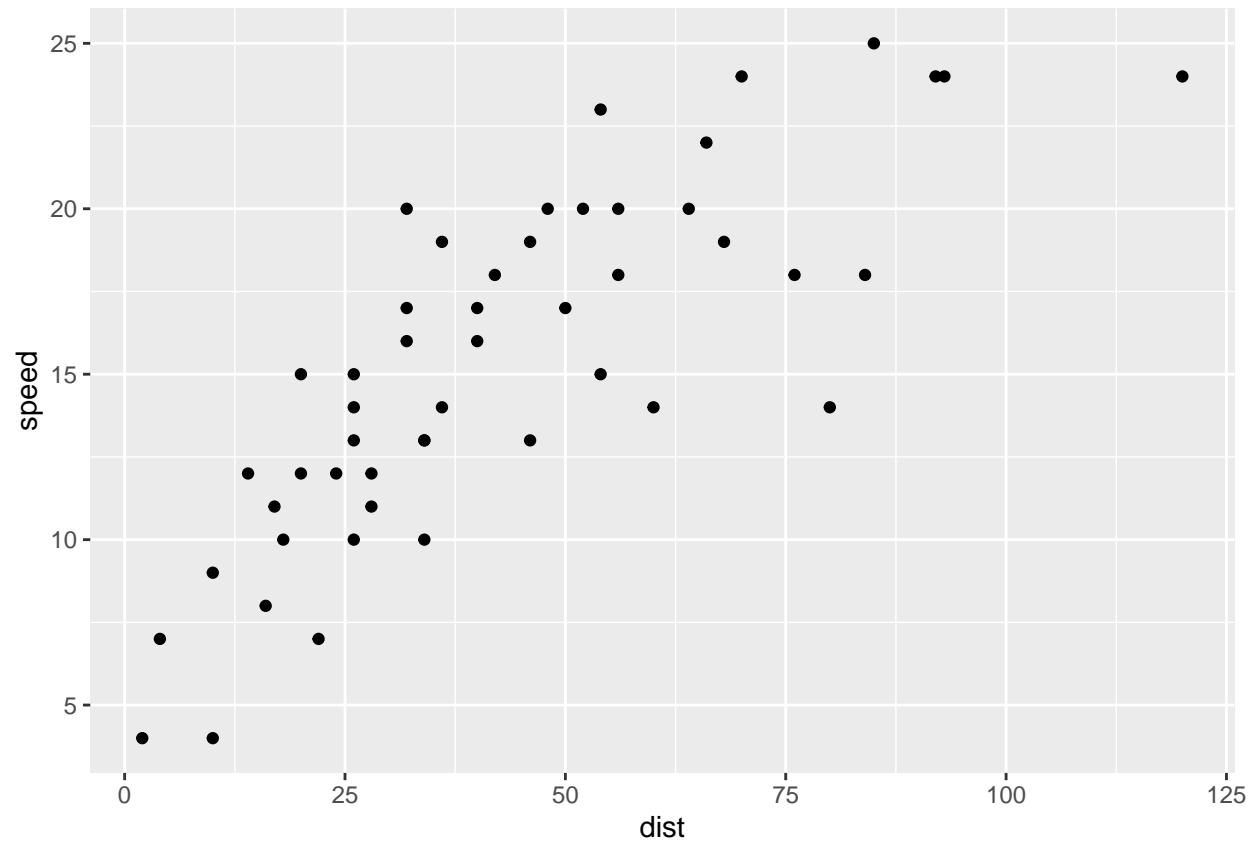
```r
# Class 05 Data Visualization

# 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)
```

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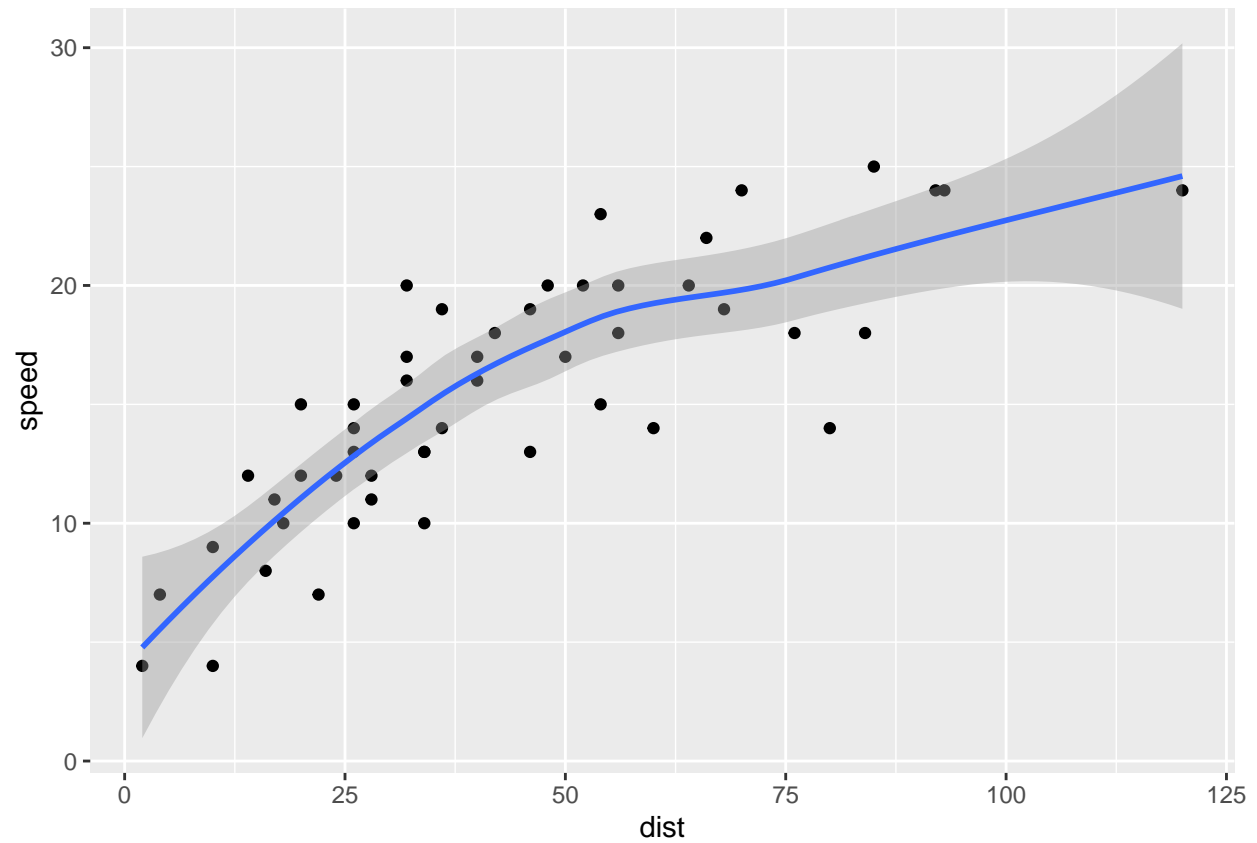


```r
gg <- ggplot(data=cars) + aes(x=dist, y=speed) + geom_point()
gg
```
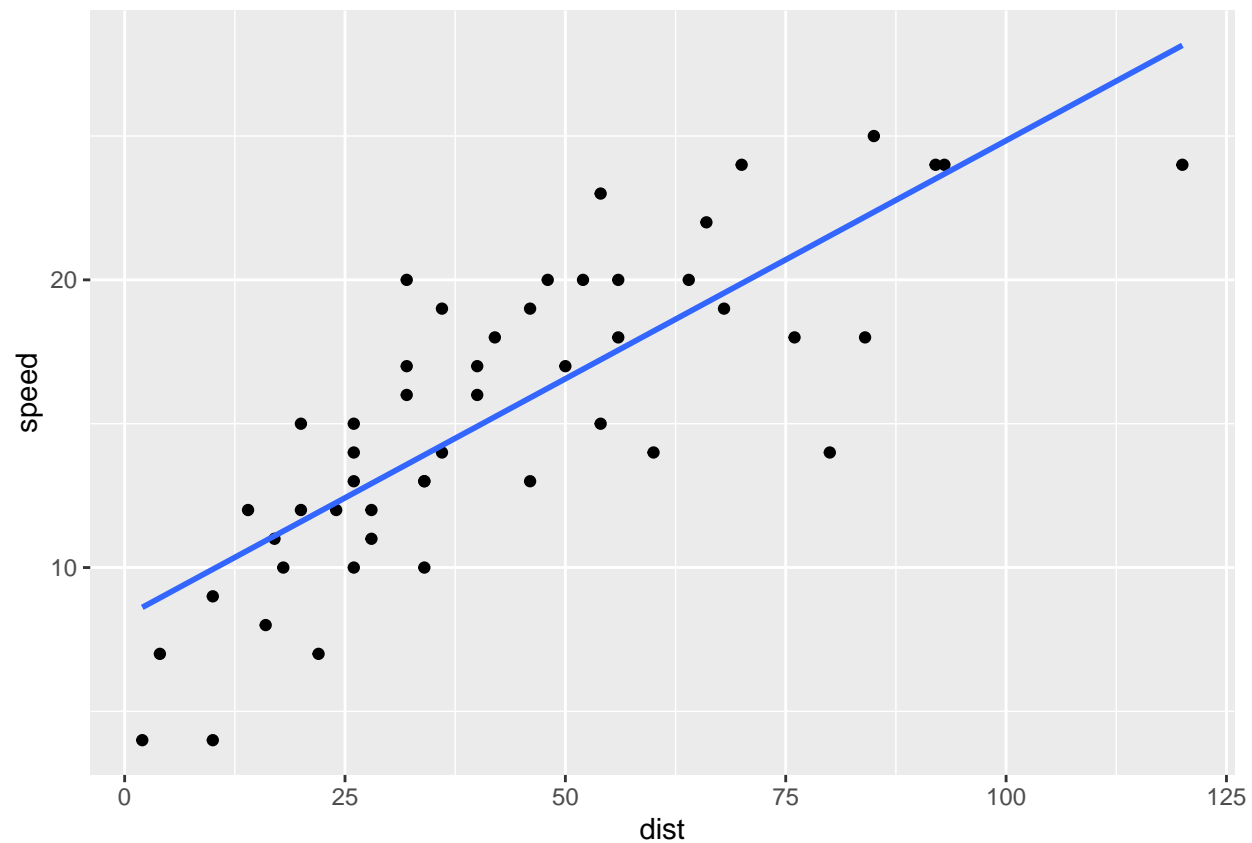
```
# One last thing. lets add a line to the data

gg + geom_smooth()
```

```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```
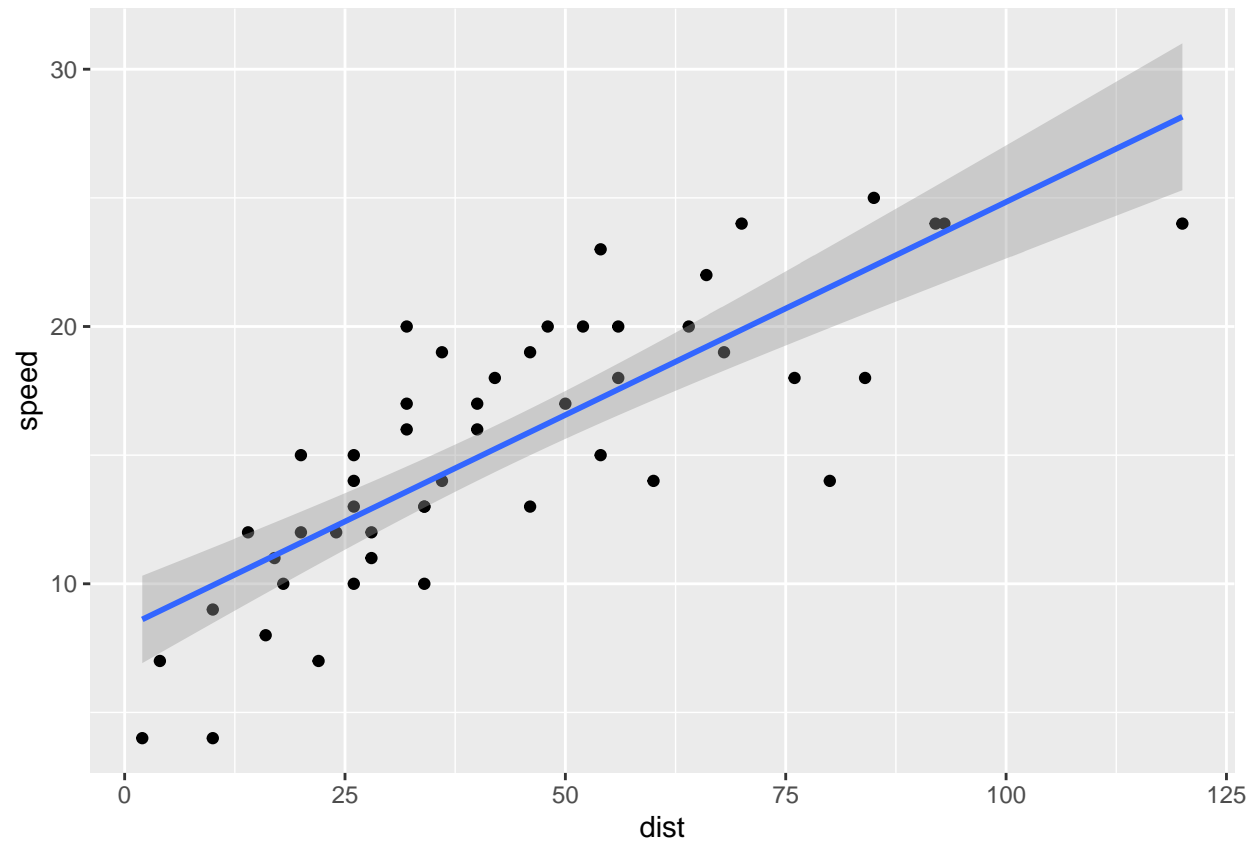
```
# I want a linear model
gg + geom_smooth(method="lm", se=FALSE)
```

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

```
ggplot(data=cars) +
  aes(x=dist, y=speed) +
  geom_point() +
  geom_smooth(method="lm")
```
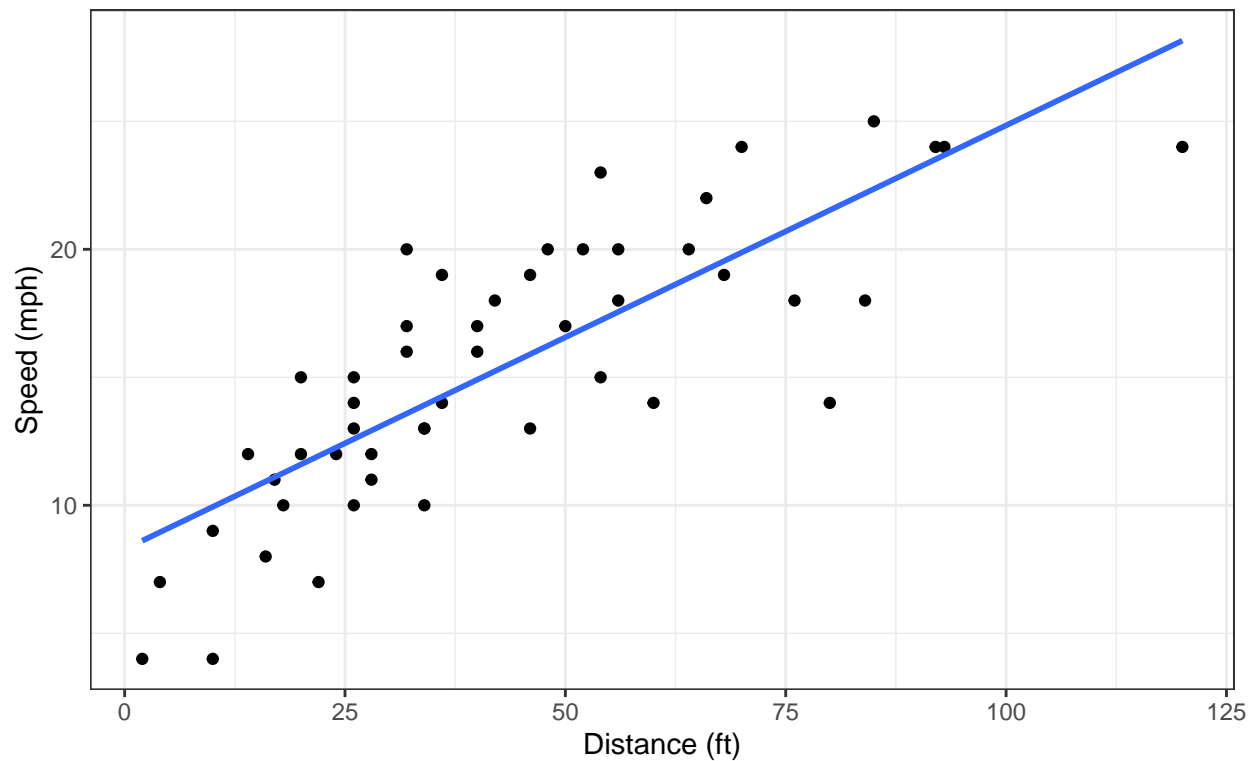
## `geom_smooth()` using formula 'y ~ x'

```
# Add more layers
gg + labs(title = "Relationship between speed and distance for cars",
          caption = "BIMM143") +
  xlab("Distance (ft)") +
  ylab("Speed (mph)")+
  theme_bw() +
  geom_smooth(method="lm", se = FALSE)
```

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

## Relationship between speed and distance for cars

```r
# 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
```

```r
nrow(genes)
```

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

```r
colnames(genes)
```

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

```
# I want to plot this result
ncol(genes)
```

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

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

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

```
round(table(genes$State)/nrow(genes) * 100, 1)
```

```
##
##       down unchanging         up
##        1.4       96.2        2.4
```

```
sum(genes$State == "up")
```

```
## [1] 127
```

```
ggplot(genes) +
  aes(x=Condition1, y=Condition2, color = State)+
  geom_point() + labs(title="Condition 1 vs Condition 2")
```