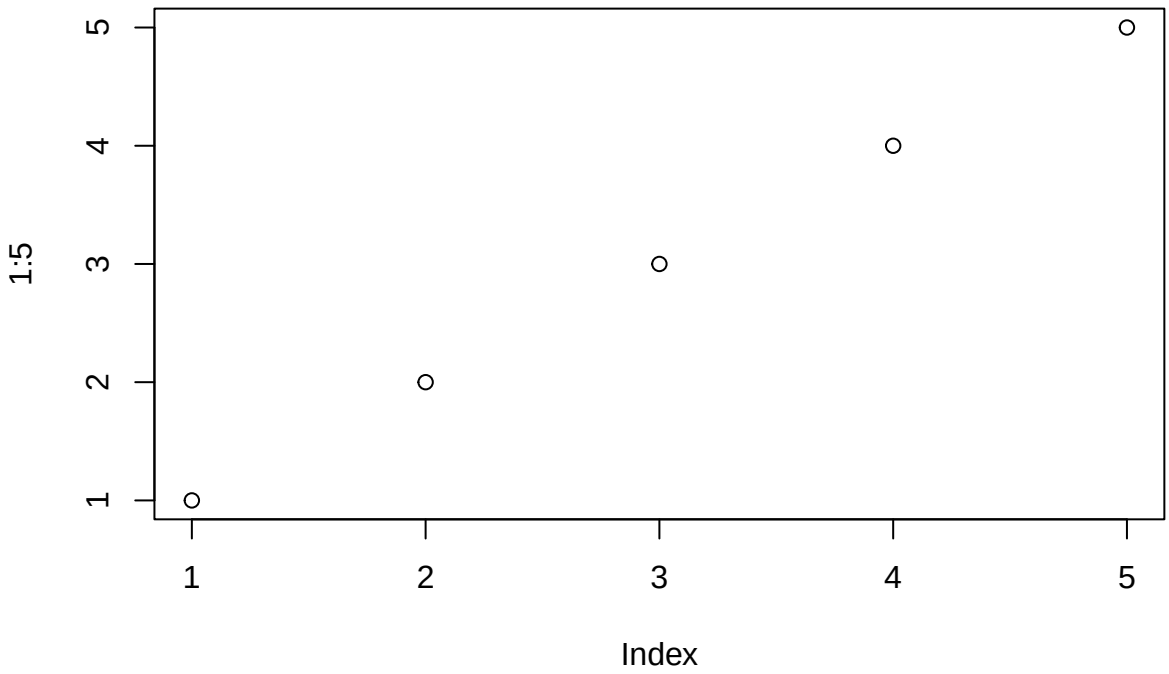
class05.R

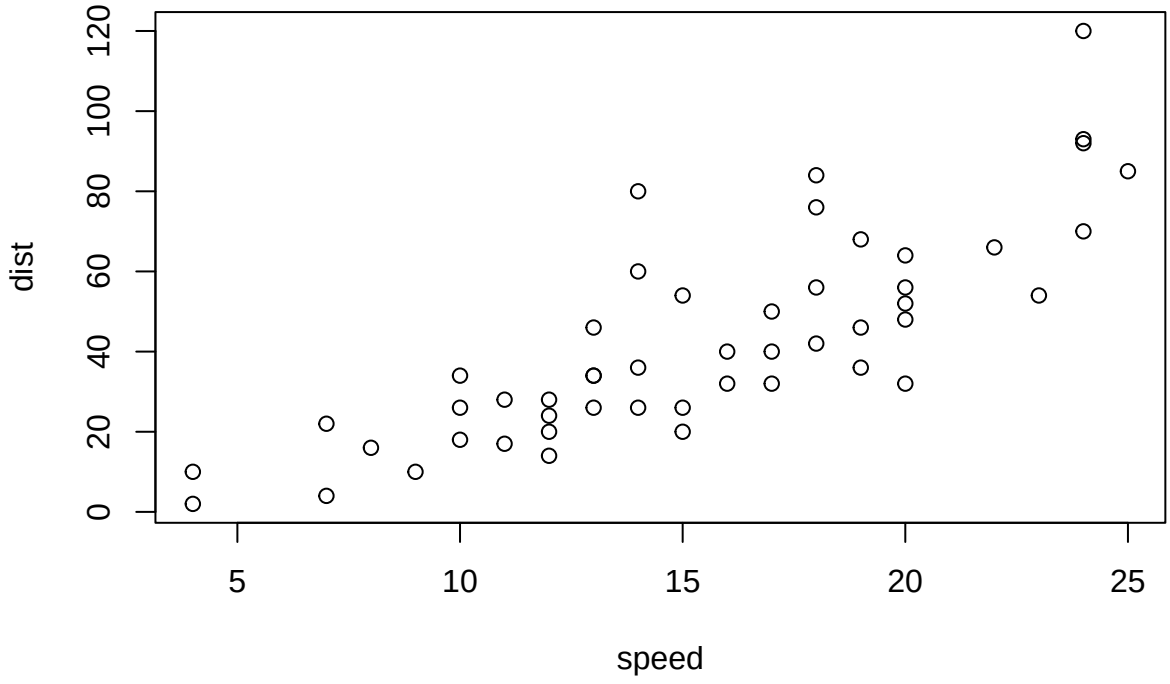
HP

2022-02-02

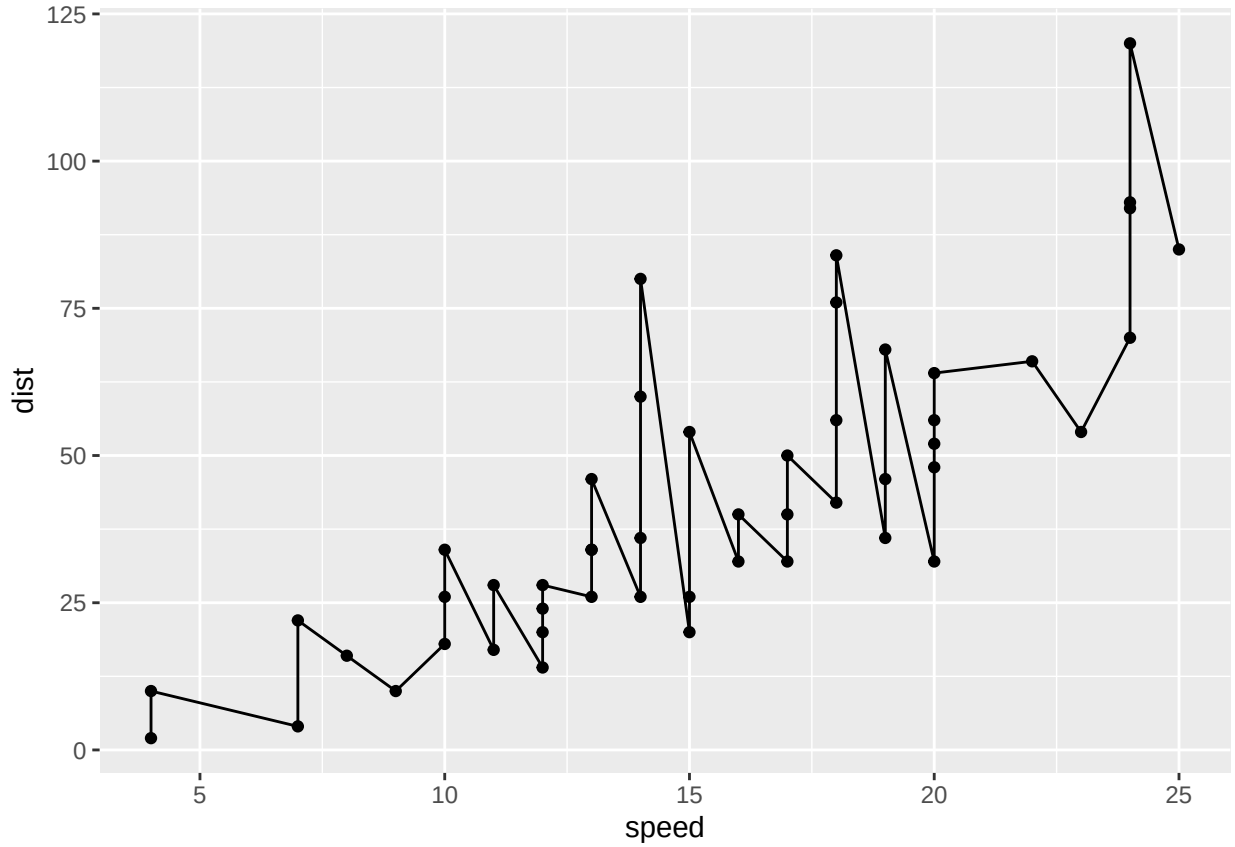
```
#class 5 Data Visualization

plot(1:5)



#That was base R plot - quick and not very nice!
#We will use an add-on package called ggplot2

# install.packages("ggplot2")

library(ggplot2)
```



```
#Before I can use any functions from this package
# I need to load it whith the library() call!
#Install: you do it only once on your computer
#library call you do every time you use it!

plot(cars)
```

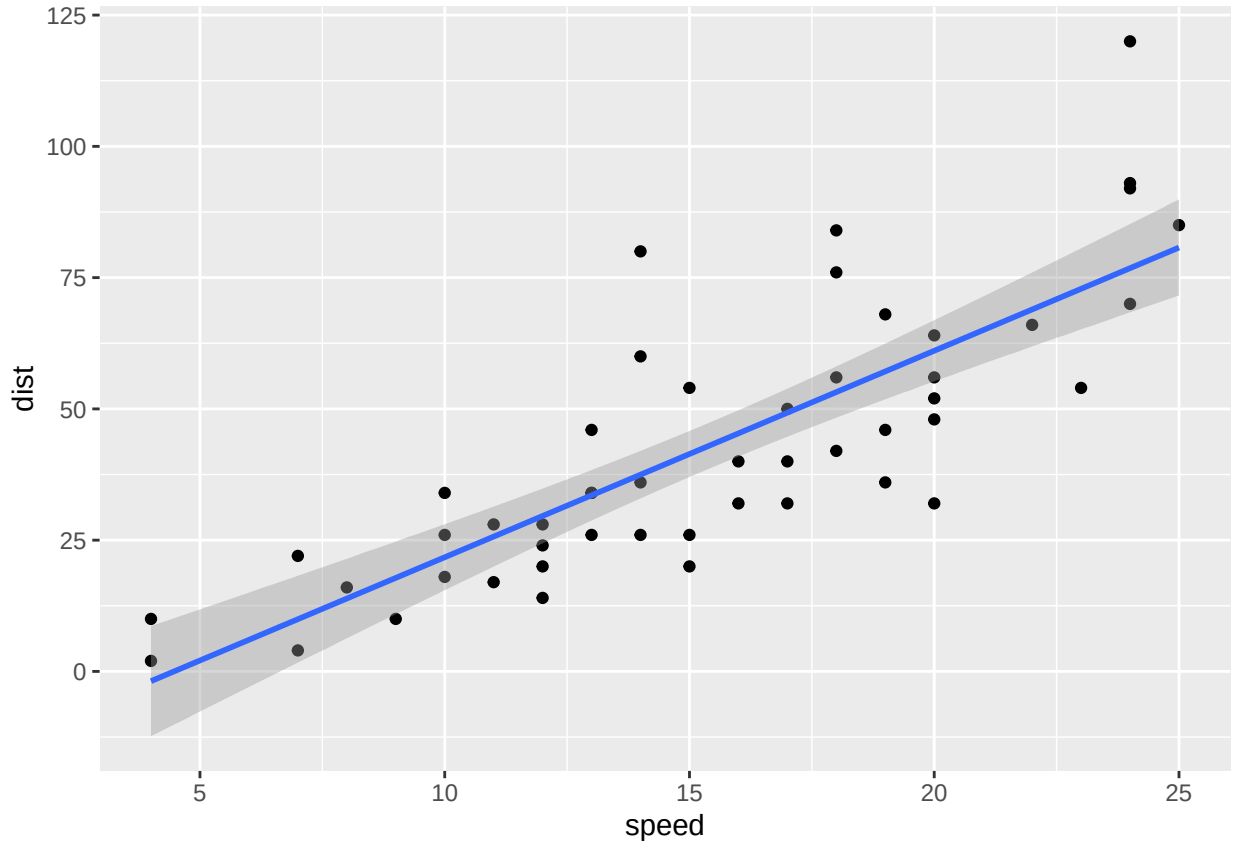



```
#Every ggplot has at least 3 layers
#data + aesthetics + geometry


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

p + geom_line()
```

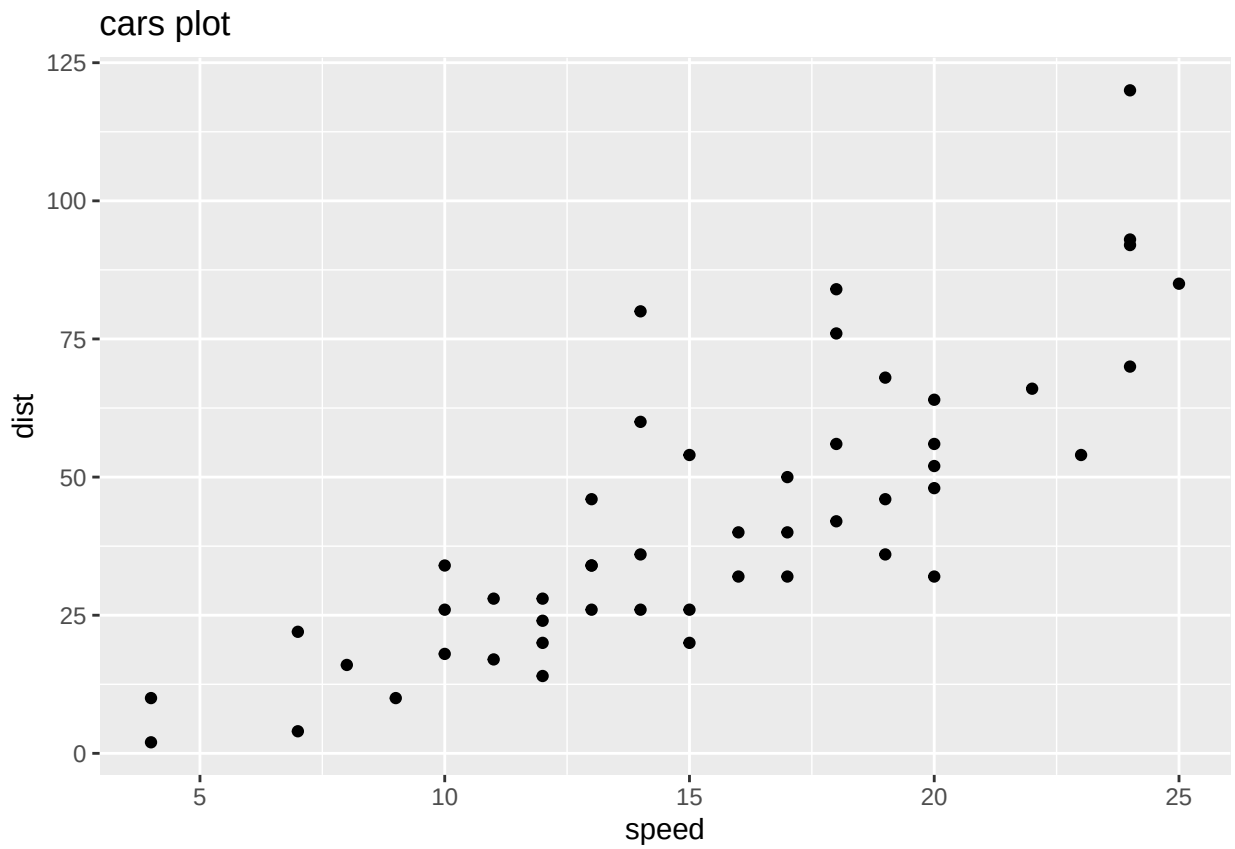



```
p + geom_smooth(method="lm")
```

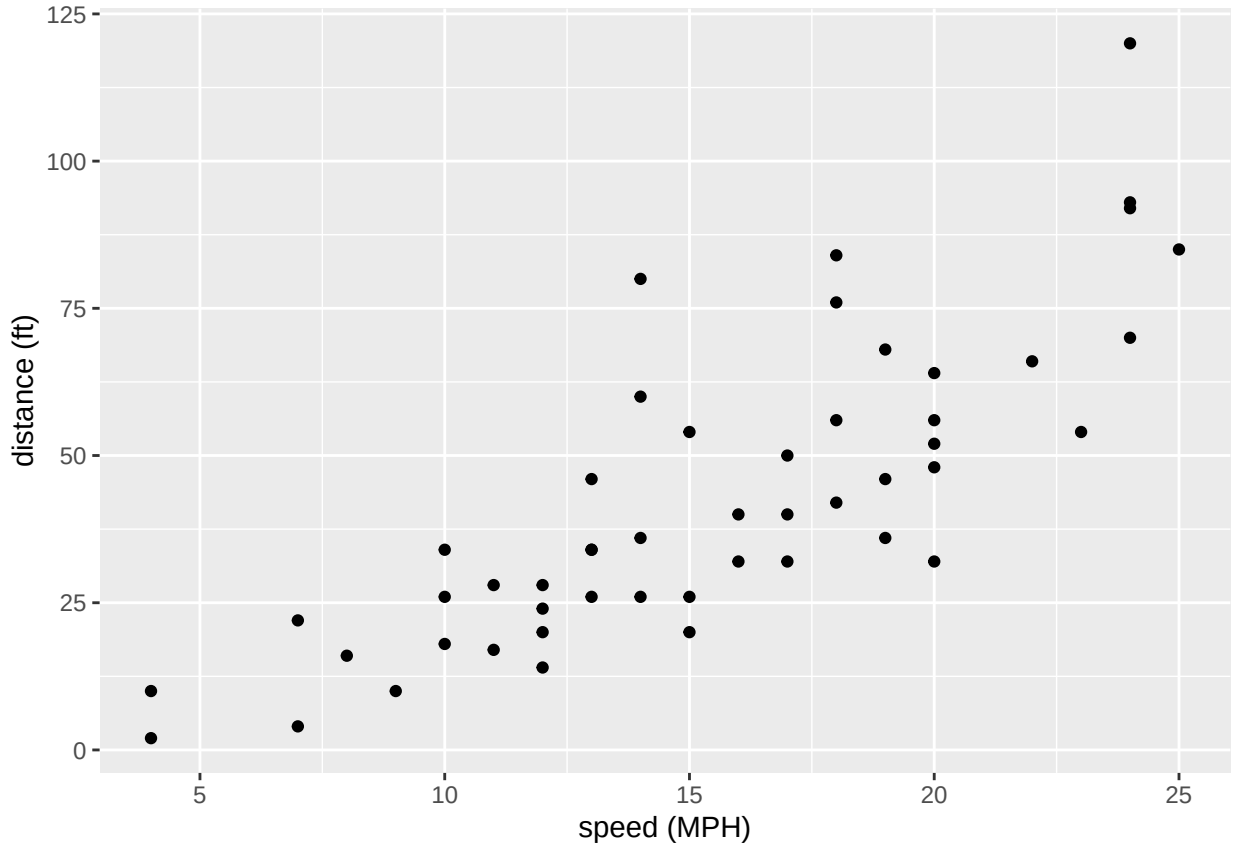
```
## `geom_smooth()` using formula 'y ~ x'
```




```
p + labs (title = "cars plot")
```



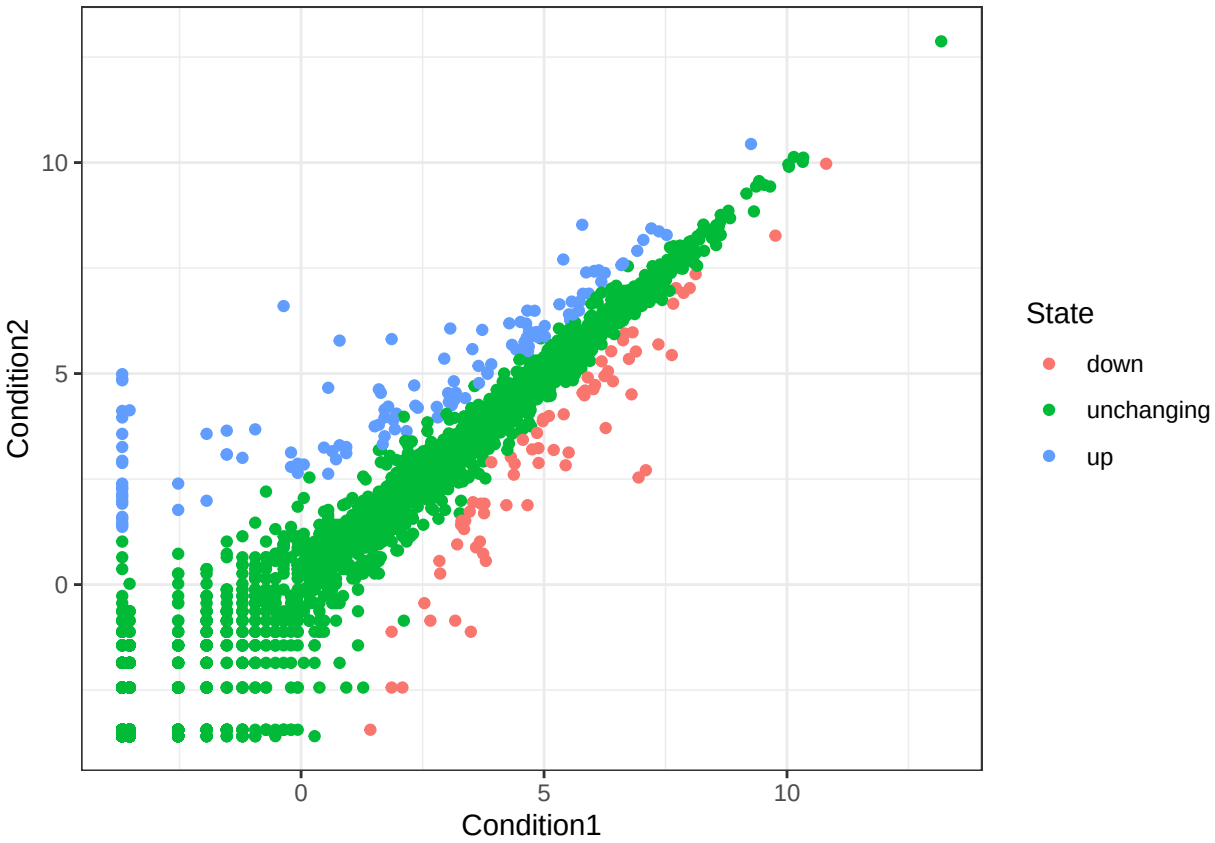

```
p + xlab ("speed (MPH)") +
ylab ("distance (ft)")
```




```
#RNA-Seq plot

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
```

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

p
```


Condition2
10
5
0
0
5
10
Condition1
State
down
unchanging
up