

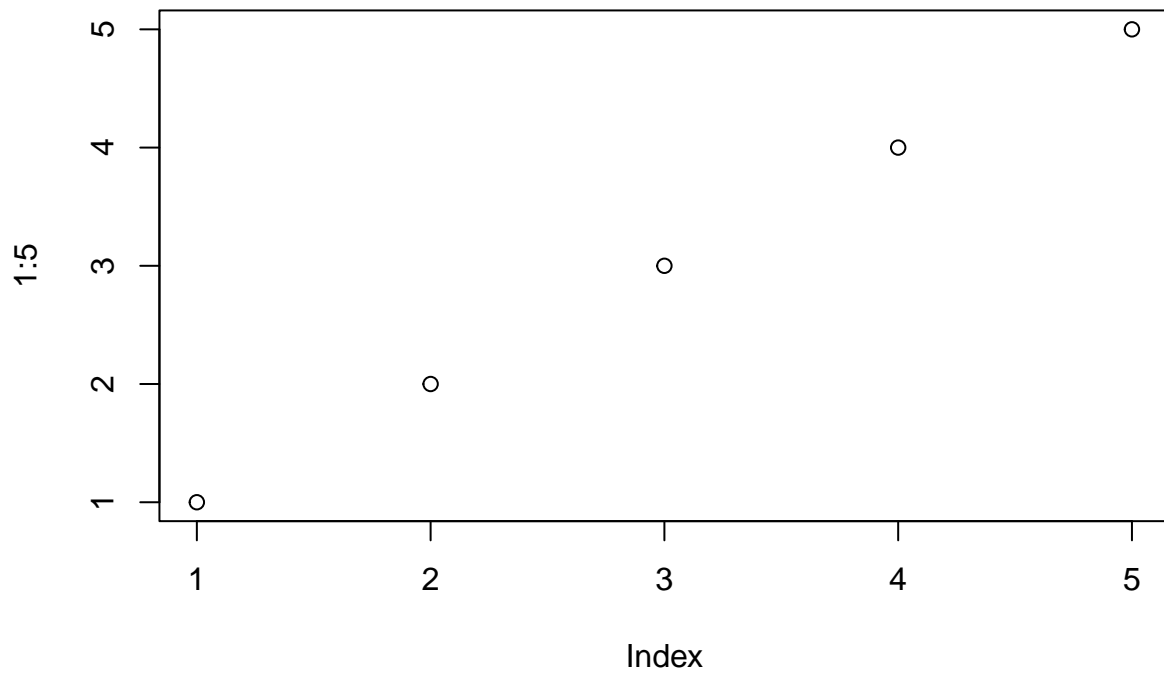
class05.R

gwcha

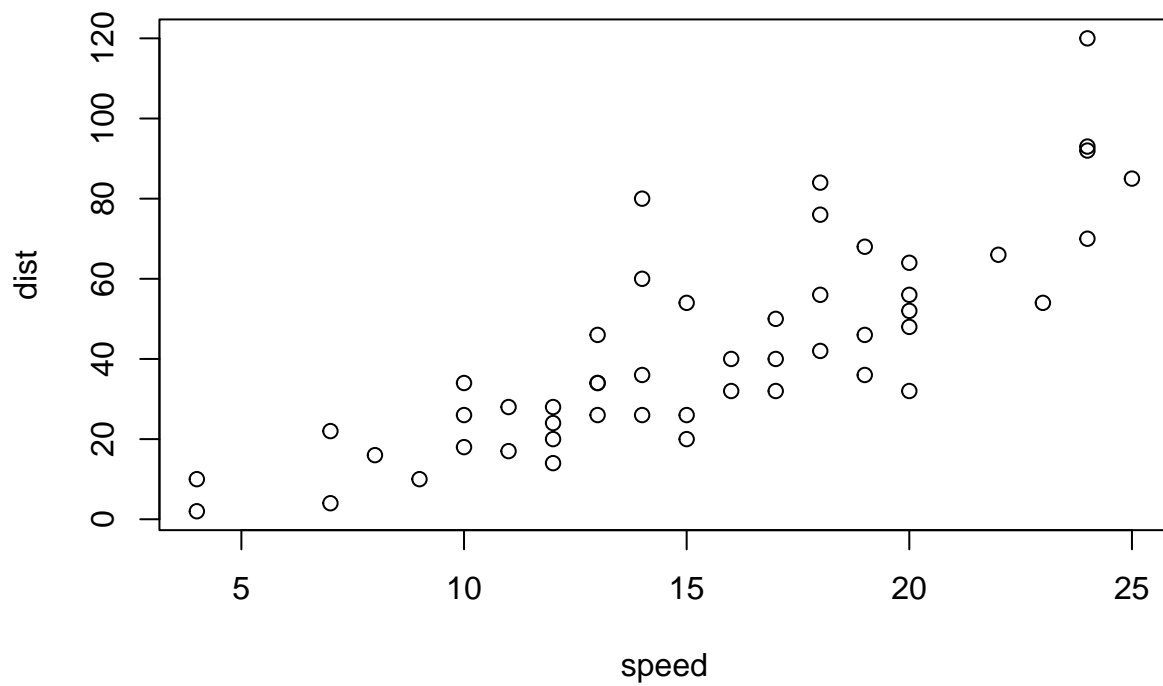
2022-02-02

```
#Class 5 Data Visualization  
#Base R graphics  
#This was more helpful than datacamp  
plot(1:5)  
  
#That was base R plot - quick and not very nice!  
#We will use an add on package called ggplot2  
#function has parentheses  
#install.packages("ggplot2")  
  
#Before I can use any functions from the package  
#I need to load it with the library  
library(ggplot2)
```

```
## Warning in register(): Can't find generic 'scale_type' in package ggplot2 to  
## register S3 method.
```



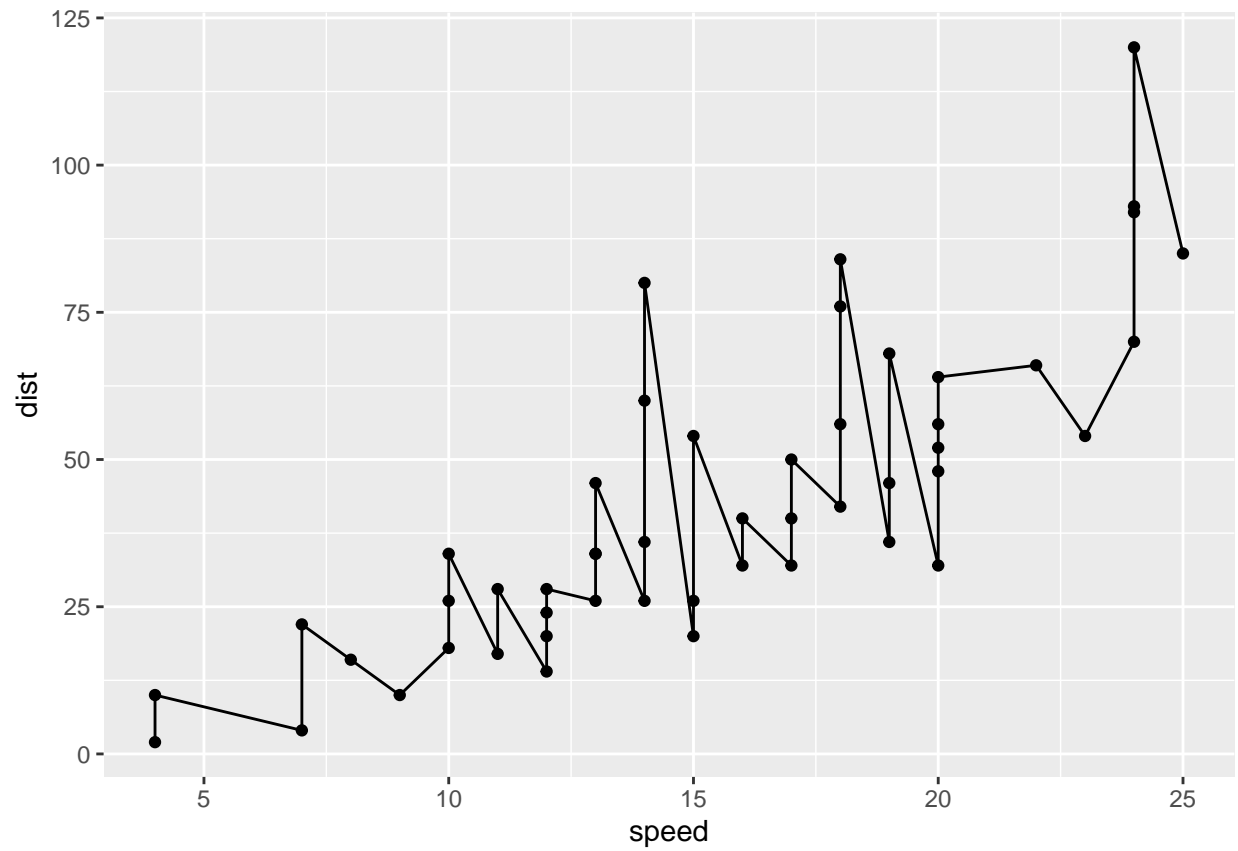
```
plot(cars)
```



```
#plot is still kind of ugly when distance vs speed
#ggplot2 will make it easier to visualize
#take data and map to aesthetics to make it look nice

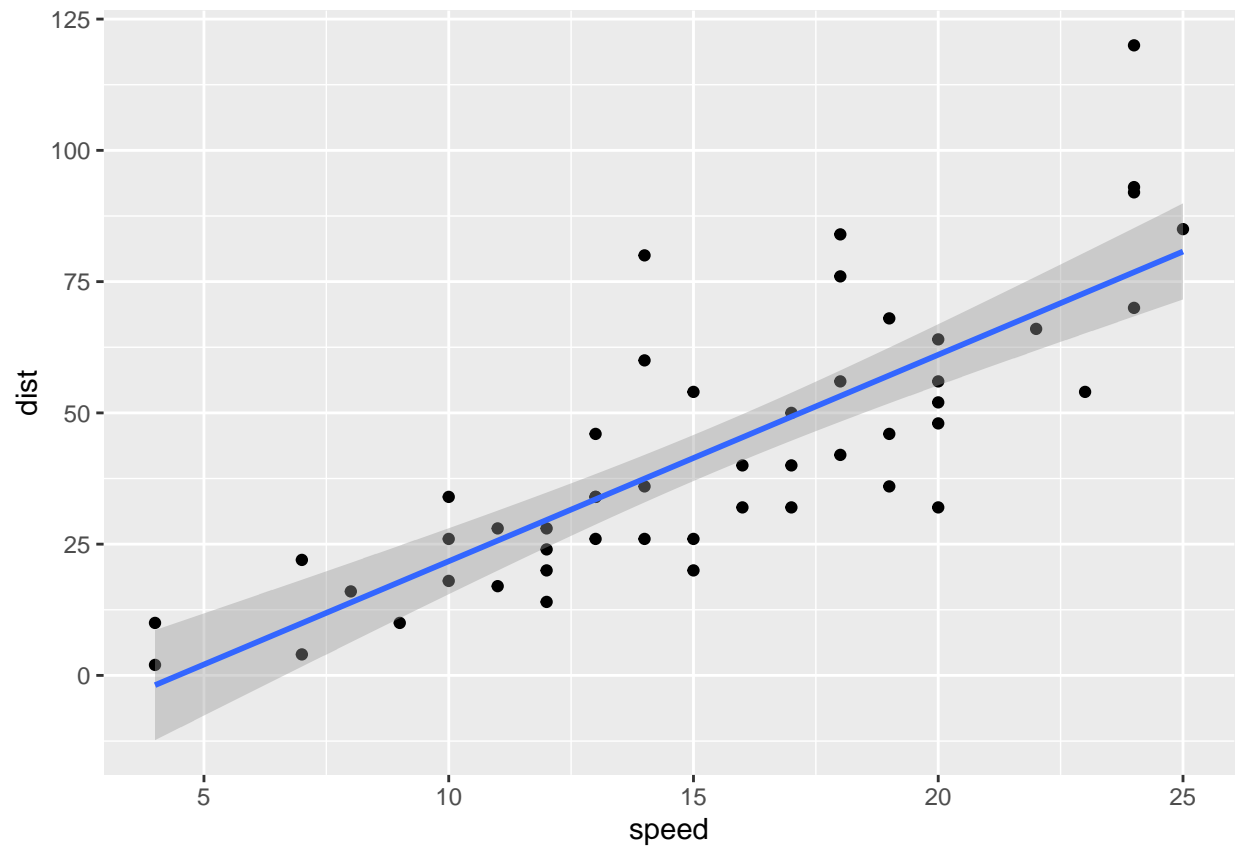
#data + aesthetics + geometrys
#data + aes + geom
#Every ggplot has at least 3 layers
#these are three main "layers" that are in every ggplot

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



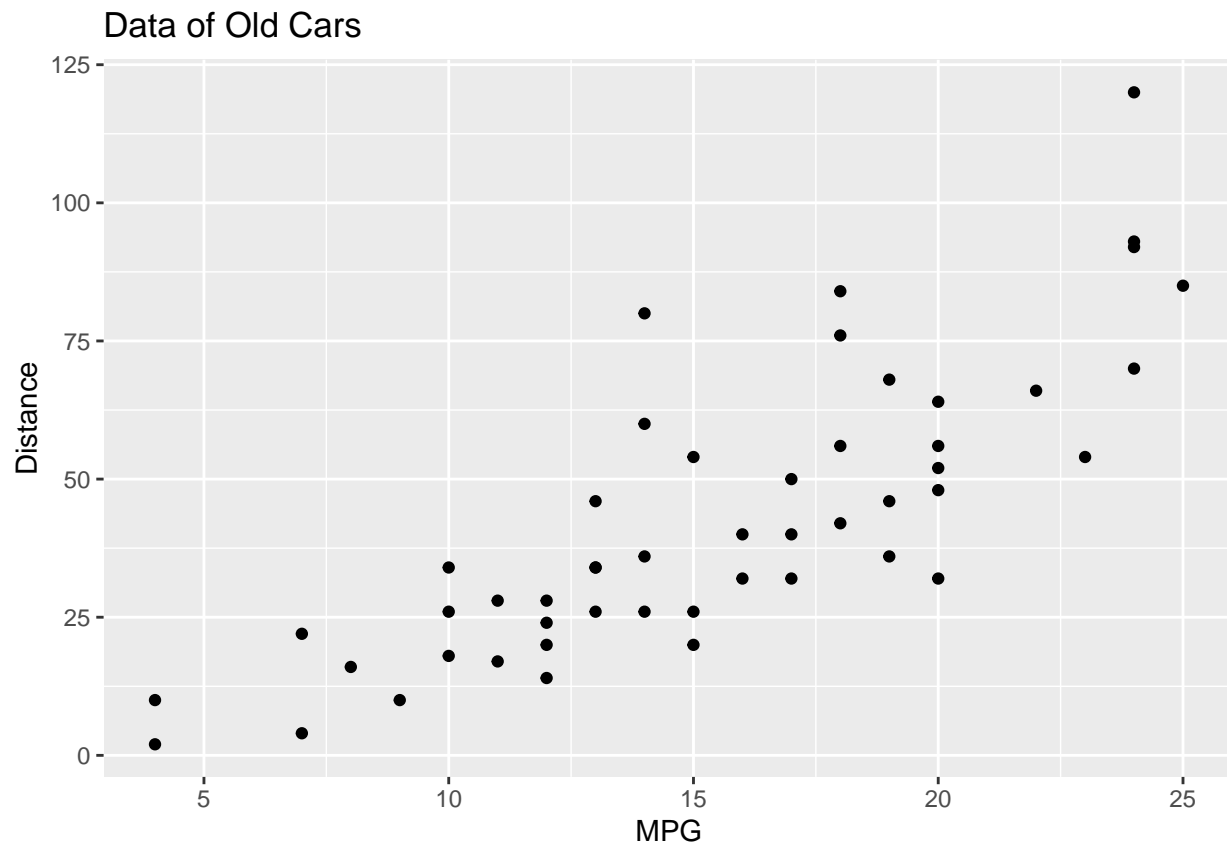
```
p+geom_smooth(method="lm")
```

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



#this is more helpful than datacamp

```
p + labs(title = "Data of Old Cars") + xlab("MPG") + ylab("Distance")
```



```
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
```

```
drugtreatment <- ggplot(data=genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point(alpha=0.2)
drugtreatment + labs(title = "RNA Seq Data") + xlab("Condition1") + ylab("Condition2") +
  scale_colour_manual( values=c("orange","gray","green") )
```

