

class05.R

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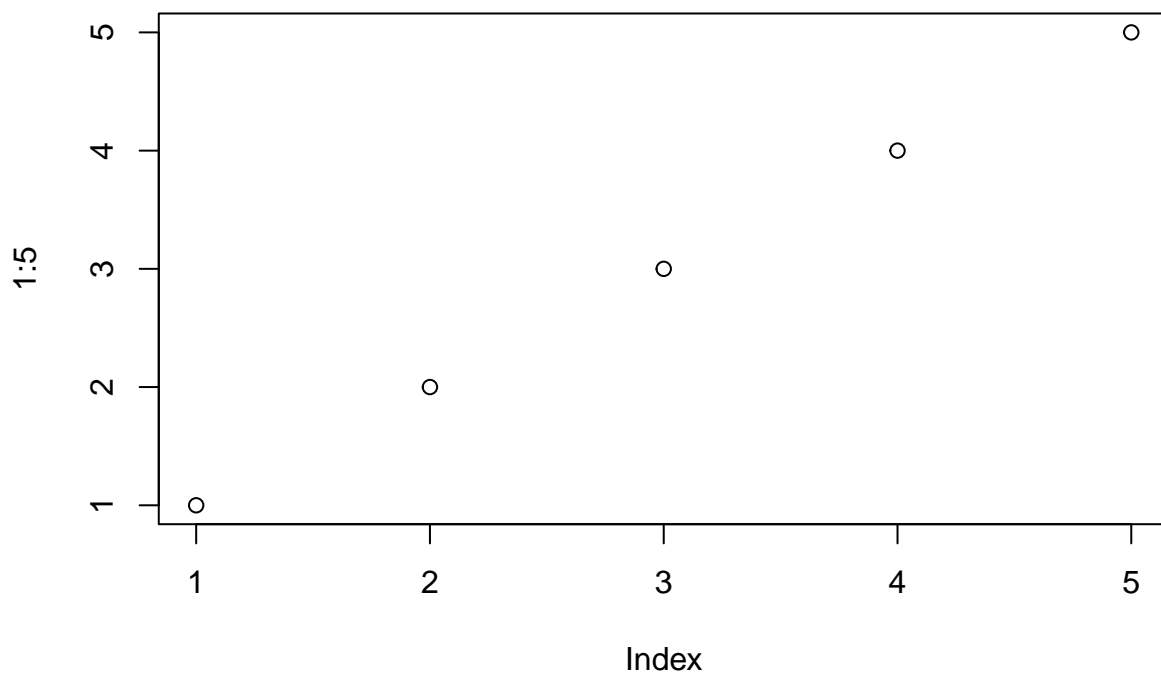
2022-02-02

```
# Class 5 Data Visualization
```

```
plot(1:5)
```

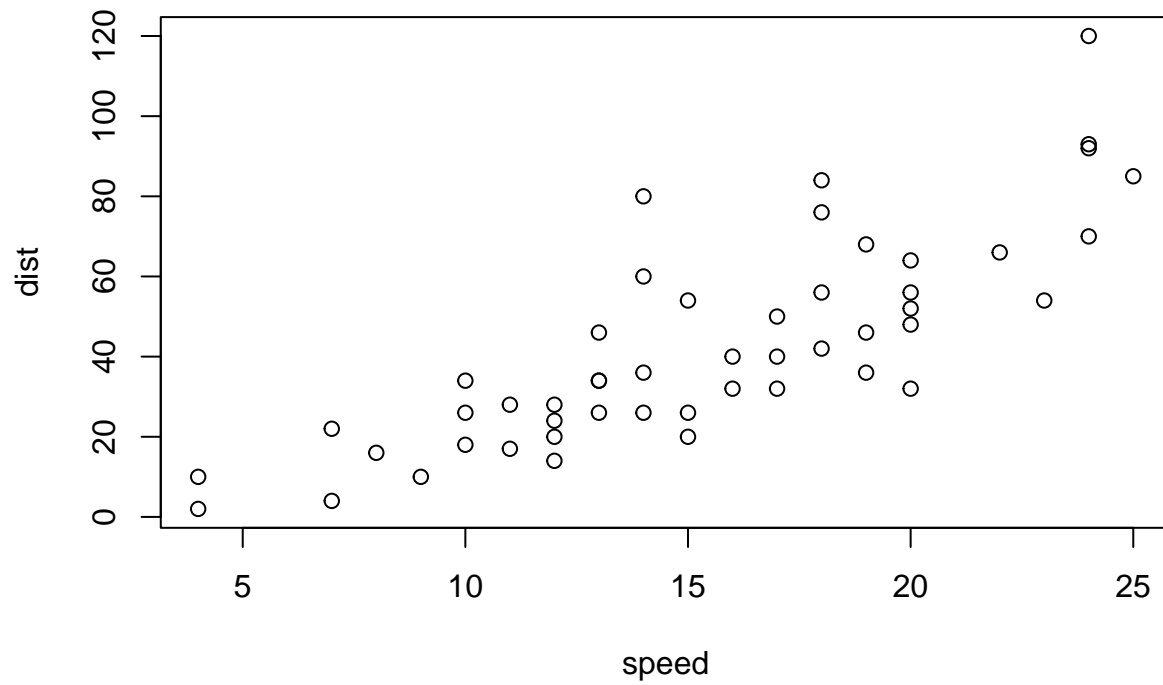
```
# That was base R plot - quick and not very nice!  
# We will use an add on package called ggplot2.
```

```
library(ggplot2)
```



```
# Before I can use any functions from this package  
# I need to load it with the library() call!
```

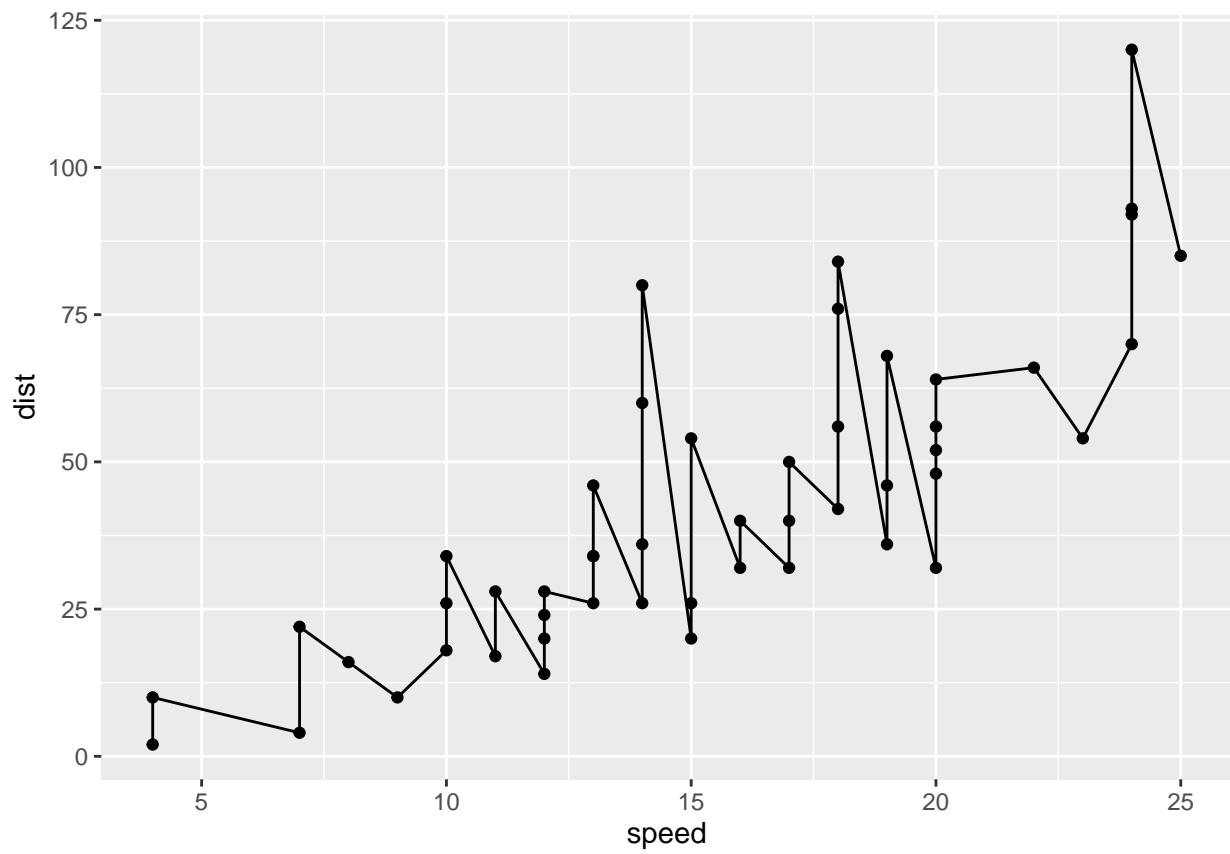
```
plot(cars)
```



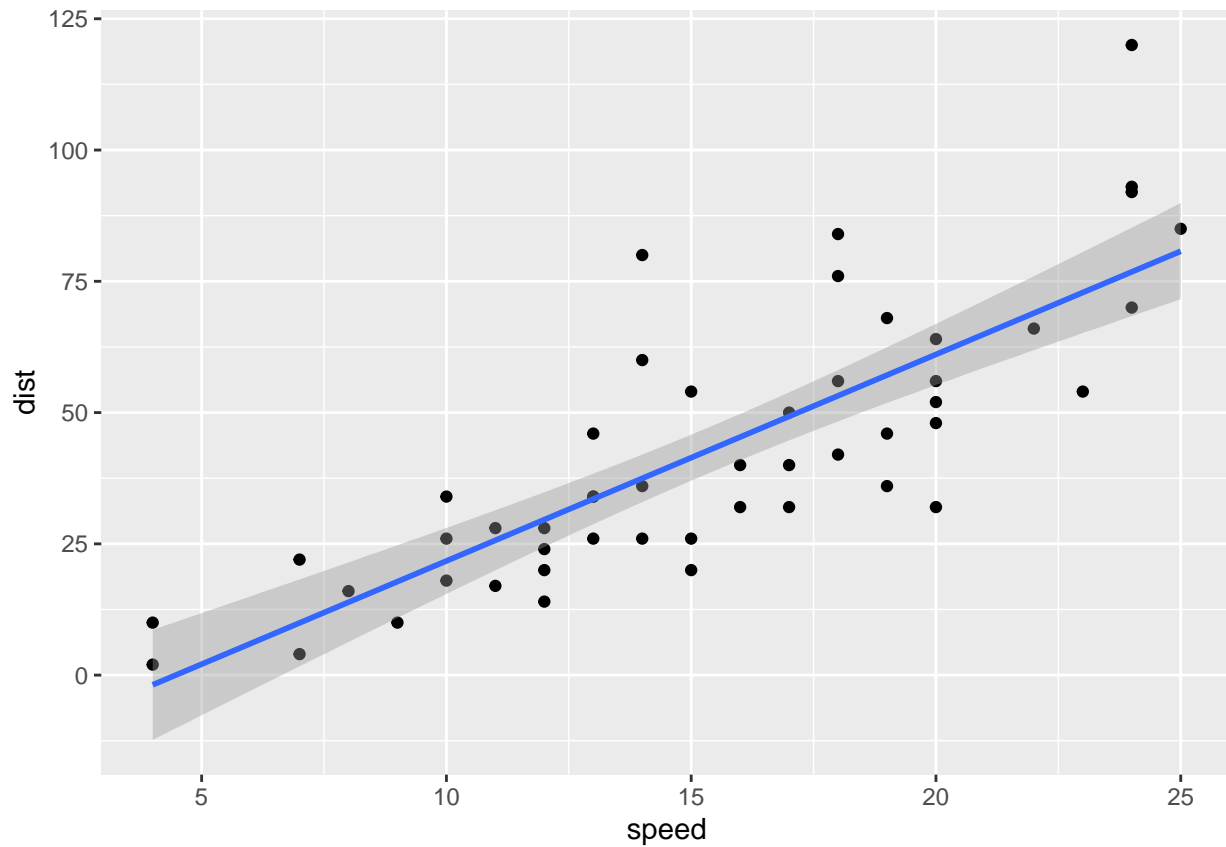
```
# Every ggplot has at least 3 layers  
# data + aes + geoms
```

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

```
p + geom_line()
```



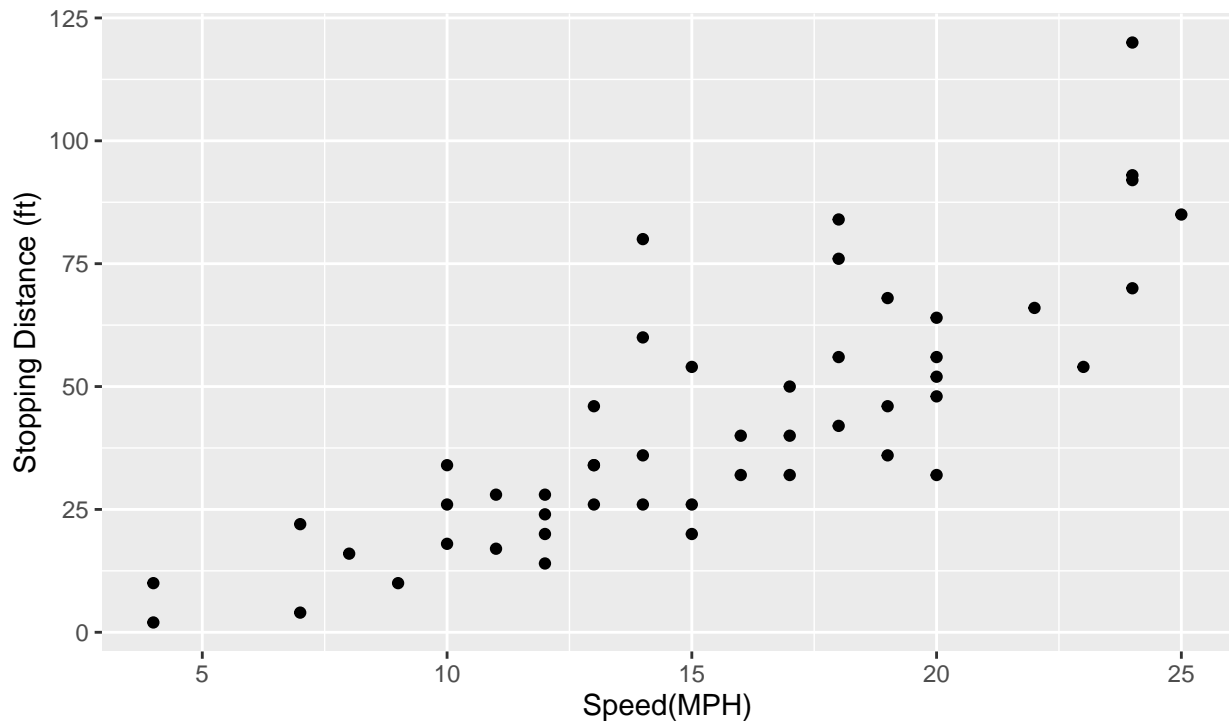
```
p + geom_smooth(method = "lm")  
  
## `geom_smooth()` using formula 'y ~ x'
```



```
p + labs(title = "Speed and Stopping Distance of Cars",  
         subtitle = "Note: We will see the code for this plot in a moment",  
         caption = "Dataset: 'cars'",  
         #x = "Speed(MPH)",  
         y = "Stopping Distance (ft)") +  
xlab("Speed(MPH)")
```

Speed and Stopping Distance of Cars

Note: We will see the code for this plot in a moment



Dataset: 'cars'

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

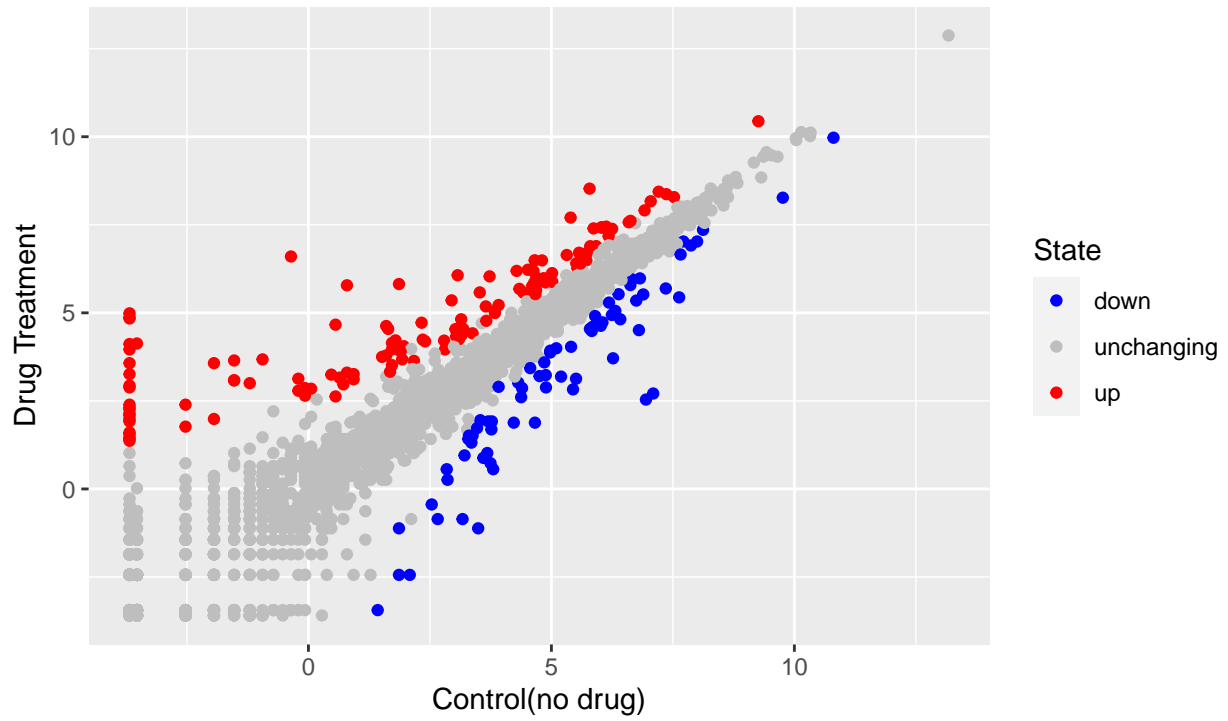
```
##      Gene Condition1 Condition2      State
## 1    A4GNT  -3.6808610 -3.4401355  unchanging
## 2    AAAS   4.5479580  4.3864126  unchanging
## 3   AASDH   3.7190695  3.4787276  unchanging
## 4    AATF   5.0784720  5.0151916  unchanging
## 5    AATK   0.4711421  0.5598642  unchanging
## 6 AB015752.4 -3.6808610 -3.5921390  unchanging
```

```
p1 <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col= State) +
  geom_point()

p1 + labs(title = "Gene Expression Changes Upon drug Treatment",
  subtitle = "Just another scater made with ggplot",
  caption = "BIMM143",
  x = "Control(no drug)",
  y = "Drug Treatment") +
  scale_colour_manual( values=c("blue","gray","red") )
```

Gene Expression Changes Upon drug Treatment

Just another scater made with ggplot



BIMM143