

class05.R

Shivam

2022-02-02

```
#class 5 data visualization
```

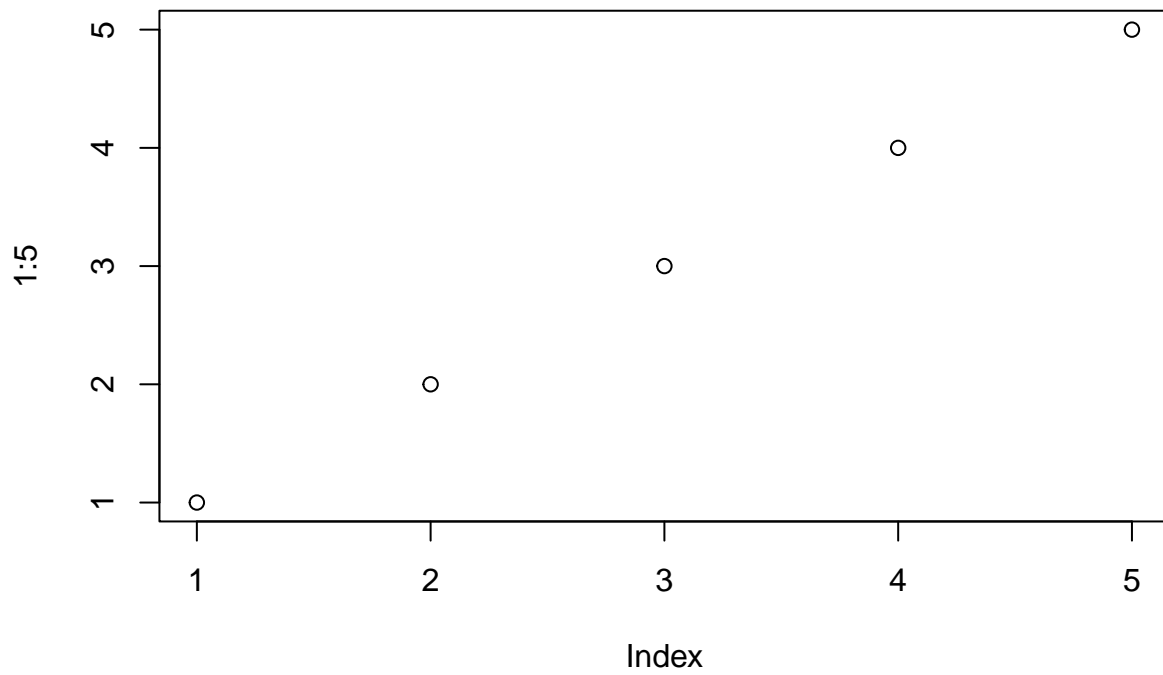
```
plot(1:5)
```

```
#Time to upgrade plots
```

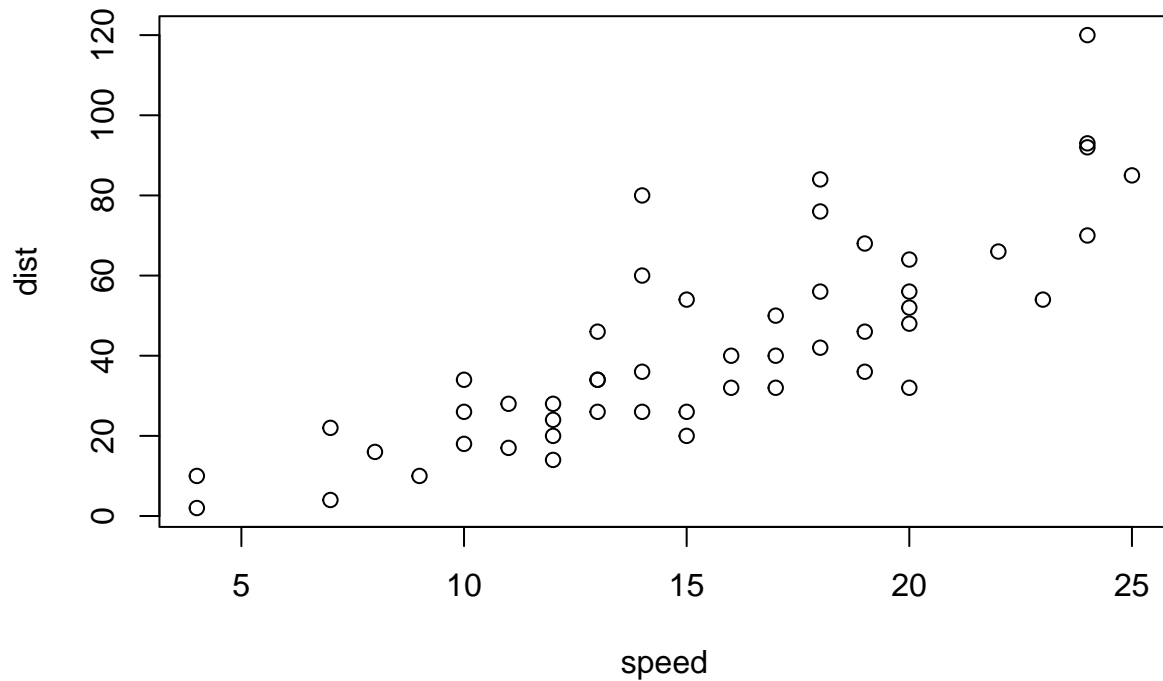
```
#Use ggplot2
```

```
#install.packages("ggplot2")
```

```
library(ggplot2)
```



```
plot(cars)
```



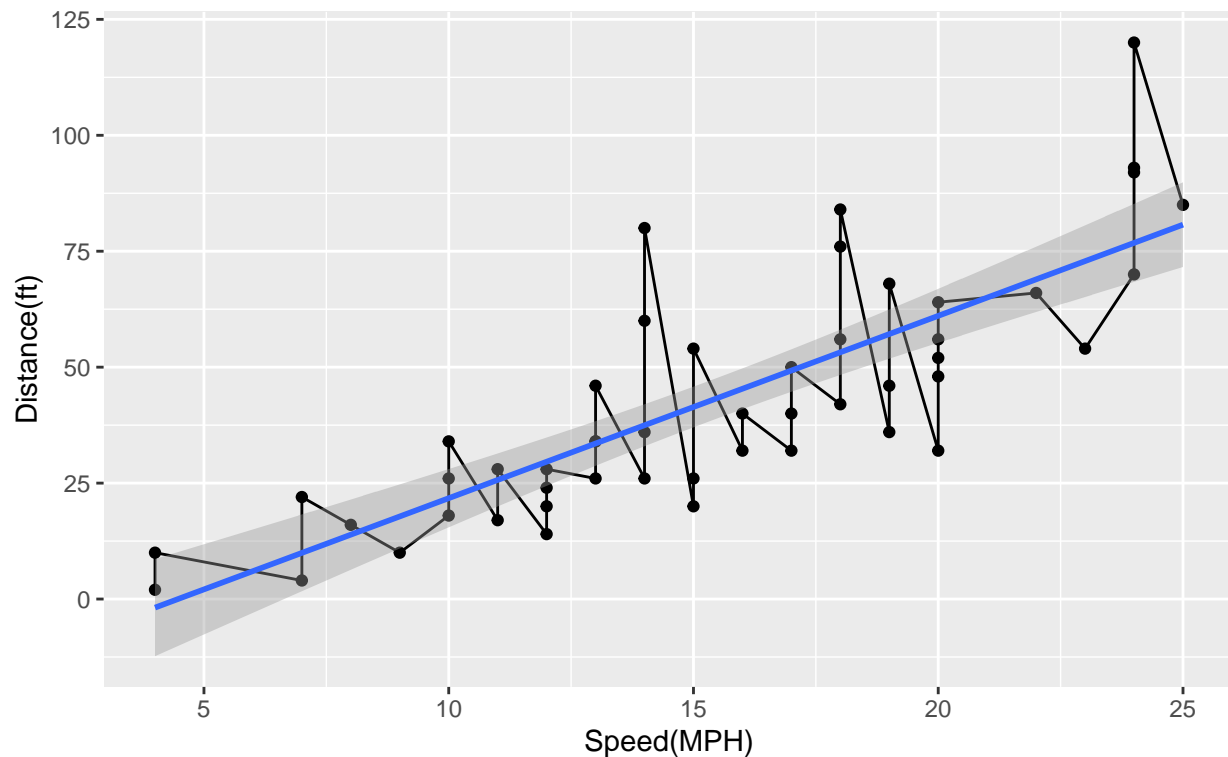
```
#data + AEsthetics + GEOMS
```

```
p <- ggplot(data = cars)+  
  aes(x=speed, y = dist) +  
  geom_point() + geom_line() + geom_smooth(method = "lm") +  
  labs(title = "Speed and stopping distance of cars", subtitle = "Note: We see this plot in some time",  
  labs( x = "Speed(MPH)", y = "Distance(ft)")  
p
```

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

Speed and stopping distance of cars

Note: We see this plot in some time



```
#load genes
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
```

```
ggplot(genes) +
  aes(Condition1, Condition2, col=State) +
  geom_point(alpha = 0.2) +
  theme_bw()
```

