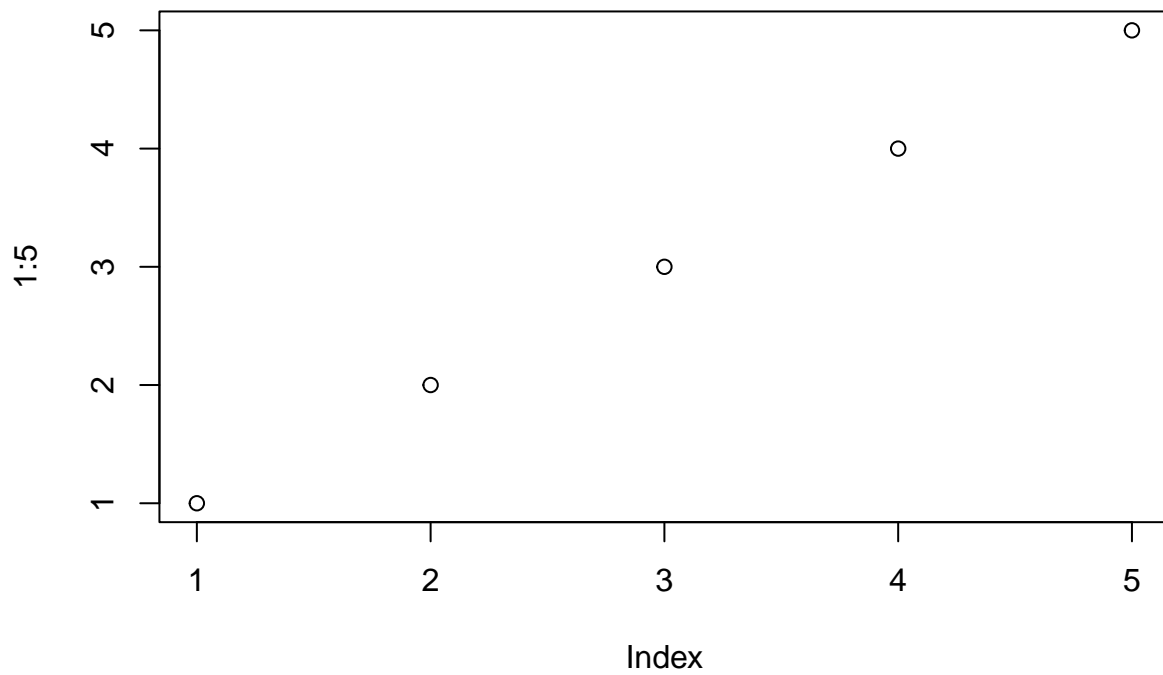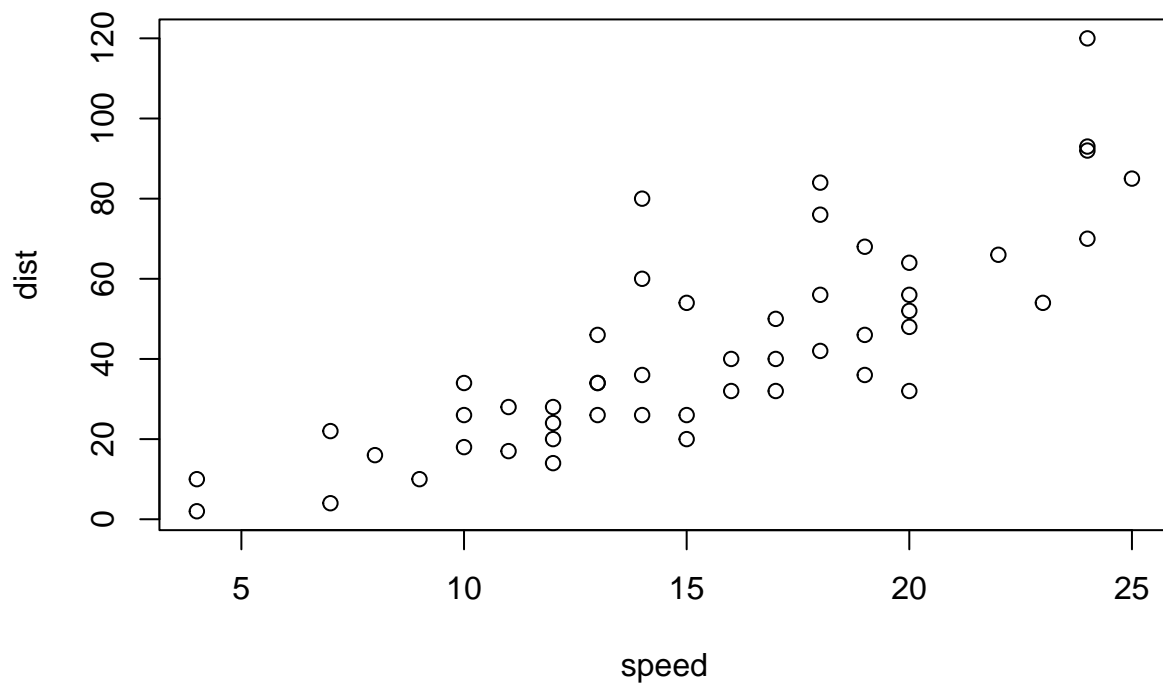# class5.R

ethanlai

2022-02-02

```r
# class 5 Data Visualization
plot(1:5)

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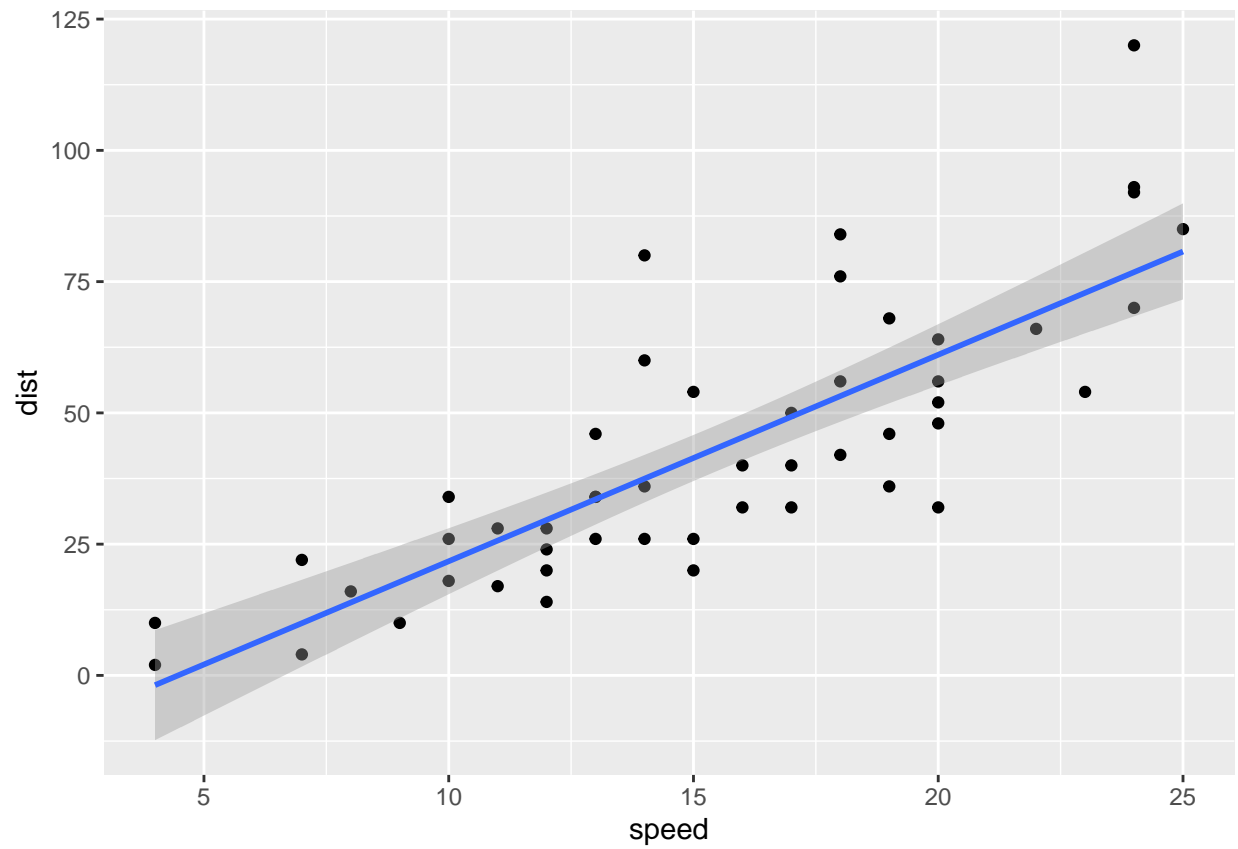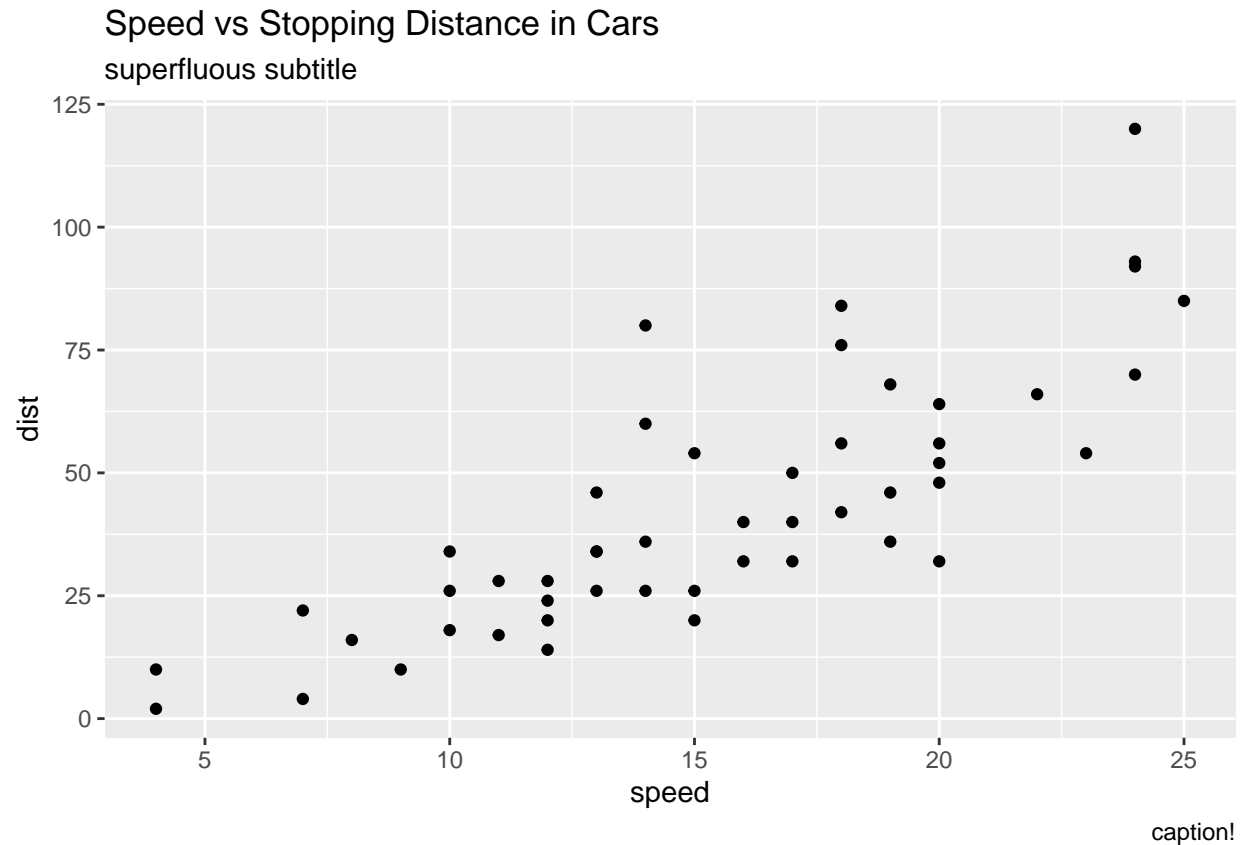


```r
plot(cars)
```

```
#every gg plot has at least 3 layers: data + aes + geoms
p<- ggplot(data = cars) +
  aes(speed, dist) +
  geom_point()

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

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

```
p+ labs(title="Speed vs Stopping Distance in Cars", subtitle = "superfluous subtitle", caption = "capti
```

Speed vs Stopping Distance in Cars
superfluous subtitle

caption!

```
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
```

```
p2<- ggplot(genes)+
  aes(Condition1, Condition2, col=State)+
  geom_point(alpha=0.5, size=0.1)+
  theme_bw()

p2 + scale_colour_manual( values=c("blue","gray","red")) + labs(title="Gene Expression")
```

Gene Expression