class05.R

weins

2022-02-02

```r
# Class 5 Data Visualization

plot(1:5)

# Base R plot is quick but kinda ugly
# We will use ggplot2, and add on package

library(ggplot2)
```
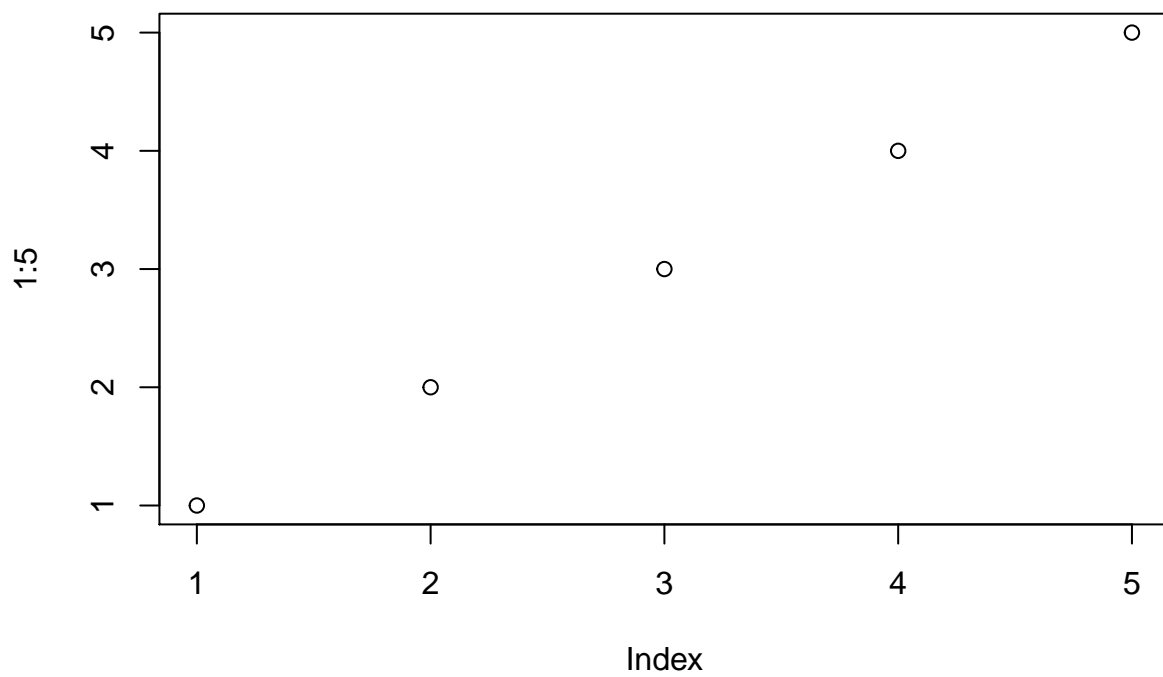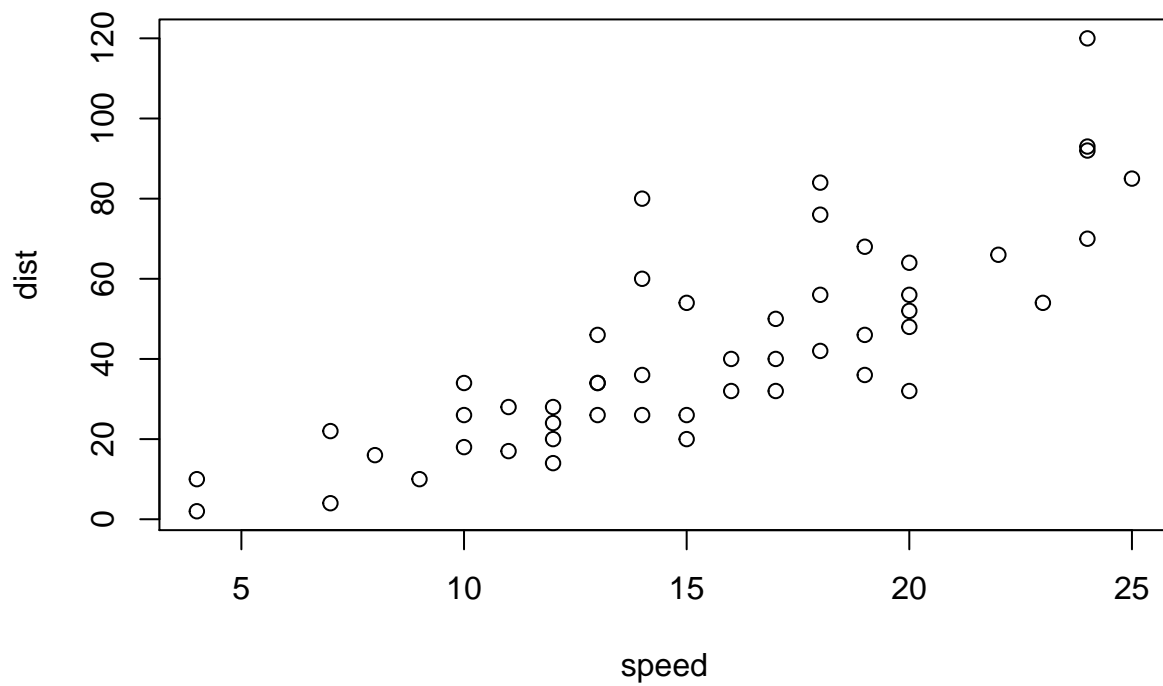
```
## Warning: package 'ggplot2' was built under R version 4.0.5
```
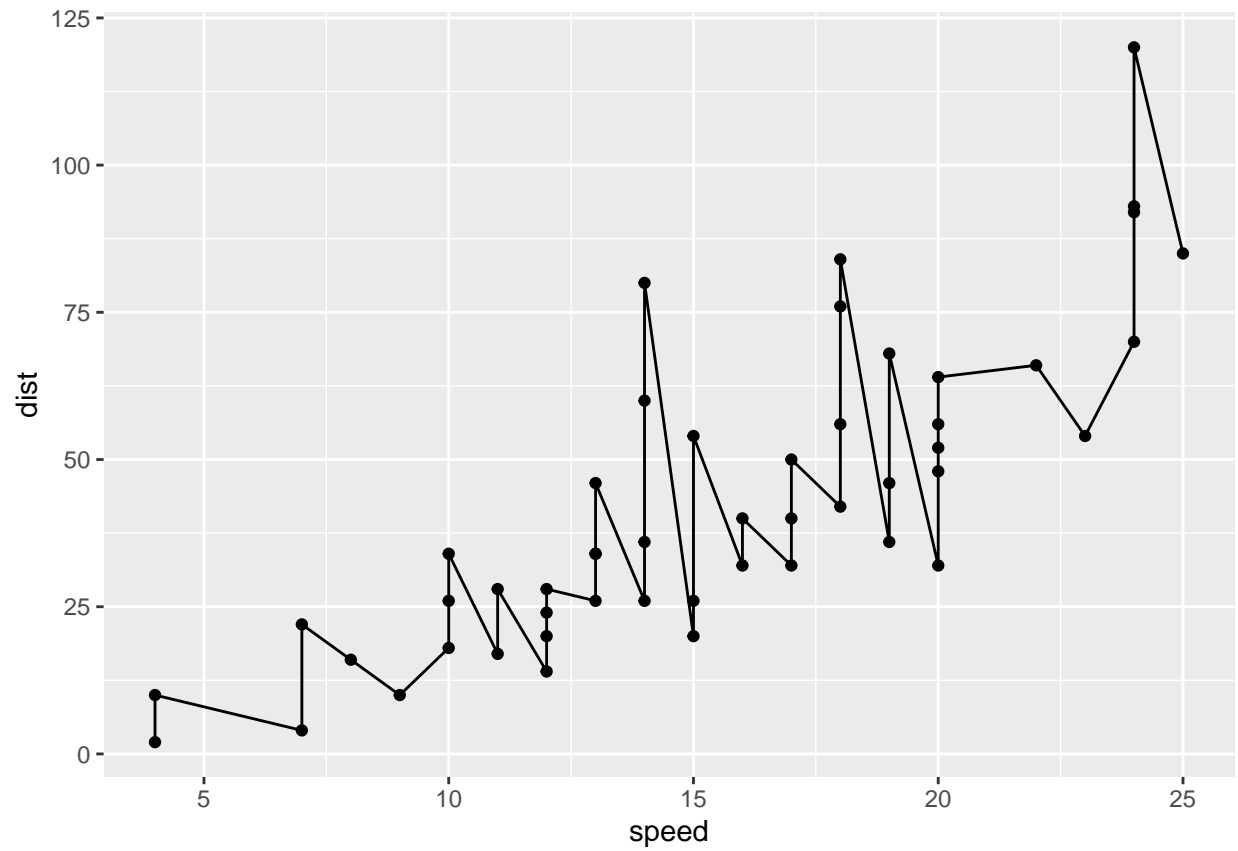
```
#must load ggplot2 to use it

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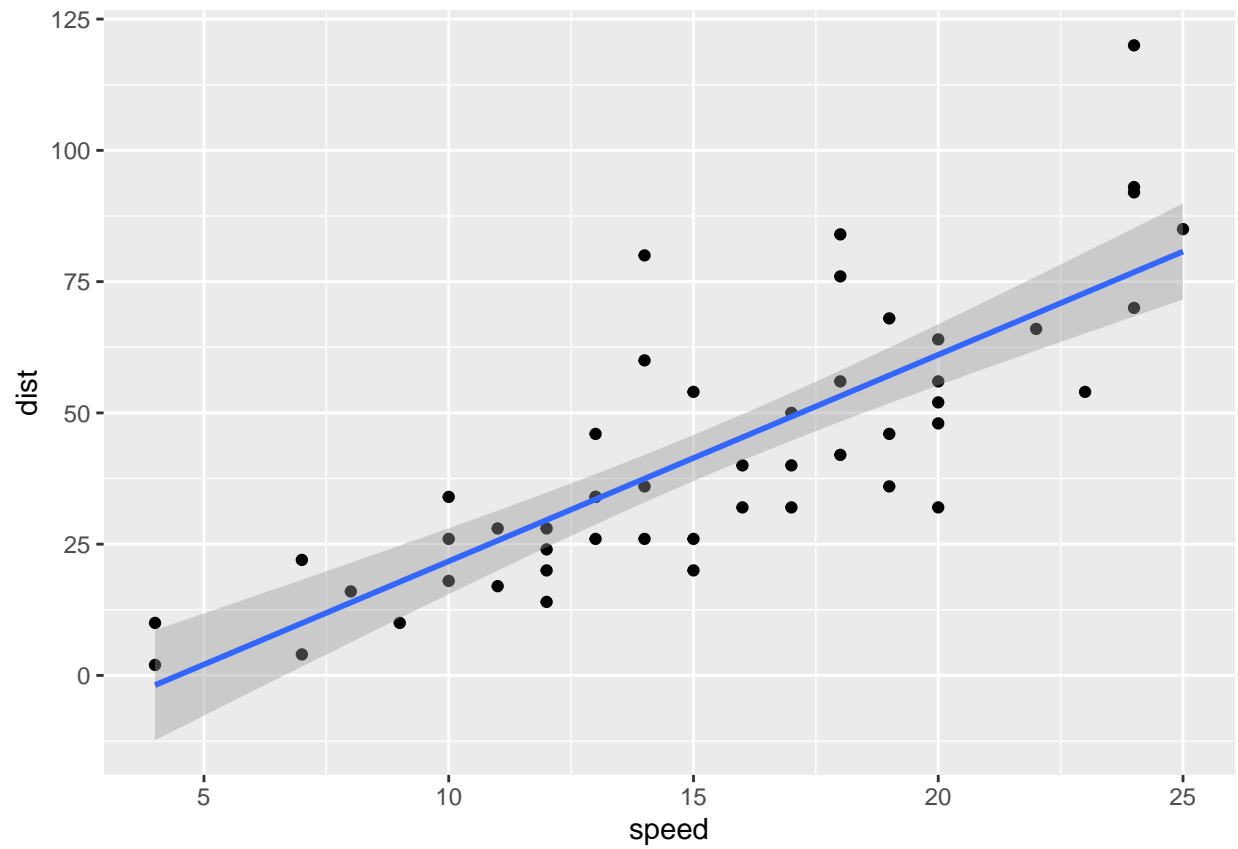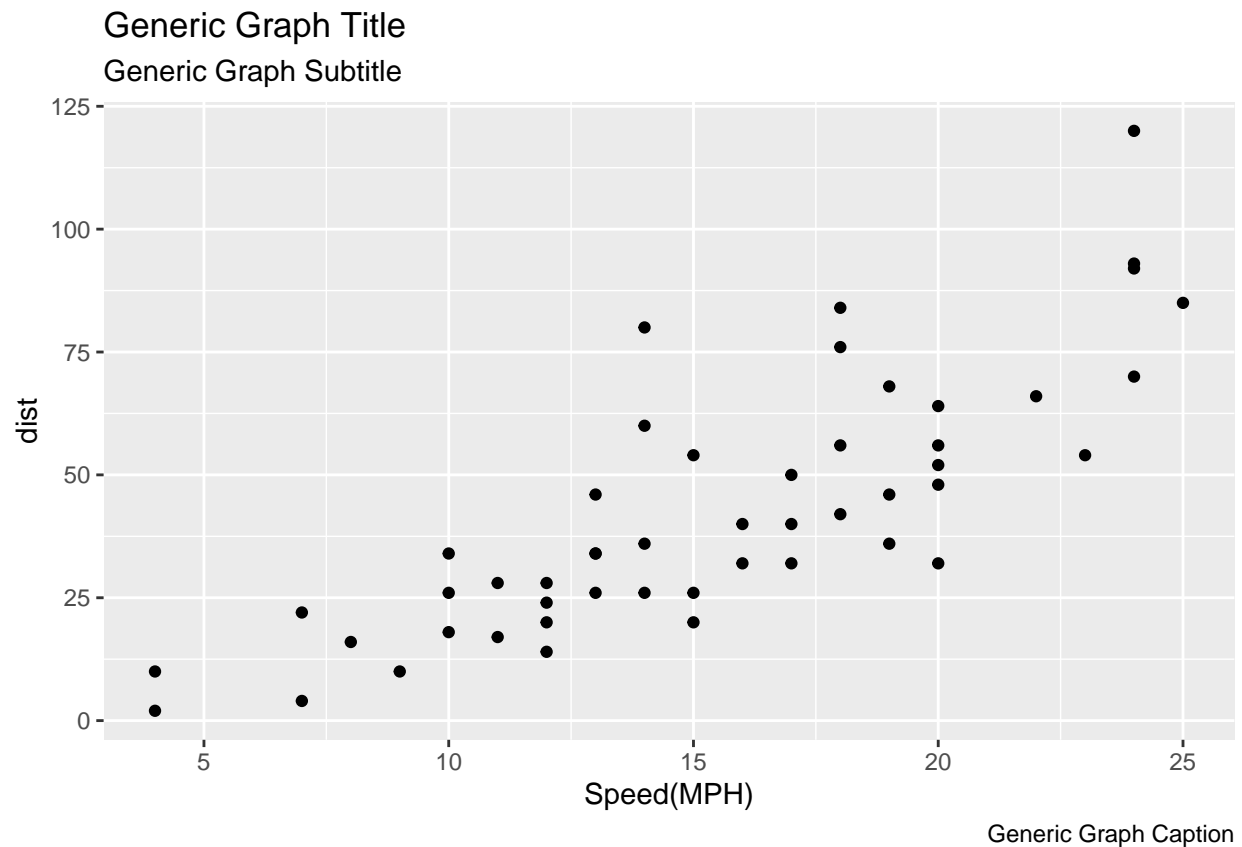
```
p + geom_smooth(method=lm)
```

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

```
p + labs(title="Generic Graph Title", subtitle="Generic Graph Subtitle", caption="Generic Graph Caption
  xlab("Speed(MPH)")
```

```r
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
```

```r
ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()+
  scale_colour_manual(values=c("blue","gray","red")) +
  labs(title="Gene Expression Changes Upon Drug Treatment",
       x="Control (no drug) ",
       y="Drug Treatment")
```

Gene Expresion Changes Upon Drug Treatment