

## Class5.R

saumy

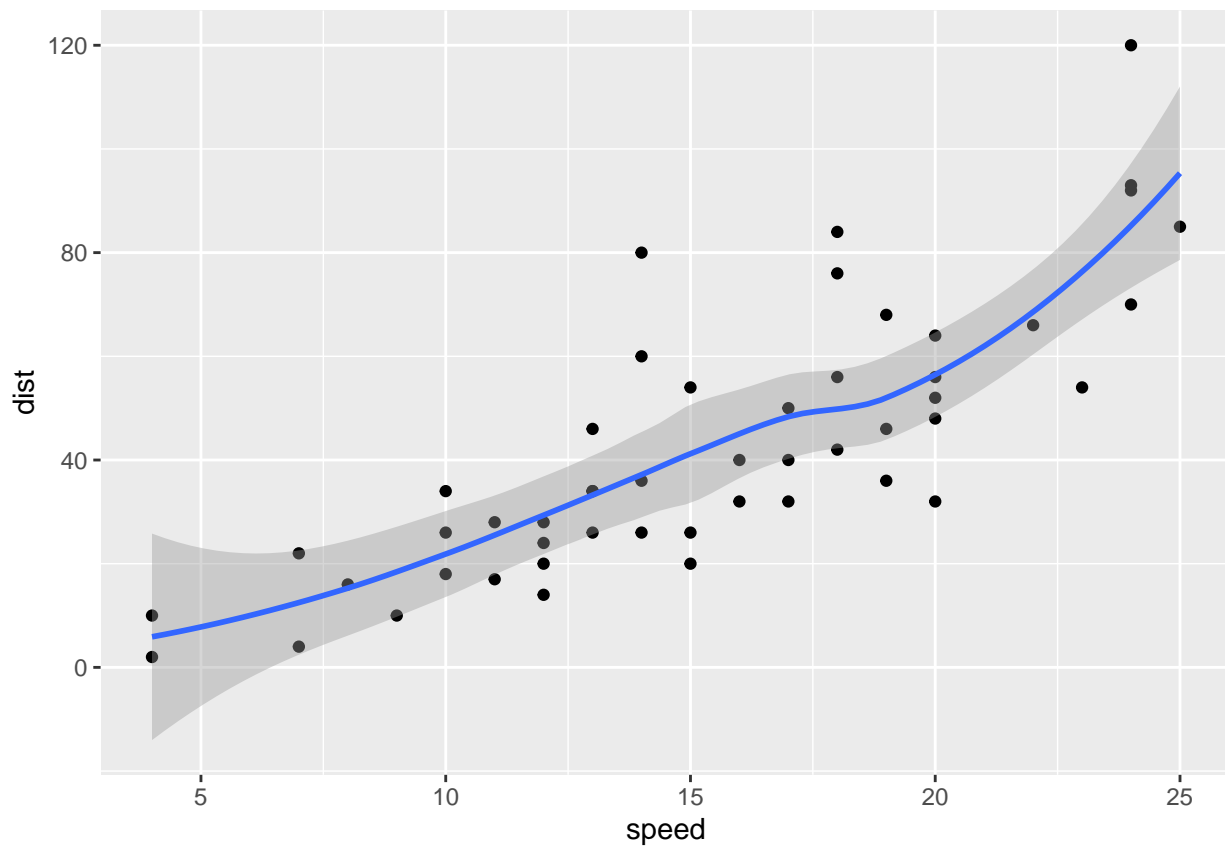
2021-10-12

```
# Installed ggplot using install.packages(ggplot2)

# Making a scatter Plot

# ggplot is data + aes + geoms
library(ggplot2)
ggplot(data=cars)+ aes(x=speed, y=dist)+ geom_point() + geom_smooth()
```

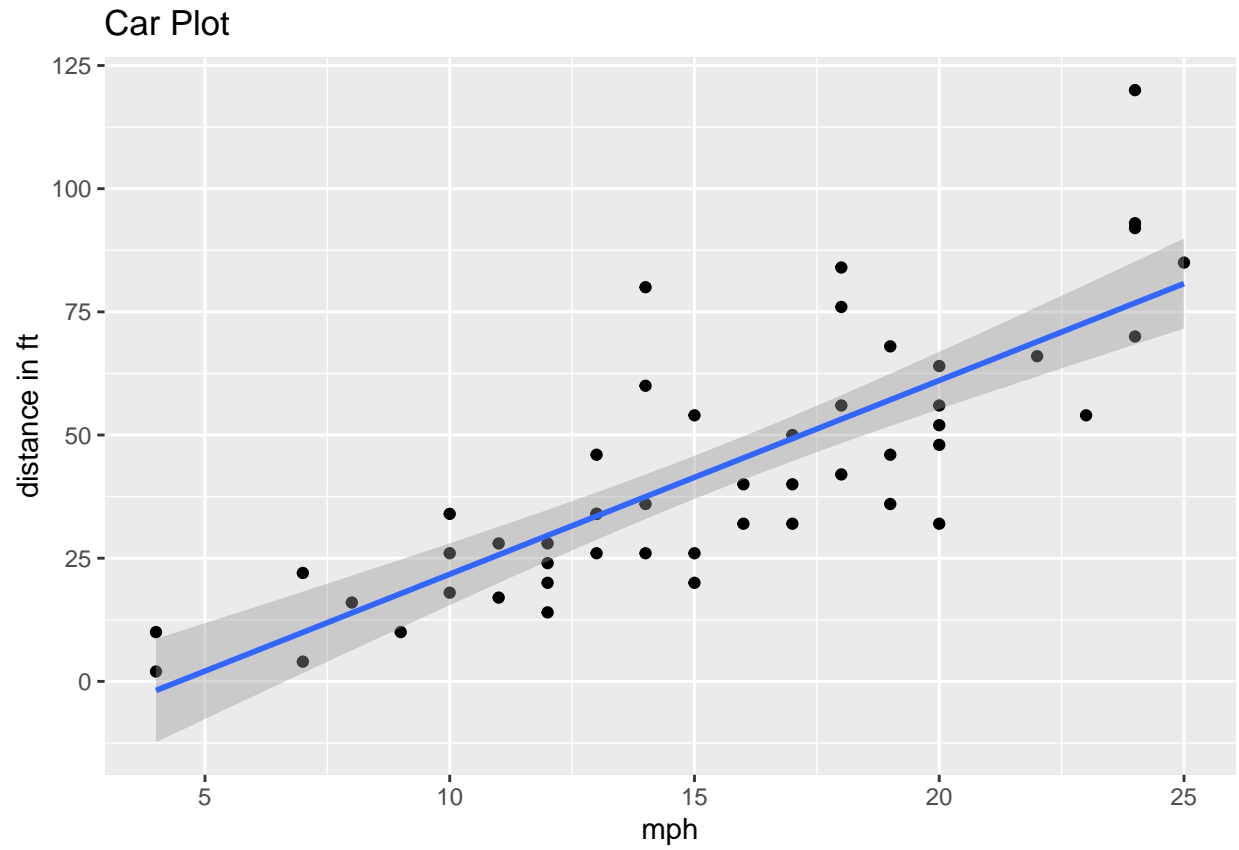
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



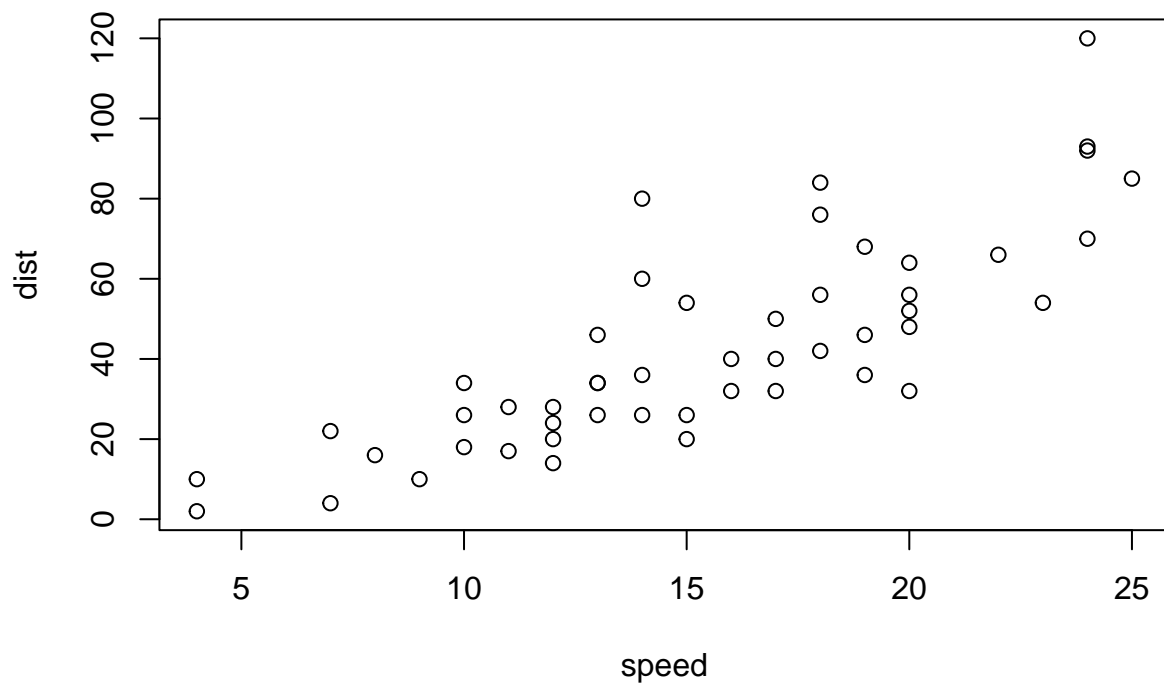
```
# change to a linear model
p <- ggplot(data=cars)+ aes(x=speed, y=dist)+ geom_point() + geom_smooth(method= "lm")
```

```
p+ labs(title="Car Plot", x= "mph", y= "distance in ft")
```

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

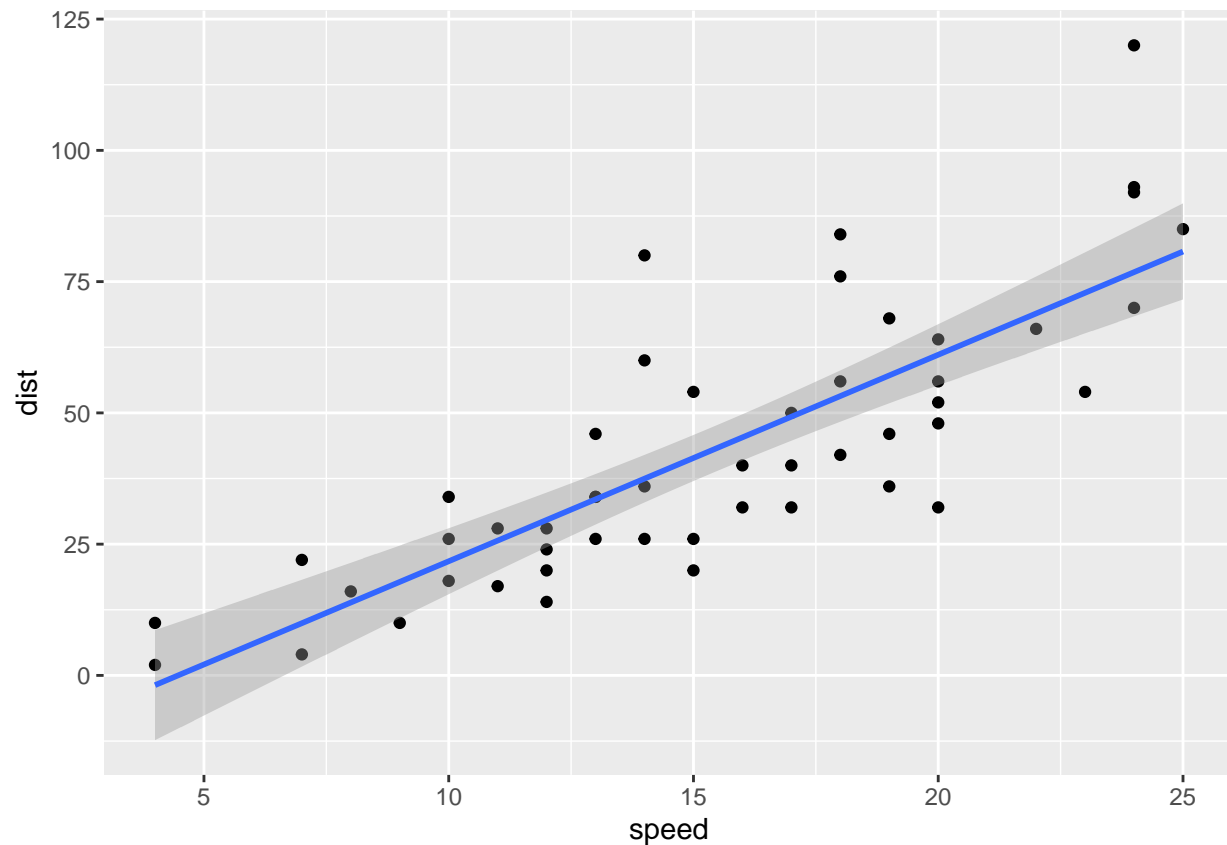


```
#Base graphics is shorter  
plot(cars)
```



p

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



```
#Adding more data section
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
```

```
#how to access State col
table(genes$State)
```

```
##
##      down unchanging      up
##      72      4997      127
```

```
# What % are up/down
prec <- table(genes$State) / nrow(genes) * 100
prec
```

```
##
##      down  unchanged      up
## 1.385681 96.170131 2.444188
```

```
round(prec, 2)
```

```
##
##      down  unchanged      up
##      1.39      96.17      2.44
```

```
#Making a scatter Plot (d for drug)
head(genes)
```

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

```
d <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
d + scale_colour_manual(values=c("blue","gray","red")) + labs(title = "Change in Gene Expression After Drug Treatment")
```

