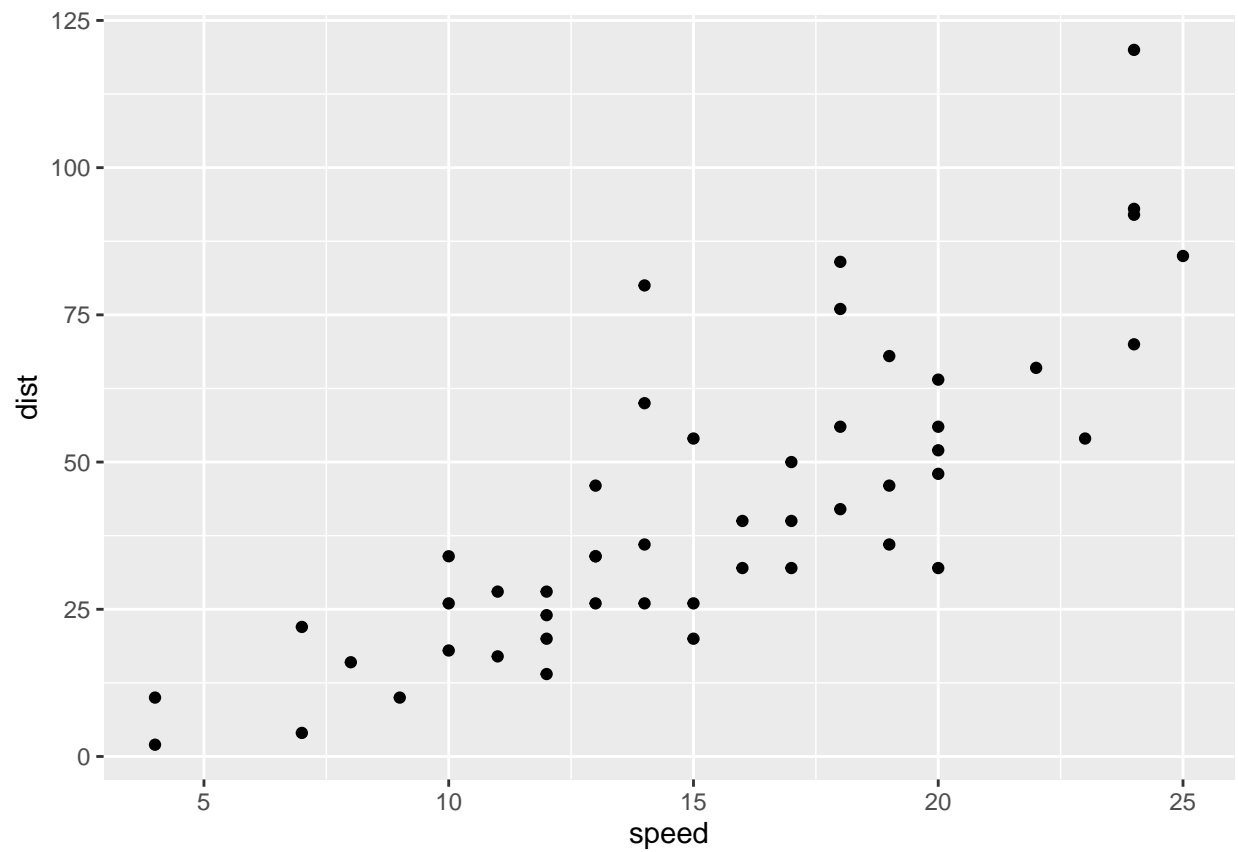


# Week 4 Data Visualization Lab

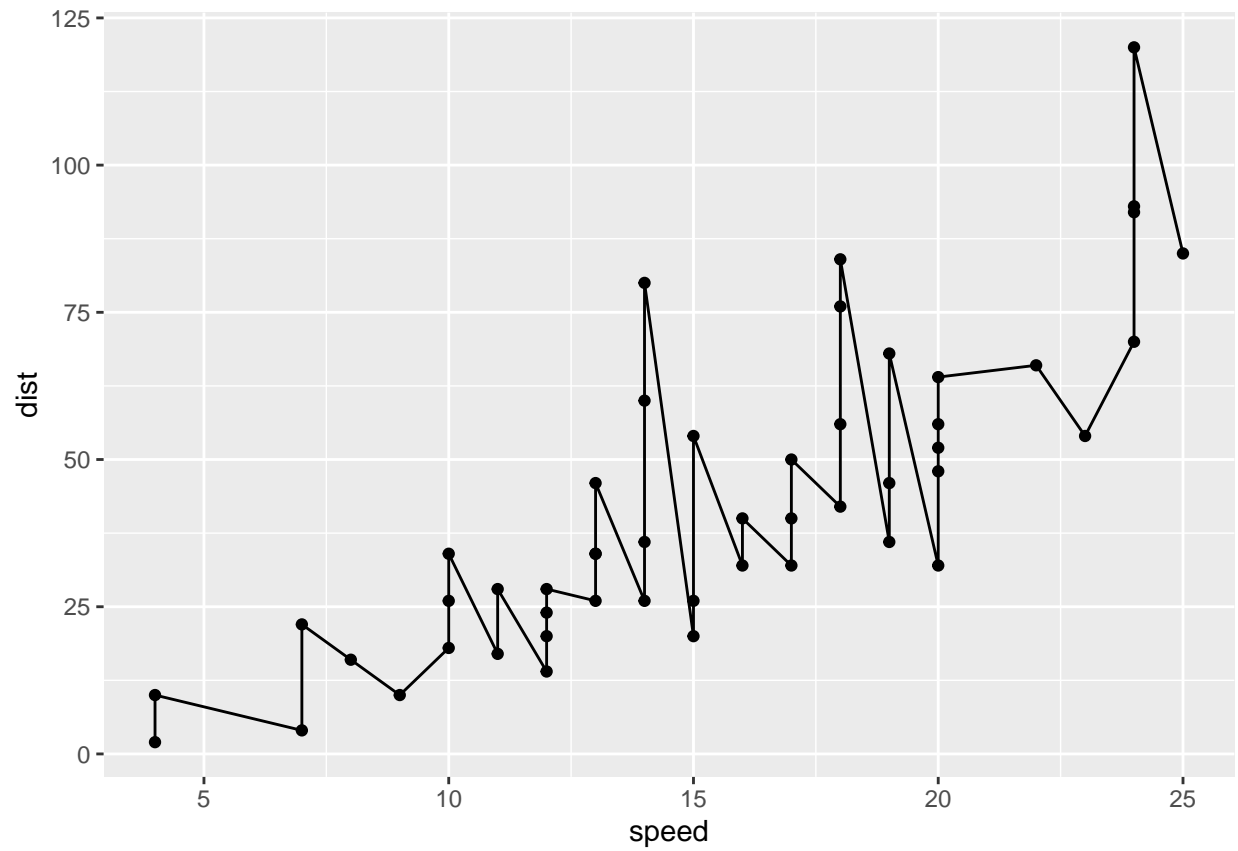
Nicholas Thiphakhinkeo A17686679

10/15/2024

```
library("ggplot2")  
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()
```

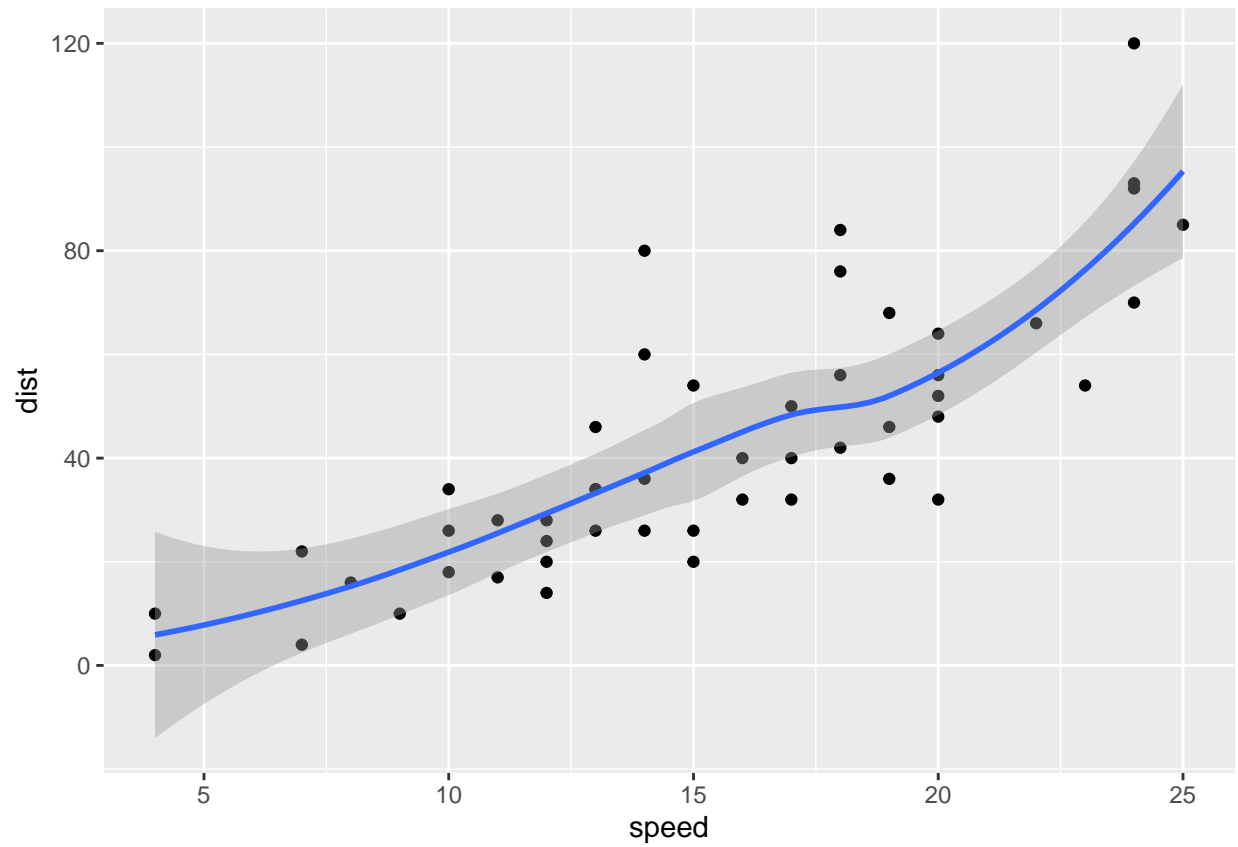


```
p <- ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()  
#adding scatter line  
p + geom_line()
```

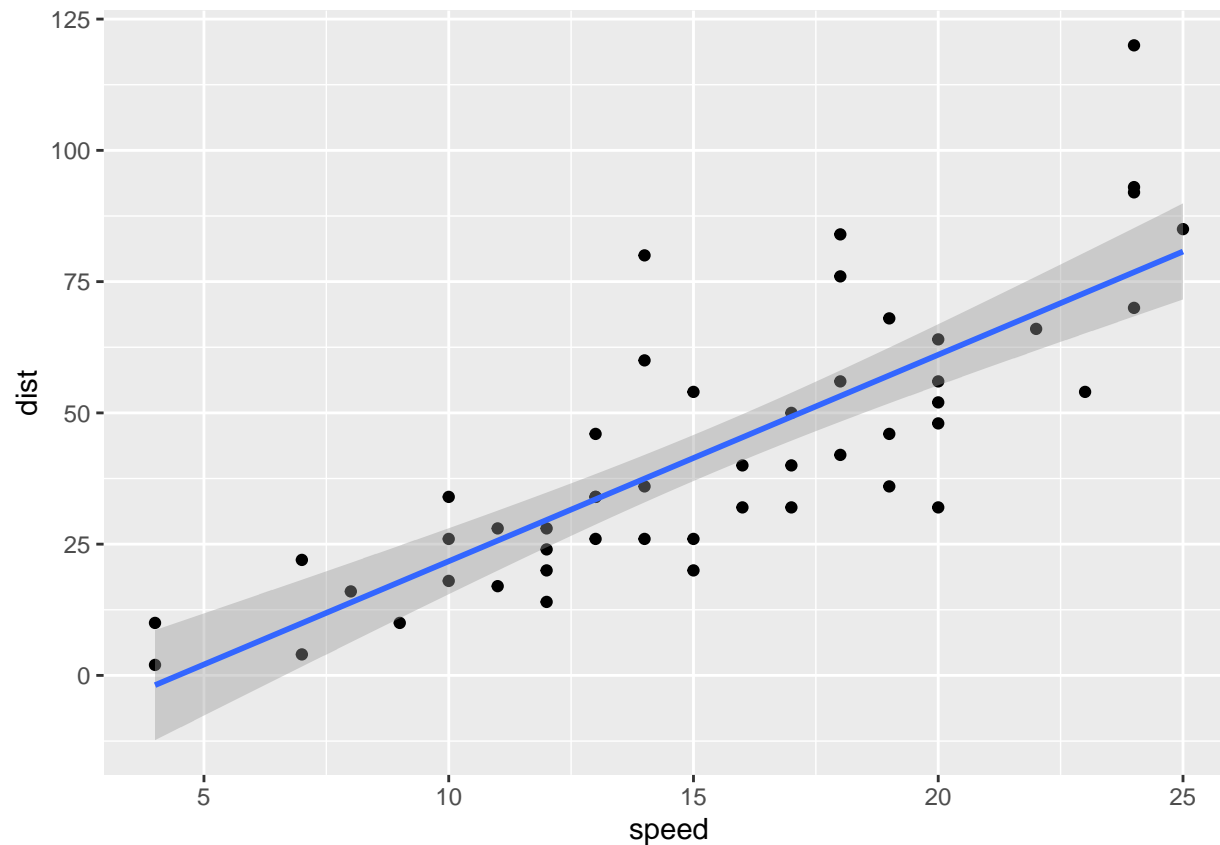


```
#adding fit line  
p + geom_smooth()
```

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



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



```
#-----
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  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
```

```
#Plot and Adding Color
g <- ggplot(data=genes) +
  aes(x=Condition1, y=Condition2,
      col=State) +
  geom_point()
#Fraction of Total Genes Up-Reg(%)
table(genes$State)/nrow(genes) * 100
```

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

```
#Rounding Value (last purple value sig fig amounts)
round(table(genes$State)/nrow(genes) * 100,3)
```

```
##
##      down  unchanged      up
##      1.386    96.170    2.444
```

```
#Changing Color
```

```
g + scale_color_manual(values=c("brown", "gray", "purple")) +
  labs(title="Gene Expression Changes Upon Drug Treatment",
        x="Control(no drug)", y="Drug Administered") +
  theme_bw()
```

