

# Week 5 Data Visualization Lab

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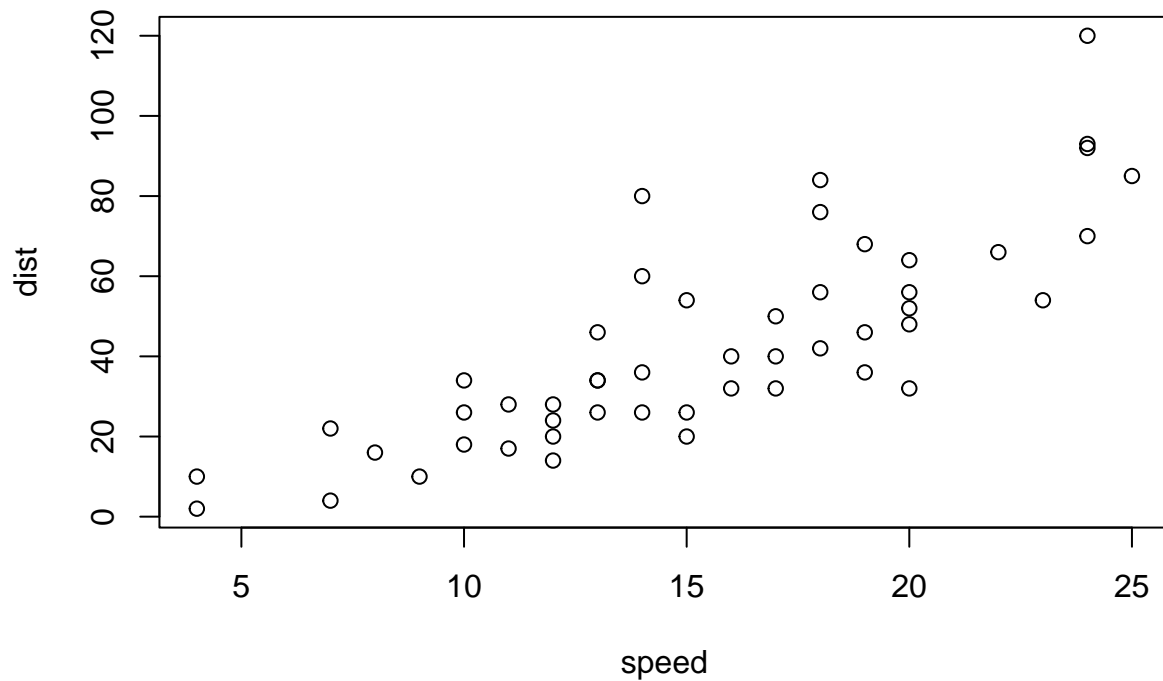
2022-02-07

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

# Anytime I want to use this package, I need to load it
library(ggplot2)

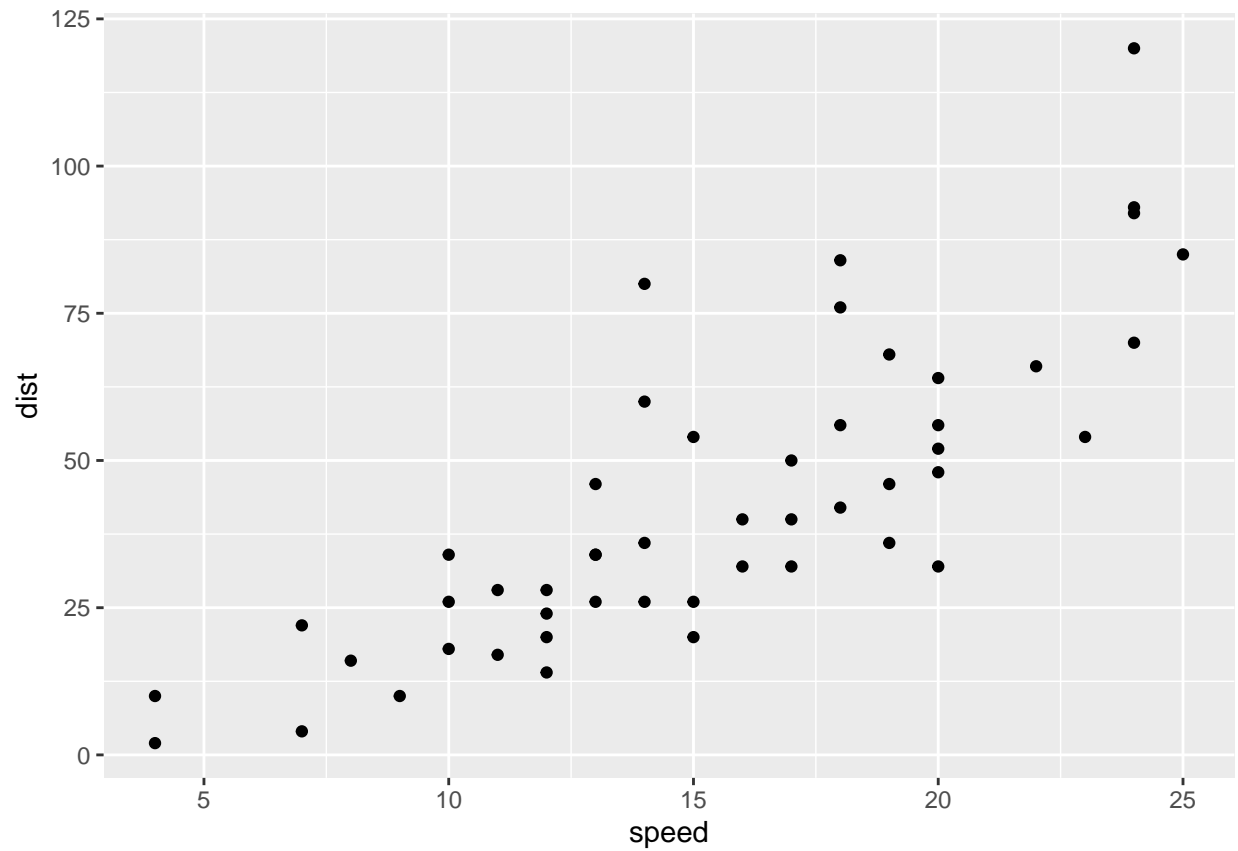
#View(cars)

# A quick base R plot - not ggplot
plot(cars)
```

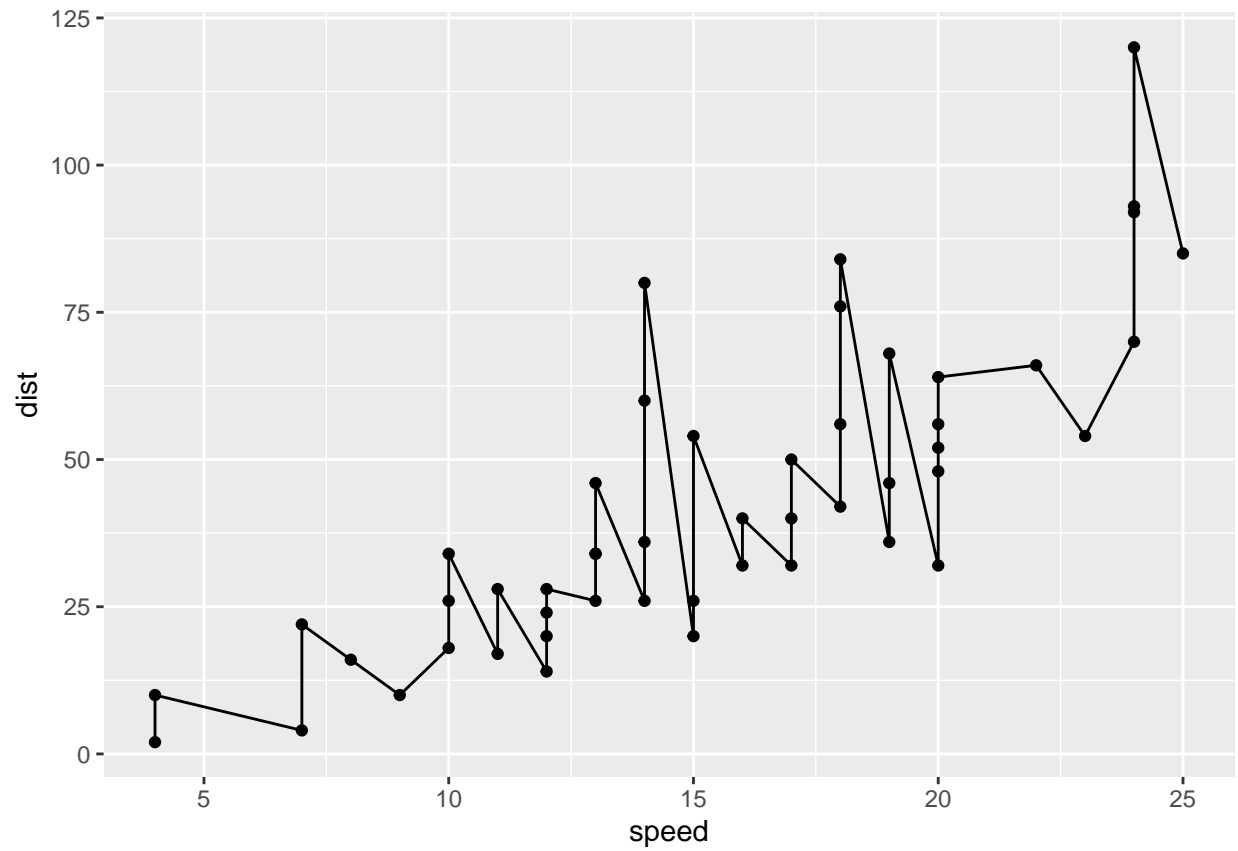


```
# Our first ggplot
# We need data + aesthetics + geometry
```

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

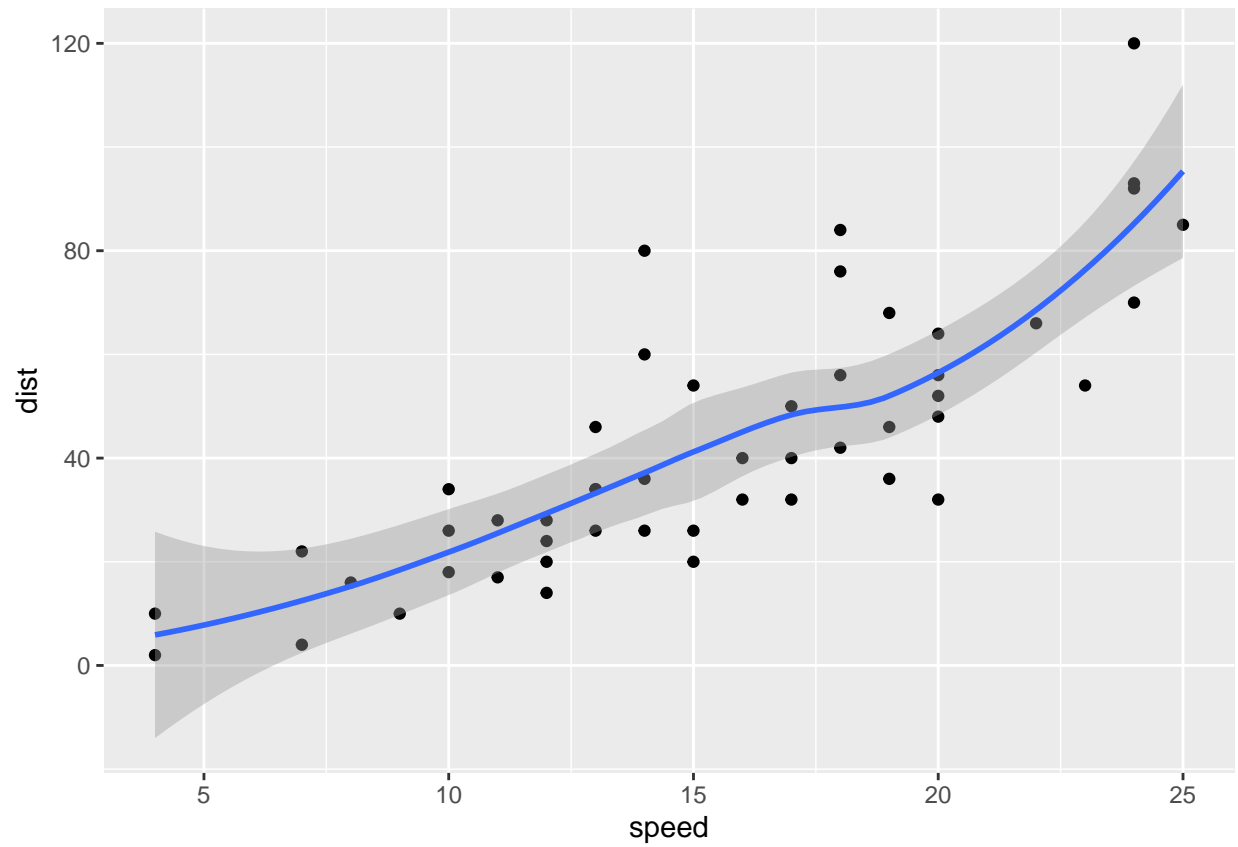


```
p <- ggplot(data=cars) +  
  aes(x=speed,y=dist) +  
  geom_point()  
  
# Add a line geom with geom_line()  
p + geom_line()
```



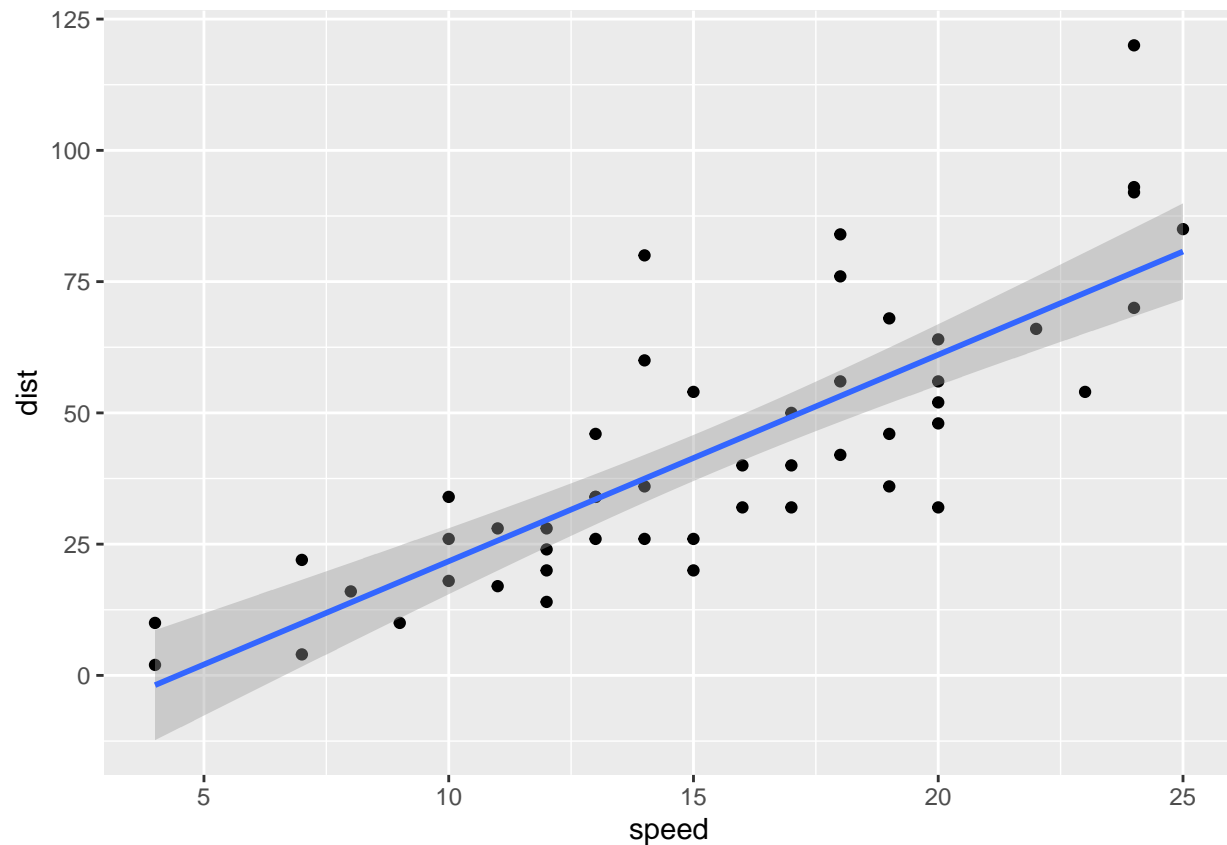
```
#Add a trend line close to the data  
p + geom_smooth()
```

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



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

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



*# Read in our drug expression data*

```
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
```

*# Make a ggplot*

```
#ggplot(data=genes)+aes(x=Condition1,y=Condition2,col=State) +geom_point()
# Add some color
```

*# How many rows in genes?*

```
nrow(genes)
```

```
## [1] 5196
```

```
# How many columns in genes?  
colnames(genes)
```

```
## [1] "Gene"      "Condition1" "Condition2" "State"
```

```
ncol(genes)
```

```
## [1] 4
```

```
# down, unchanging and up of State  
table(genes$State)
```

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

```
# Fraction of total genes are up-regulated  
round(table(genes$State)/nrow(genes)*100,2)
```

```
##  
##      down unchanging      up  
##      1.39      96.17      2.44
```

```
# Change color  
#g + scale_colour_manual(values=c("blue","gray","red")) +  
#labs(title="Gene Expression Changes Upon Drug Treatment",  
#x="Control (no drug)",  
#y="Drug Treatment")
```