

Week 5 Data Visualization Lab

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```
# Week 5 Data Visualization Lab
```

```
# Use "cars" data included with downloaded R package
```

```
View(cars)
```

```
## Warning in system2("/usr/bin/otool", c("-L", shQuote(DSO)), stdout = TRUE)
```

```
:
```

```
## running command ''/usr/bin/otool' -L '/Library/Frameworks/R.framework/Resources/
```

```
## modules/R_de.so'' had status 1
```

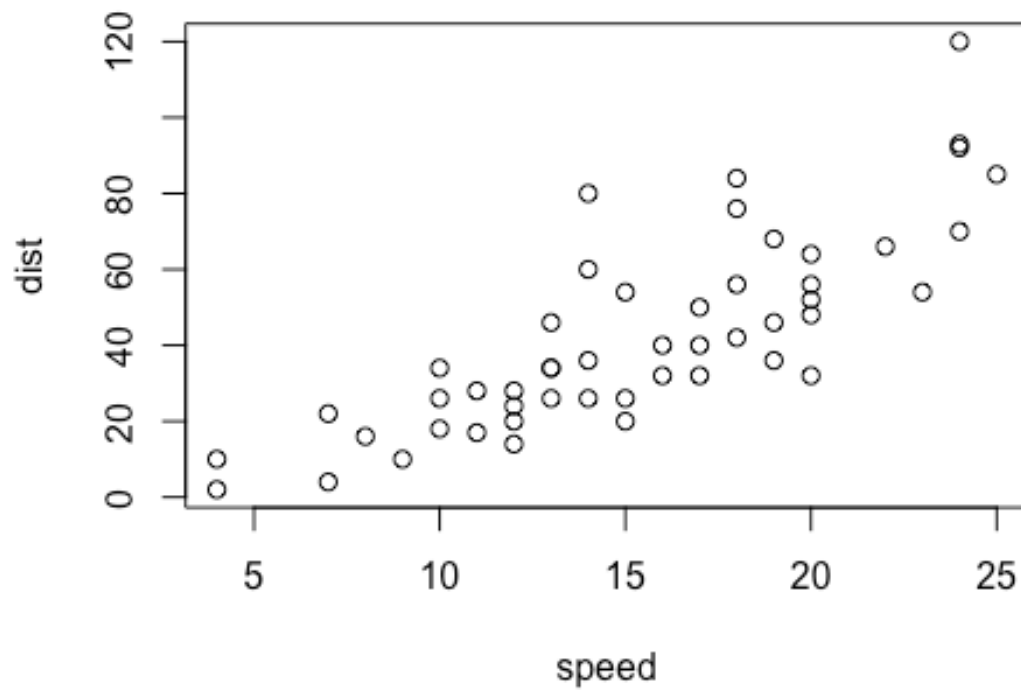
```
plot(cars)
```

```
# ggplot2 has already been installed on this device
```

```
library(ggplot2)
```

```
## Warning in register(): Can't find generic `scale_type` in package ggplot2  
to
```

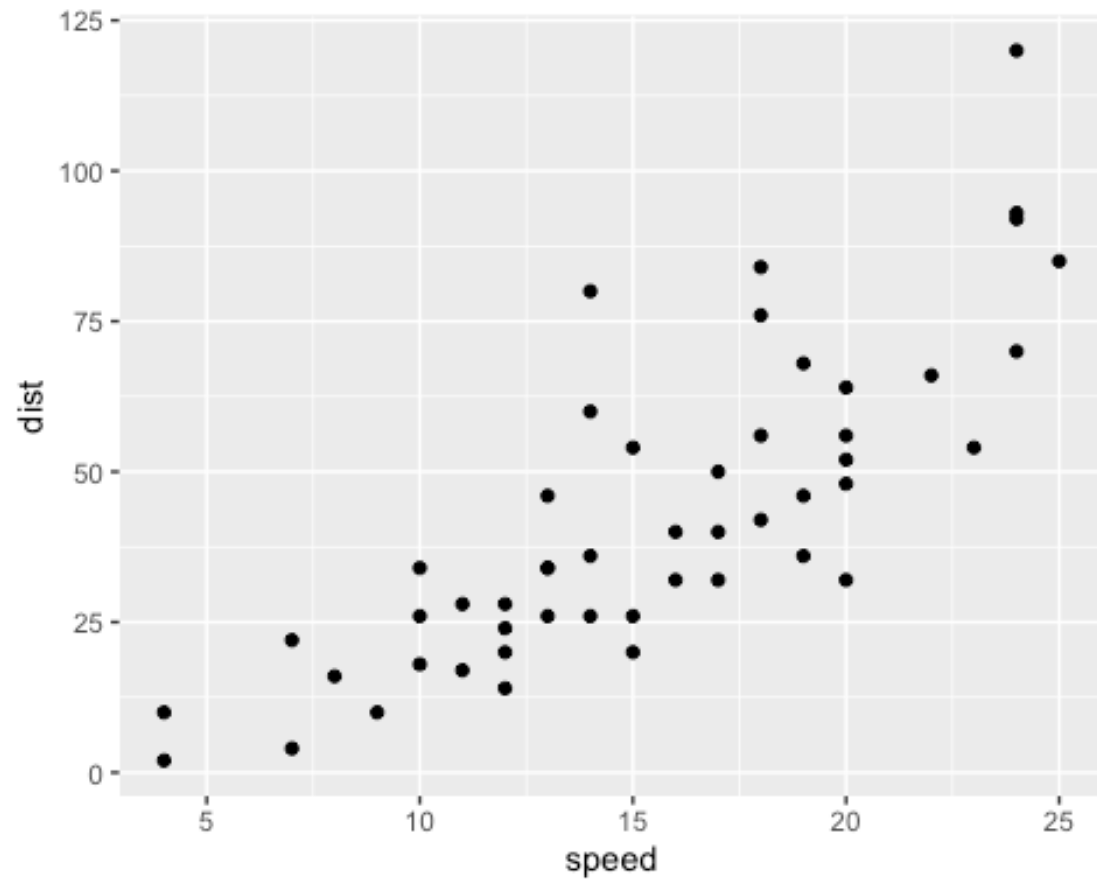
```
## register S3 method.
```



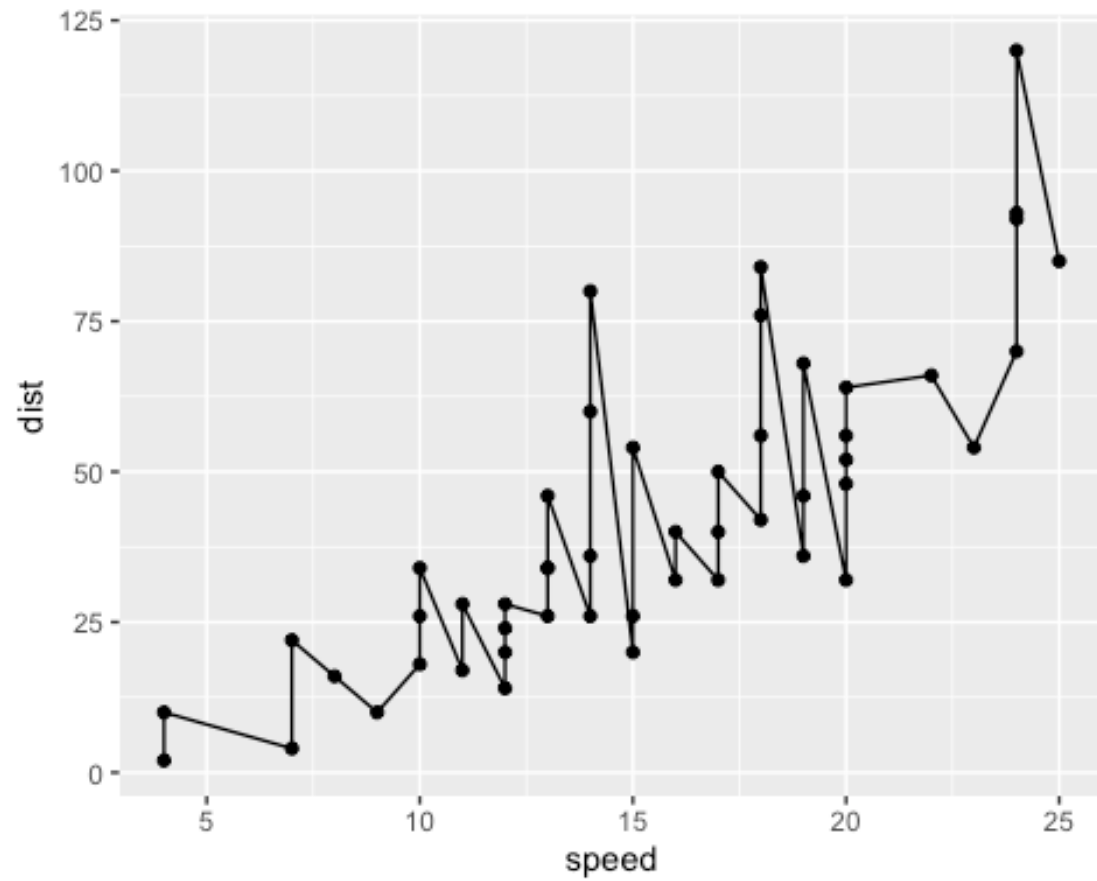
```
# Use ggplot to graph "cars" data
```

```
p <- ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point()
```

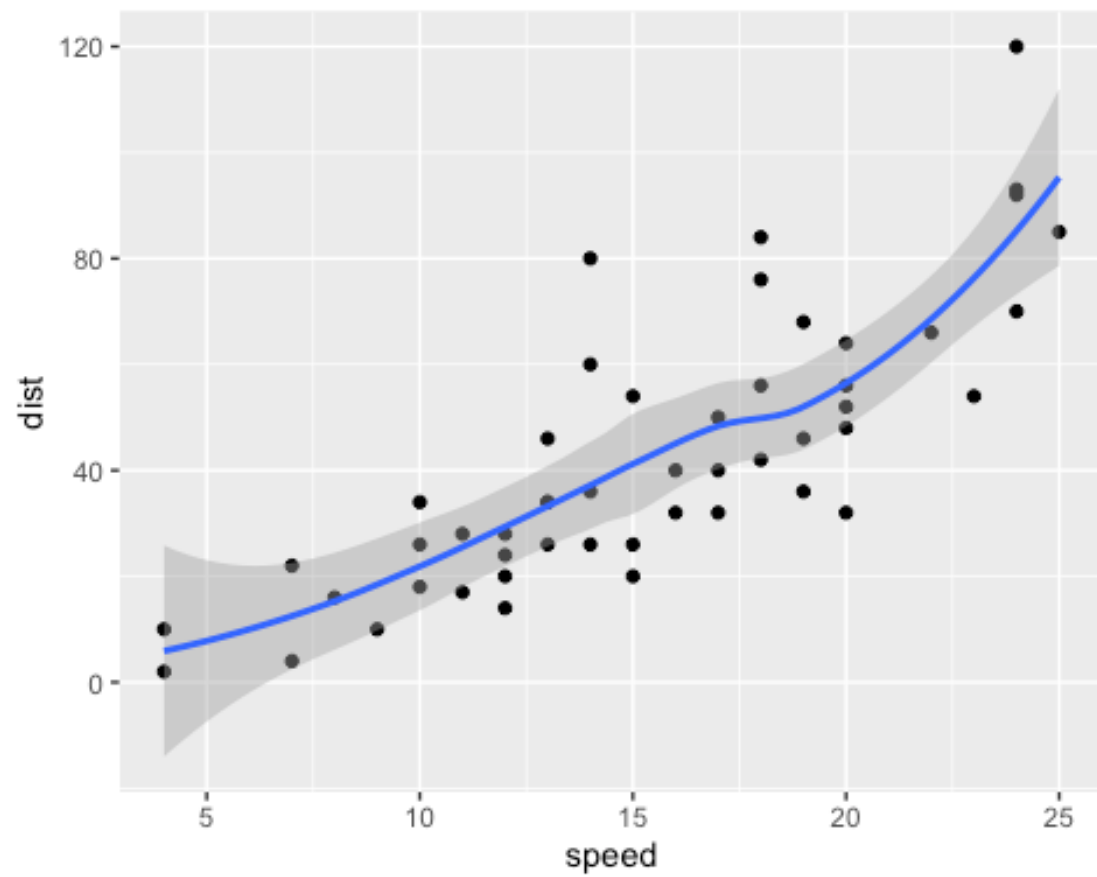
```
p
```



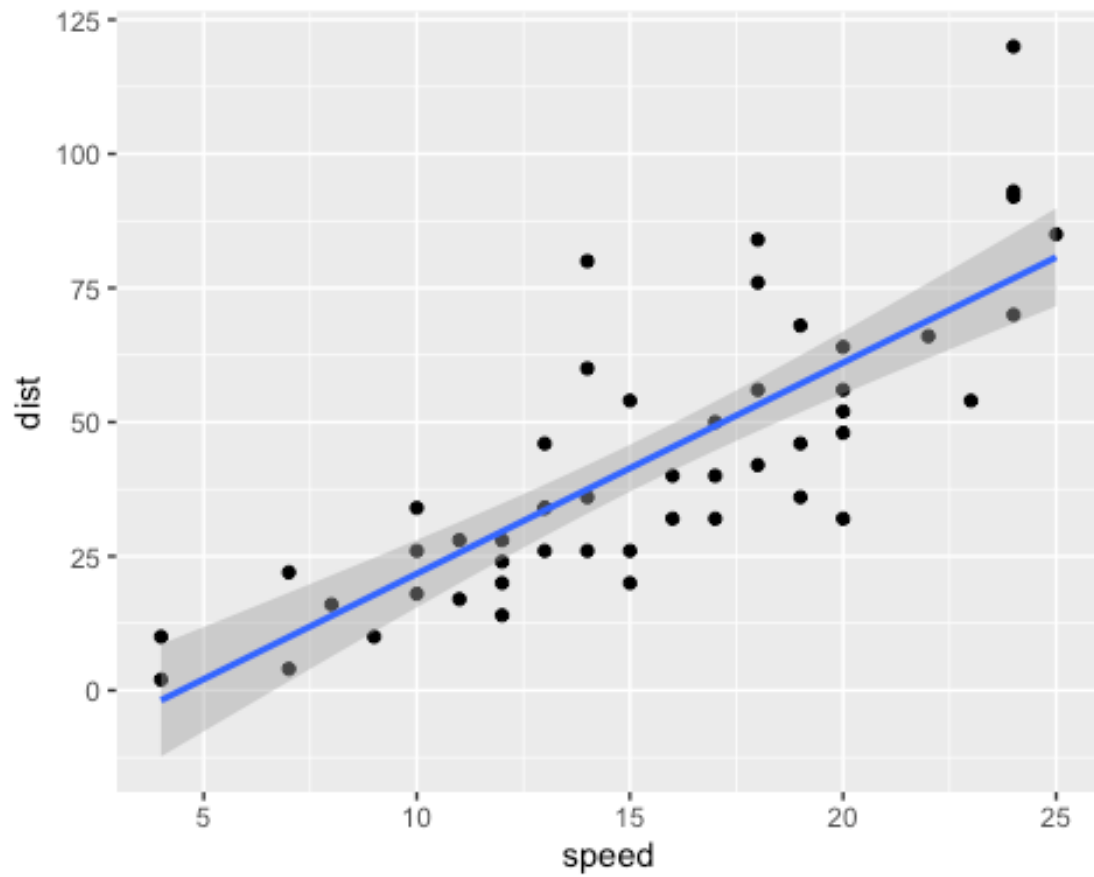
```
p + geom_line()
```



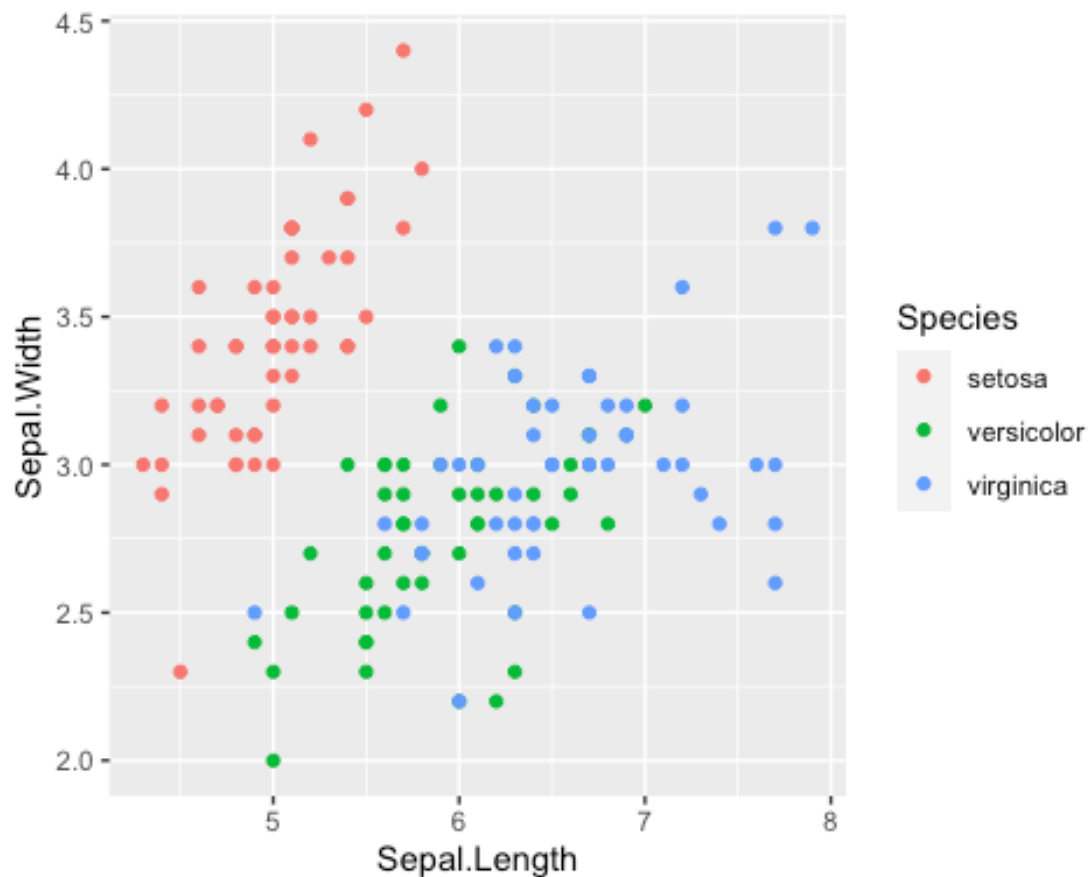
```
p + geom_smooth()  
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



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



```
#Create plot using "iris" data)  
ggplot(iris, aes(x=Sepal.Length,  
                 y=Sepal.Width,  
                 col=Species)) +  
  geom_point()
```



```
View(iris)

## Warning in system2("/usr/bin/otool", c("-L", shQuote(DSO)), stdout = TRUE)
:
## running command ''/usr/bin/otool' -L '/Library/Frameworks/R.framework/Reso
urces/
## modules/R_de.so'' had status 1

# Import data from website and assign to "genes"
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expressi
on.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

# View "genes" data
View(genes)
```

```
## Warning in system2("/usr/bin/otool", c("-L", shQuote(DSO)), stdout = TRUE)
:
## running command ''/usr/bin/otool' -L '/Library/Frameworks/R.framework/Reso
urces/
## modules/R_de.so'' had status 1

nrow(genes)

## [1] 5196

table(genes$State)

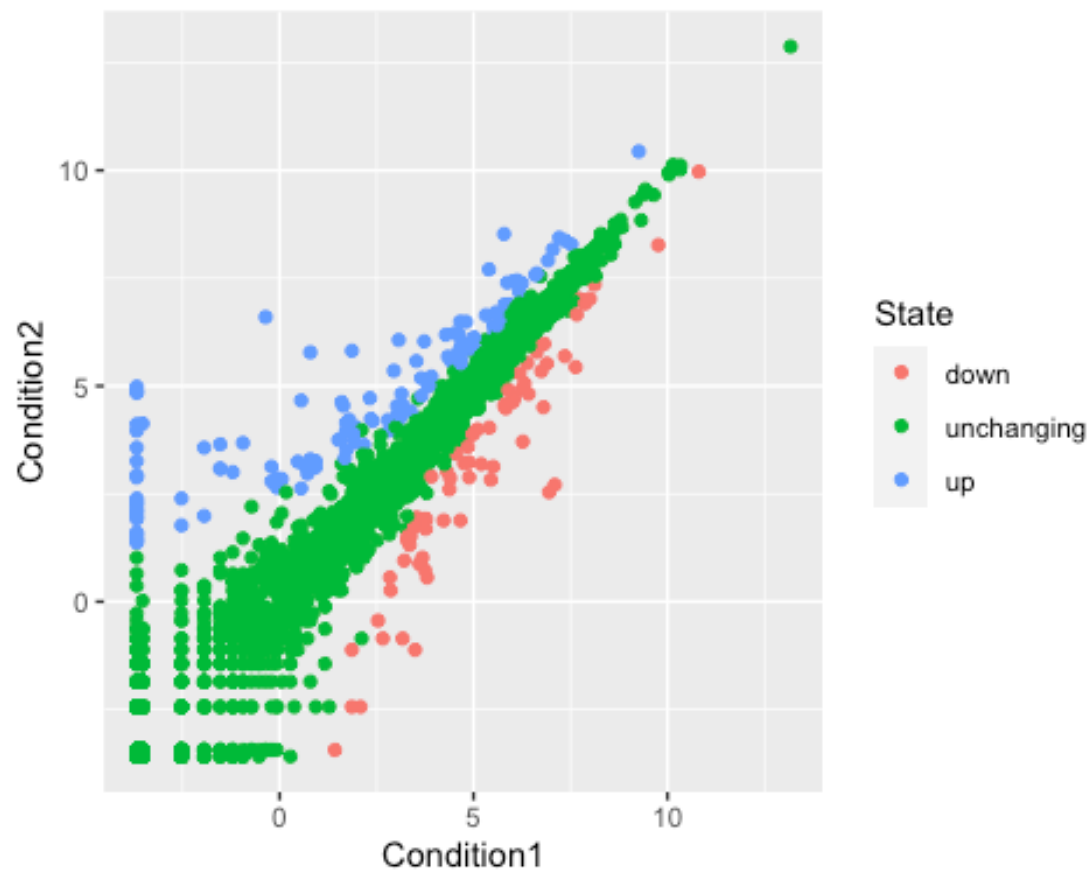
##
##      down  unchanging      up
##      72      4997      127

round((table(genes$State)/nrow(genes))*100, 2)

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

# Use ggplot to plot "genes" data
g <- ggplot(genes)+
  aes(x=Condition1,
      y=Condition2,
      col=State)+
  geom_point()

g
```

```
# Adjust ggplot of "genes" data
g + theme_bw() +
  scale_color_manual(values=c("blue","gray","red"))+
  labs(x="Control (no drug)",
       y="Drug treated",
       title="Gene expression changes example plot")
```

Gene expression changes example plot

