Week 5 Data Visualization Lab

Kiley Hooker (PID A15441609)

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```r
# Week 4 Data Visualization Lab

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

# Any time I want to use this package I need to load it
library(ggplot2)

View(cars)
```
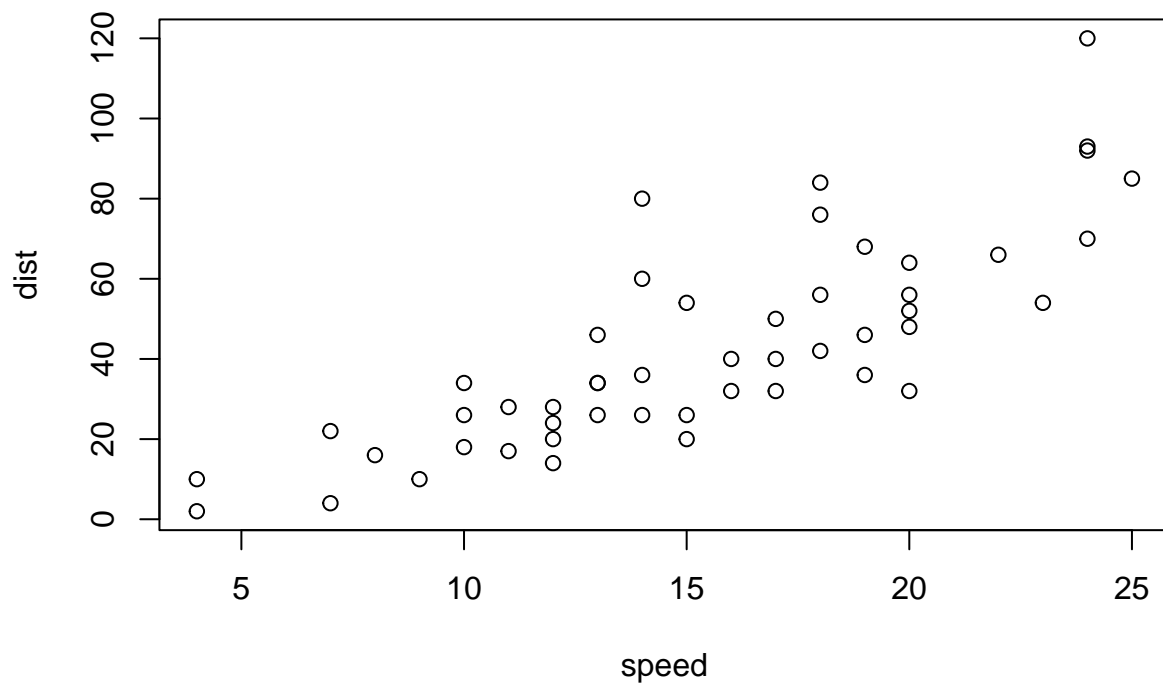
```
## Warning in system2("/usr/bin/otool", c("-L", shQuote(DSO)), stdout = TRUE):
## running command ''/usr/bin/otool' -L '/Library/Frameworks/R.framework/Resources/
## modules/R_de.so'' had status 1
```
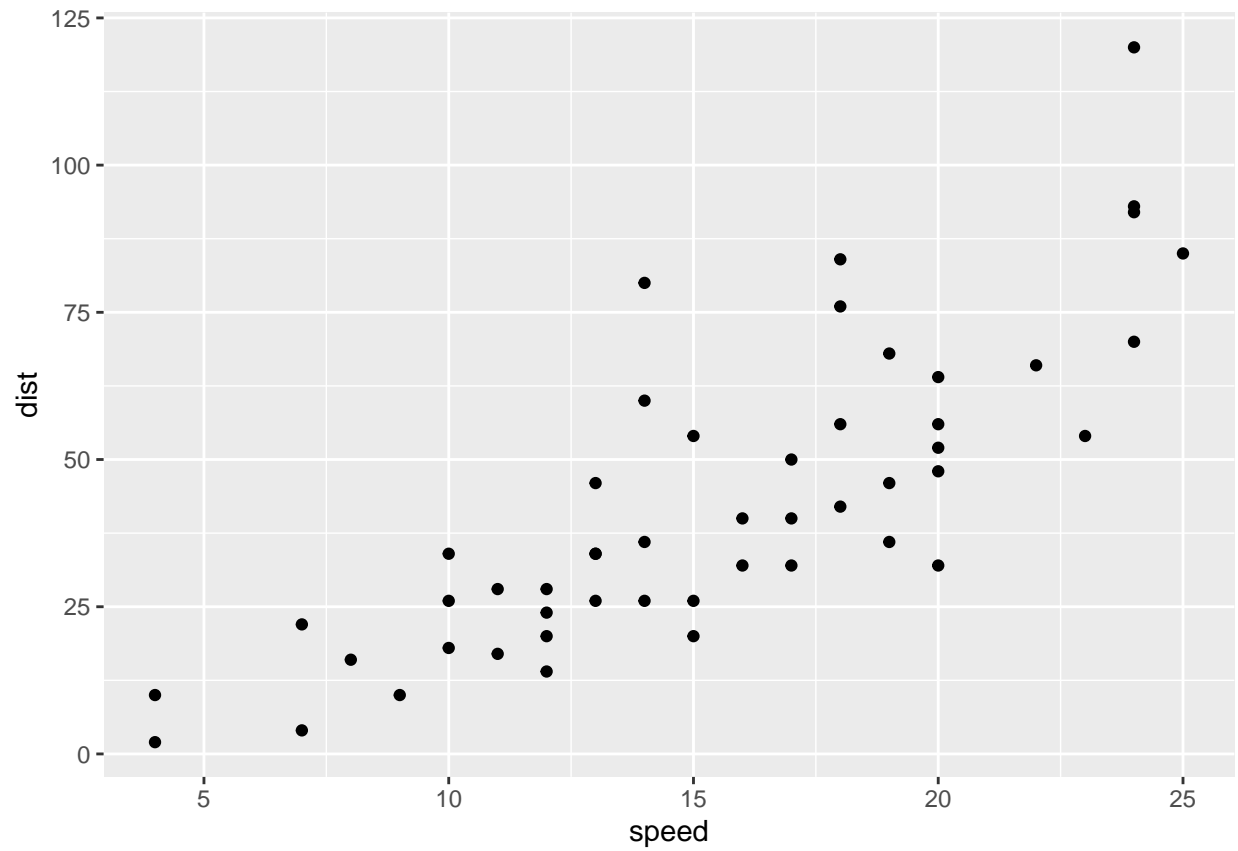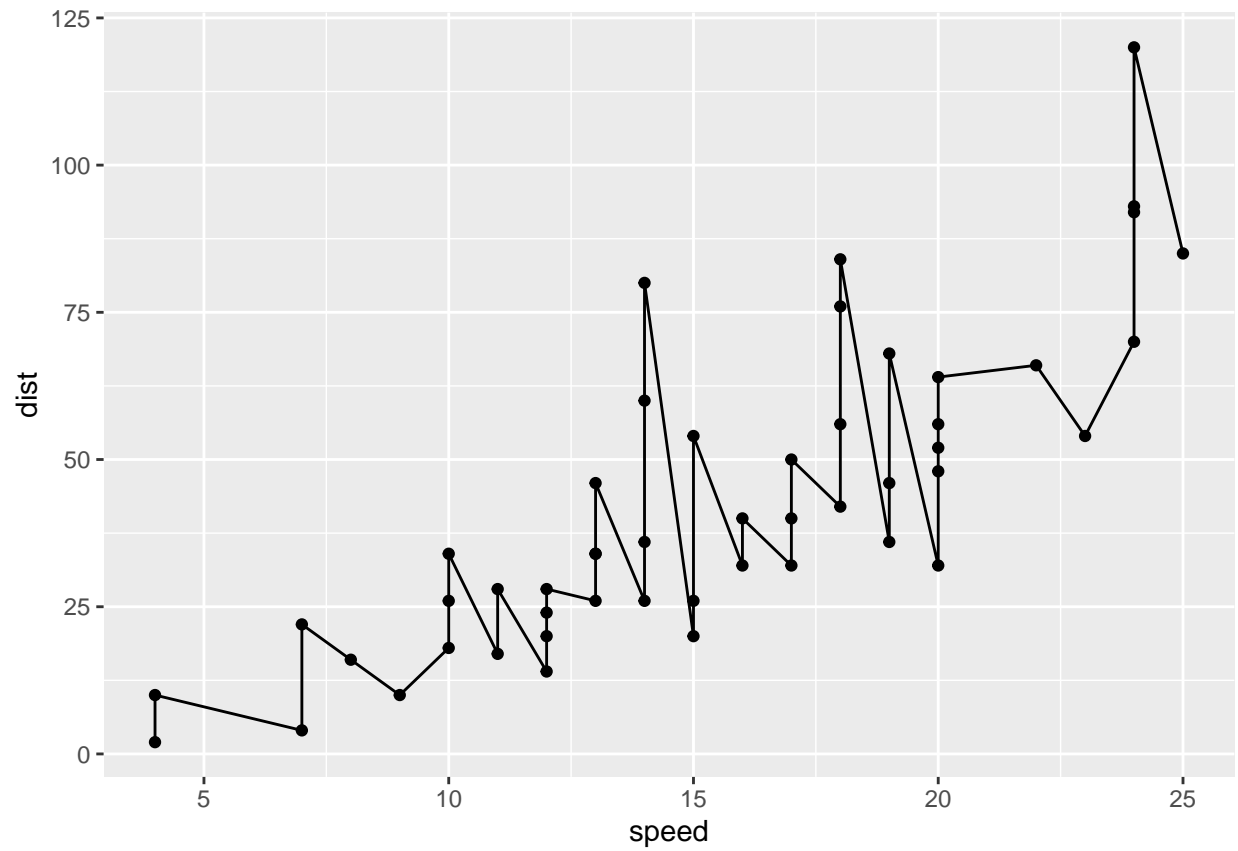
```r
# A quick base R plot - this is not ggplot
plot(cars)
```

```r
# Our first ggplot
# we need data + aes + geoms
ggplot(data=cars)  +
  aes(x=speed, y=dist) +
  geom_point()
```
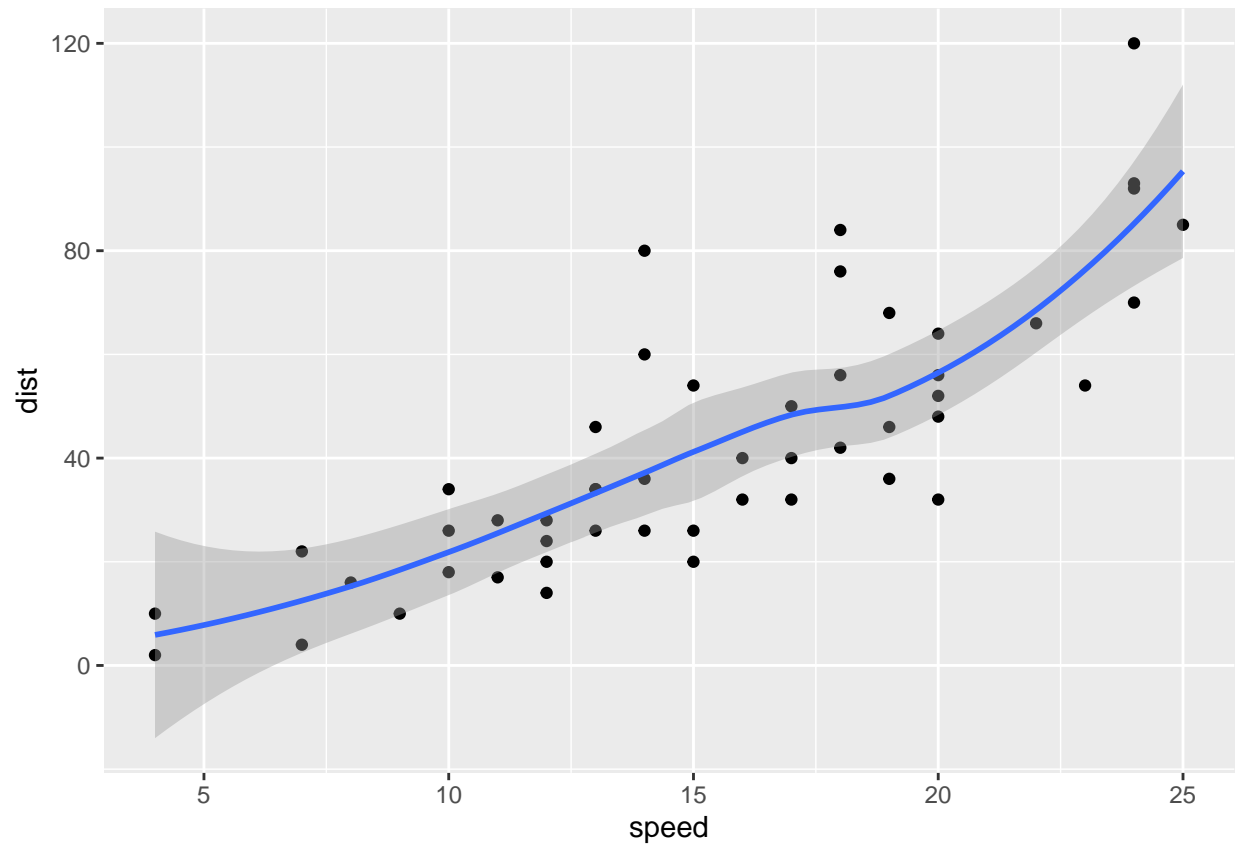
```
p <- ggplot(data=cars)  +
  aes(x=speed, y=dist) +
  geom_point()

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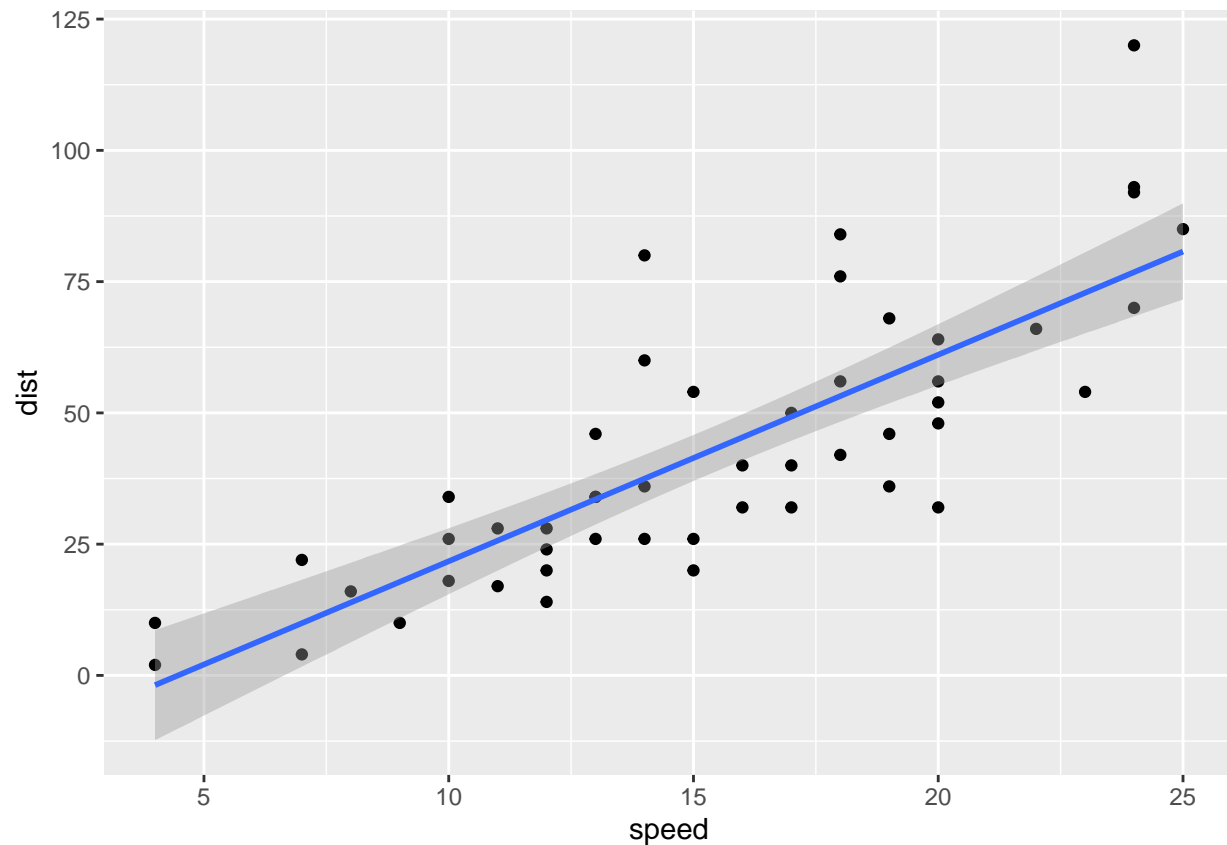
```
# Add a trend line close to the data
p + geom_smooth()
```

```
## `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
```

```
# Q. How many genes in this dataset
nrow(genes)
```

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

```
# 5196 genes

# Q. How many 'up' regulated genes
table(genes$State)
```

```
##
```

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

```r
# 127 up

# Q. What fraction of total genes is
#     up-regulated
round((table(genes$State) / nrow(genes)) * 100, 2)
```

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

```r
# Let's make a first plot attempt
g <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()

#g

# Add some color
# g + scale_color_manual(values=c("blue", "gray", "red")) +
#   labs(title="Gene Expression Changes Upon Drug Treatment",
#       x="Control (no drug)", y="Drug Treatment") +
#   theme_bw()
# Had issues with the last plot when compiling which is why I added #
```