Week 3: Visualization Lab

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October 19, 2025
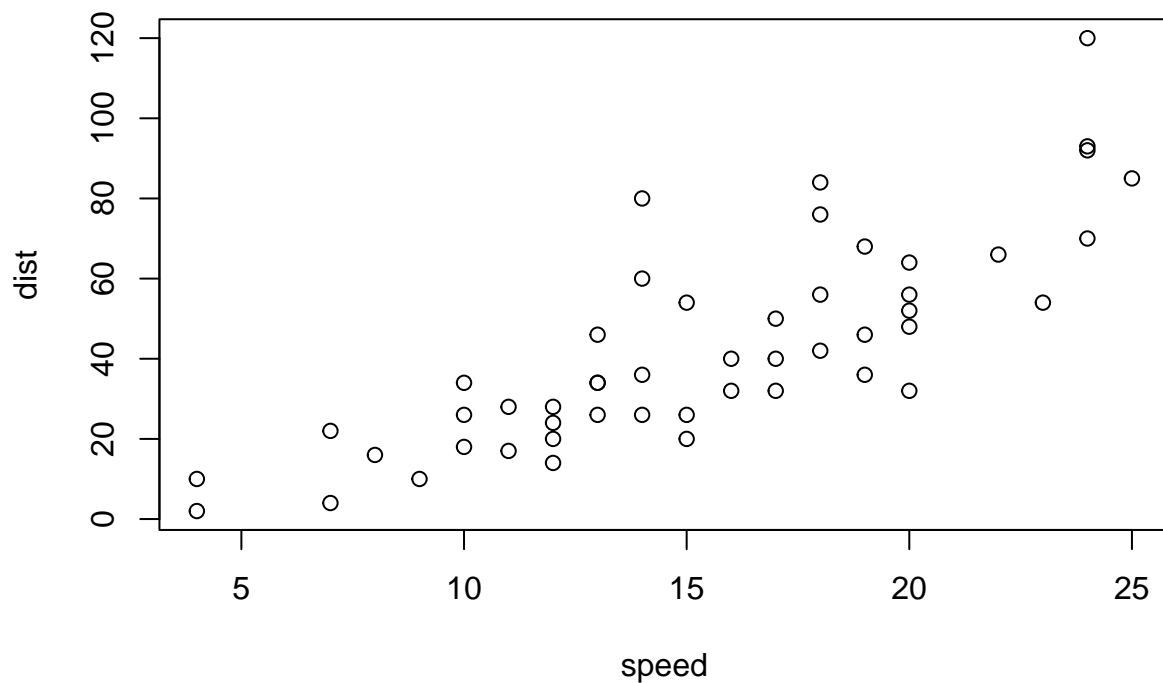
```r
# Week 3 Data Visualization Lab

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

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

View(cars)

# A quick base R plot - this is not ggplot
plot(cars)
```
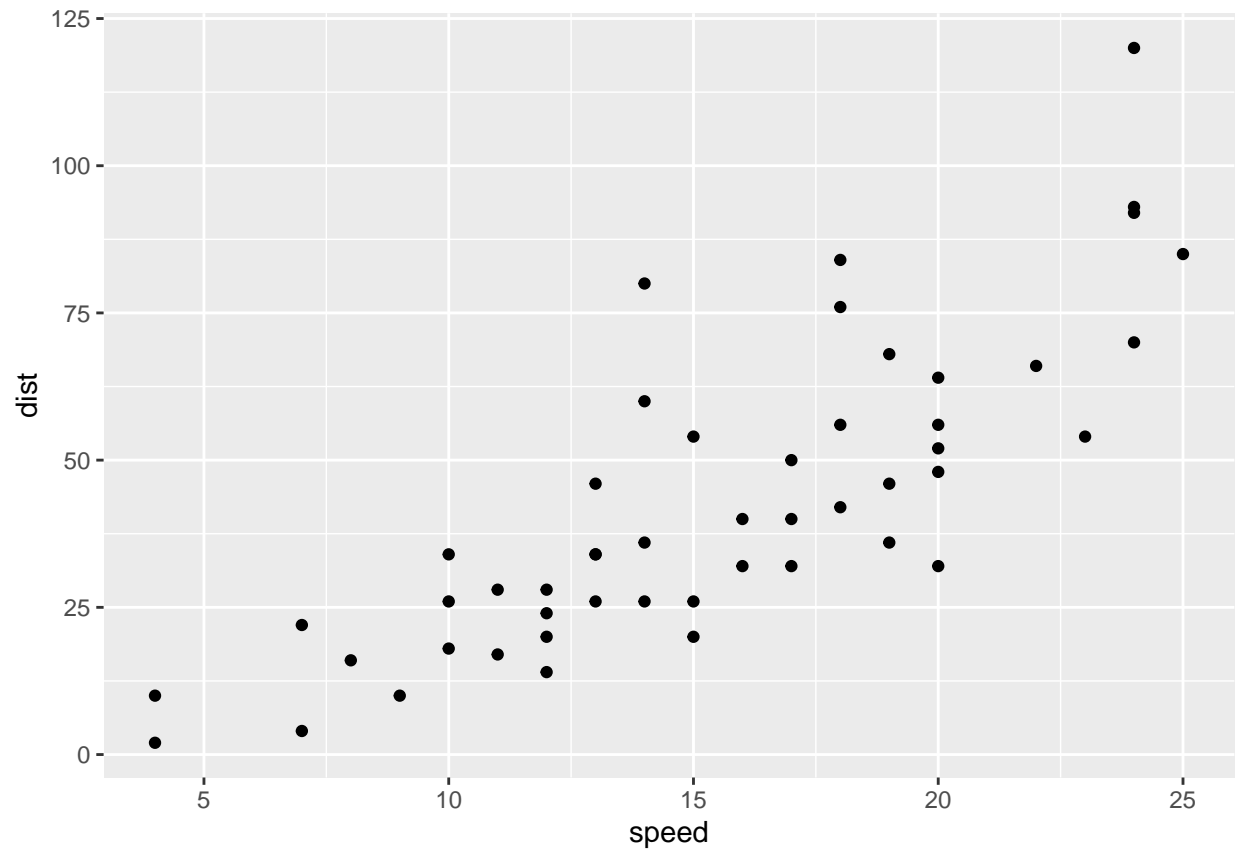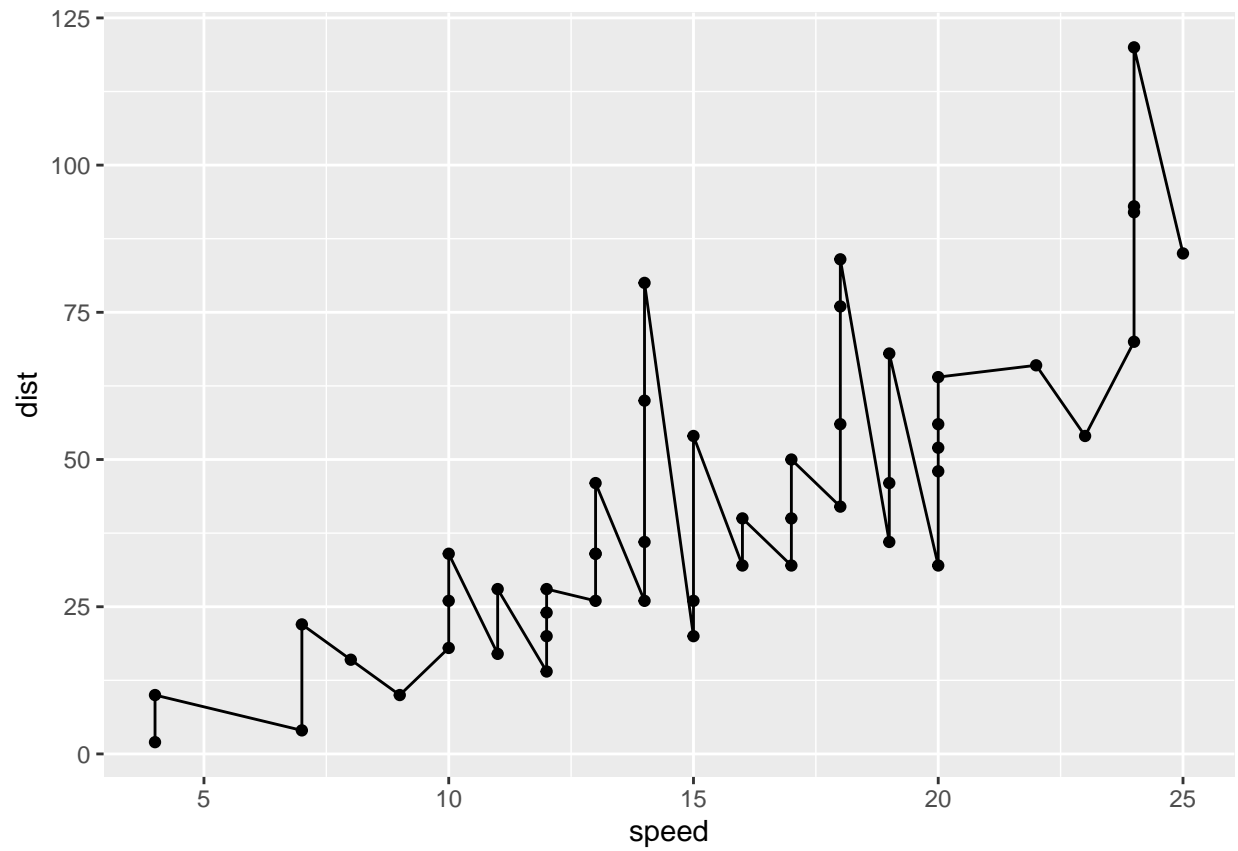
```r
# Our first ggplot
# we need data + aes + geoms
ggplot(data=cars)+
  aes(x=speed, y=dist) +
  geom_point()
```
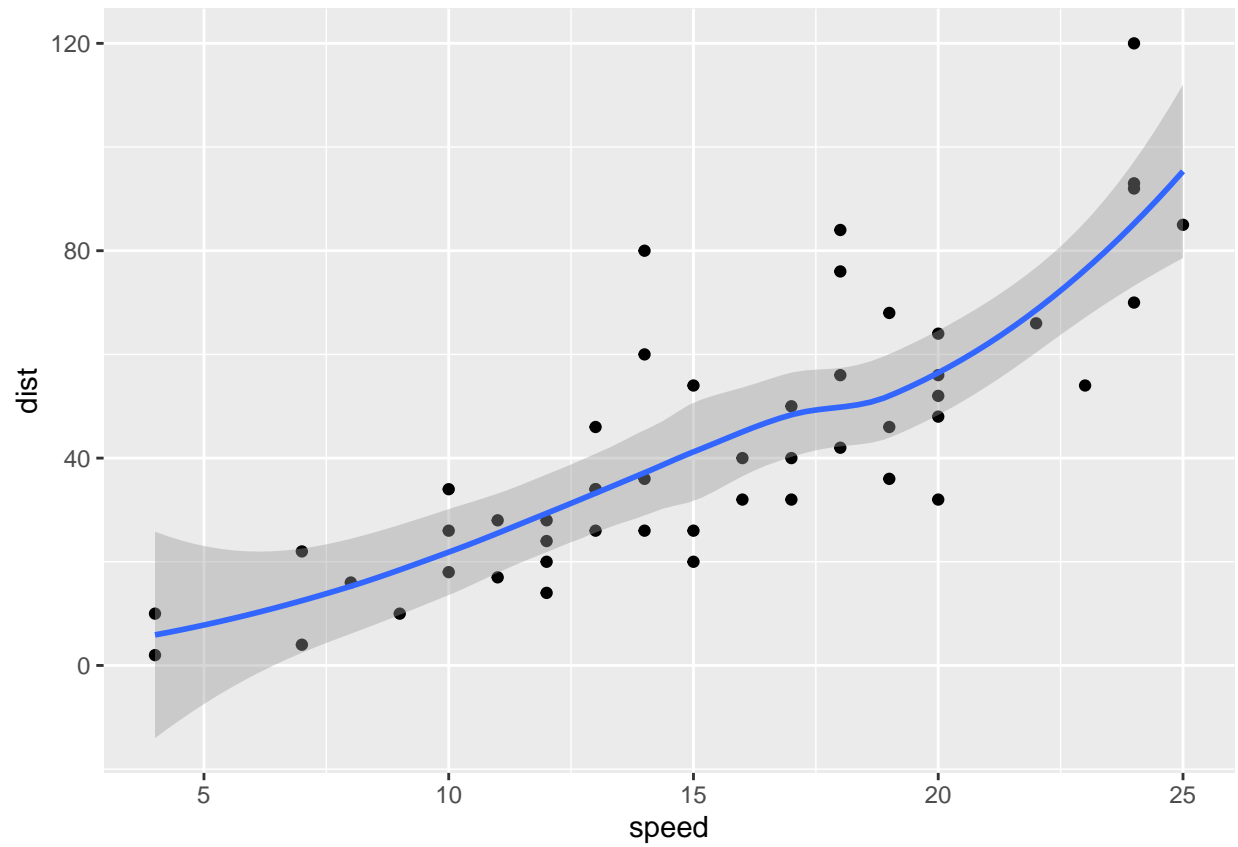


```r
p<-ggplot(data=cars)+
  aes(x=speed, y=dist) +
  geom_point()

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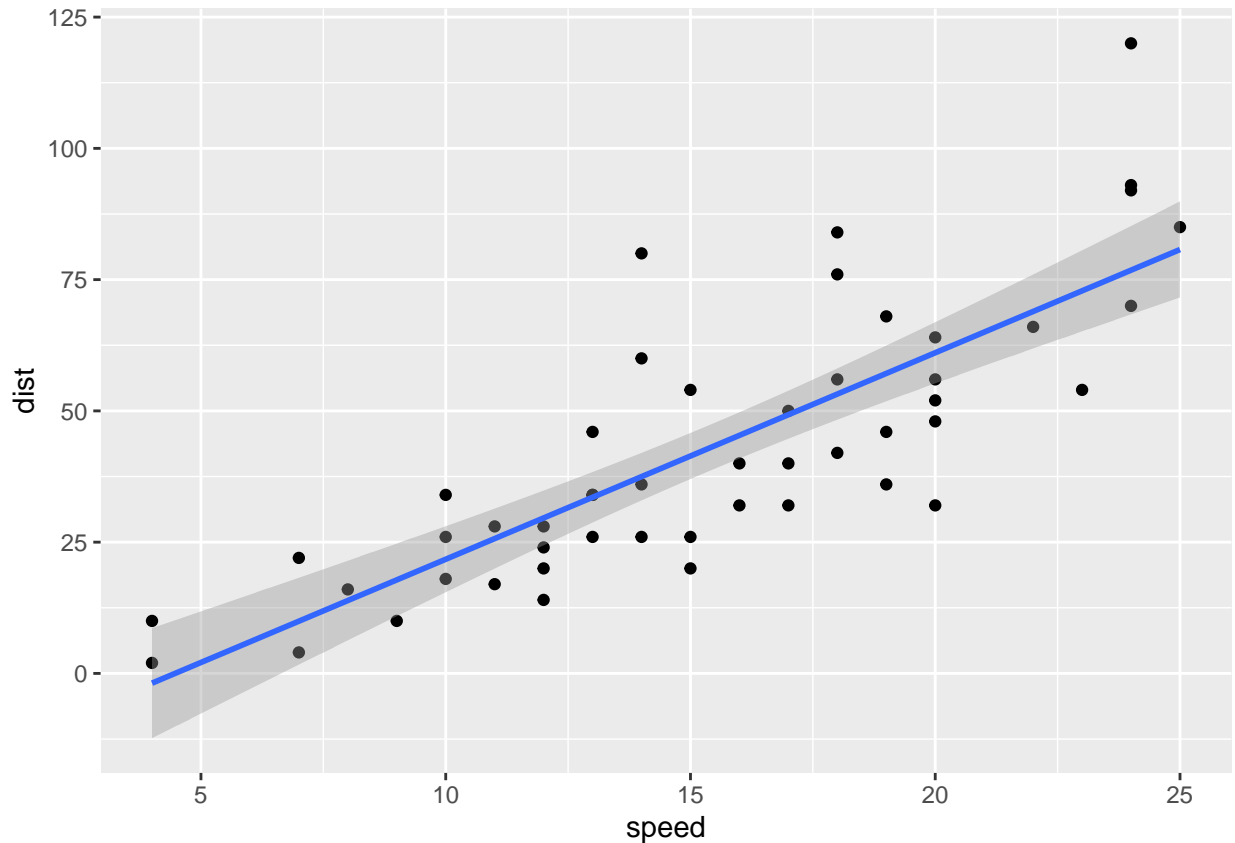
```
# Add a trend line close to the data
p + geom_smooth()
```

```
## `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 are in this dataset
nrow(genes)
```

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

```
# Q. how many columns did you find?
colnames(genes)
```

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

5

```
ncol(genes)
```

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

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

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

```
# Q. What fraction of total genes is up-regulated?
round( (table(genes$State) / nrow(genes)) * 100, 2)
```
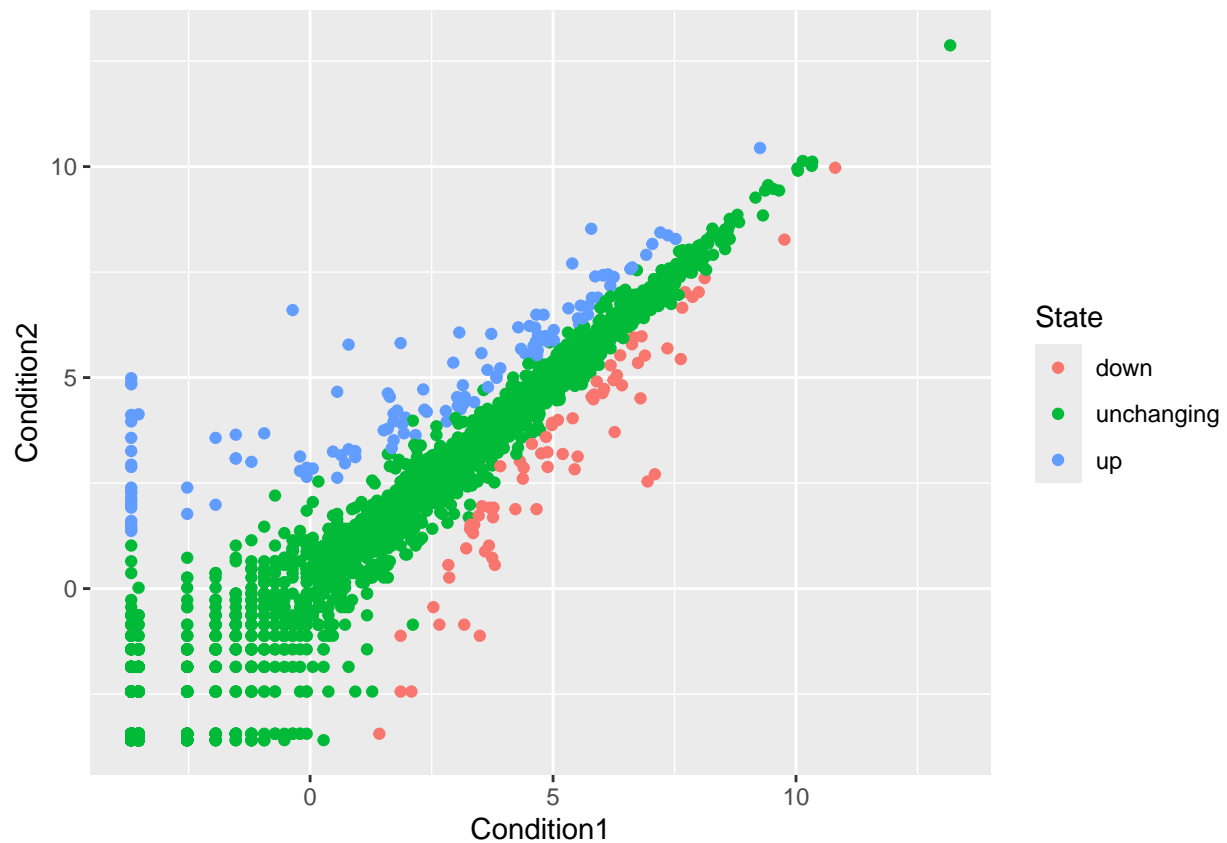
```
##
##       down unchanging          up
##       1.39      96.17        2.44
```

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

g
```

```
# Add some color
g + scale_color_manual(values=c("blue","grey","red"))+
  labs(title="Gene Expression Changes Upon Drug Treatments",
        x="Control (no drug)", y="Drug Treatment") +
        theme_bw()
```

Gene Expression Changes Upon Drug Treatments