

Class05

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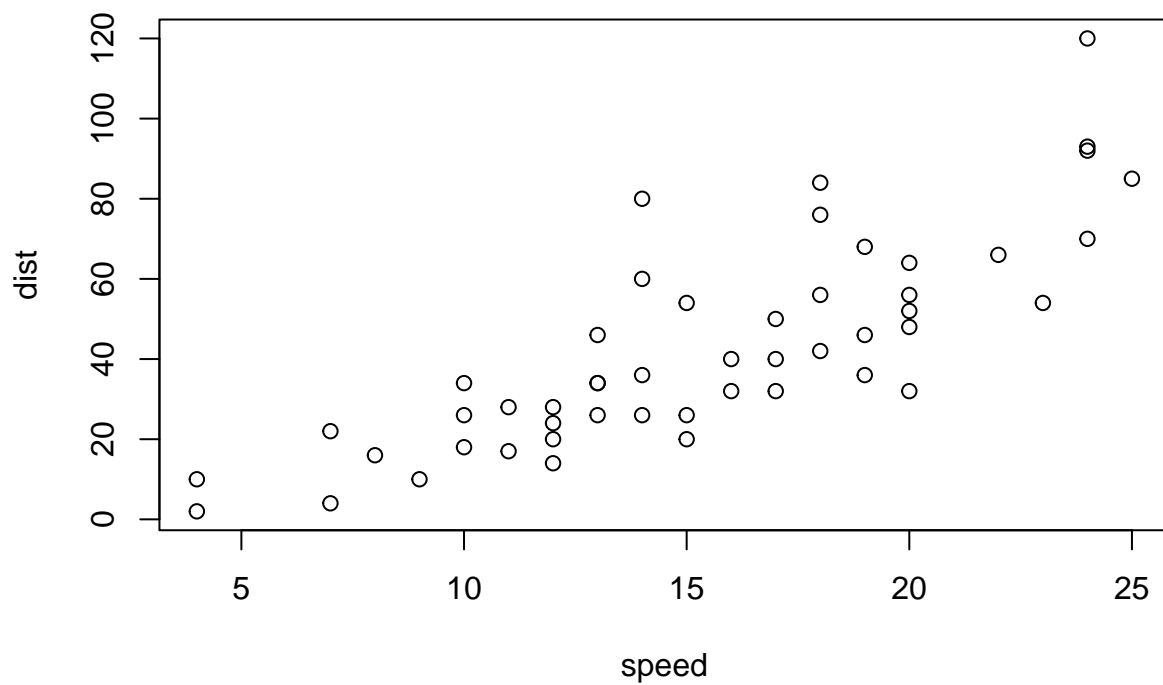
```
# Class 5 Data Visualization Lab

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

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

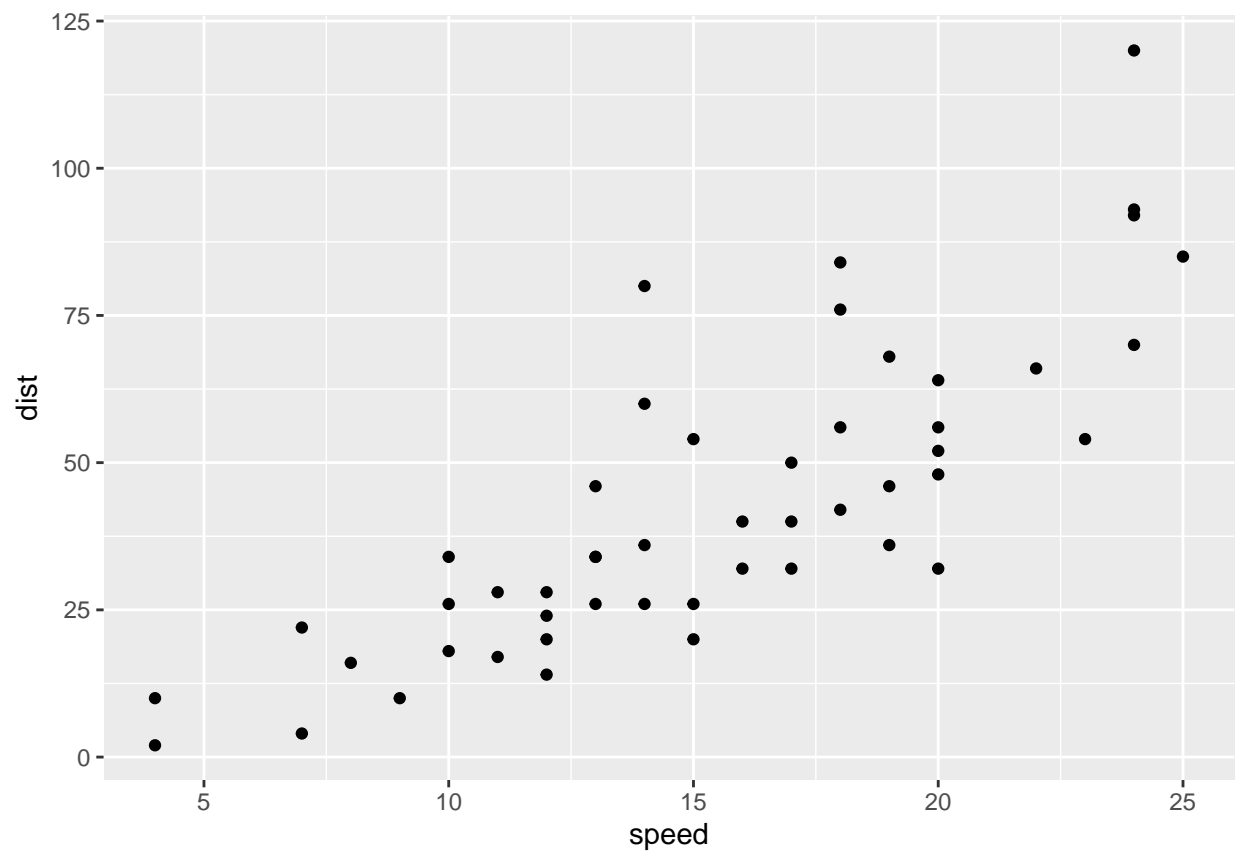
View(cars)

# a quick base R plot - this is not ggplot
plot(cars)
```

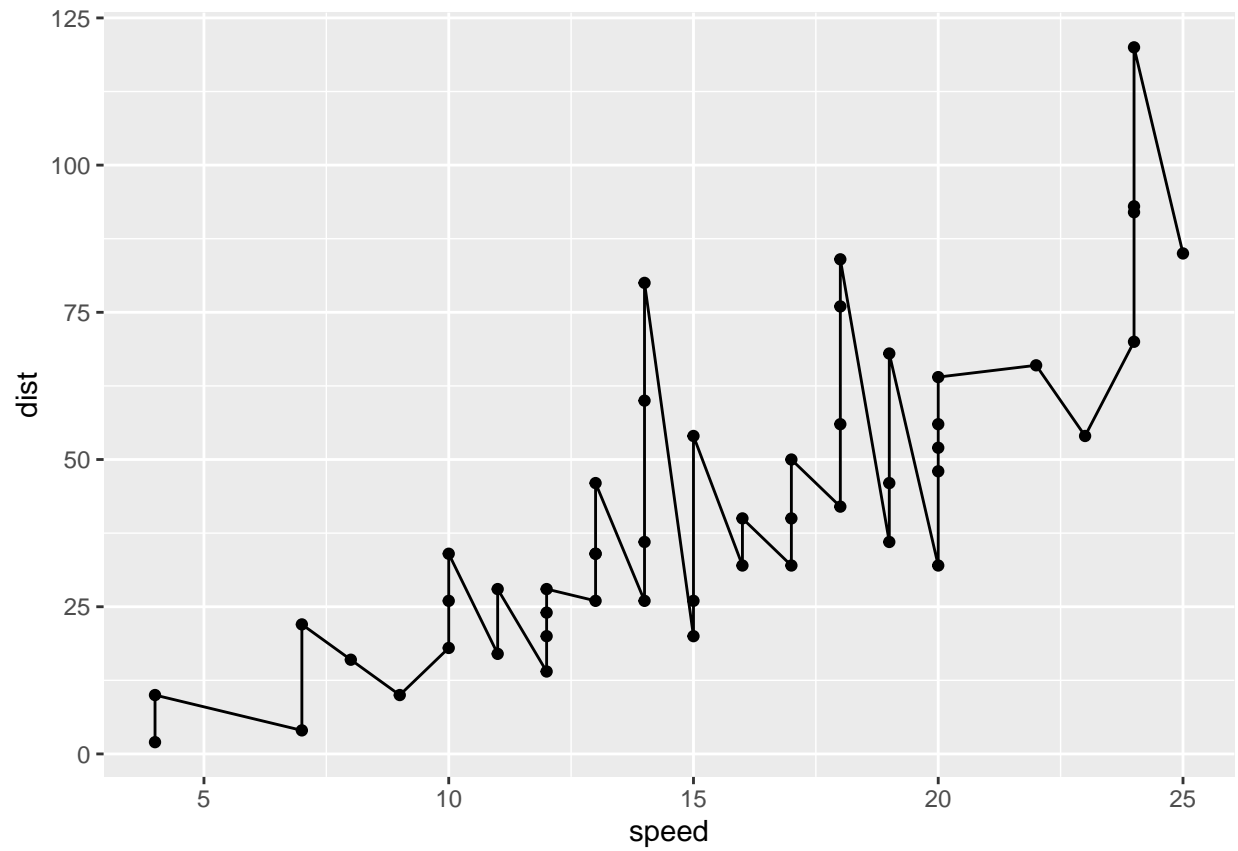


```
# Our first ggplot
# We need data + aes + geoms
```

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



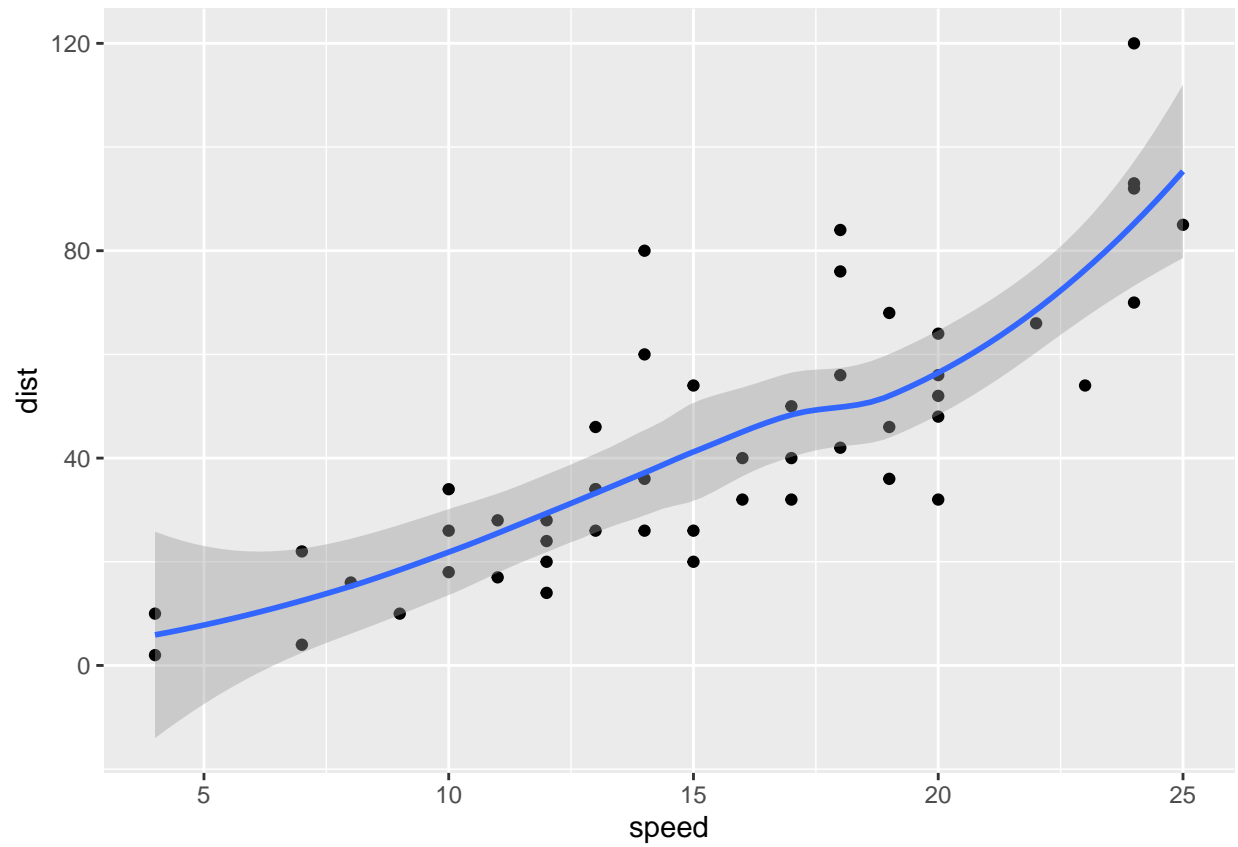
```
p <- ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()  
  
# Add a line geom with geom_line()  
p + geom_line()
```



```
# Add a trendline close to the data
```

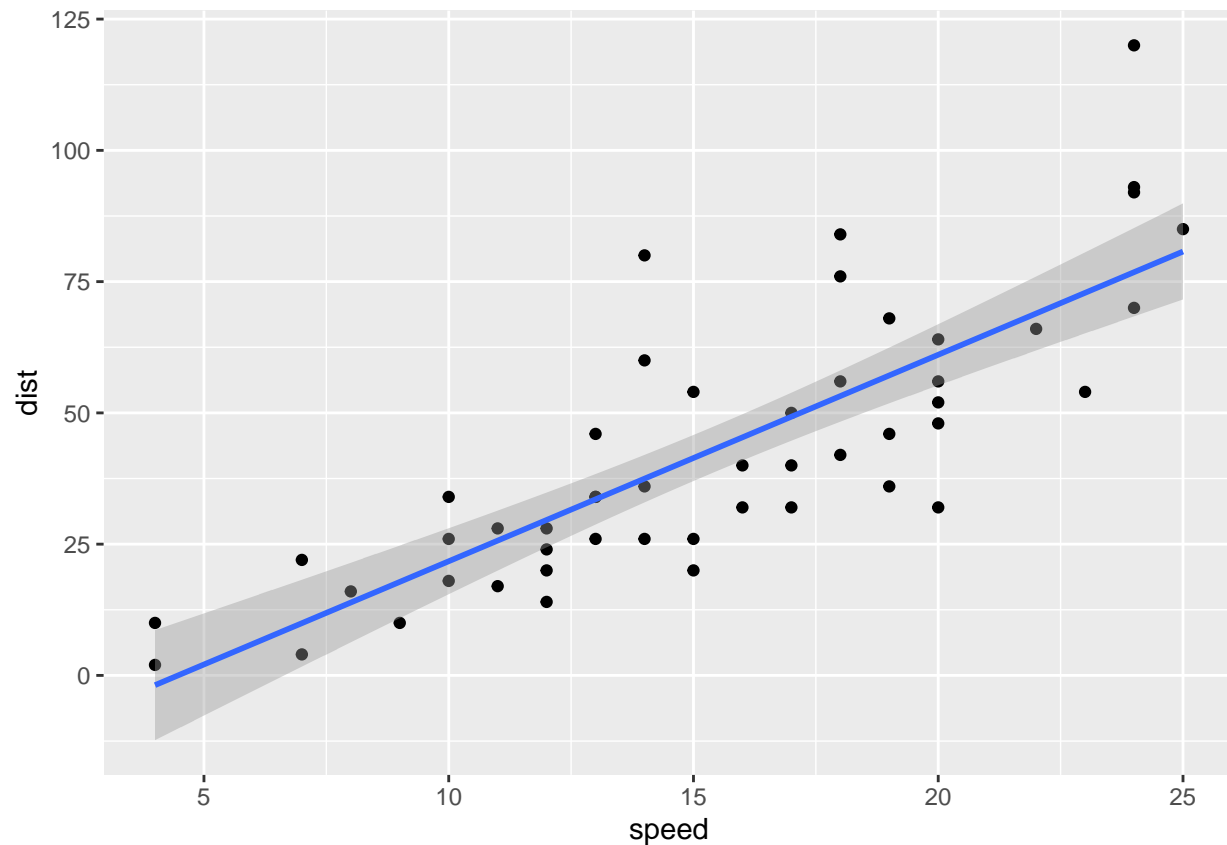
```
p + geom_smooth()
```

```
## `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
```

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

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

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

```
# Q. How many columns did you find?
ncol(genes)
```

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

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

```
##
##      down  unchanged      up
##      72      4997      127
```

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

```
##
##      down  unchanged      up
##      1.39      96.17      2.44
```

```
# Add some color
g + scale_color_manual(values=c("blue", "gray", "purple")) +
  labs(title="Gene expression changes upon drug treatment",
       x="Control(no drug)",
       y="Drug Treatment") +
  theme_bw()
```

