week03_class05.R

David Alvarez

2023-10-22

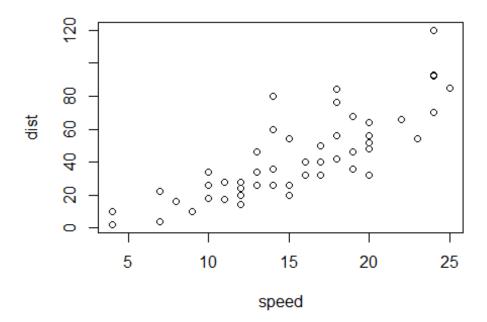
```
# Week 3 Data Visualization Lab 5

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

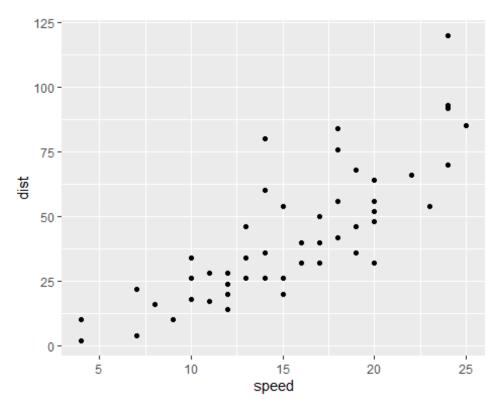
# Install the package ggplot2
# install.packages("ggplot2")

View(cars)

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

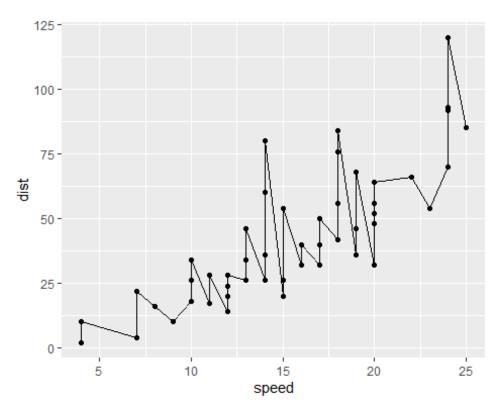


```
# First ggplot
# Need data + aes + geoms
ggplot(data =cars) + aes(x=speed, y=dist) + geom_point()
```

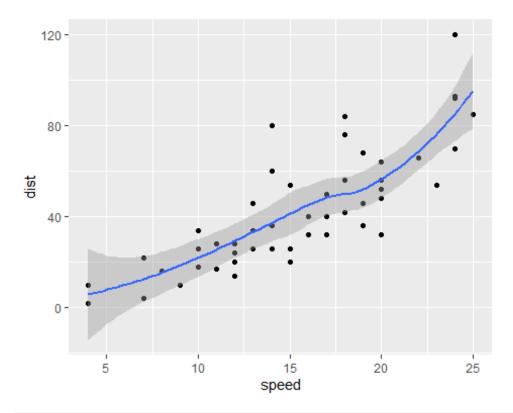


```
p <- ggplot(data =cars) + aes(x=speed, y=dist) + geom_point()

# Add a line geom with geom_line()
p + geom_line()</pre>
```

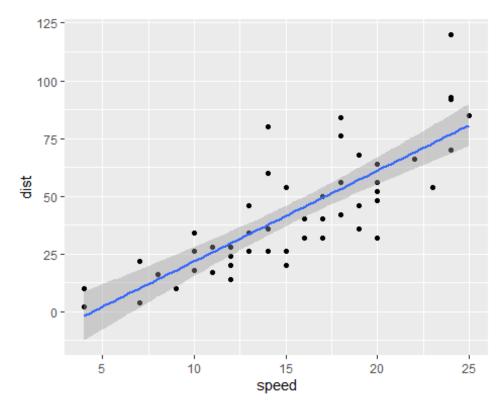


```
# Add a trend line close to the data
p + geom_smooth()
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



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-</pre>
material/up_down_expression.txt"
genes <- read.delim(url)</pre>
head(genes)
##
           Gene Condition1 Condition2
                                            State
## 1
          A4GNT -3.6808610 -3.4401355 unchanging
          AAAS 4.5479580 4.3864126 unchanging
## 2
## 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 are in this dataset
ncol(genes)
## [1] 4
# Q. How many 'up' regulated genes
table(genes$State)
##
##
         down unchanging
                                 up
##
                    4997
           72
                                 127
# Q. What fraction of total genes is up-regulated
round( (table(genes$State) / nrow(genes)) * 100, 2 )
##
##
         down unchanging
                                  up
##
                   96.17
         1.39
                                2.44
library(ggplot2)
# First plot attempt
g <- ggplot(data=genes) + aes(x=Condition1, y=Condition2, col=State) +</pre>
geom_point()
```

```
# Adding 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()
```