

Week 4 ggplot RMB submission

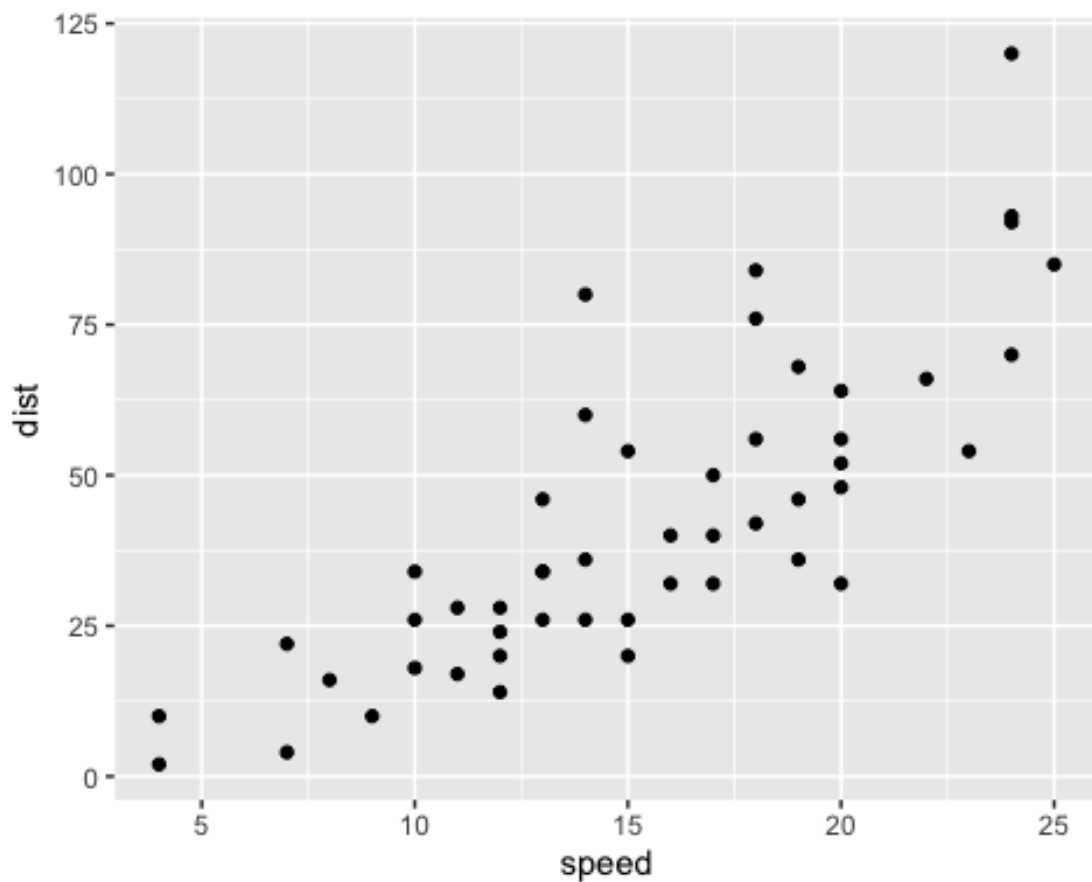
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```
library(ggplot2)
install.packages("ggplot2", repos = "http://cran.us.r-project.org")

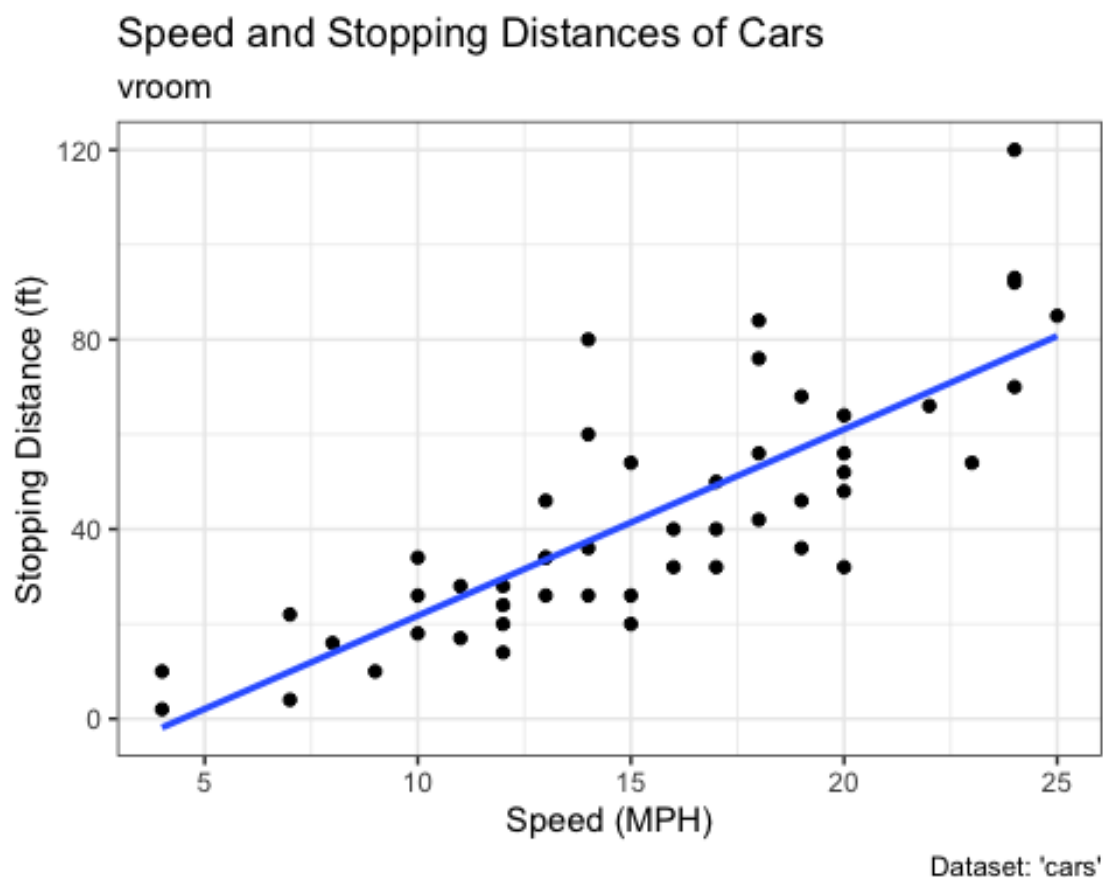
##
## The downloaded binary packages are in
##
/var/folders/x6/5z1hfstd7x3880lk3c9rx8yr0000gn/T//RtmpkvwE02/downloaded_packages

# 1st geom_point() plot of cars data
library(ggplot2)
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()
```



```
# Full plot attempt for cars
library(ggplot2)
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  labs(title="Speed and Stopping Distances of Cars",
       x="Speed (MPH)",
       y="Stopping Distance (ft)",
       subtitle = "vroom",
       caption="Dataset: 'cars'") +
  geom_smooth(method="lm", se=FALSE) +
  theme_bw()

## `geom_smooth()` using formula 'y ~ x'
```



```
# moving on to data set genes
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
```

```
p <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
p + scale_colour_manual(values=c("blue","gray","red")) +
  labs(title="Gene Expression Changes Upon Drug Treatment",
       x="Control (no drug) ",
       y="Drug Treatment")
```

