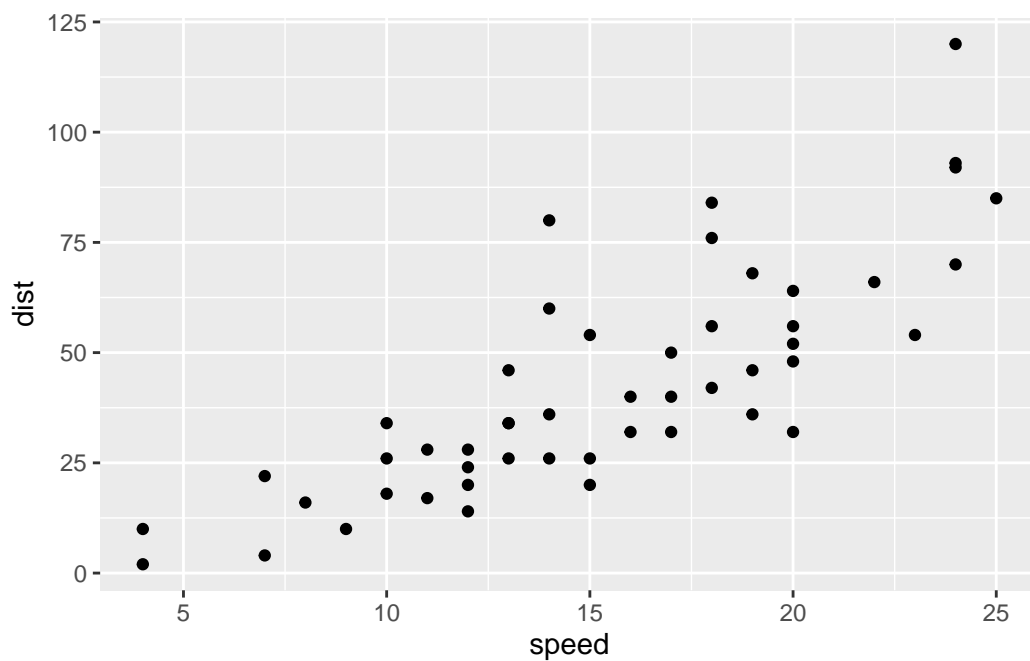


# Class 5 Lab

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```
#install.packages("ggplot2")
library(ggplot2)

#Dot plot of cars mapping distance versus speed
ggplot(cars, aes(x = speed, y = dist)) +
  geom_point()
```



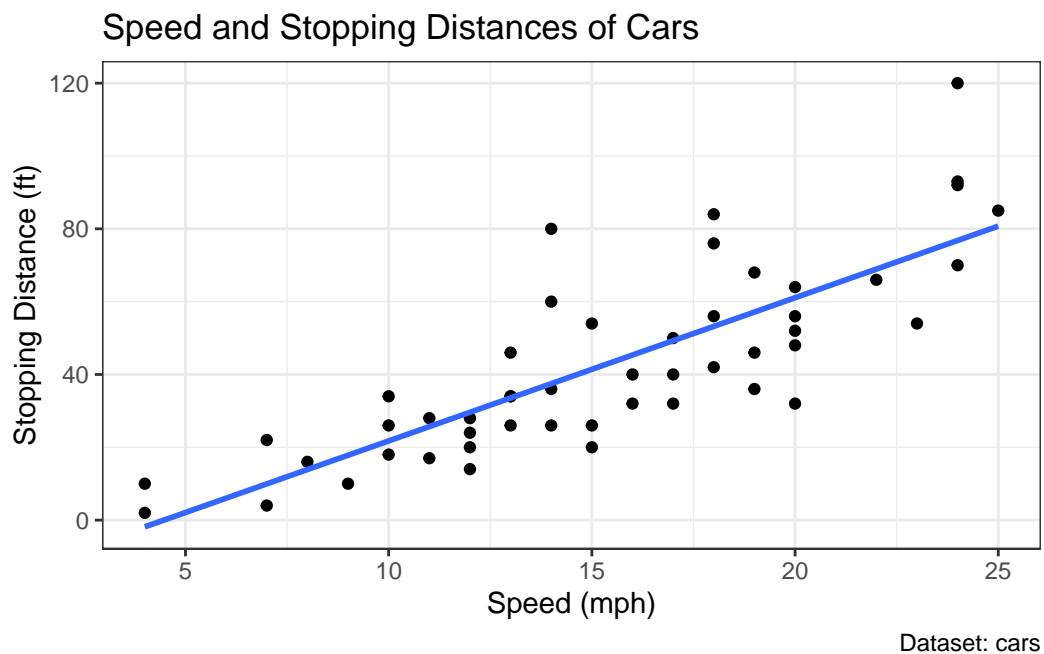
```
#Dot plot and linear model of cars mapping distance versus speed

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

```
#Linear model
geom_smooth(method = "lm", se = FALSE) +

#Label
labs(title = "Speed and Stopping Distances of Cars",
      x = "Speed (mph)",
      y = "Stopping Distance (ft)",
      caption = "Dataset: cars") +
theme_bw()
```

`geom\_smooth()` using formula = 'y ~ x'



```
# Gene expression profile of anti-viral drug treatment
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

```

```

#Plotting gene expression increase (red) and decrease (blue) of anti-viral drug treatment
ggplot(genes, aes(x = Condition1, y = Condition2, color = State)) +
  geom_point() +
  scale_color_manual(values = c("blue", "gray", "red")) +
  labs(title = "Gene Expression Changes Upon Drug Treatment",
       x = "Control (no drug)",
       y = "Drug Treatment")

```

