

class05

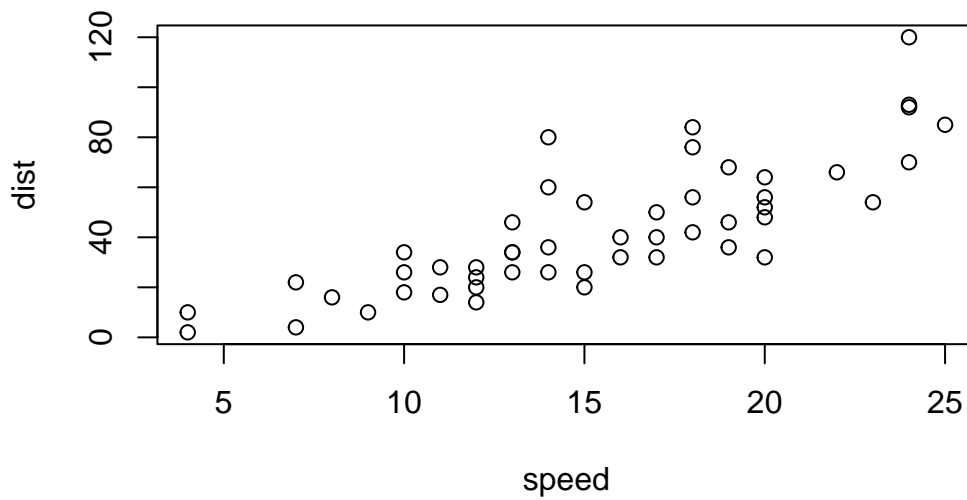
Nate Tran

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

```
head(cars, 10)
```

	speed	dist
1	4	2
2	4	10
3	7	4
4	7	22
5	8	16
6	9	10
7	10	18
8	10	26
9	10	34
10	11	17

```
plot(cars)
```

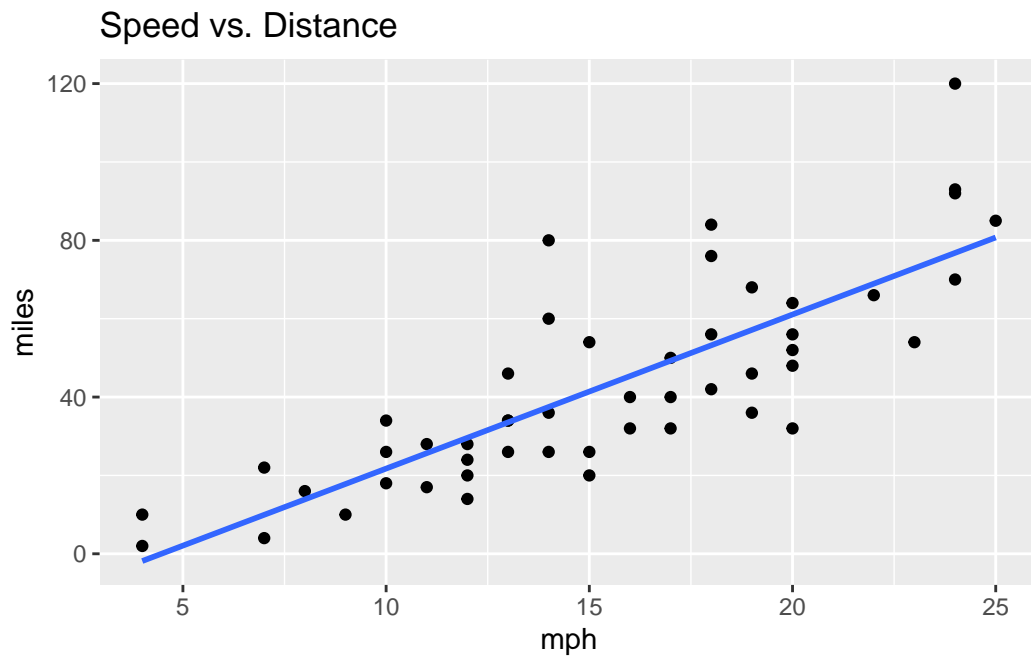


ggplot requires 3 components:

1. **Data** (in the form of a data.frame)
2. **Aesthetics** (aes() for short)
3. **Geometries** (e.g. geom_point() or geom_line())

```
library(ggplot2)
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method = "lm", se = F) +
  labs(title = "Speed vs. Distance") +
  xlab("mph") +
  ylab("miles")
```

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



Gene Expression

```
genes <- read.delim("https://bioboot.github.io/bimm143_S20/class-material/up_down_expressi
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

```
nrow(genes)
```

```
[1] 5196
```

```
colnames(genes)
```

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

```
ncol(genes)
```

```
[1] 4
```

```
table(genes$State)
```

down	unchanging	up
72	4997	127

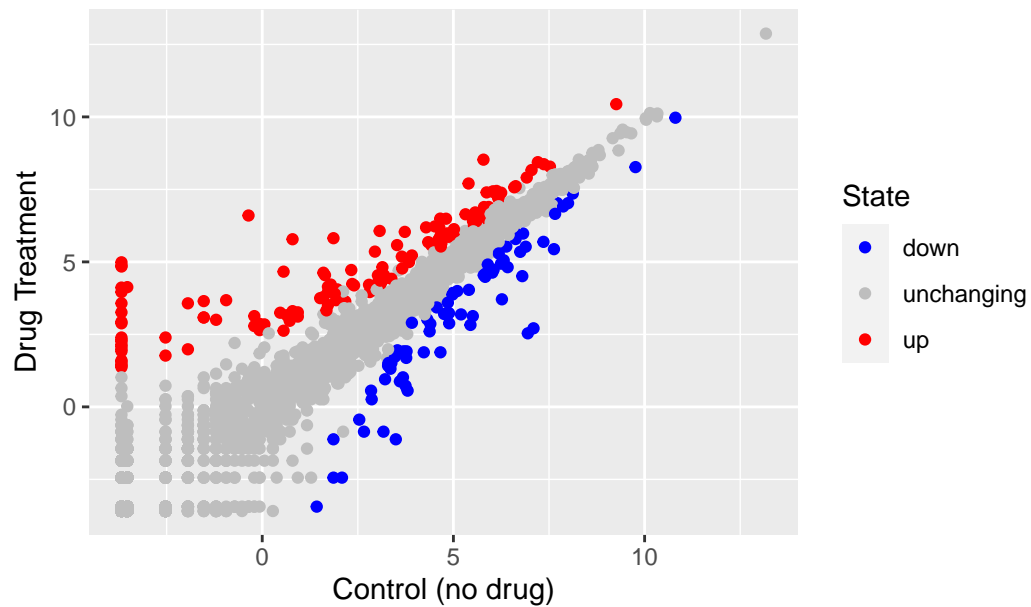
```
round((table(genes$State)/nrow(genes))*100, 2)
```

down	unchanging	up
1.39	96.17	2.44

There are 5196 genes in this dataset.

```
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") +  
  xlab("Control (no drug)") +  
  ylab("Drug Treatment")
```

Gene Expression Changes upon Drug Treatment



Gapminder

```
library(gapminder)
length(unique(gapminder$country))
```

```
[1] 142
```

```
gapminder[which.min(gapminder$pop), "country"]
```

```
# A tibble: 1 x 1
  country
  <fct>
1 Sao Tome and Principe
```

```
gapminder[which.min(gapminder$pop),]
```

```
# A tibble: 1 x 6
  country continent year lifeExp pop gdpPercap
```

	<fct>	<fct>	<int>	<dbl>	<int>	<dbl>
1	Sao Tome and Principe	Africa	1952	46.5	60011	880.

```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.4) +
  facet_wrap("continent")
```

