Class05: Data Viz with GGPLOT

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Today we are playing with plotting and graphing in R.

There are lots of ways to make cool figures in R. There is "base" R graphics ('plot()', 'hist()', 'boxplot()', etc.)

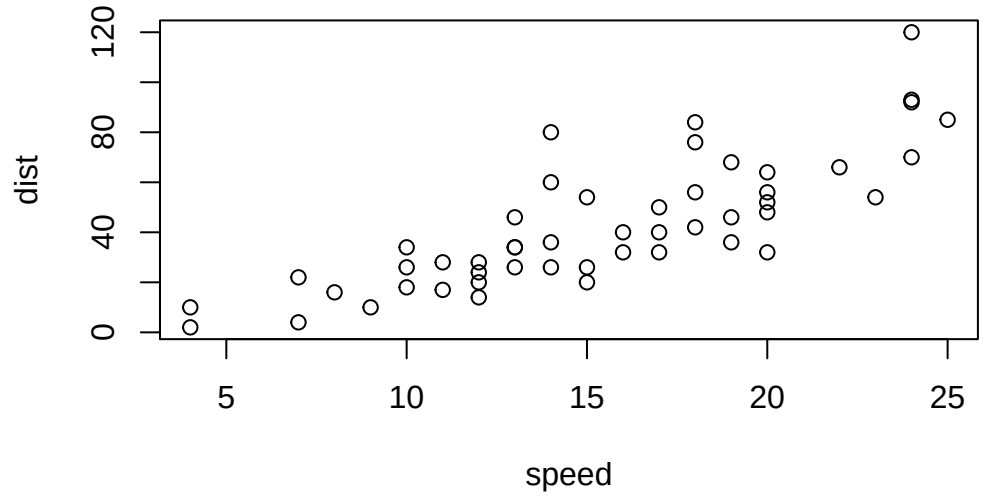
There is also add-on packages, like **ggplot**.

```
head(cars,3)
```

```
  speed dist
1     4    2
2     4   10
3     7    4
```

Let's plot this with "base" R:

```
plot(cars)
```

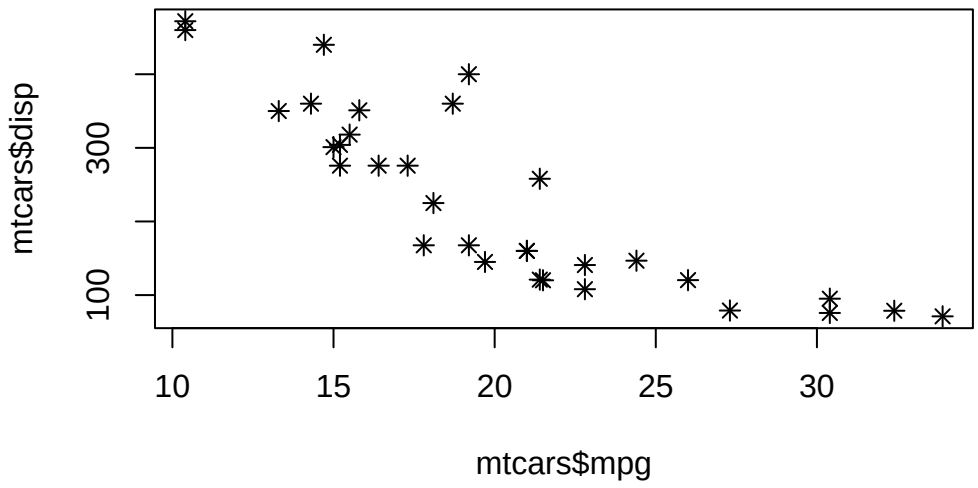



```
head(mtcars)
```

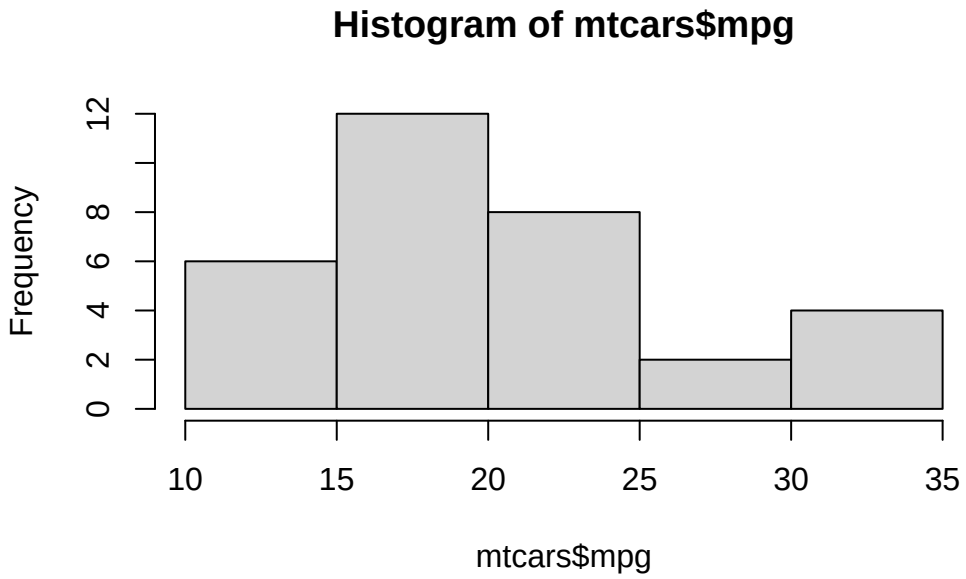
```
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

Let's plot 'mpg' vs. 'disp'

```
plot(mtcars$mpg,mtcars$disp, pch=8)
```




```
hist(mtcars$mpg)
```

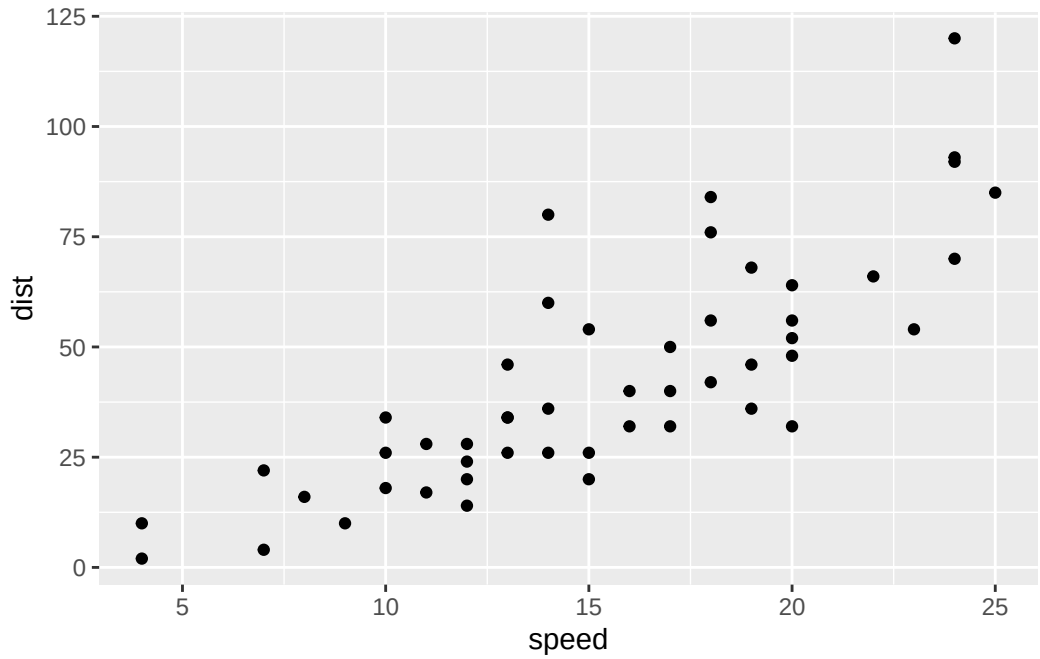


GGPLOT

The main function in the ggplot2 package is 'ggplot()'. First I need to install the **ggplot2** package. I can install any package with the function 'install.(packages)'. You don't want to keep downloading ggplot over and over again. *In order to not download the software package over and over again, type this code in the console.*

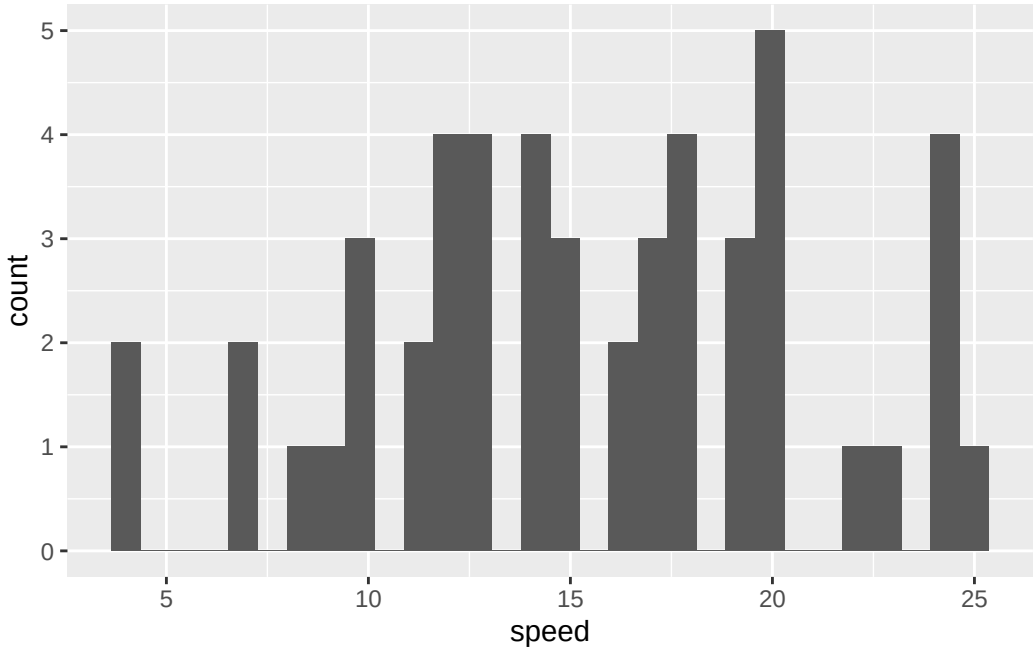
N.B. I never want to run 'install.packages()' in my quarto source document girl!

```
library(ggplot2)
ggplot(cars) +
  aes(x=speed, y=dist)+
  geom_point()
```




```
ggplot(cars)+
  aes(speed)+
  geom_histogram()
```

```
`stat_bin()` using `bins = 30`. Pick better value `binwidth`.
```



Every ggplot needs at least 3 things:

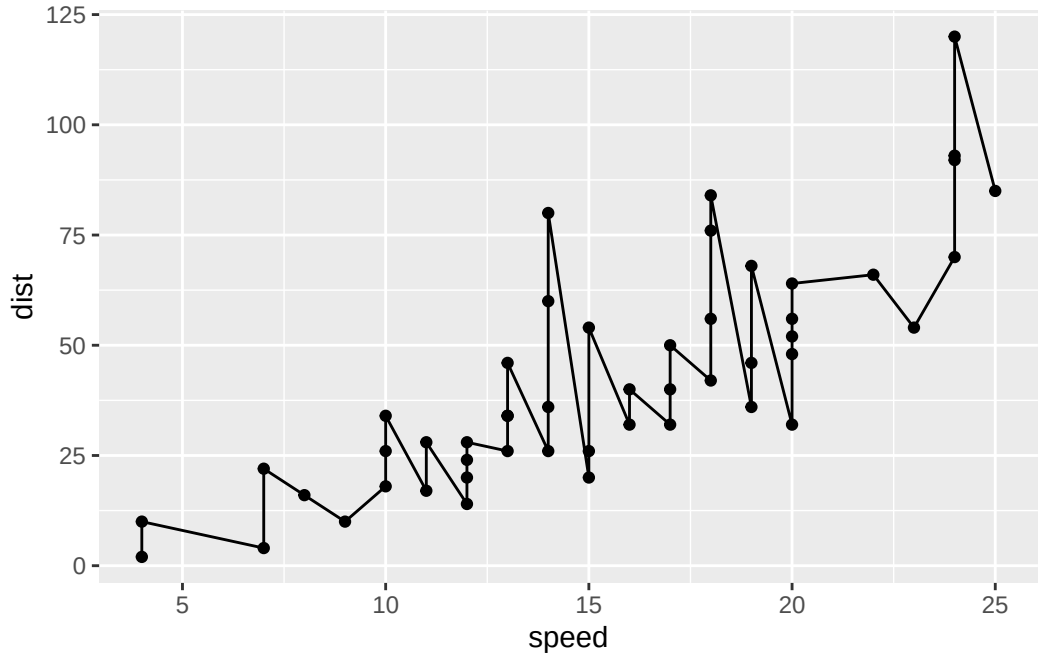
- The **data** (given with 'ggplot(cars)')
- The **aesthetics** mapping (given with 'aes()')
- The **geometry** (given with geom_point)

  For simple canned graphs "base" R is nearly always faster

Adding more layers

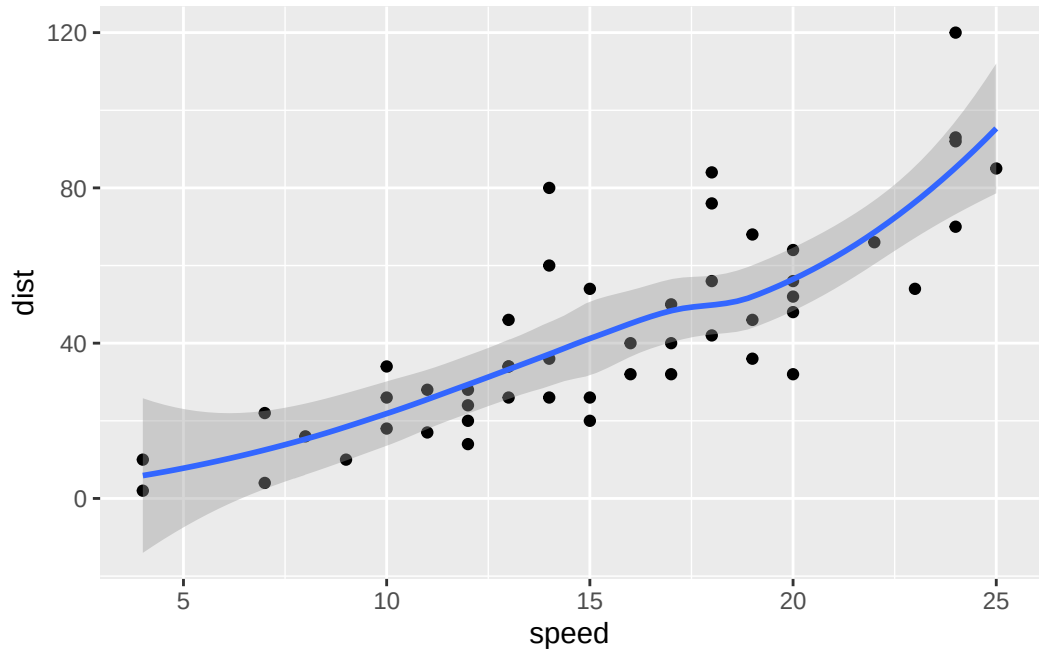
Let's add a line and a title, subtitle and caption as well as custom axis labels.

```
library(ggplot2)
ggplot(cars) +
  aes(x=speed, y=dist)+
  geom_point() +
  geom_line ()
```



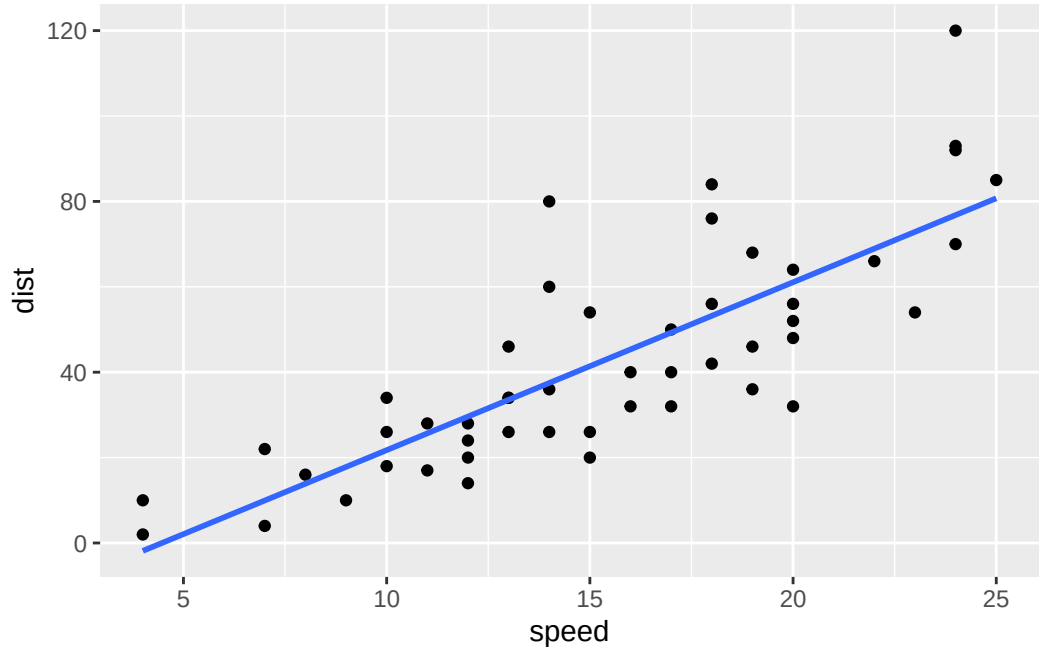

```
library(ggplot2)
ggplot(cars) +
  aes(x=speed, y=dist)+
  geom_point() +
  geom_smooth ()
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



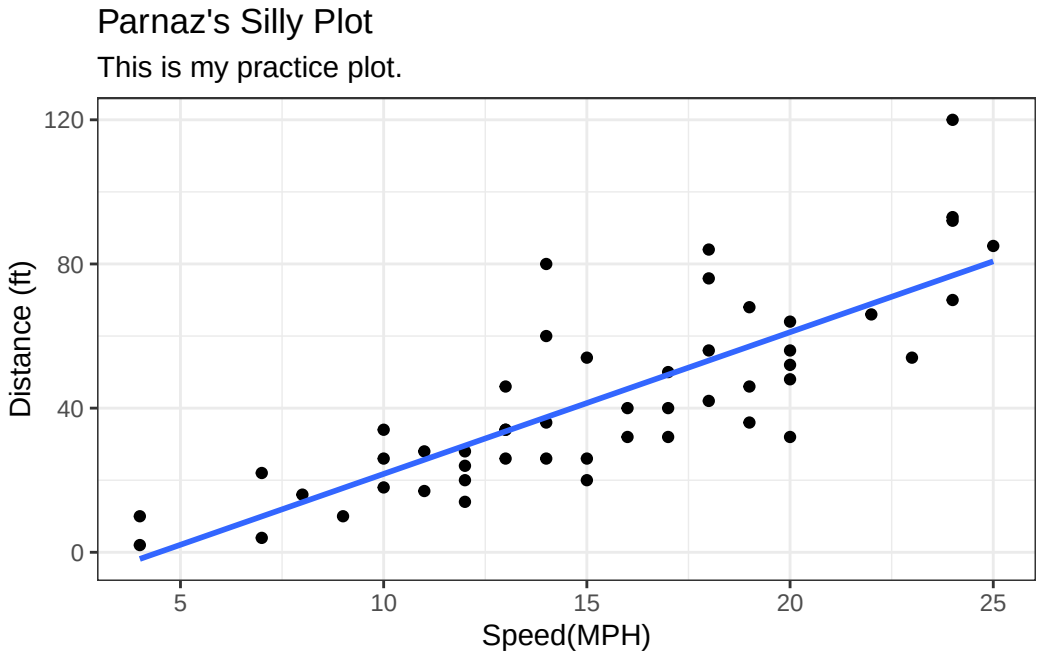

```
library(ggplot2)
ggplot(cars) +
  aes(x=speed, y=dist)+
  geom_point() +
  geom_smooth (method="lm", se=FALSE)
```

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




```
library(ggplot2)
ggplot(cars) +
  aes(x=speed, y=dist)+
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  labs (
    title= "Parnaz's Silly Plot",
    subtitle = "This is my practice plot.",
    x="Speed(MPH)",
    y="Distance (ft)")+
    theme_bw()
```

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



##Plot some expression data

Read data file from online URL

```
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
```

Q1. How many genes are in this wee dataset?

There are 5196 in this dataset.

Q2. How many "up" regulated genes are there?

```
sum(genes$State == "up")
```

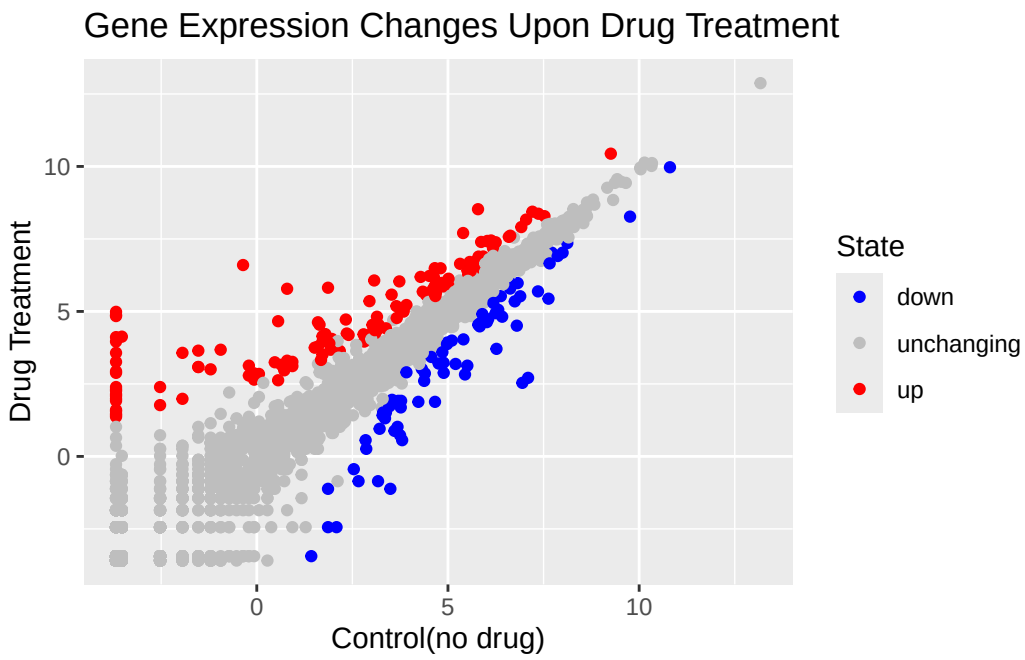
```
[1] 127
```

These are 127 genes.

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

```
      down unchanging         up
        72       4997        127
```

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

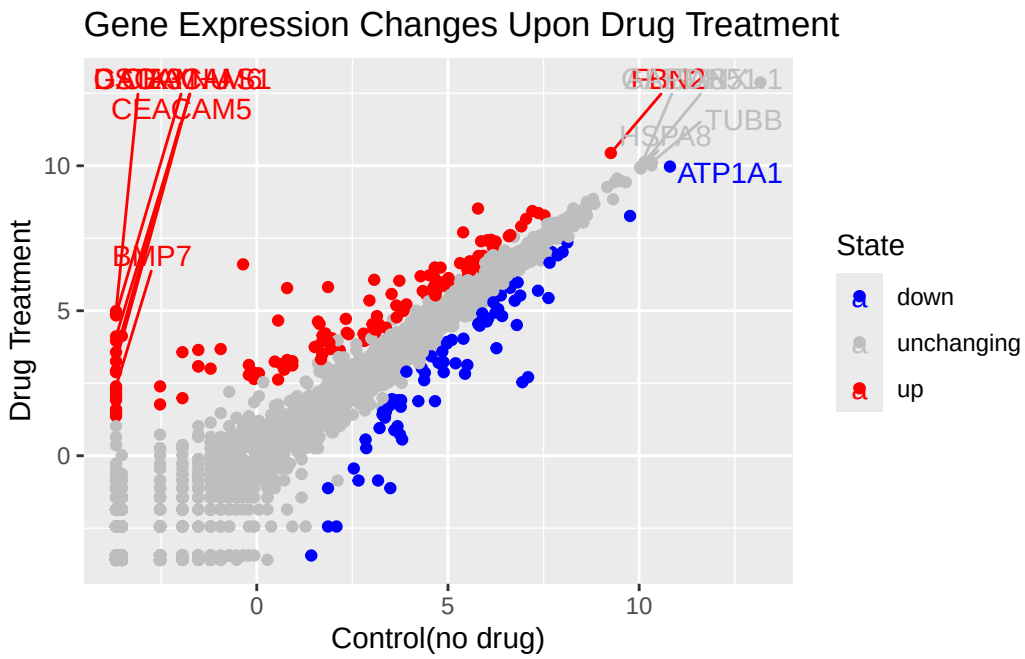


Silly example of adding labels

```
library(ggrepel)

ggplot(genes)+
  aes(x=Condition1, y=Condition2, col=State,label=Gene)+
  geom_point()+
  scale_colour_manual( values=c("blue","gray","red") )+
   labs (
    title= "Gene Expression Changes Upon Drug Treatment",
    x="Control(no drug)",
    y="Drug Treatment")+
  geom_text_repel(max.overlaps = 100)
```

```
Warning: ggrepel: 5183 unlabeled data points (too many overlaps). Consider
increasing max.overlaps
```



Going Further

Playing with some different layers and the gapmider dataset...

```r
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.tsv

gapminder <- read.delim(url)
```

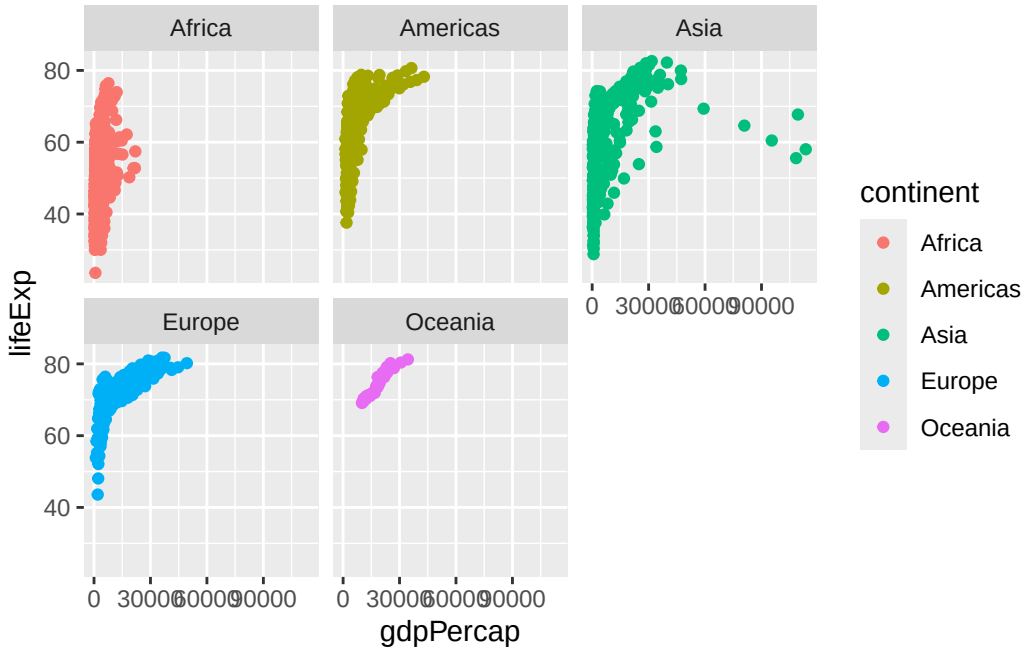
```r
head(gapminder)
```

```
      country continent year lifeExp      pop gdpPercap
1 Afghanistan      Asia 1952  28.801  8425333  779.4453
2 Afghanistan      Asia 1957  30.332  9240934  820.8530
3 Afghanistan      Asia 1962  31.997 10267083  853.1007
4 Afghanistan      Asia 1967  34.020 11537966  836.1971
5 Afghanistan      Asia 1972  36.088 13079460  739.9811
6 Afghanistan      Asia 1977  38.438 14880372  786.1134
```

```r
tail(gapminder)
```

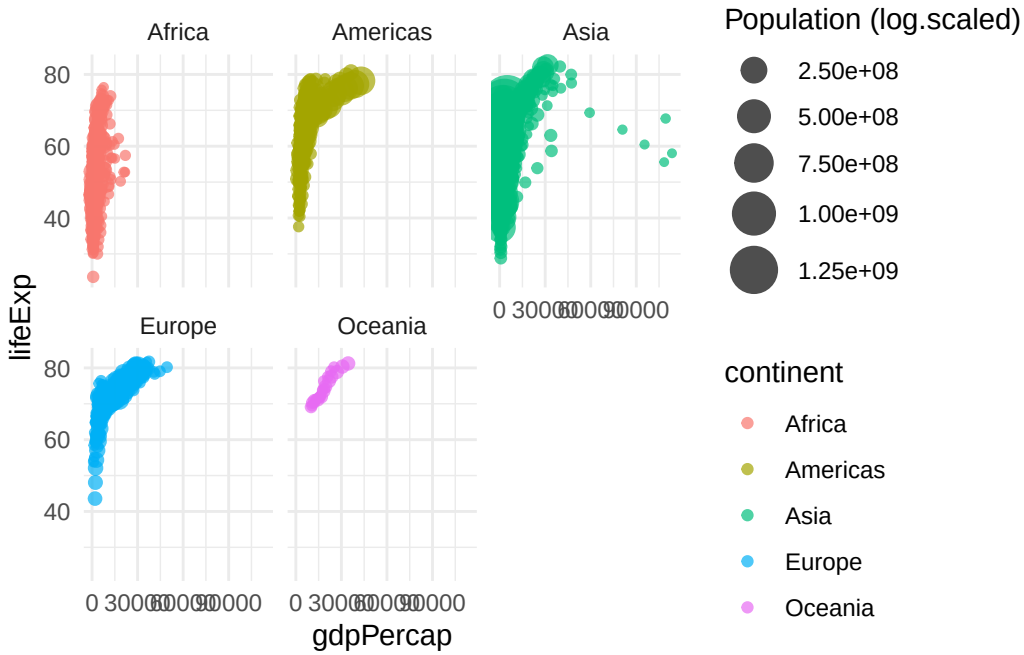
```
      country continent year lifeExp      pop gdpPercap
1699 Zimbabwe    Africa 1982  60.363  7636524  788.8550
1700 Zimbabwe    Africa 1987  62.351  9216418  706.1573
1701 Zimbabwe    Africa 1992  60.377 10704340  693.4208
1702 Zimbabwe    Africa 1997  46.809 11404948  792.4500
1703 Zimbabwe    Africa 2002  39.989 11926563  672.0386
1704 Zimbabwe    Africa 2007  43.487 12311143  469.7093
```

```r
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, col=continent) +
  geom_point()+
  facet_wrap(~continent)
```



Insert fun plot here:

```
ggplot(gapminder) +
  aes(x = gdpPercap, y = lifeExp,
      col = continent,
      size = pop) +                  # bubble size reflects population
  geom_point(alpha = 0.7) +
  facet_wrap(~continent) +
  scale_size(range = c(1, 8)) +      # keep bubbles readable
  labs(size = "Population (log-scaled)") +
  theme_minimal()
```


Africa
Americas
Asia
Europe
Oceania
lifeExp
gdpPercap
80
60
40
0
30000
60000
90000
Population (log.scaled)
2.50e+08
5.00e+08
7.50e+08
1.00e+09
1.25e+09
continent
Africa
Americas
Asia
Europe
Oceania