Class 5: Data Viz with ggplot

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Background

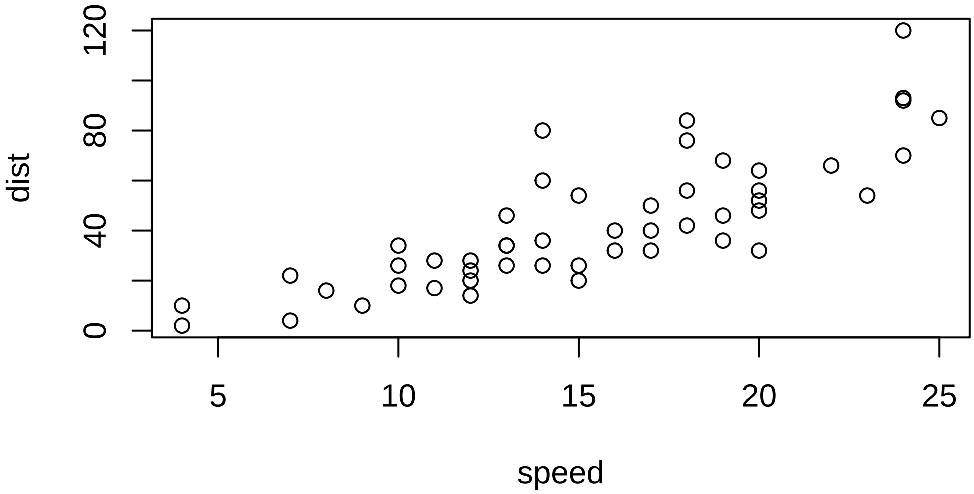
There are lots of ways to make figures in R. These include so-called "base R" graphics (e.g. `plot()`) and tones of add-on packages like **ggplot2**.

For example here we make the same plot with both:

```
head(cars)
```

```
  speed dist
1     4    2
2     4   10
3     7    4
4     7   22
5     8   16
6     9   10
```

```
plot(cars)
```



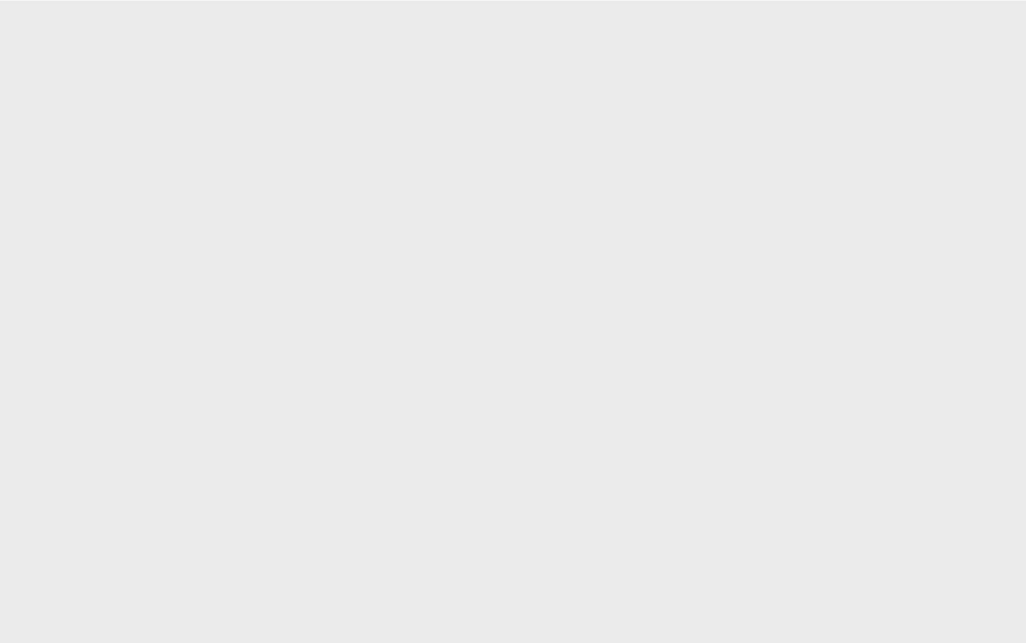
First I need to install the package with command `install.packages()`

> **N.B.** We never run an install cmd in a quarto code chubnk or we will end up re-installing packages many many times - which is not what we want!

Every time we want to use one of these "add-on" packages we need to load it up in R with the `library()` function:

```
library(ggplot2)
```

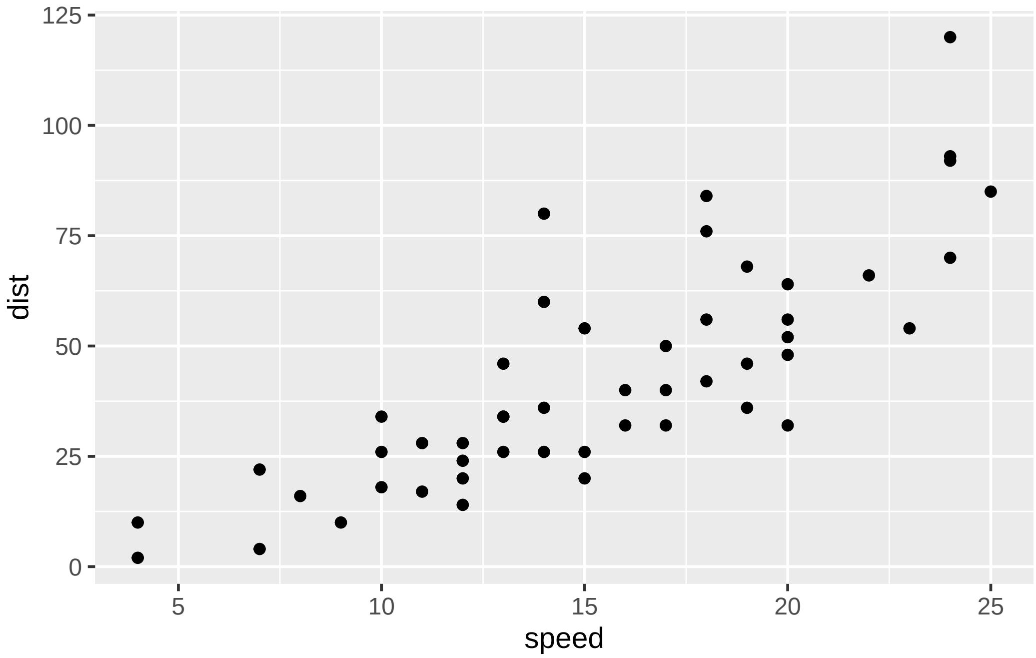
```
ggplot(cars)
```



Every ggplot needs at least 3 things:

- The **data**, the stuff you want plotted
- The **aes**thitics, how the data map to the plot
- The **geom**emtry, the type of plot

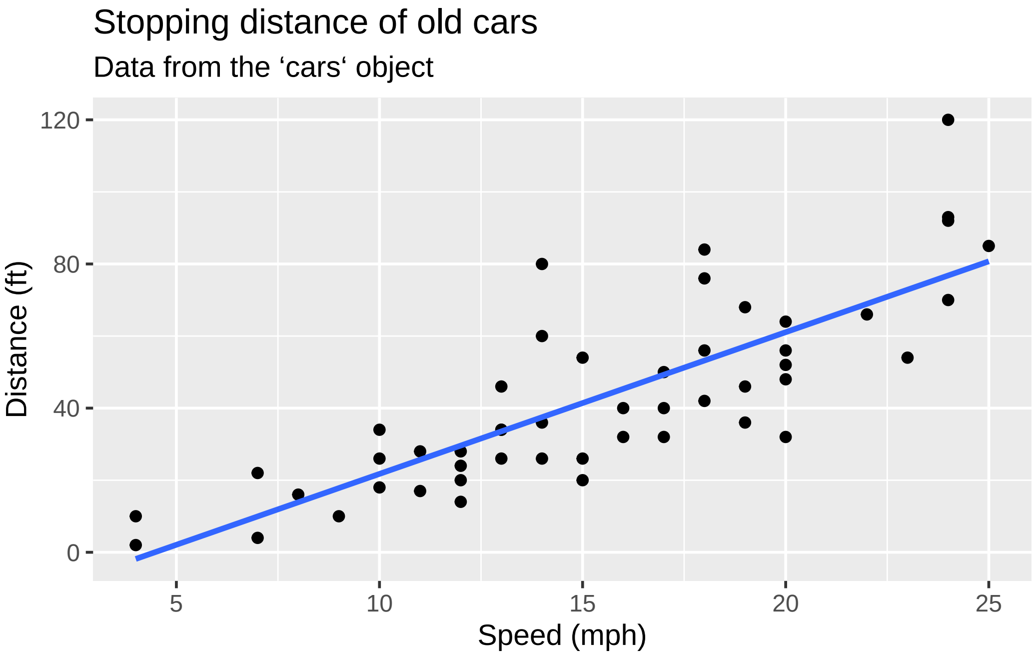
```r
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()
```



Add a line to better show relationship between speed and dist

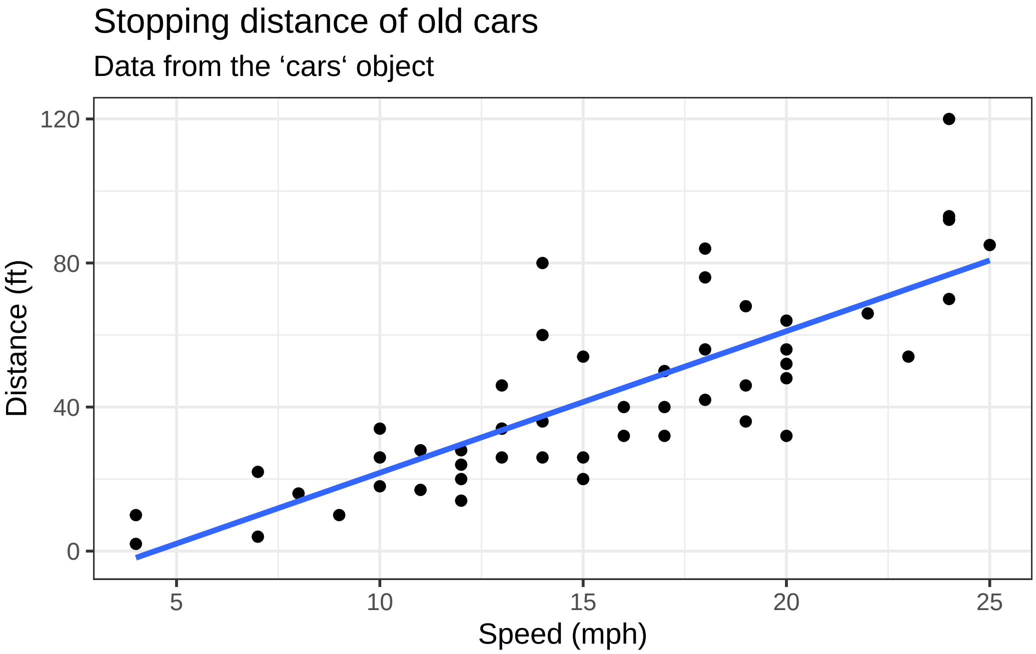
```
p <- ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  labs(
    title="Stopping distance of old cars",
subtitle = "Data from the `cars` object",
  x="Speed (mph)",
  y="Distance (ft)"
  )

p
```

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



```
p + theme_bw()
```

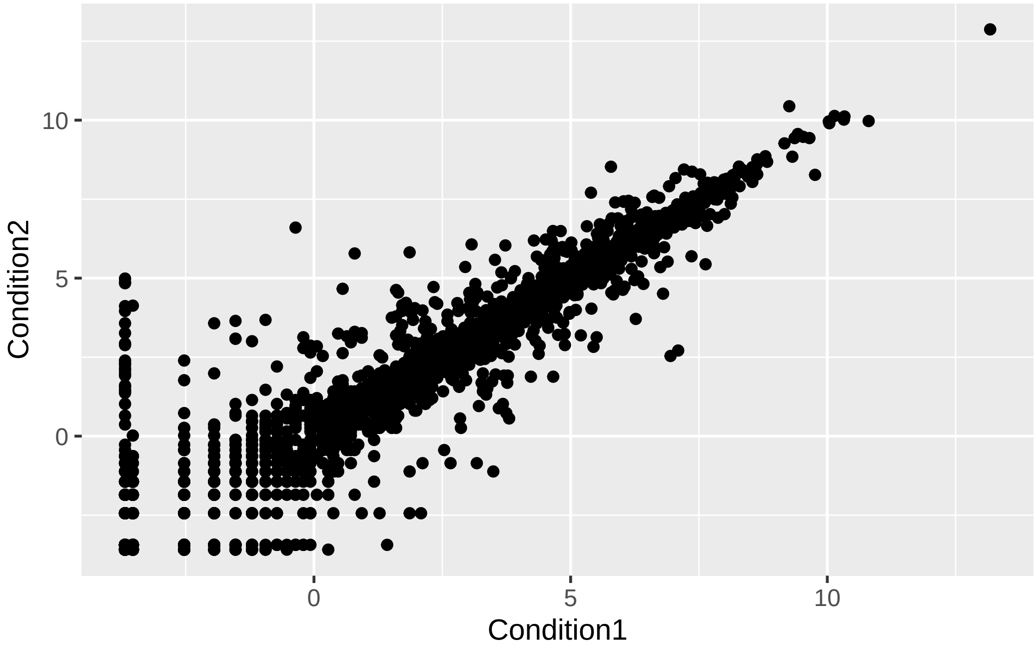
```
`geom_smooth()` using formula = 'y ~ x'
```



```
## Gene expression plot


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
```

```
ggplot(genes) +
aes(Condition1, Condition2) +
geom_point()
```

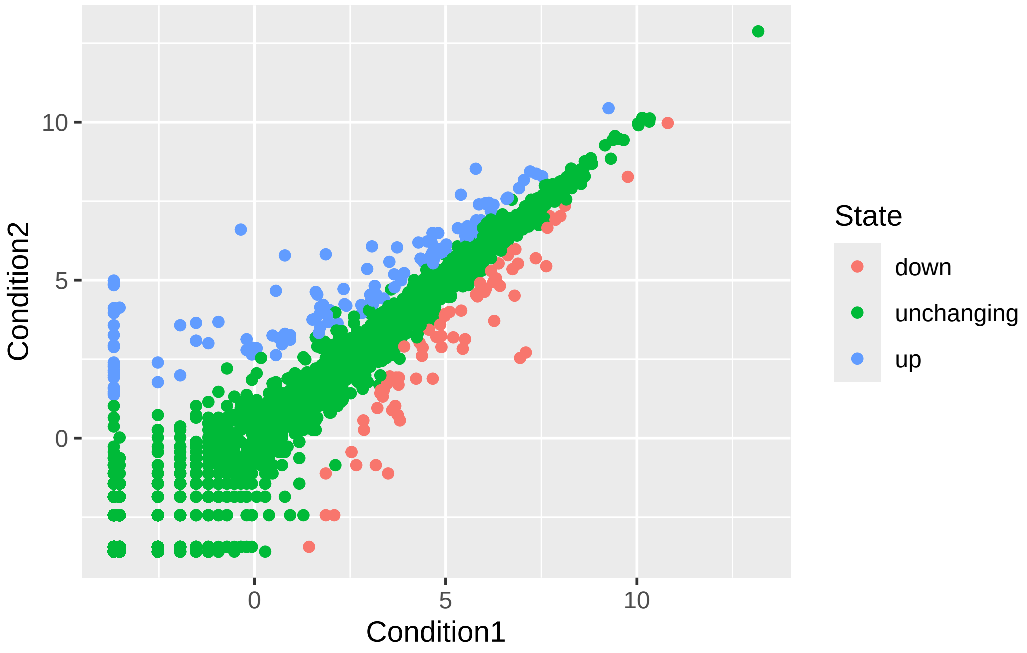


```
table(genes$State)
```

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

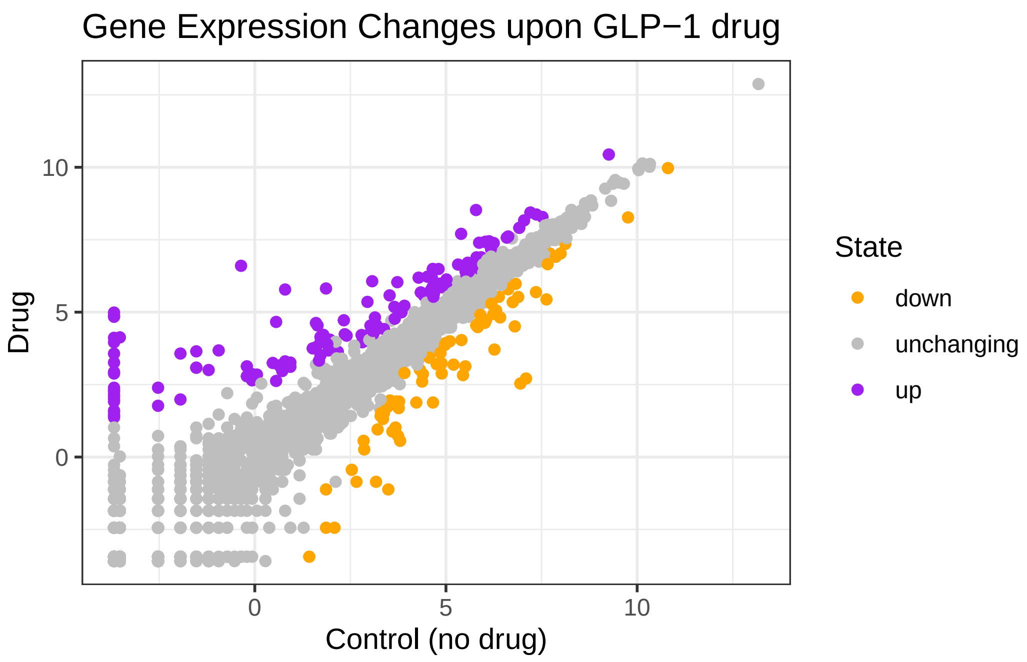
Version 2 let's color by `State` so we can see the "up" and "down" significant genes compared to all the "unchanging" genes

```
ggplot(genes) +
aes(Condition1, Condition2, col=State) +
geom_point()
```



Version 3 plot, let's modify the default colors to something we like

```
ggplot(genes) +
aes(Condition1, Condition2, col=State) + geom_point() +
  scale_colour_manual(values=c("orange", "gray", "purple"))+
labs(x="Control (no drug)",
y="Drug",
title= "Gene Expression Changes upon GLP-1 drug") + theme_bw()
```



##Going Further

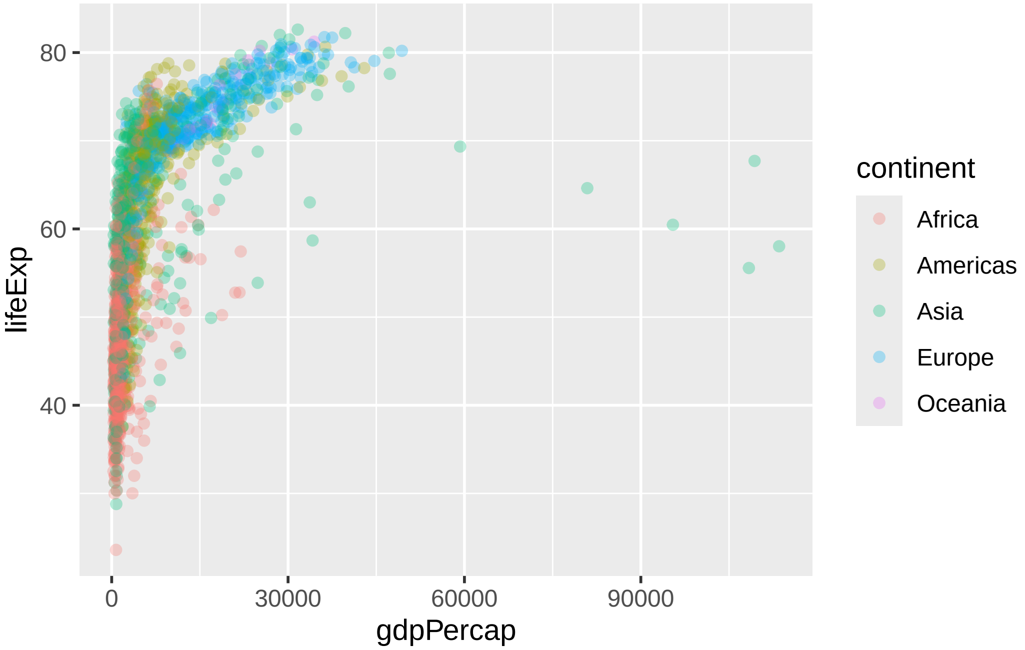
Let's have a look at the famous

```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.ts

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

```
head(gapminder, 3)
```

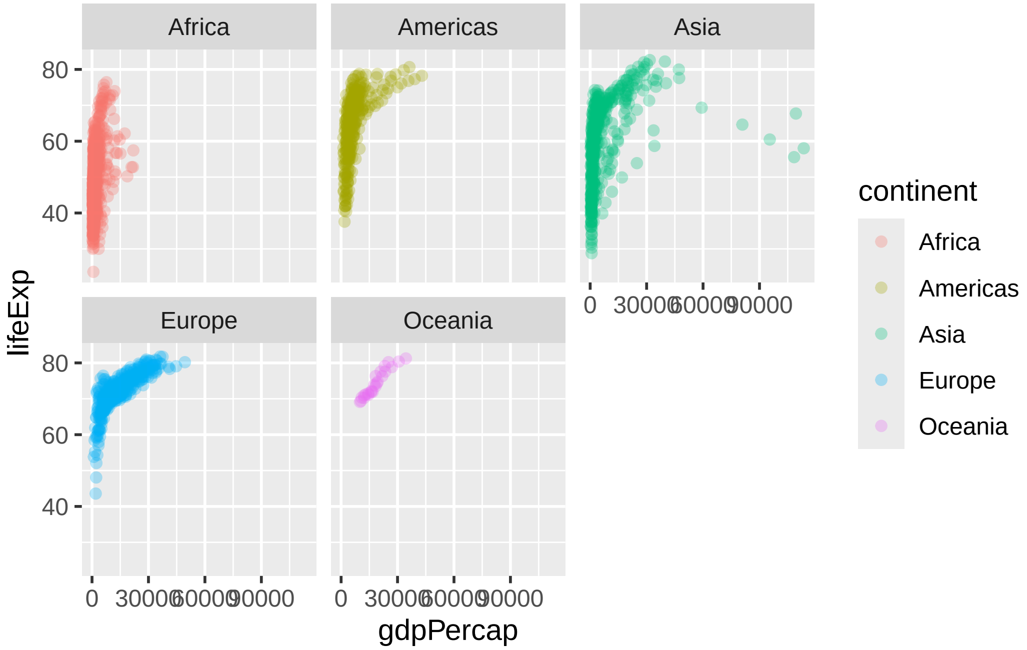
```
      country continent year lifeExp      pop gdpPercap
1 Afghanistan      Asia 1952  28.801  8425333  779.4453
2 Afghanistan      Asia 1957  30.332  9240934  820.8530
3 Afghanistan      Asia 1962  31.997 10267083  853.1007
```

```
ggplot(data=gapminder) +
  aes(x=gdpPercap, y=lifeExp, col=continent) +
  geom_point(alpha=0.3)
```



Let's "facet" (i.e. make a separate plot) by continent rather than the big hot mess above.

```
ggplot(data=gapminder) +
  aes(x=gdpPercap, y=lifeExp, col=continent) +
  geom_point(alpha=0.3) +
  facet_wrap(~continent)
```



Custom plots

How big is this gapminder dataset?

```r
nrow(gapminder)
```

```
[1] 1704
```

I want to "filter" down to a subset of data. I will use the **dplyr** package to help me.

First I need to install it and load it up.. `install.packages("dplyr")` and then `library(dplyr)`

```r
library(dplyr)
```

```


Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

    filter, lag
```

```
The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

```
gapminder_2007 <- filter(gapminder, year==2007)
head(gapminder_2007)
```

```
      country continent year lifeExp      pop  gdpPercap
1 Afghanistan      Asia 2007  43.828 31889923   974.5803
2     Albania    Europe 2007  76.423  3600523  5937.0295
3     Algeria    Africa 2007  72.301 33333216  6223.3675
4      Angola    Africa 2007  42.731 12420476  4797.2313
5   Argentina  Americas 2007  75.320 40301927 12779.3796
6   Australia   Oceania 2007  81.235 20434176 34435.3674
```

```
filter(gapminder_2007, country=="Ireland")
```

```
  country continent year lifeExp     pop gdpPercap
1 Ireland    Europe 2007  78.885 4109086     40676
```

```
filter(gapminder, year==2007, country=="Ireland")
```

```
  country continent year lifeExp     pop gdpPercap
1 Ireland    Europe 2007  78.885 4109086     40676
```

```
filter(gapminder, year==1977, country=="United States")
```

```
        country continent year lifeExp       pop gdpPercap
1 United States  Americas 1977   73.38 220239000  24072.63
```

```
filter(gapminder, year==1977, country=="Ireland")
```

```
  country continent year lifeExp     pop gdpPercap
1 Ireland    Europe 1977   72.03 3271900  11150.98
```

```
filter(gapminder, year==2007, country=="United States")
```

```
        country continent year lifeExp       pop gdpPercap
1 United States  Americas 2007  78.242 301139947  42951.65
```

Q. Make a plot comparing 1977 and 2007 for all countries

```
input <- filter(gapminder, year %in% c(1977, 2007))
head(input)
```

```
      country continent year lifeExp      pop gdpPercap
1 Afghanistan      Asia 1977  38.438 14880372  786.1134
2 Afghanistan      Asia 2007  43.828 31889923  974.5803
3     Albania    Europe 1977  68.930  2509048 3533.0039
4     Albania    Europe 2007  76.423  3600523 5937.0295
5     Algeria    Africa 1977  58.014 17152804 4910.4168
6     Algeria    Africa 2007  72.301 33333216 6223.3675
```

```
gapminder_1977 <- gapminder %>% filter(year==1977 | year==2007)
ggplot(gapminder_1977) +
  geom_point(aes(x = gdpPercap, y = lifeExp, color=continent,
              alpha=0.7)) +
  facet_wrap(~year)
```