class05:DataVisualization_GGPLOT

Leah Johnson

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Background

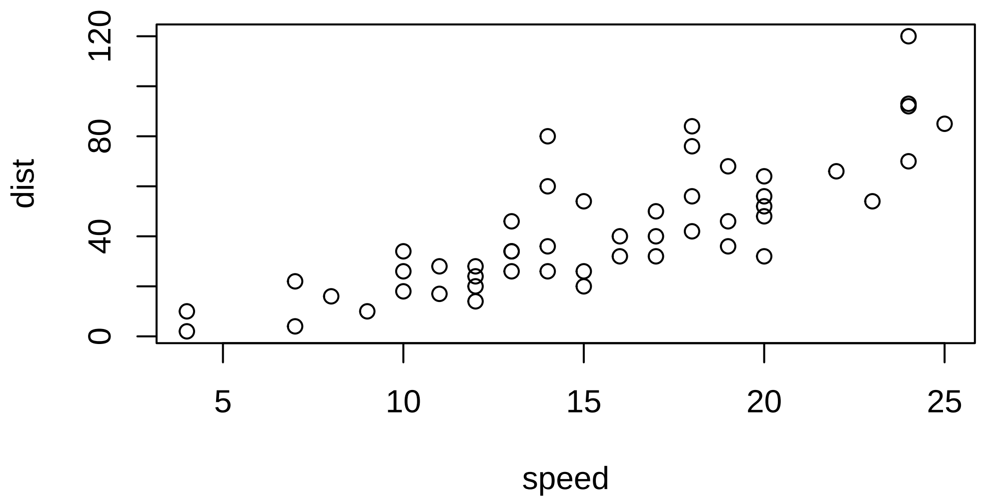
There are lots of ways to make figures in R. These include so-called "base R" graphics (e.g. 'plot()') and tons of add-on packages like **ggplot2**.

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)
```



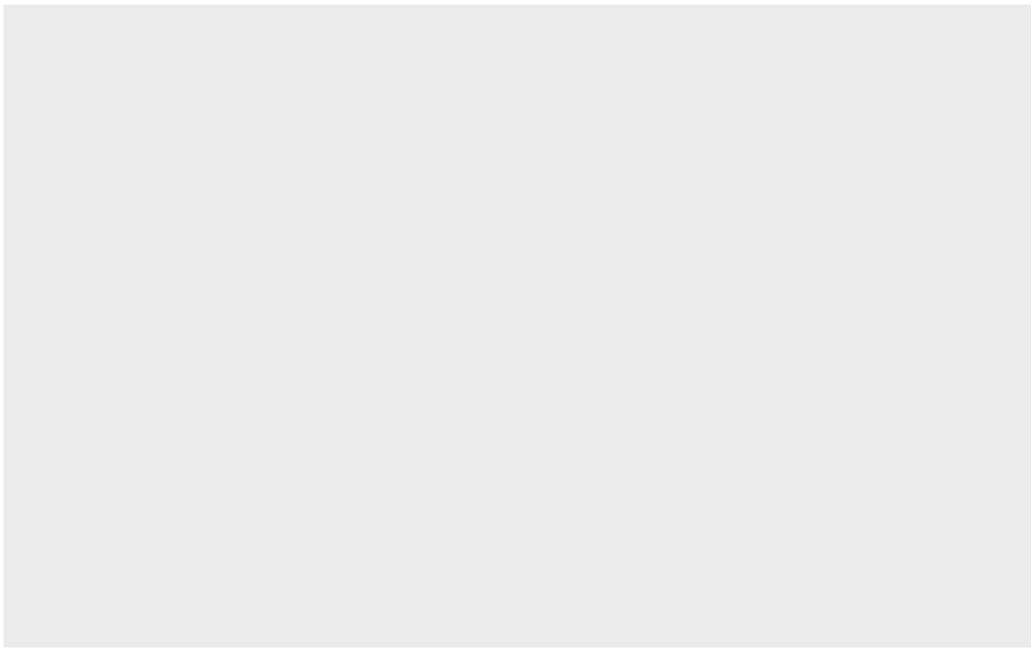
First I need to install the package with the command install.packages().

> **N.B.** We never run an install cmd in a quarto code chunk 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)
```

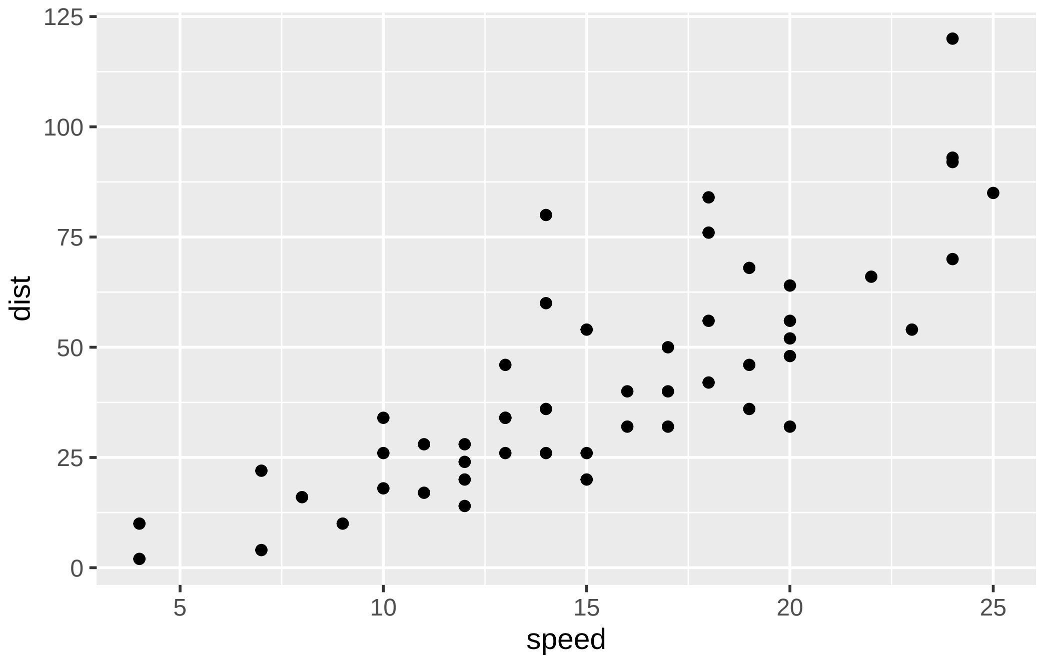
```
ggplot(cars)
```



Every ggplot needs at least 3 things:

- The **data**, the stuff you want plotted
- The **aes**thetics, how the data maps to the plot
- The **geom**etry, the type of plot

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

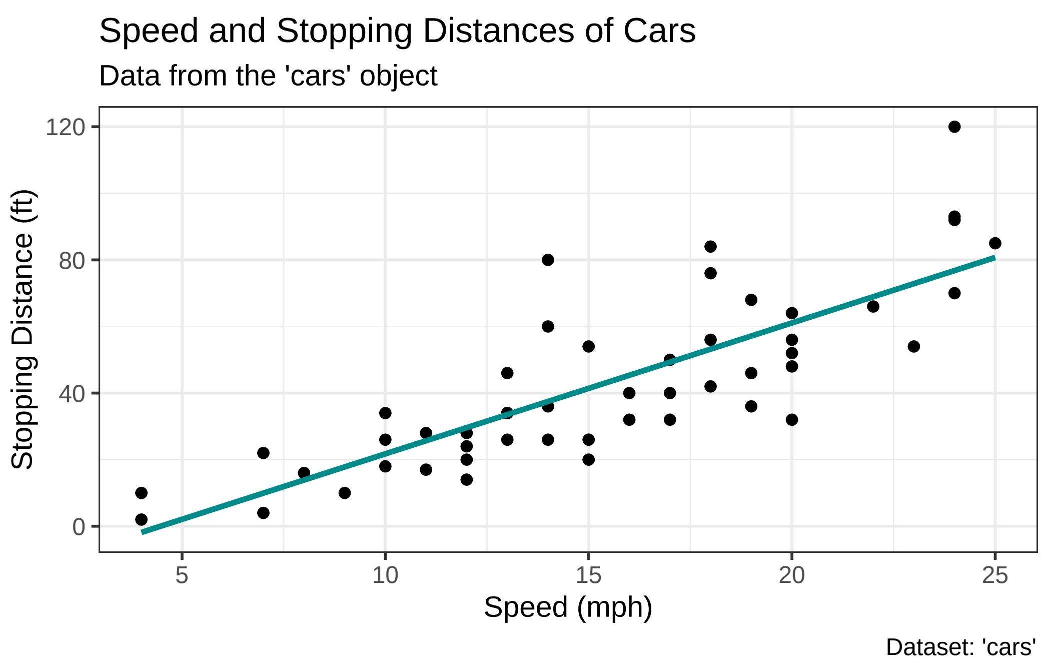


```
p <- ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  labs(title="Speed and Stopping Distances of Cars",
       x="Speed (mph)",
       y="Stopping Distance (ft)",
       subtitle="Data from the 'cars' object",
       caption="Dataset: 'cars'") +
  geom_smooth(method="lm", se=FALSE, col="cyan4") +
  theme_bw()
```

render it out

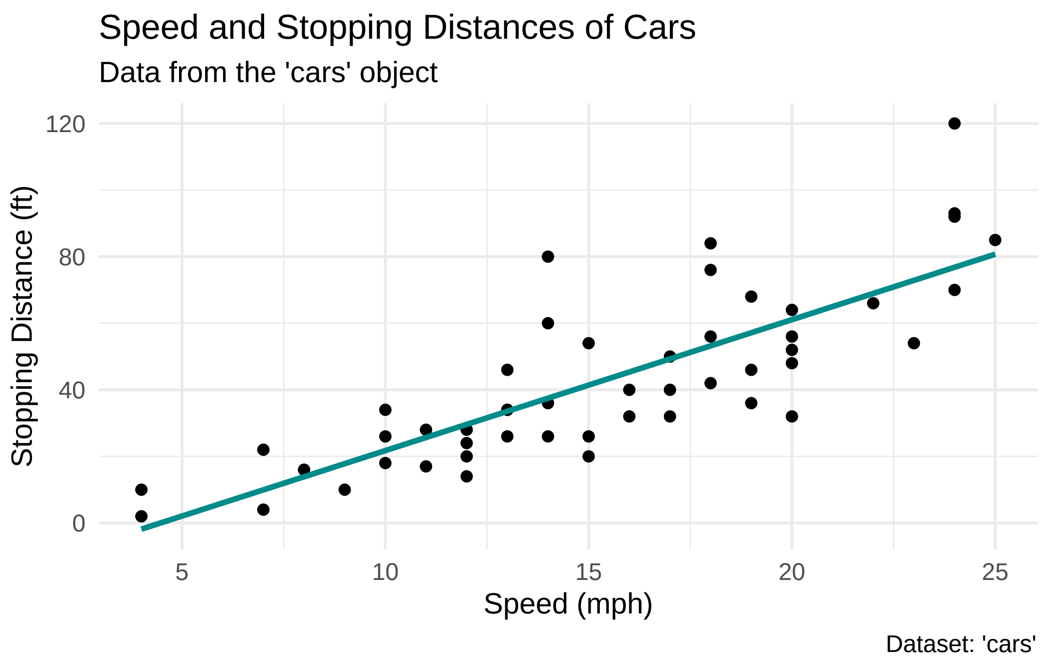
```
p
```

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



```r
p + theme_minimal()
```

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



Gene expression plot

We can read the input data from the class website.

```
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
```

```
nrow(genes)
```

```
[1] 5196
```

```
colnames(genes)
```

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

```
ncol(genes)
```

```
[1] 4
```

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

```

      down unchanging         up 
        72       4997        127 
```

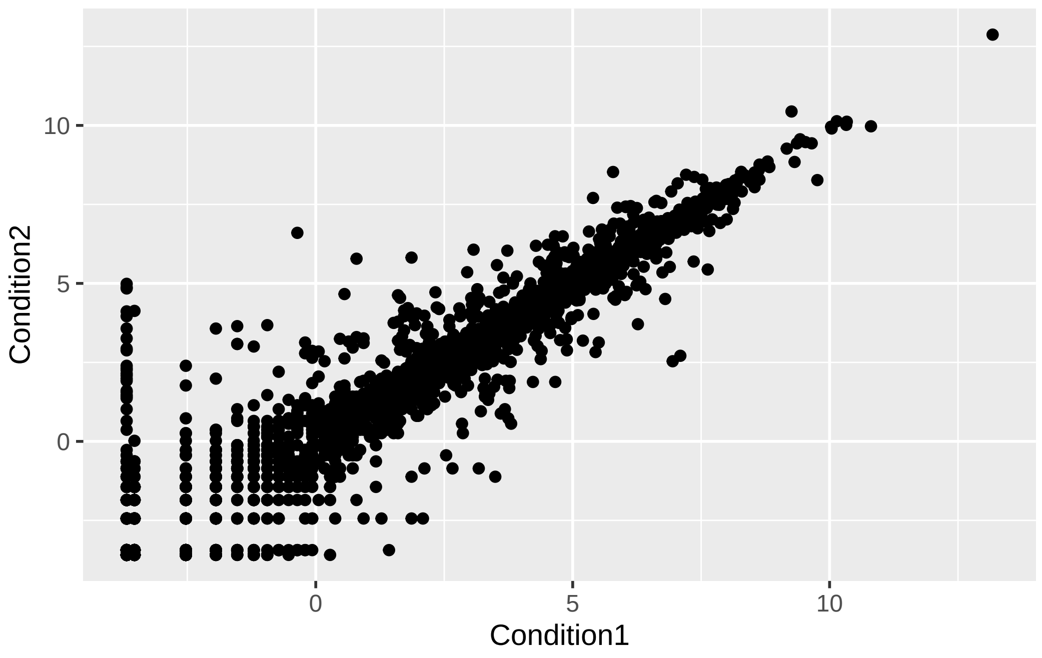
```
round(table(genes$State)/nrow(genes) * 100, 2)
```

```

      down unchanging         up 
      1.39      96.17       2.44 
```

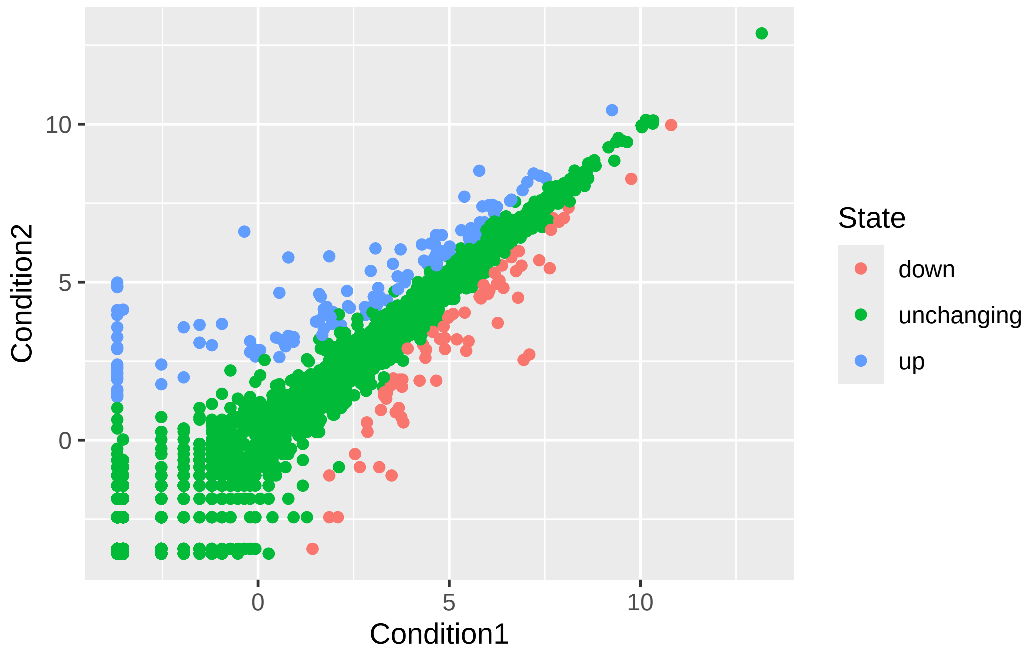
Version 1 plot:

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



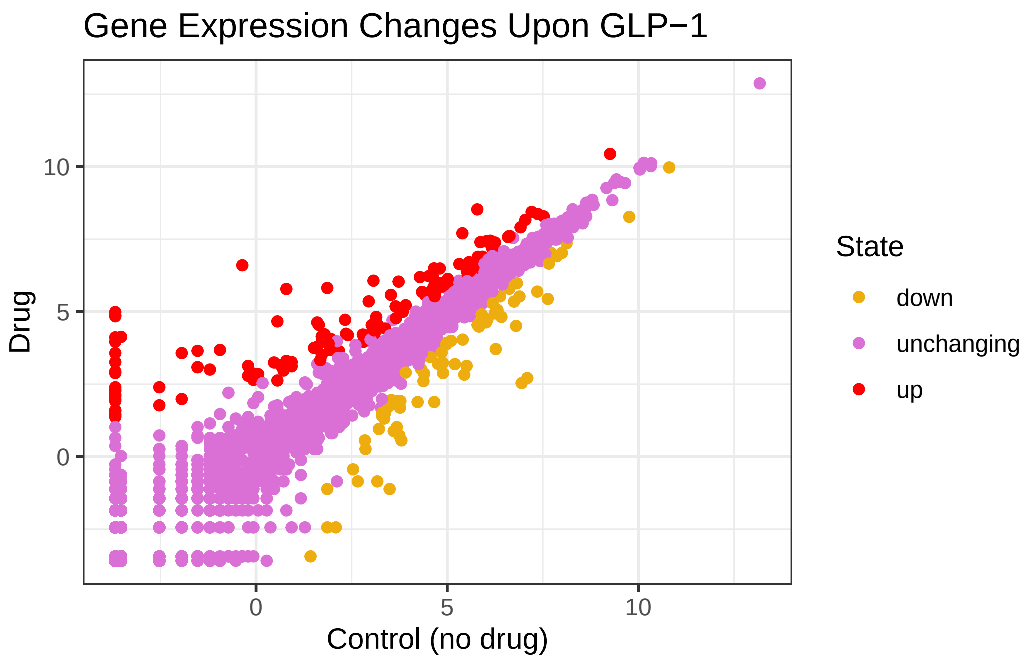
Version 2 plot: Let's color by State so we can see the "up" and "down" significant genes compared to the "unchanging" genes.

```
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("darkgoldenrod2", "orchid", "red")) +
  labs(x="Control (no drug)",
       y="Drug",
       title="Gene Expression Changes Upon GLP-1") +
  theme_bw()
```



Going Further

Let’s have a look at the famous **gapminder**

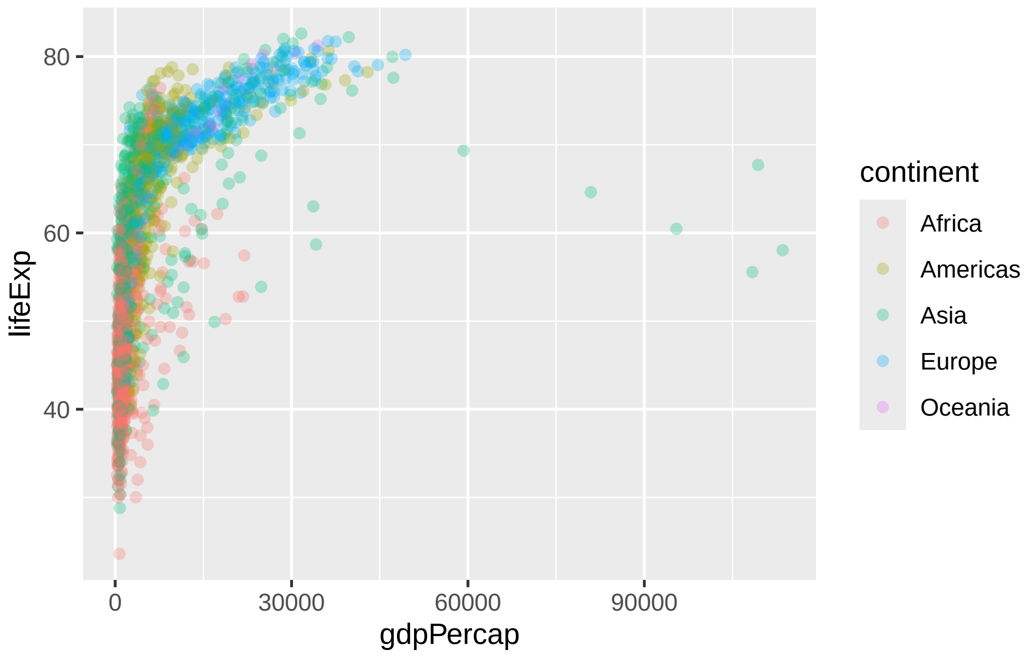
```
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.ts

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

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

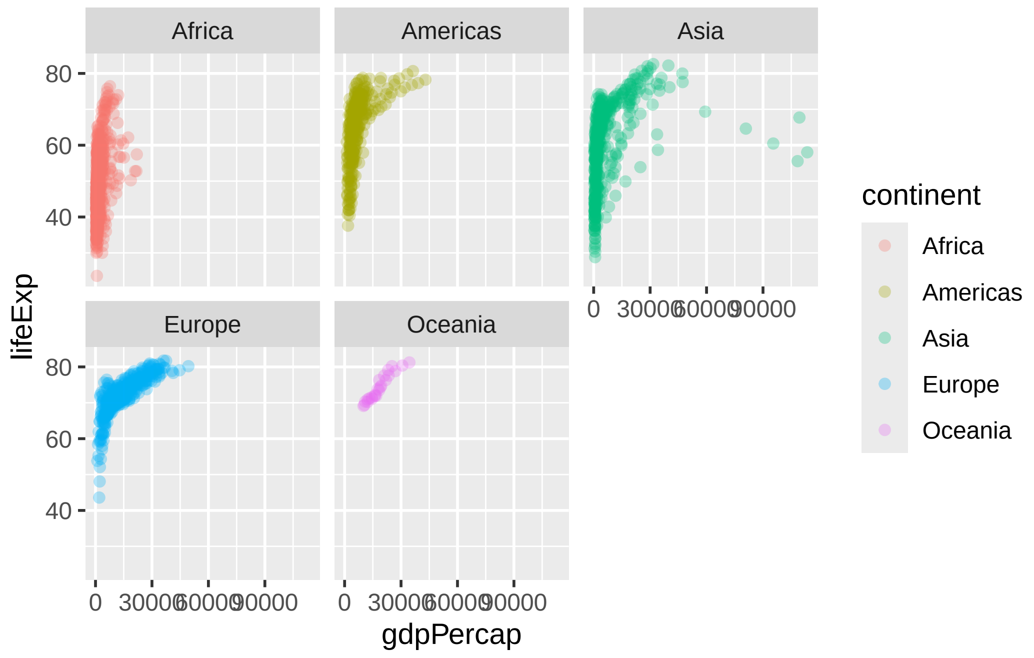
```
      country continent year lifeExp      pop gdpPercap
1 Afghanistan      Asia 1952  28.801  8425333  779.4453
2 Afghanistan      Asia 1957  30.332  9240934  820.8530
3 Afghanistan      Asia 1962  31.997 10267083  853.1007
```

```
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 hot mess above.

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



Custom Plots

How large is this gapminder dataset()

```
nrow(gapminder)
```

```
[1] 1704
```

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

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

```
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")
```

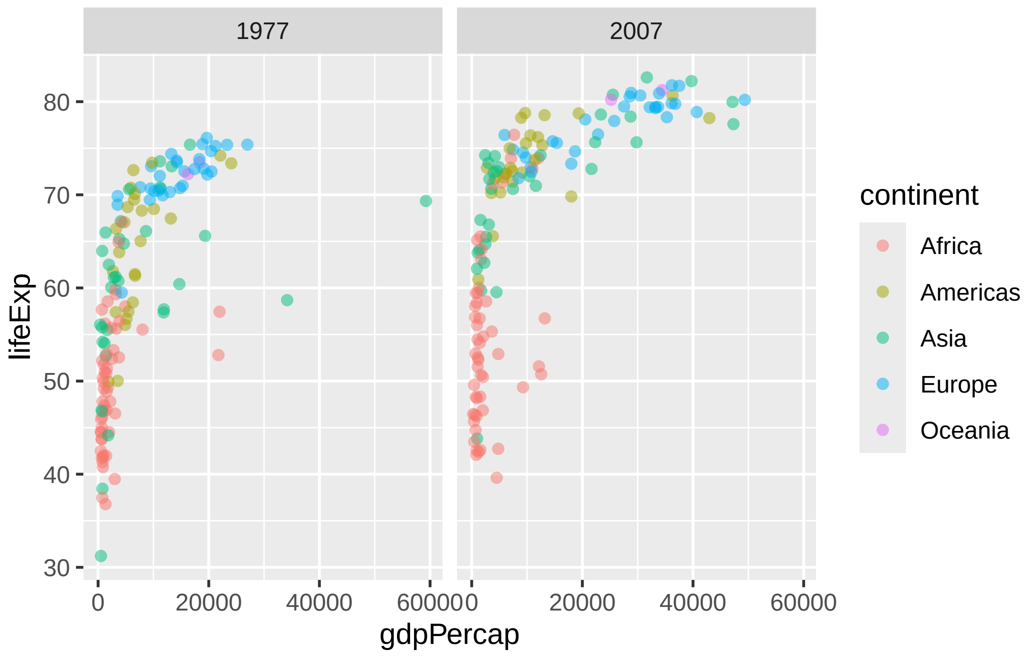
```
  country continent year lifeExp     pop gdpPercap
1 Ireland    Europe 2007  78.885 4109086     40676
```

```
filter(gapminder_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))
ggplot(input) +
  aes(x=gdpPercap, y=lifeExp, col=continent) +
  geom_point(alpha=0.5) +
  facet_wrap(~year)
```


1977
2007
lifeExp
80
70
60
50
40
30
0
20000
40000
60000
gdpPercap
continent
Africa
Americas
Asia
Europe
Oceania