Lab 5: Intro to ggplot

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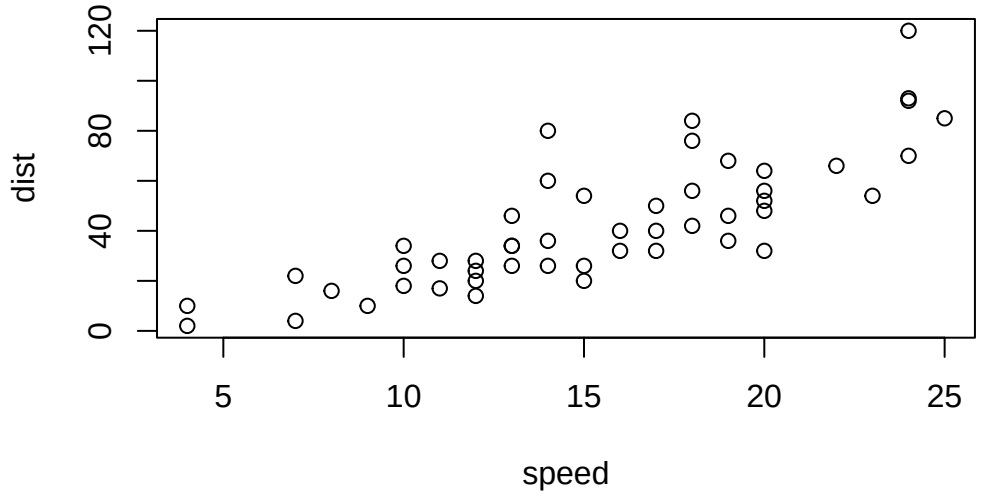
Plotting in R

(Test typing random **bolded** *italicized* words and sentences to see if it is replicated onto the **rendered** results.) Quarto enables you to weave together content and executable code into a finished document. To learn more about Quarto see https://quarto.org.

Testing Running Code

```
plot(cars)
```



This is a *base* R plot of the in-built `cars` dataset that has only two columns:

```
head(cars)
```

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

Q. How would we plot this dataset with **ggplot2**?

All ggplot figures have at least 3 layers:

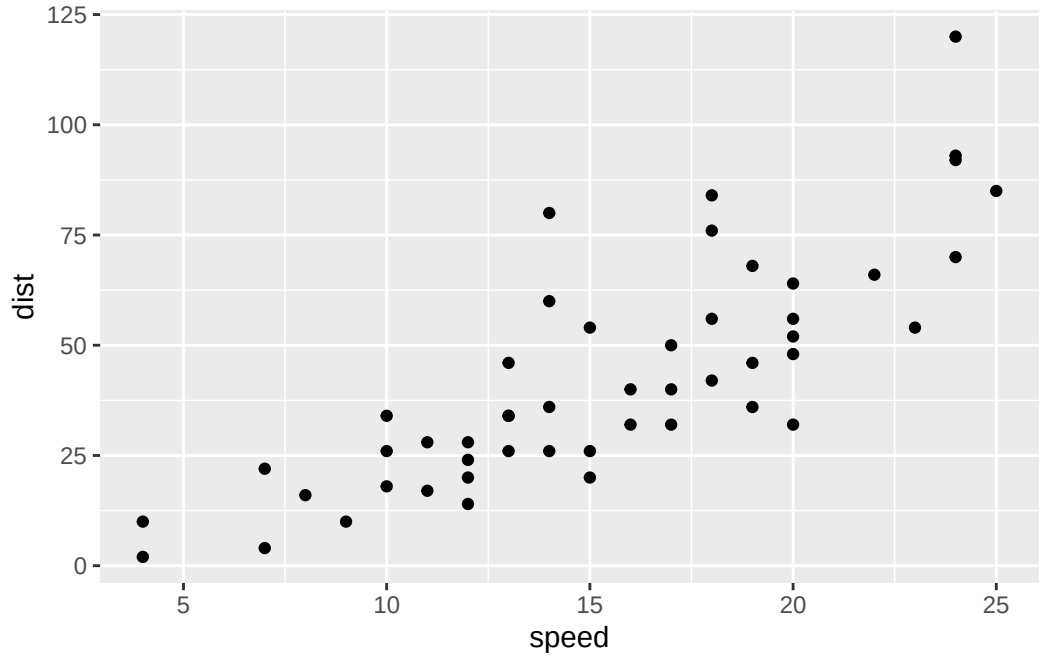
- data -aes (how the data map to the plot) -geoms (how we draw the plot)

Before I use any new package, I need to download and install it with the `install.packages()` command.

I never use `install.packages()` within my quarto document otherwise I will install the package over and over and over again - which is silly!

Once a package is installed, I can load it up with the `library()` function.

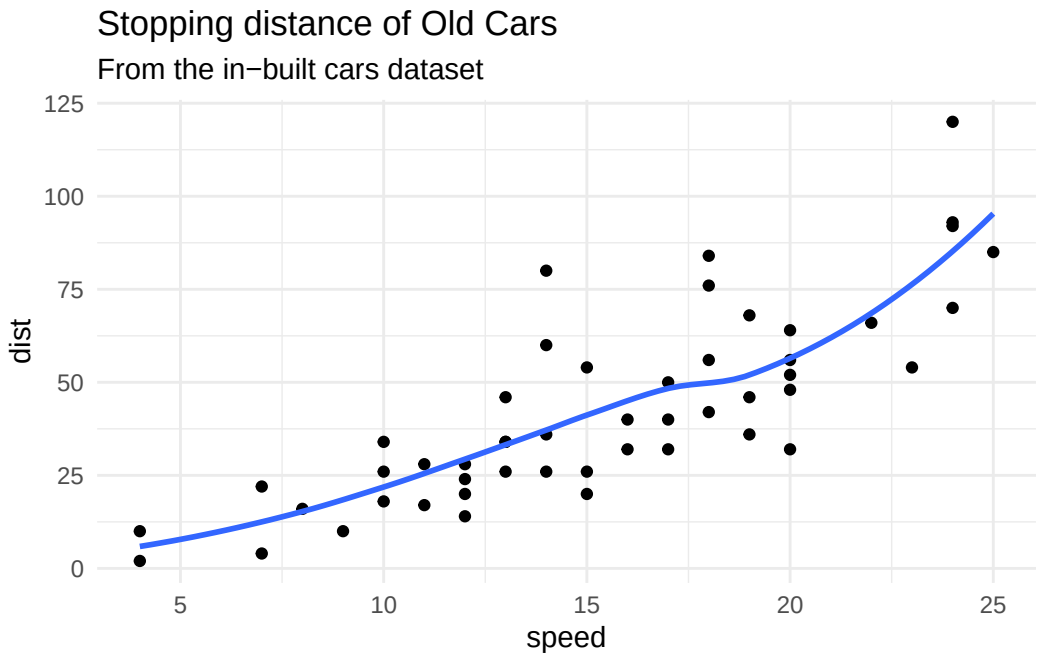
```
# install.packages("tidyverse")
# Before you use it every time, you need library(ggplot2) to call the installed packages to l
library(ggplot2)

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



Key-point: For simple plots (like the one above) ggplot is more verbose (we need to do more typing; "fancier"), but as plots get more complicated ggplot starts to be more clear and simple than base R plot().

```
# "p <- ggplot()" used to save the plot.
ggplot(cars) +
  aes(speed,dist) +
  geom_point() +
  geom_smooth(se=F, na.rm=T) +
  labs(title="Stopping distance of Old Cars",
       subtitle = "From the in-built cars dataset",
       ytitle = "distance",
       xtitle = "Speedy Speed Speed") +
  theme_minimal()
```

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



Running Code

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
nrow(genes)
```

```
[1] 5196
```

```
colnames(genes)
```

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

```
ncol(genes)
```

```
[1] 4
```

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

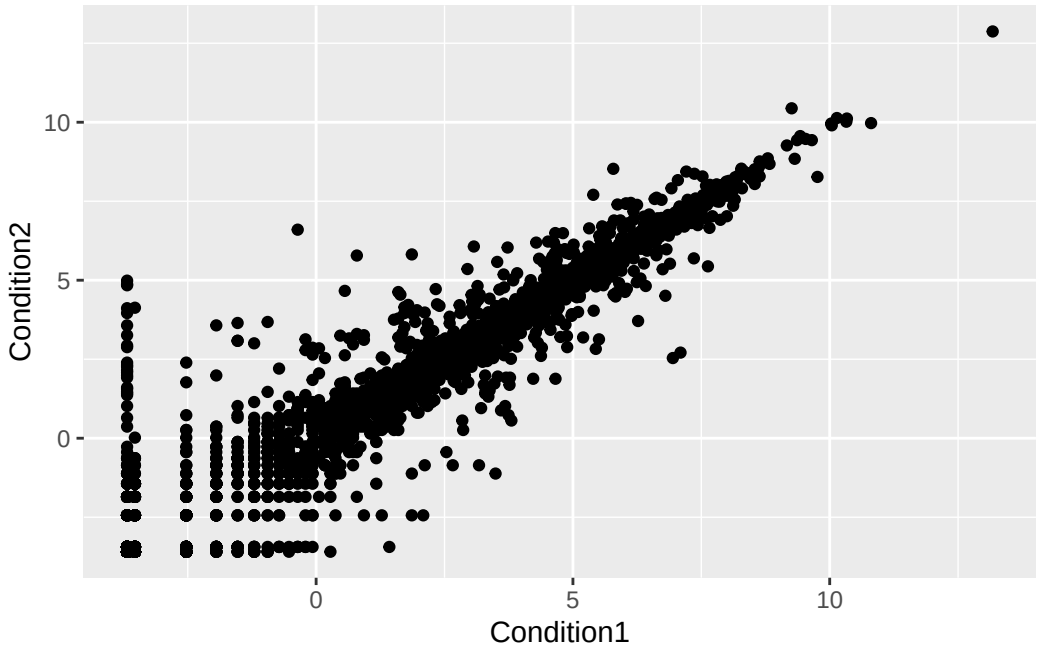
```
      down unchanging         up
        72       4997        127
```

```
# or round( table(genes$State)/nrow(genes), 2)
```

The key functions here where:

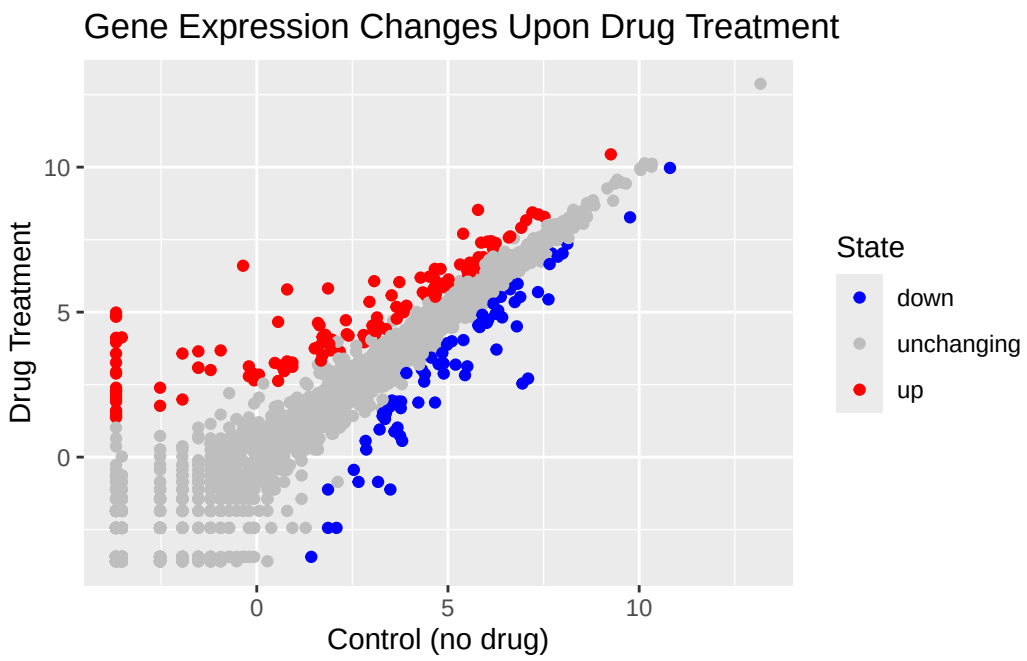
`nrow()` and `ncol()` `table()` is very useful for getting counts finally `round()`

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
p <- ggplot(genes) +
    aes(x=Condition1, y=Condition2) +
    geom_point()
p + scale_colour_manual(values=c("blue","gray","red") )
```




```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
p <- ggplot(genes) +
    aes(x=Condition1, y=Condition2, col=State) +
    geom_point()
```

```
p + scale_colour_manual( values=c("blue","gray","red") ) +
  # Question: Nice, now add some plot annotations to the p object with the labs() function so
  labs(title="Gene Expression Changes Upon Drug Treatment",
       x="Control (no drug)",
       y = "Drug Treatment")
```

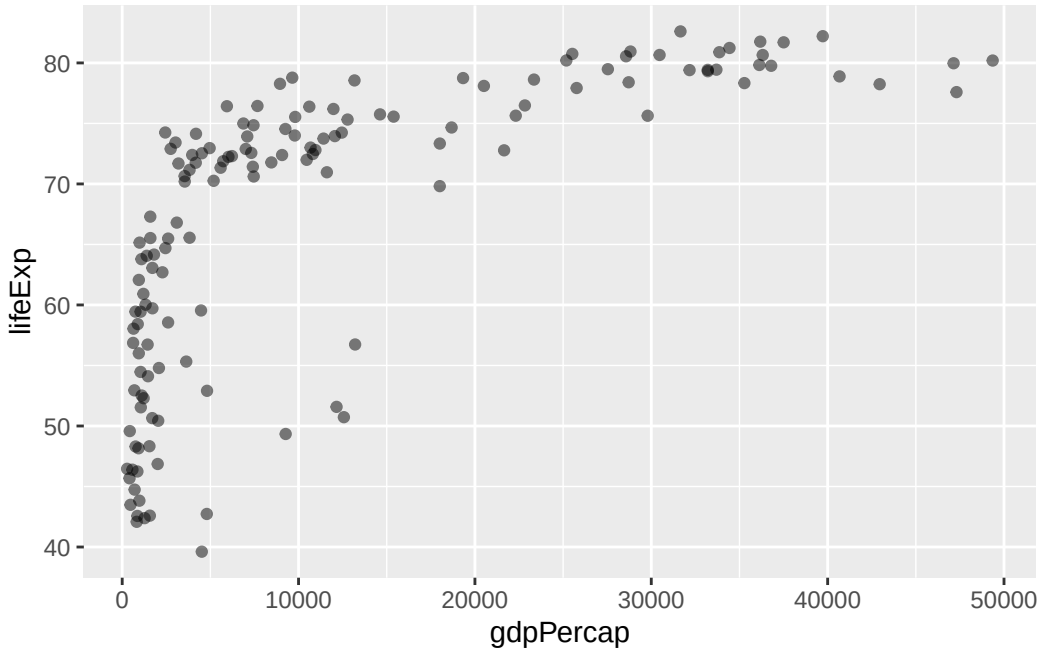



```
# install.packages("gapminder")
library(gapminder)
# Or Read File location online
# url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.t
#
# gapminder <- read.delim(url)
# install.packages("dplyr")
library(dplyr)
```

```
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 <- gapminder %>% filter(year==2007)
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.5)
```




```
# Shows how many unique years there are in the dataset
length( unique(gapminder$year))
```

```
[1] 12
```

```
# filter to countries
filter(gapminder, country =="United States")
```

```
# A tibble: 12 x 6
   country       continent  year lifeExp       pop gdpPercap
   <fct>         <fct>     <int>   <dbl>     <int>     <dbl>
 1 United States Americas   1952    68.4 157553000    13990.
```

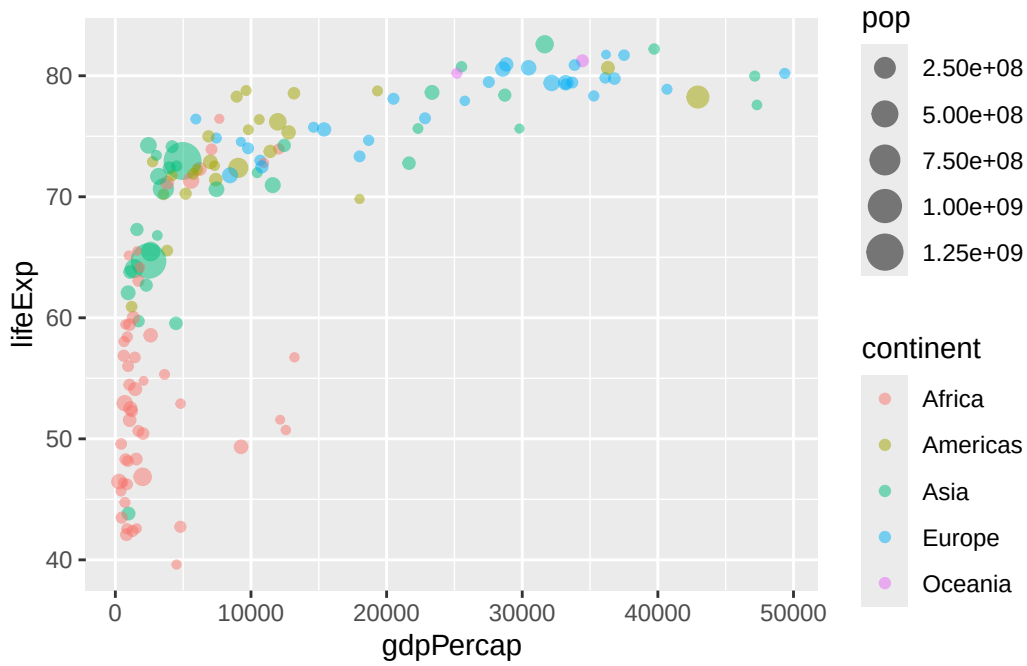
```
 2 United States Americas   1957    69.5 171984000    14847.
 3 United States Americas   1962    70.2 186538000    16173.
 4 United States Americas   1967    70.8 198712000    19530.
 5 United States Americas   1972    71.3 209896000    21806.
 6 United States Americas   1977    73.4 220239000    24073.
 7 United States Americas   1982    74.6 232187835    25010.
 8 United States Americas   1987    75.0 242803533    29884.
 9 United States Americas   1992    76.1 256894189    32004.
10 United States Americas   1997    76.8 272911760    35767.
11 United States Americas   2002    77.3 287675526    39097.
12 United States Americas   2007    78.2 301139947    42952.
```

```r
# What countries in data set had pop smaller than Ireland in 2007?
# First limit/subset the dataset to the year 2007
# Then find the pop value for Ireland
# Then extract all rows with pop less than Ireland
# Claude AI RESPONSE
# First, let's find Ireland's population in 2007
ireland_pop_2007 <- gapminder %>%
  filter(country == "Ireland", year == 2007) %>%
  pull(pop)

# Now, let's find countries with smaller populations in 2007
smaller_countries <- gapminder %>%
  filter(year == 2007, pop < ireland_pop_2007) %>%
  select(country, pop) %>%
  arrange(desc(pop))

# View the results
print(smaller_countries)
```

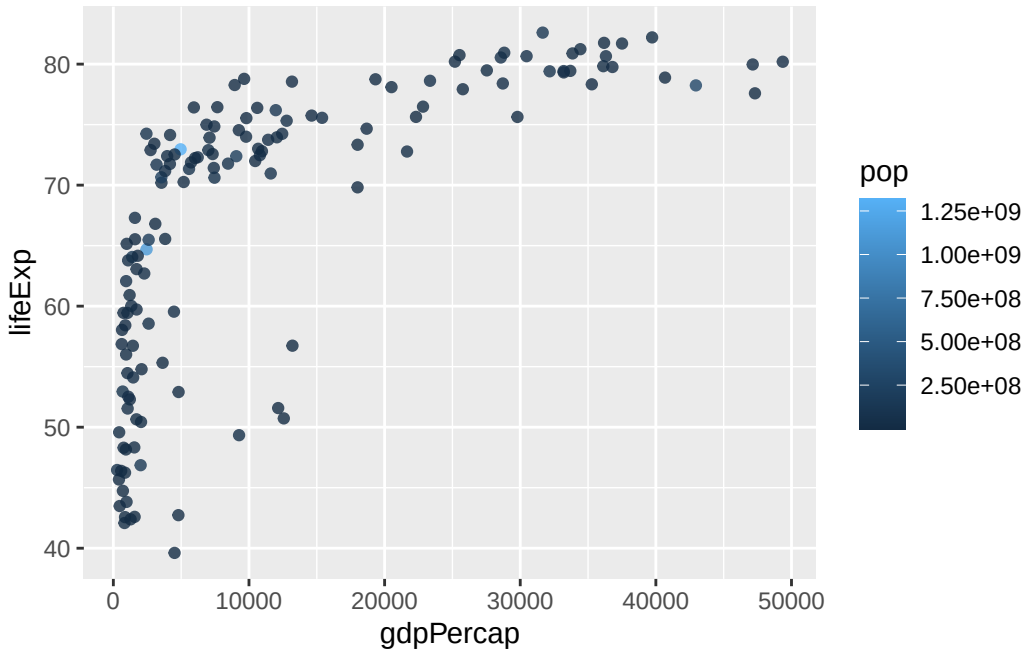
```
# A tibble: 31 x 2
   country                pop
   <fct>                <int>
 1 West Bank and Gaza 4018332
 2 Puerto Rico        3942491
 3 Lebanon            3921278
 4 Congo, Rep.        3800610
 5 Albania            3600523
 6 Uruguay            3447496
 7 Mauritania         3270065
 8 Panama             3242173
```

```
 9 Oman                3204897
10 Liberia             3193942
# i 21 more rows
```

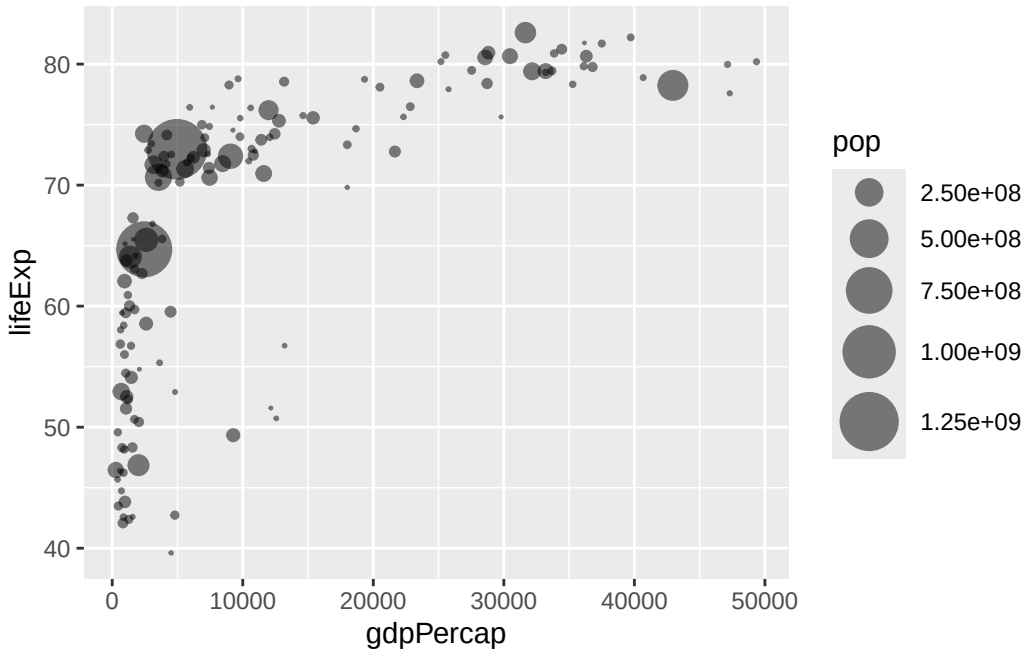
```
library(gapminder)
library(dplyr)
gapminder_2007 <- gapminder %>% filter(year==2007)
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)
```



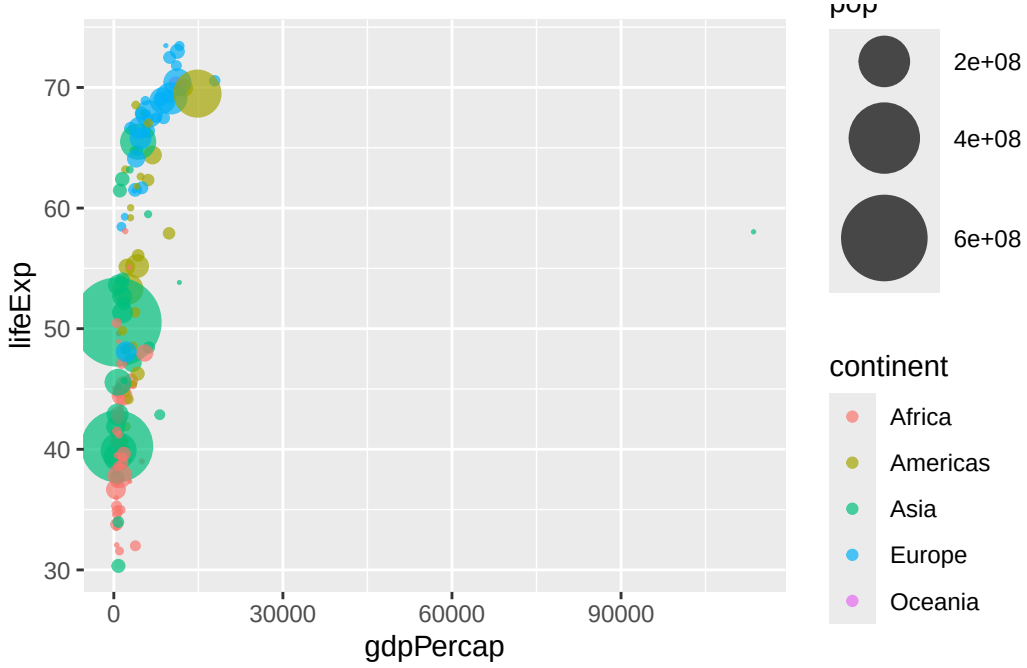

```
library(gapminder)
library(dplyr)
gapminder_2007 <- gapminder %>% filter(year==2007)
ggplot(gapminder_2007) +
  aes(x = gdpPercap, y = lifeExp, color = pop) +
  geom_point(alpha=0.8)
```



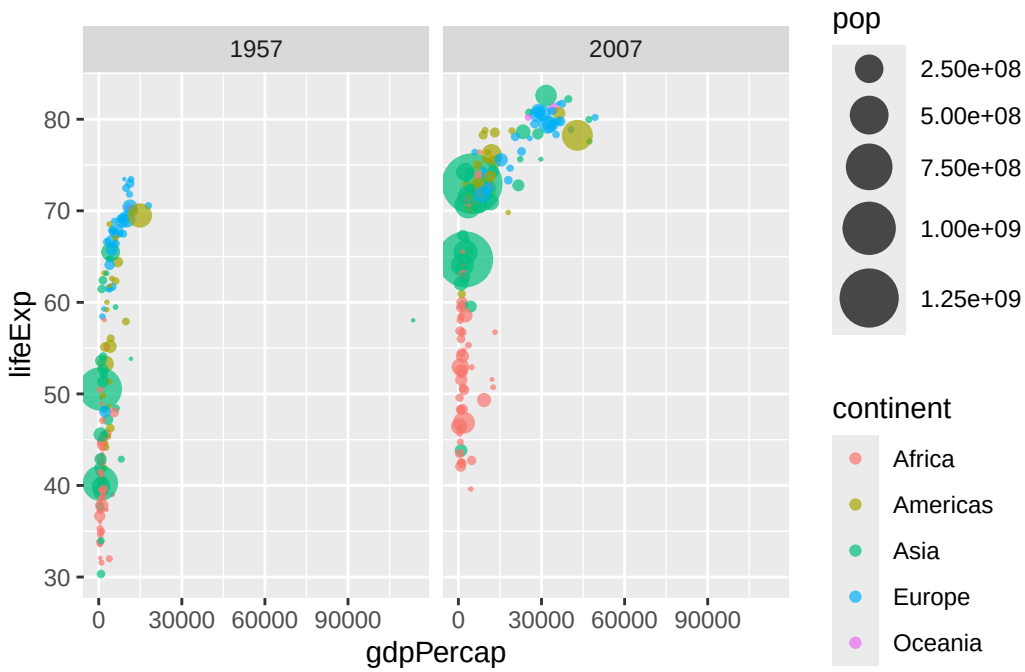

```
library(gapminder)
library(dplyr)
gapminder_2007 <- gapminder %>% filter(year==2007)
ggplot(gapminder_2007) +
  # use scale_size_area() to reflect the actual population differences by the point size
  geom_point(aes(x = gdpPercap, y = lifeExp,
                 size = pop), alpha=0.5) +
  scale_size_area(max_size = 10)
```




```
# Q. Can you adapt the code you have learned thus far to reproduce our gapminder scatter plot
library(gapminder)
library(dplyr)
gapminder_1957 <- gapminder %>% filter(year==1957)
ggplot(gapminder_1957) +
  geom_point(aes(x=gdpPercap, y=lifeExp, col=continent, size=pop), alpha=0.7) +
  scale_size_area(max_size = 15)
```




```
# Q. Do the same steps above but include 1957 and 2007 in your input dataset for ggplot(). Yo
library(gapminder)
library(dplyr)
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)
p <- ggplot(gapminder_1957) +
  geom_point(aes(x=gdpPercap, y=lifeExp, col=continent, size=pop), alpha=0.7) +
  scale_size_area(max_size = 10)
p +
   facet_wrap(~year)
```

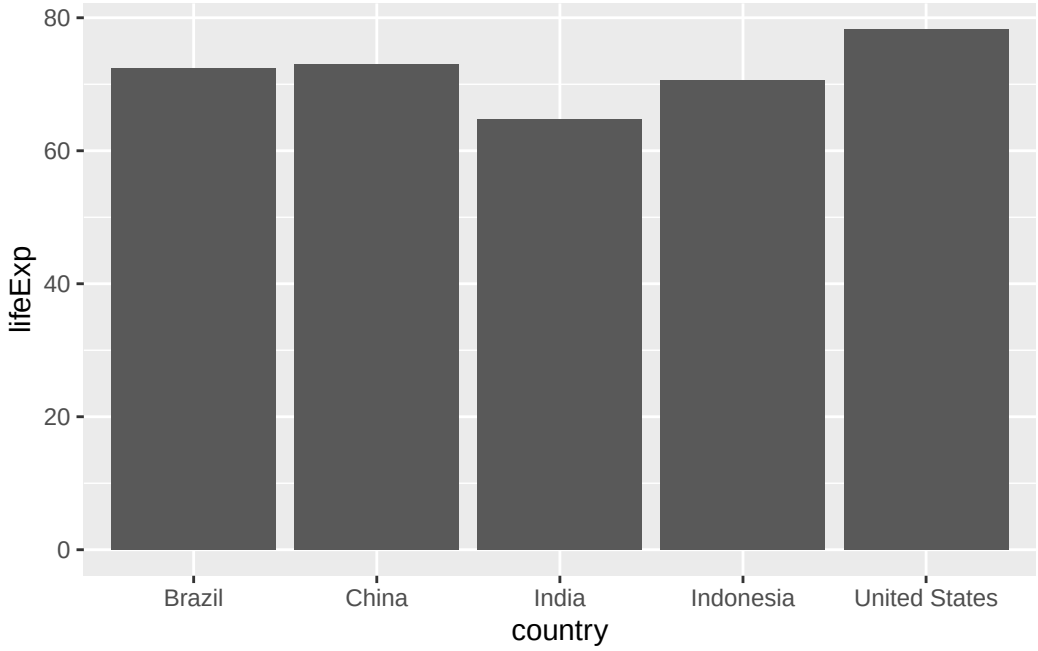


##OPTIONAL SECTIONS

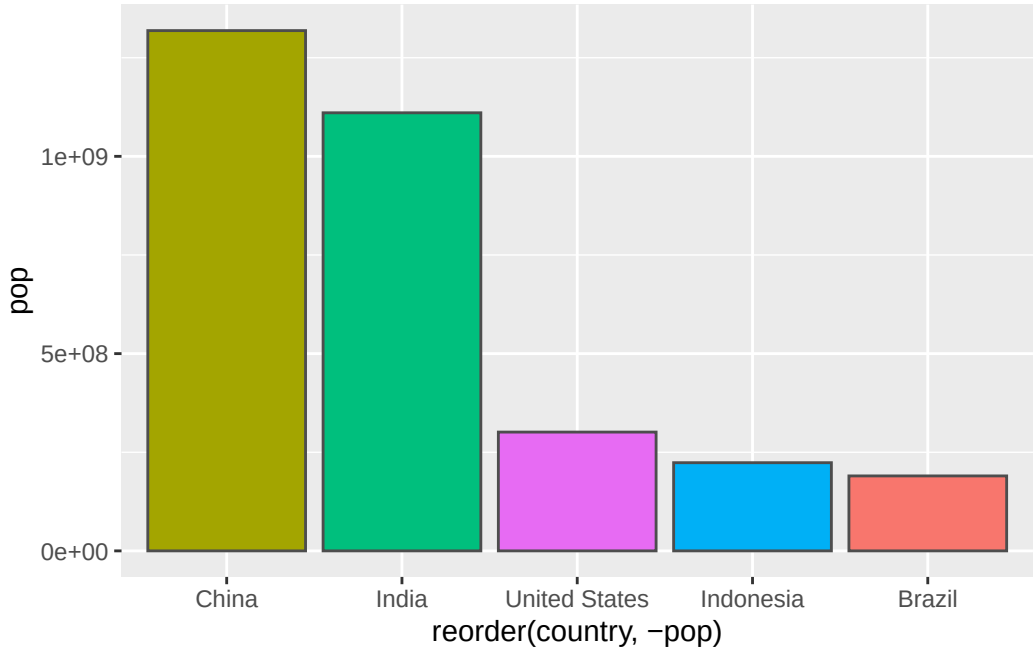
```
# Bar Chart Introduction
# Q Create a bar chart showing the life expectancy of the five biggest countries by populatio
library(gapminder)
library(dplyr)
gapminder_top5 <- gapminder %>%
  filter(year==2007) %>%
  arrange(desc(pop)) %>%
  top_n(5, pop)

gapminder_top5
```

```
# A tibble: 5 x 6
  country       continent  year lifeExp        pop gdpPercap
  <fct>         <fct>     <int>   <dbl>      <int>     <dbl>
1 China         Asia       2007    73.0 1318683096     4959.
2 India         Asia       2007    64.7 1110396331     2452.
3 United States Americas   2007    78.2  301139947    42952.
4 Indonesia     Asia       2007    70.6  223547000     3541.
5 Brazil        Americas   2007    72.4  190010647     9066.
```

```
ggplot(gapminder_top5) +
  geom_col(aes(x=country, y=lifeExp))
```



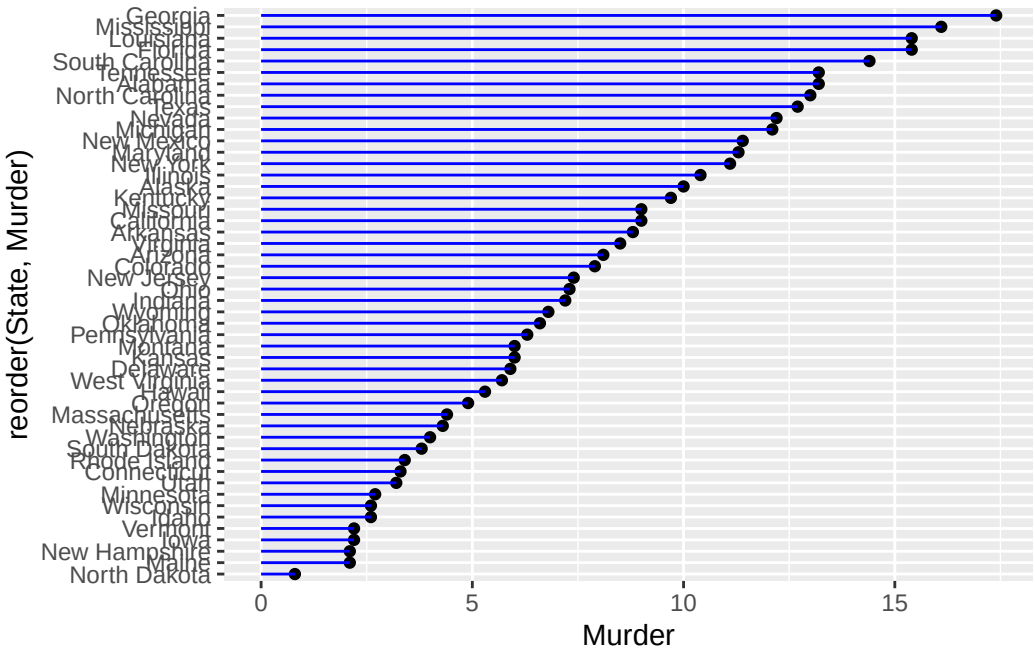

```
# Q. Plot population size by country. Create a bar chart showing the population (in millions)

ggplot(gapminder_top5) +
  aes(x=reorder(country, -pop), y=pop, fill=country) +
  geom_col(col="gray30") +
  guides(fill="none")
```




```
# Flipped Bar Charts
head(USArrests)
```

```
           Murder Assault UrbanPop Rape
Alabama      13.2     236       58 21.2
Alaska       10.0     263       48 44.5
Arizona       8.1     294       80 31.0
Arkansas      8.8     190       50 19.5
California    9.0     276       91 40.6
Colorado      7.9     204       78 38.7
```

```
# using geom_point() and geom_segment() cleans up the aesthetics and makes the chart easier c

USArrests$State <- rownames(USArrests)
ggplot(USArrests) +
  aes(x=reorder(State,Murder), y=Murder) +
  geom_point() +
  geom_segment(aes(x=State,
                   xend=State,
                   y=0,
                   yend=Murder), color="blue") +
  coord_flip()
```



Default Text

When you click the **Render** button a document will be generated that includes both content and the output of embedded code. You can embed code like this:

```
1 + 1
```

```
[1] 2
```

You can add options to executable code like this

```
[1] 4
```

The `echo: false` option disables the printing of code (only output is displayed).