Class 5: Data visualization with ggplot2

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

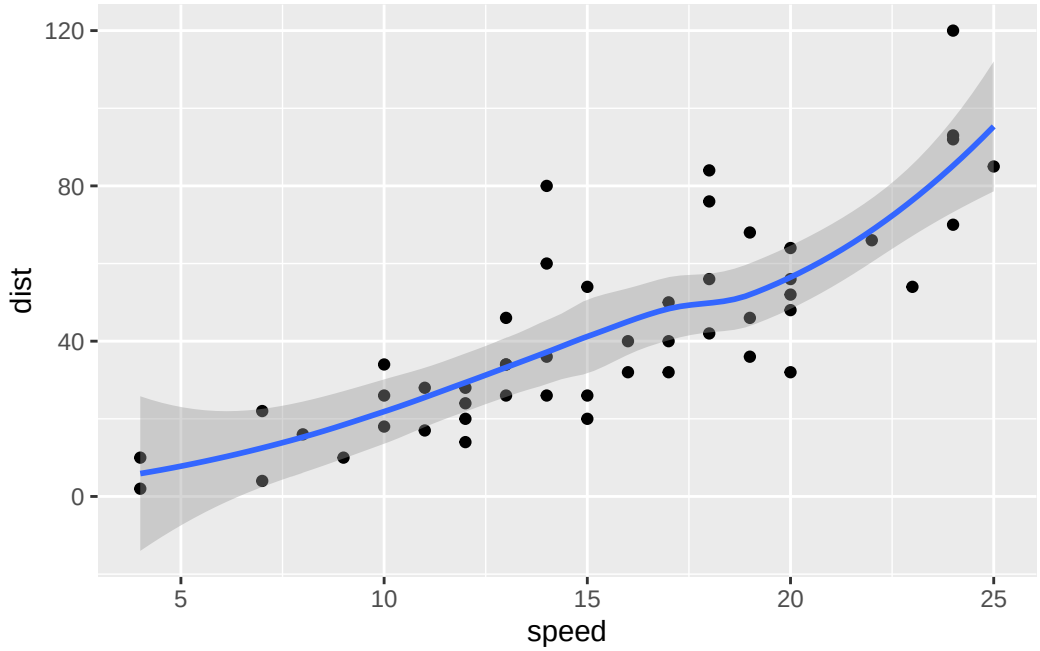
Section 6. Creating Scatter Plots

Specifing a geom layer with geom_point()

Q. In your own RStudio can you add a trend line layer to help show the relationship between the plot variables with the geom_smooth() function?

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

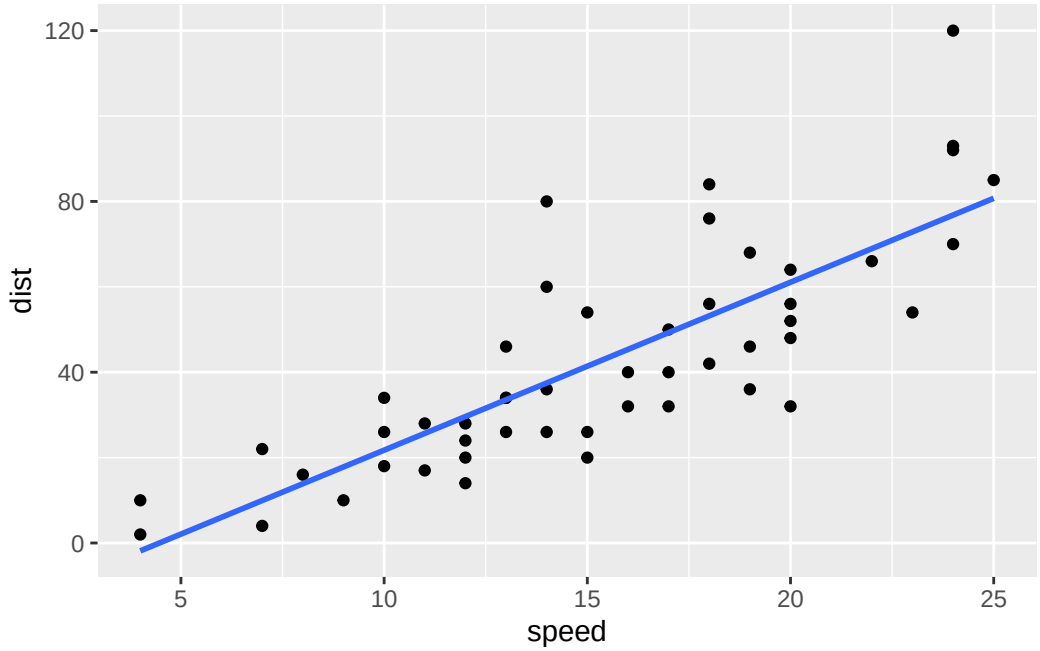
```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



Q. Argue with geom_smooth() to add a straight line from a linear model without the shaded standard error region?

```
# set the method to "linear model", and don't show the confidence interval (se = FALSE)
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method = "lm", se = F)
```

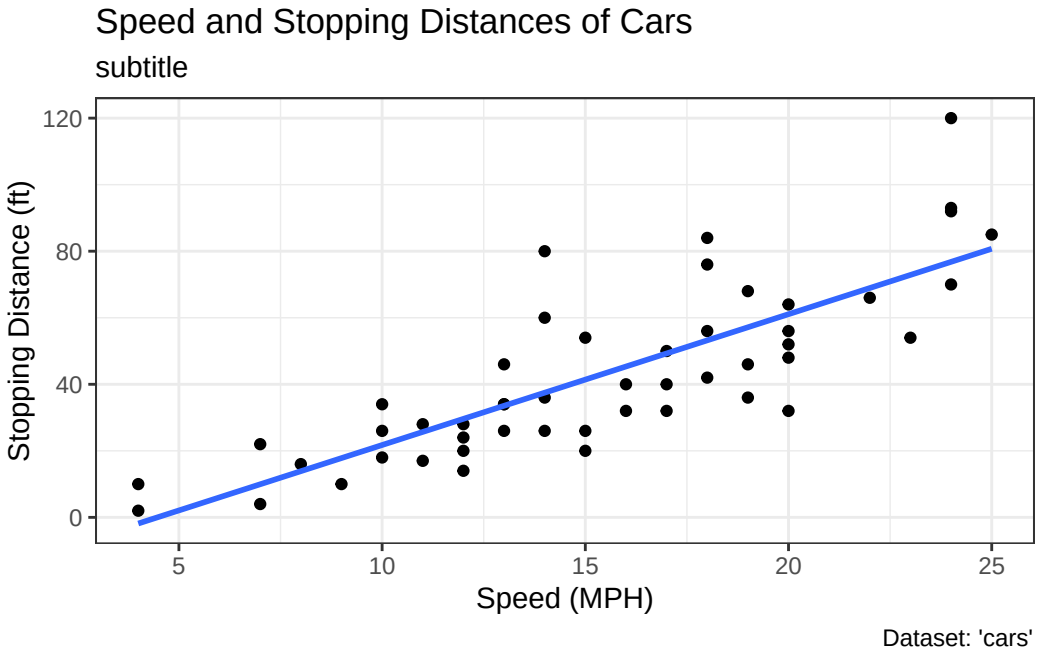
```
`geom_smooth()` using formula = 'y ~ x'
```



Q. Can you finish this plot by adding various label annotations with the labs() function and changing the plot look to a more conservative "black & white" theme by adding the theme_bw() function:

```
# Add label annotations by labs().
# theme_bw(): build-in theme, white background and thin grey grid lines
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method = "lm", se = F) +
  labs(title="Speed and Stopping Distances of Cars",
       x="Speed (MPH)",
       y="Stopping Distance (ft)",
       subtitle = "subtitle",
       caption="Dataset: 'cars'") +
  theme_bw()
```

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



Adding more plot aesthetics through aes()

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
# read.delim() function is used to read delimited text files
genes <- read.delim(url)
# head() function is used to display the first n rows present in the input data frame.
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
```

```
# colnames() function returns or sets the names of the columns in a data frame.
colnames(genes)
```

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

```
# nrow()/ncol() function returns the number of rows/columns in a data frame.
nrow(genes)
```

```
[1] 5196
```

```
ncol(genes)
```

```
[1] 4
```

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

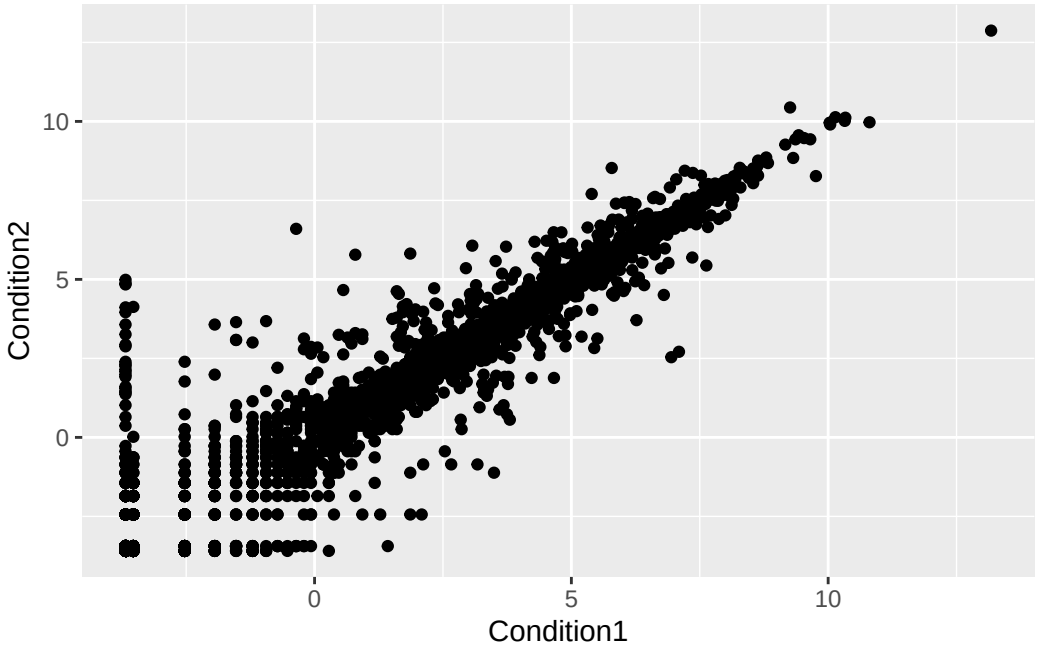
```
      down unchanging         up
        72       4997        127
```

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

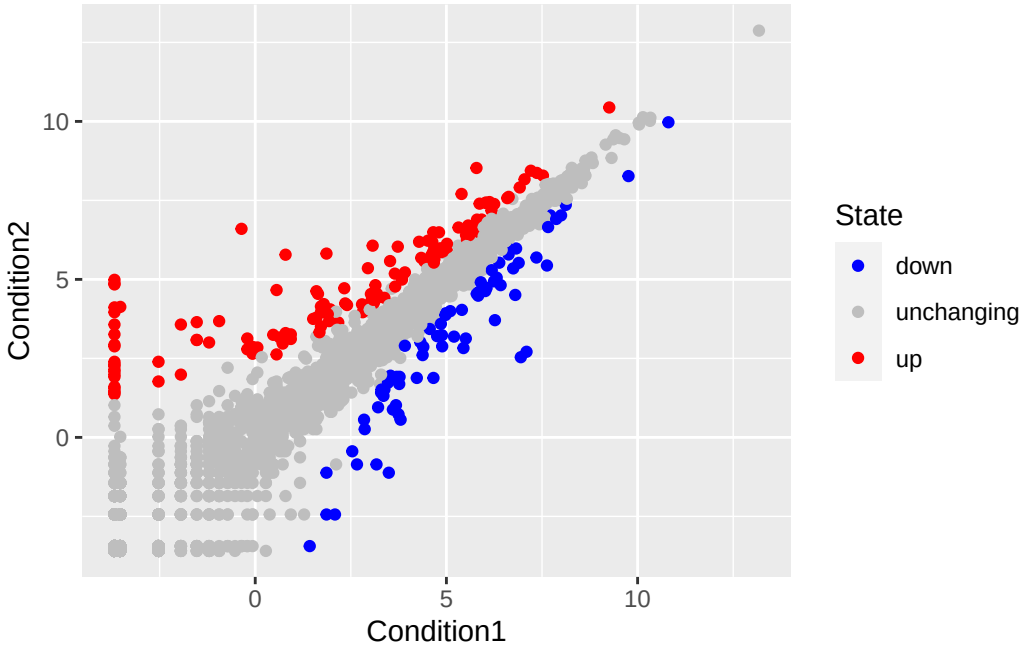
```
      down unchanging         up
      1.39      96.17       2.44
```

Q. Complete the code below to produce the following plot

```
ggplot(genes) +
    aes(x=Condition1, y=Condition2) +
    geom_point()
```

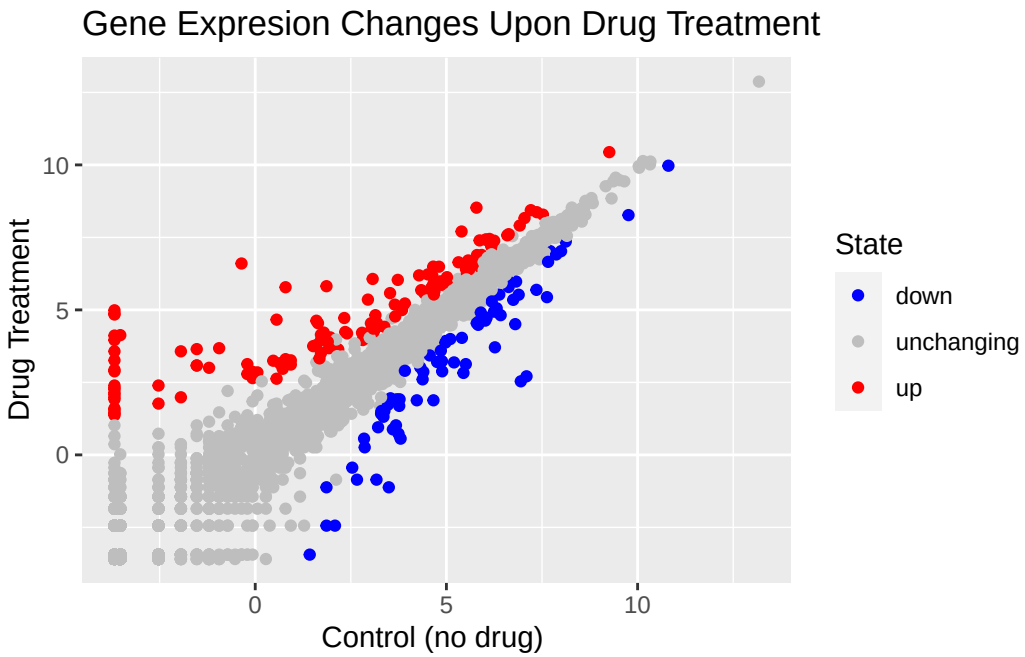



```
p <- ggplot(genes) +
    aes(x=Condition1, y=Condition2, col=State) +
    geom_point()
# scale_colour_manual(): Create your own discrete scale
p + scale_colour_manual( values=c("blue","gray","red") )
```



Q. Nice, now add some plot annotations to the p object with the labs() function so your plot looks like the following:

```
# Add label annotations by labs().
p2 <- p + scale_colour_manual(values=c("blue","gray","red")) +
    labs(title="Gene Expresion Changes Upon Drug Treatment",
         x="Control (no drug) ",
         y="Drug Treatment")
p2
```




```
# plotly library makes interactive graphs
library(plotly)
# ggplotly(p2)
```

Section 7. Going Further

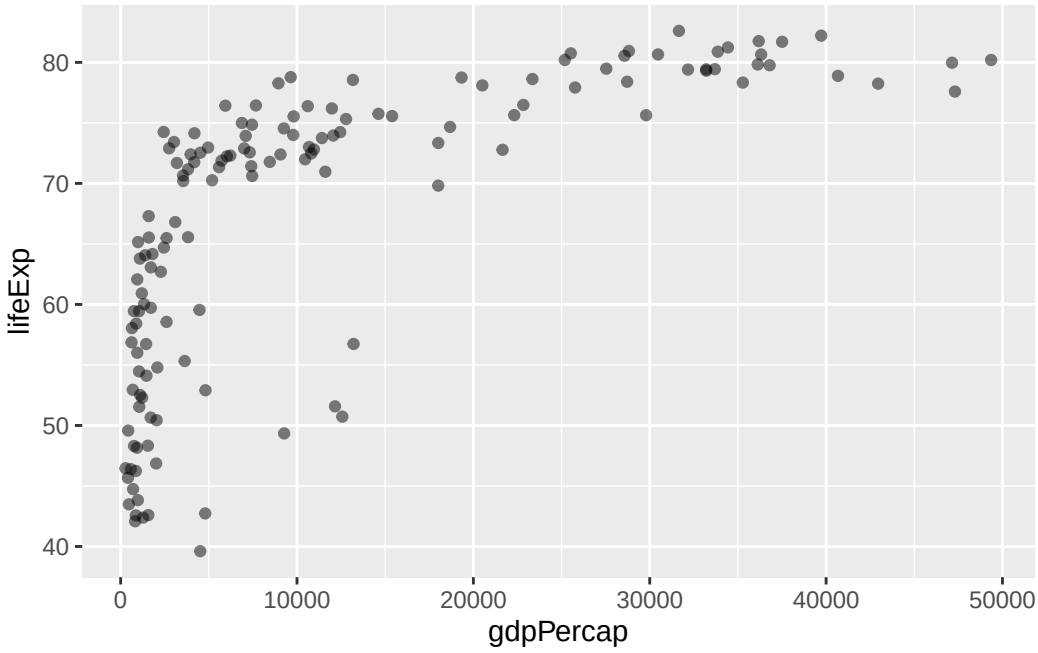
```
# install.packages("gapminder")
# install.packages("dplyr")
library(gapminder)
library(dplyr)

gapminder_2007 <- gapminder %>% filter(year==2007)
head(gapminder_2007, 2)
```

```
# A tibble: 2 x 6
  country     continent  year lifeExp      pop gdpPercap
  <fct>       <fct>     <int>   <dbl>    <int>     <dbl>
1 Afghanistan Asia       2007    43.8 31889923      975.
2 Albania     Europe     2007    76.4  3600523     5937.
```

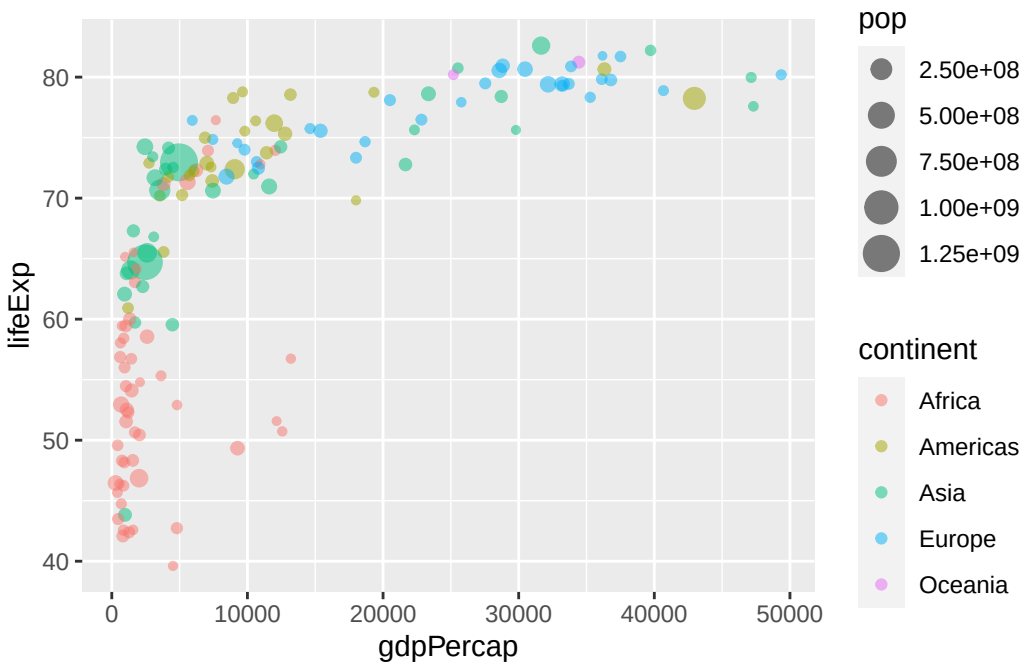
Q. Complete the code below to produce a first basic scater plot of this gapminder_2007 dataset:

```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.5)
```



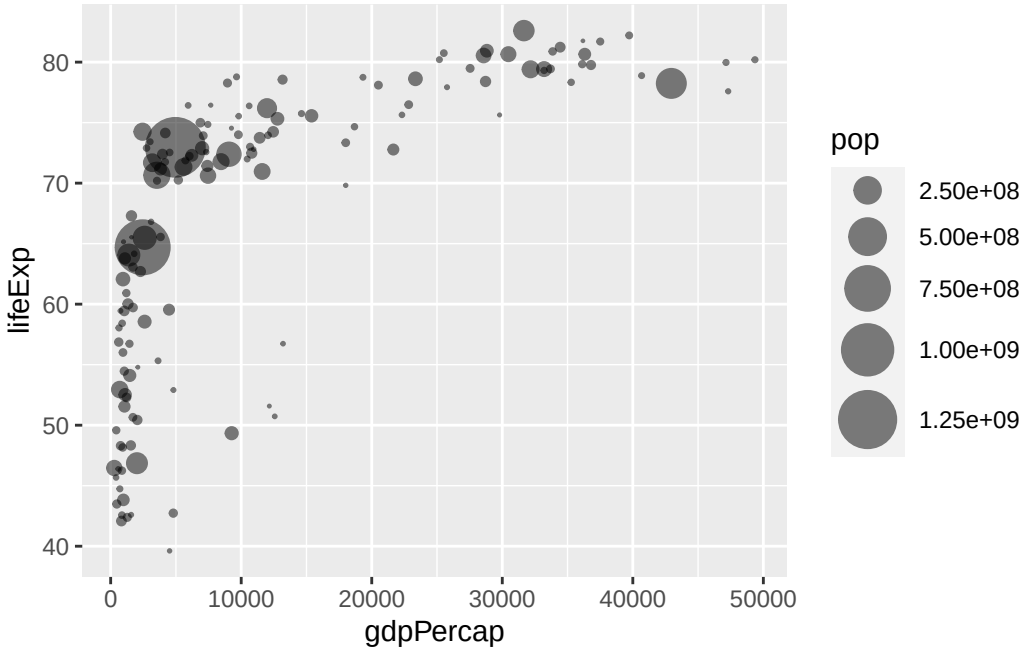
Adding more varables to aes()

```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)
```



Adjusting point size

```
ggplot(gapminder_2007) +
  geom_point(aes(x = gdpPercap, y = lifeExp,
                 size = pop), alpha=0.5) +
  scale_size_area(max_size = 10)
```

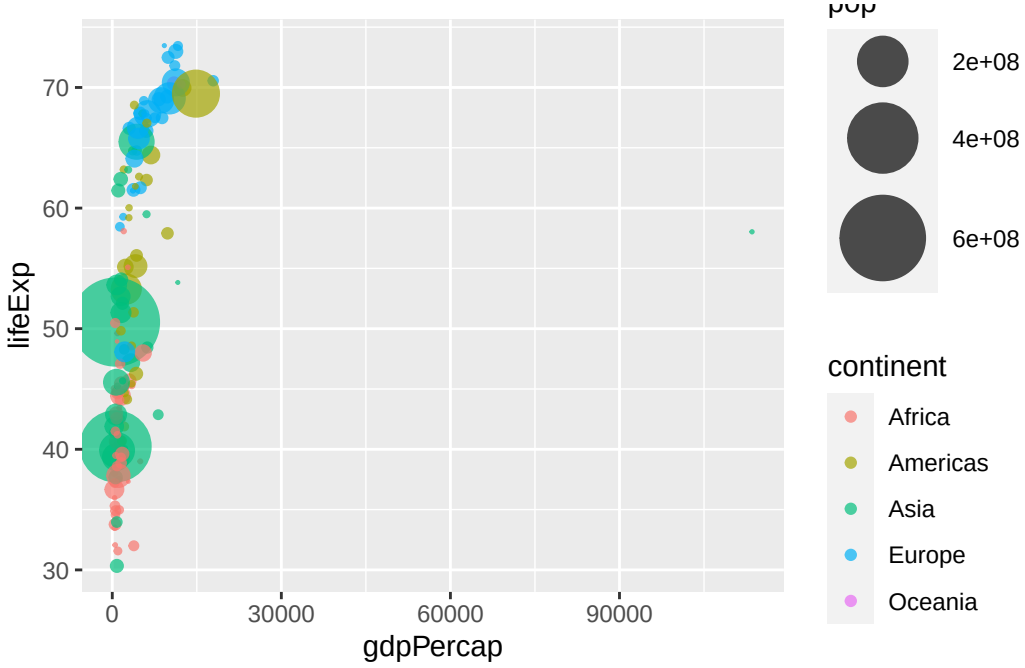


Q. Can you adapt the code you have learned thus far to reproduce our gapminder scatter plot for the year 1957? What do you notice about this plot is it easy to compare with the one for 2007?

```
gapminder_1957 <- gapminder %>% filter(year==1957)
head(gapminder_1957, 2)
```

```
# A tibble: 2 x 6
  country     continent  year lifeExp     pop gdpPercap
  <fct>       <fct>     <int>   <dbl>   <int>     <dbl>
1 Afghanistan Asia       1957    30.3 9240934      821.
2 Albania     Europe     1957    59.3 1476505     1942.
```

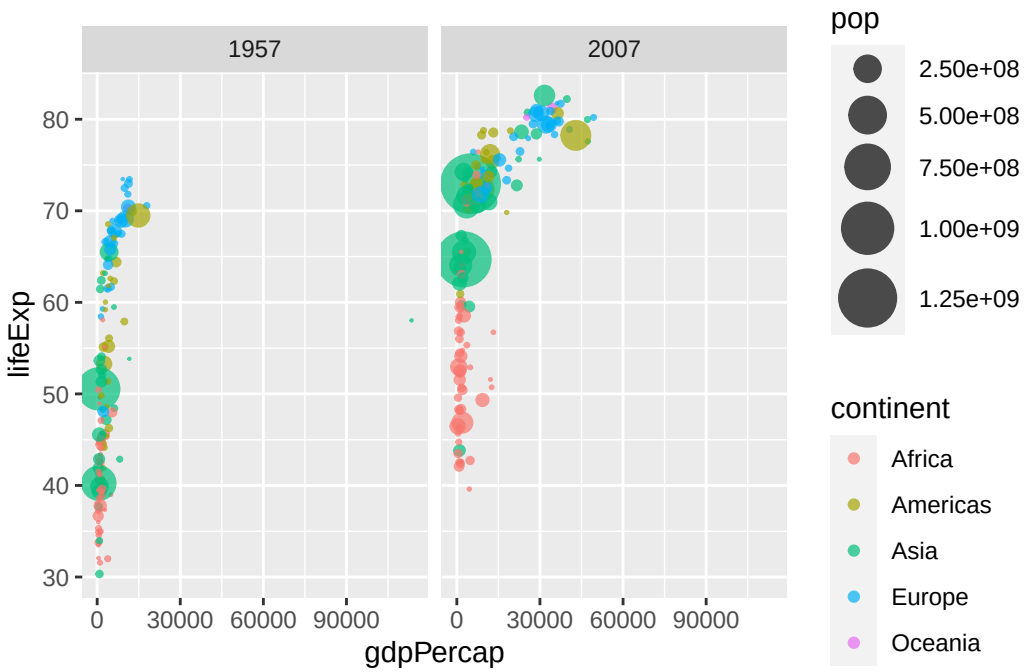
```
ggplot(gapminder_1957, aes(gdpPercap, lifeExp, color = continent, size = pop)) +
  geom_point(alpha = 0.7) +
  scale_size_area(max_size = 15)
```



Q. Do the same steps above but include 1957 and 2007 in your input dataset for ggplot(). You should now include the layer facet_wrap(~year) to produce the following plot:

```
gapminder_1957_2007 <- gapminder %>% filter(year==1957 | year==2007)

ggplot(gapminder_1957_2007) +
  geom_point(aes(x = gdpPercap, y = lifeExp, color=continent,
                 size = pop), alpha=0.7) +
  scale_size_area(max_size = 10) +
  facet_wrap(~year)
```



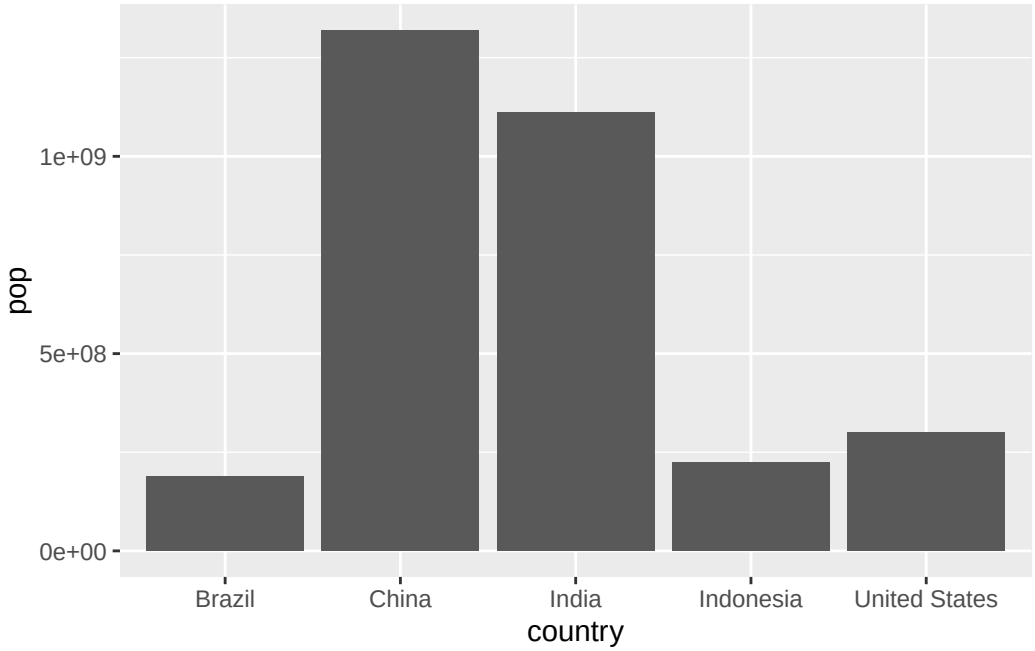
8. OPTIONAL: Bar Charts

```
gapminder_top5 <- gapminder %>%
  filter(year==2007) %>%
  arrange(desc(pop)) %>%
  top_n(5, pop)

gapminder_top5
```

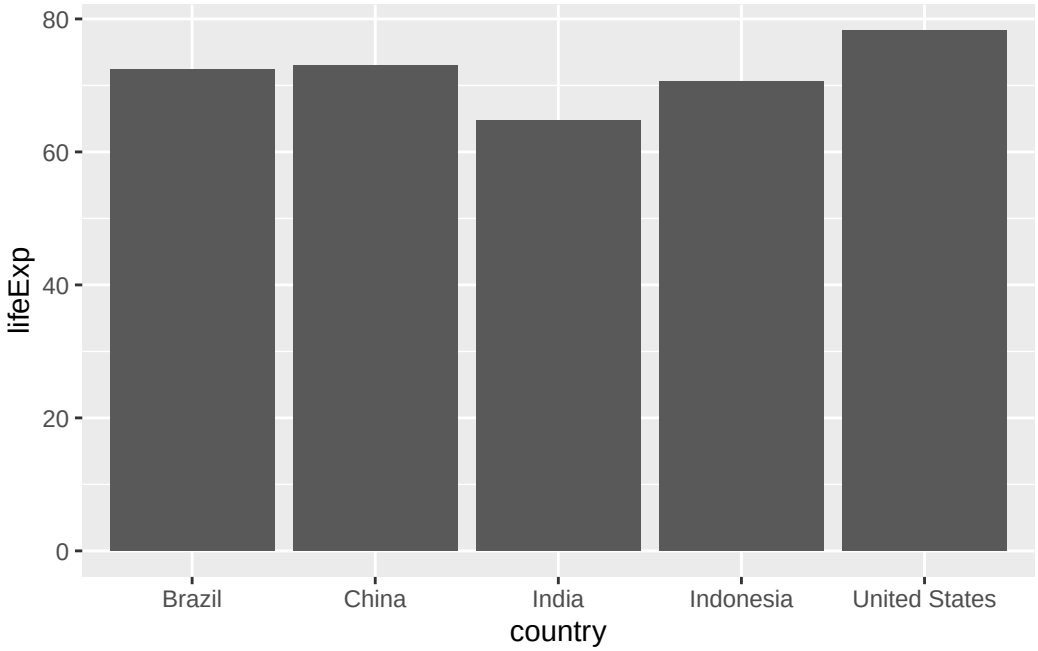
```
# A tibble: 5 x 6
  country       continent  year lifeExp        pop gdpPercap
  <fct>         <fct>     <int>   <dbl>      <int>     <dbl>
1 China         Asia       2007    73.0 1318683096     4959.
2 India         Asia       2007    64.7 1110396331     2452.
3 United States Americas   2007    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 = pop))
```



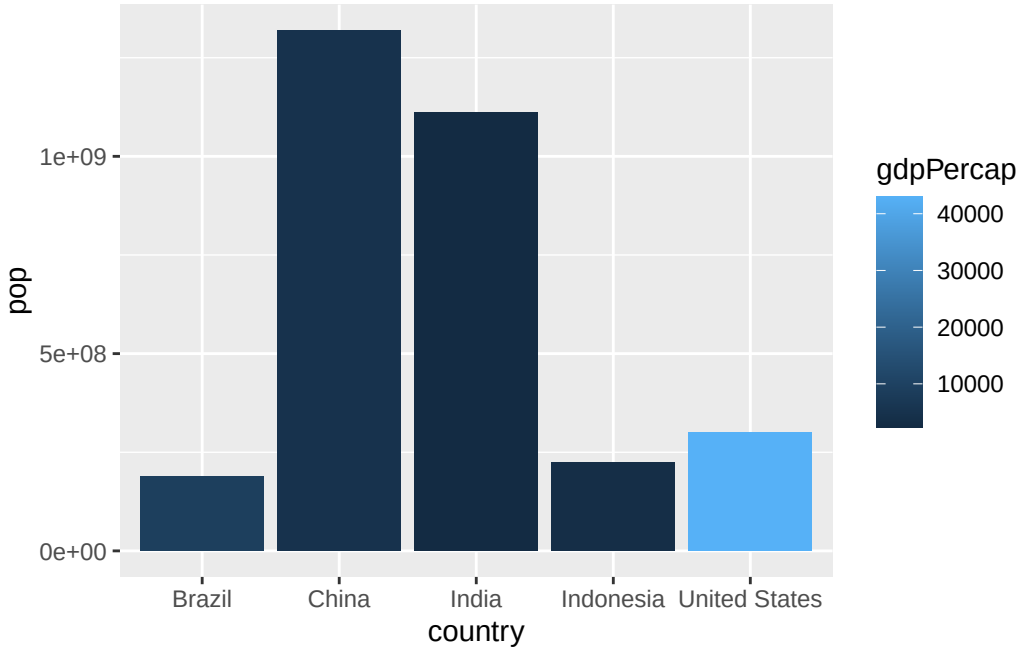
Q Create a bar chart showing the life expectancy of the five biggest countries by population in 2007.

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

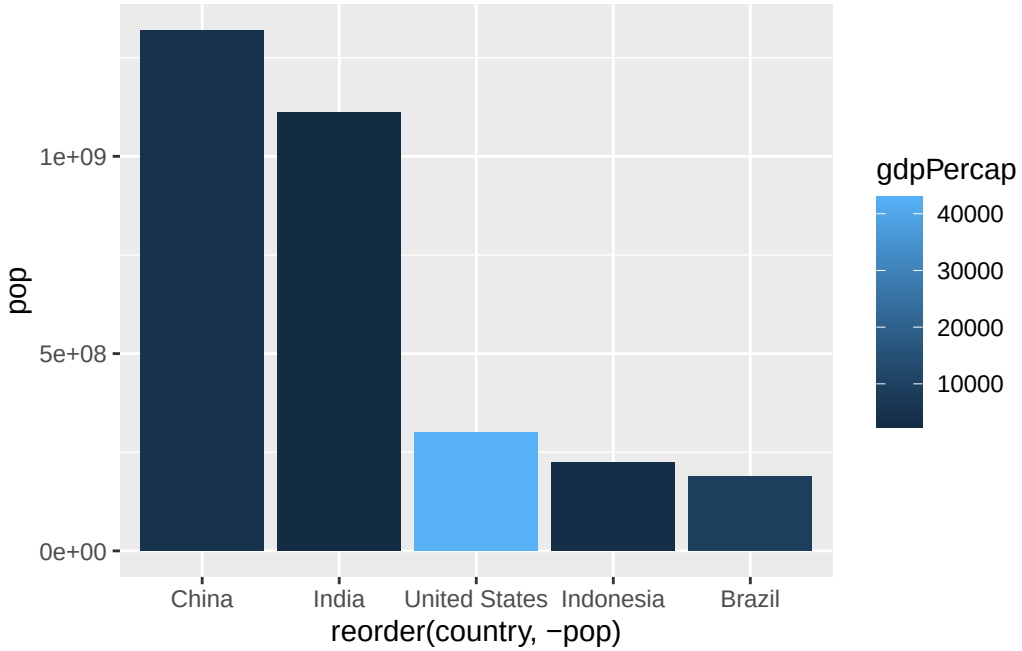


Q. Plot population size by country. Create a bar chart showing the population (in millions) of the five biggest countries by population in 2007.

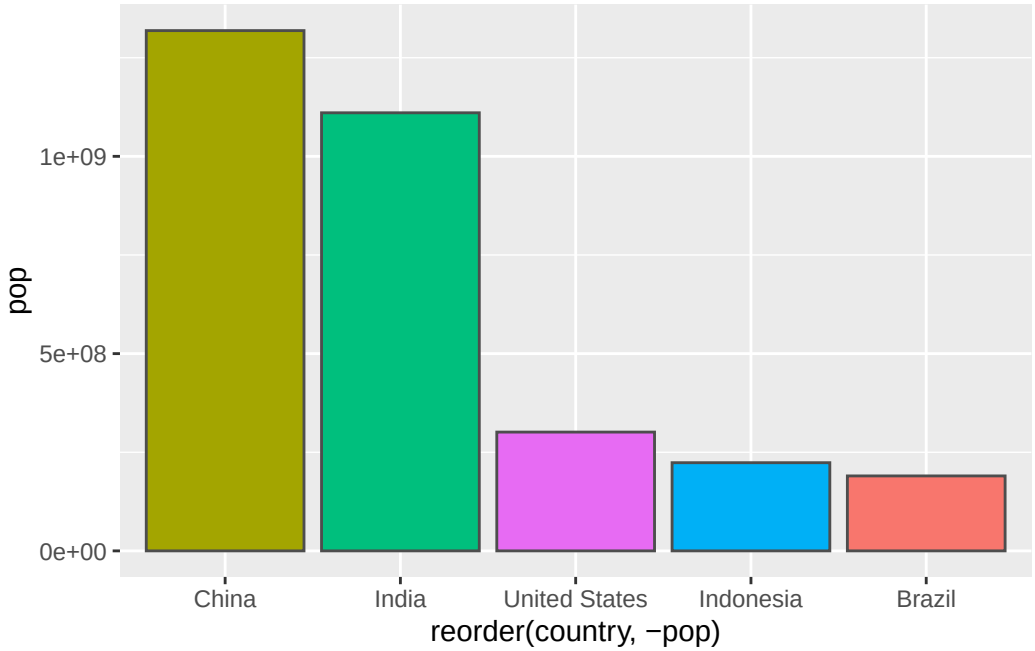
```
ggplot(gapminder_top5) +
  aes(x=country, y=pop, fill=gdpPercap) +
  geom_col()
```




```
ggplot(gapminder_top5) +
  aes(x=reorder(country, -pop), y=pop, fill=gdpPercap) +
  geom_col()
```




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


1e+09
5e+08
0e+00
pop
China
India
United States
Indonesia
Brazil
reorder(country, −pop)