class05

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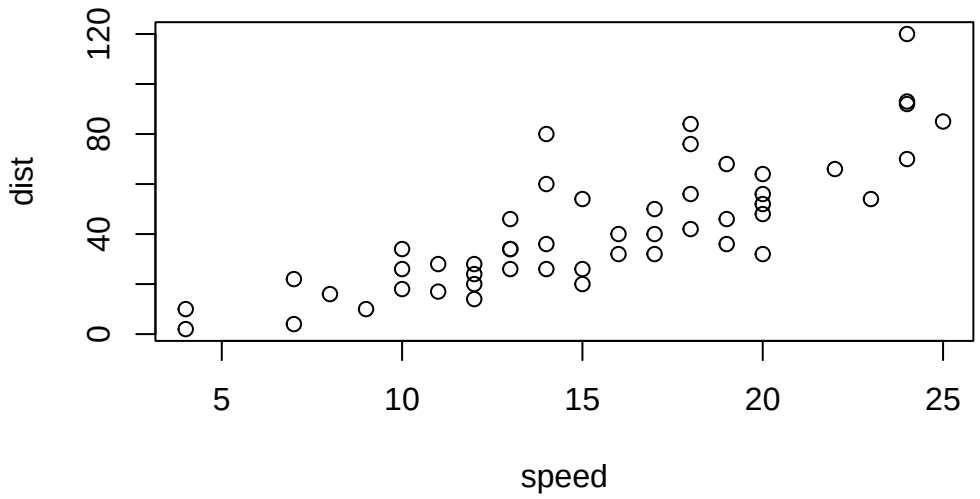
4/19/23

Base R Plotting

We are going to start by generating the plot of class 04. This code is plotting the **cars** dataset.

```
plot(cars)
```



Q1. For which phases is data visualization important in our scientific workflows?

Communication of results, EDA and detection of outliers, etc.

Q2. True or False? The ggplot2 package comes already installed with R?

False.

Ggplot2

First, we need to install the package. We do this by using the install.packages command.

```
# install.packages('ggplot2')
```

After that, we need to load the package.

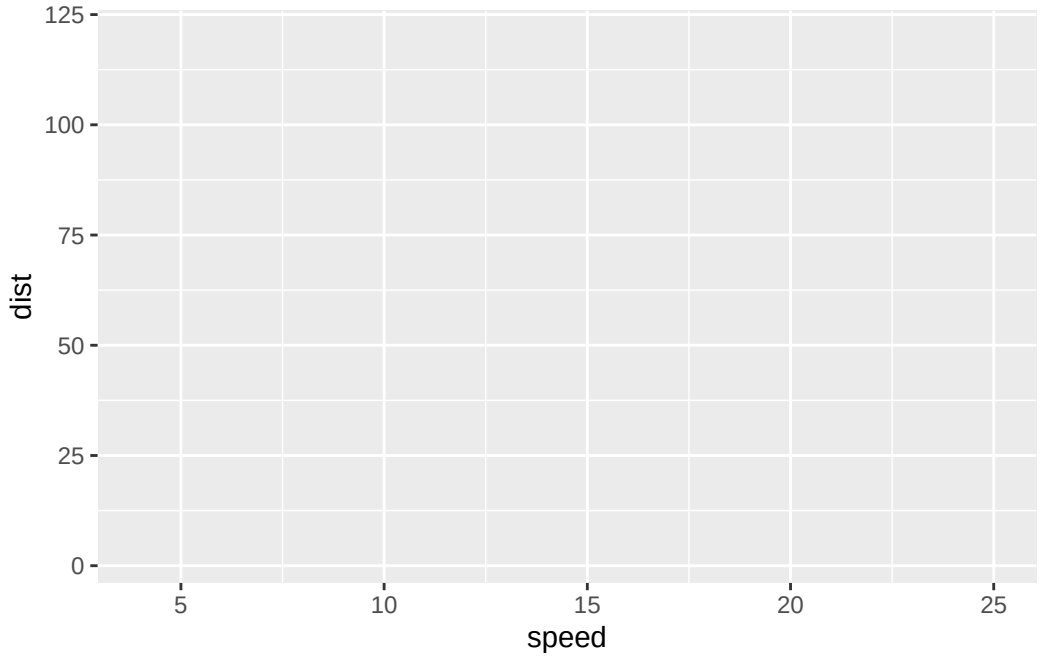
```
library(ggplot2)
```

We are going to build the plot of the cars dataframe by using ggplot.

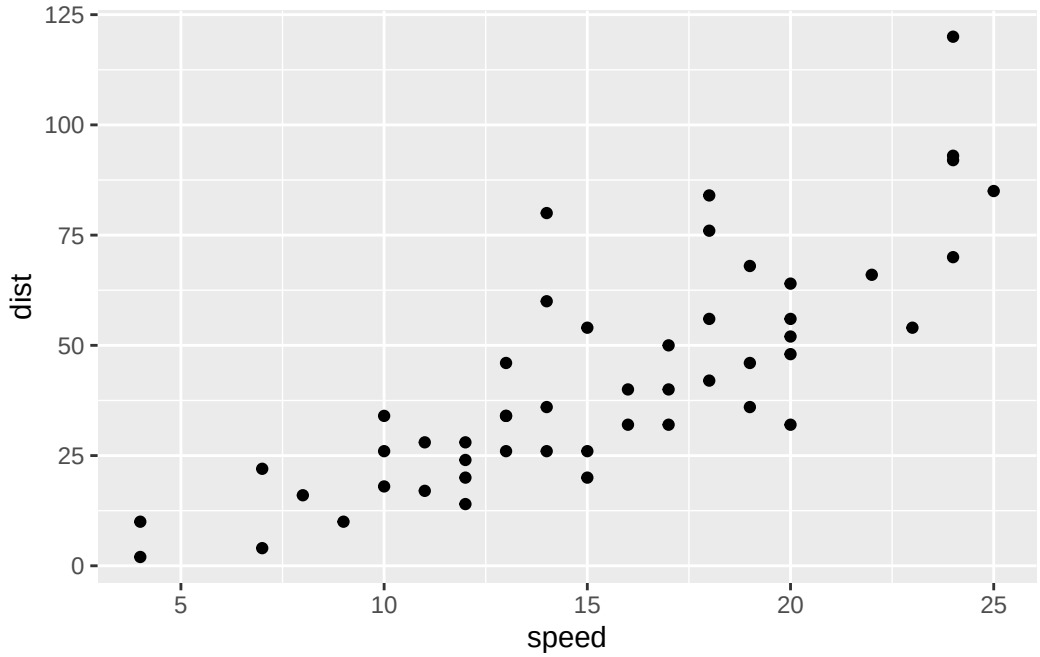
```
ggplot(data = cars)
```



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

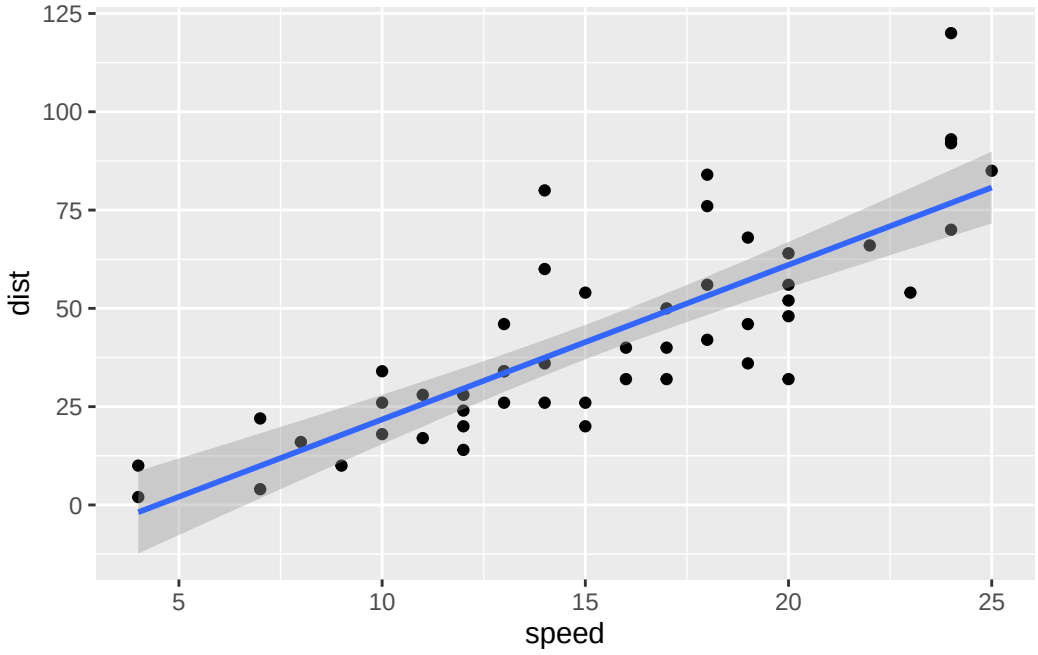



```
ggplot(data = cars) + aes(x=speed, y=dist) + geom_point()
```



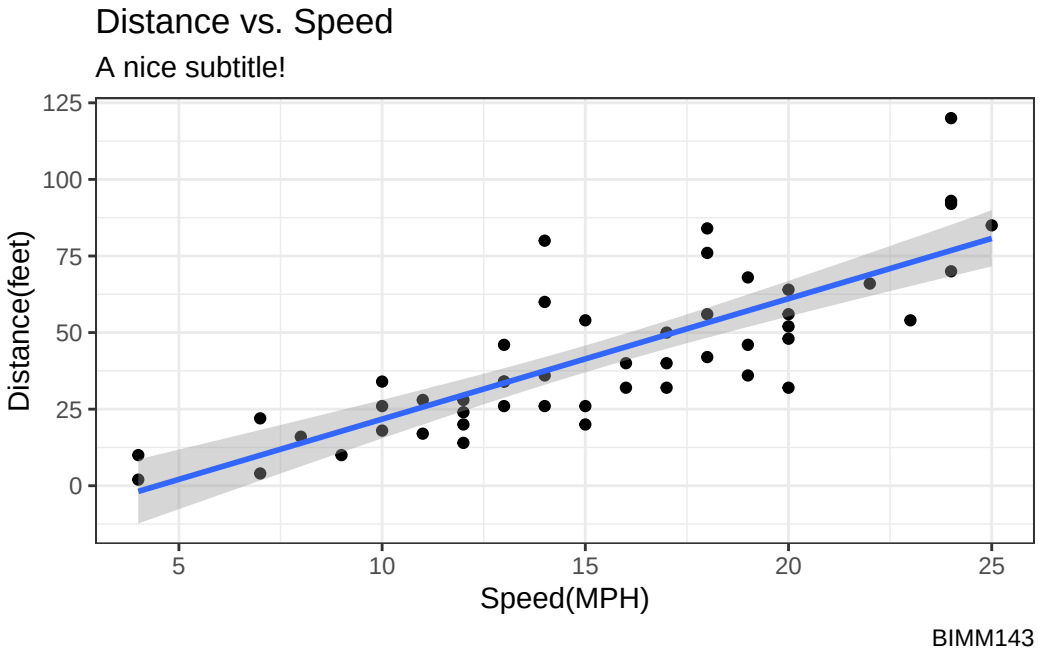
```
ggplot(data = cars) + aes(x=speed, y=dist) + geom_point() + geom_smooth(method = 'lm')
```

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




```
ggplot(data = cars) + aes(x=speed, y=dist) + geom_point() + geom_smooth(method = 'lm') + l
```

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



Q3. Which plot types are typically NOT used to compare distributions of numeric variables?

Network graphs.

Q4. Which statement about data visualization with ggplot2 is incorrect?

ggplot2 is the only way to create plots in R.

Q5. Which geometric layer should be used to create scatter plots in ggplot2?

geom_point()

Q6. 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?

Yes.

Q7. Argue with geom_smooth() to add a straight line from a linear model without the shaded standard error region?

add geom_smooth(method = 'lm')

Q8. 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?

Yes.

Plotting expression data

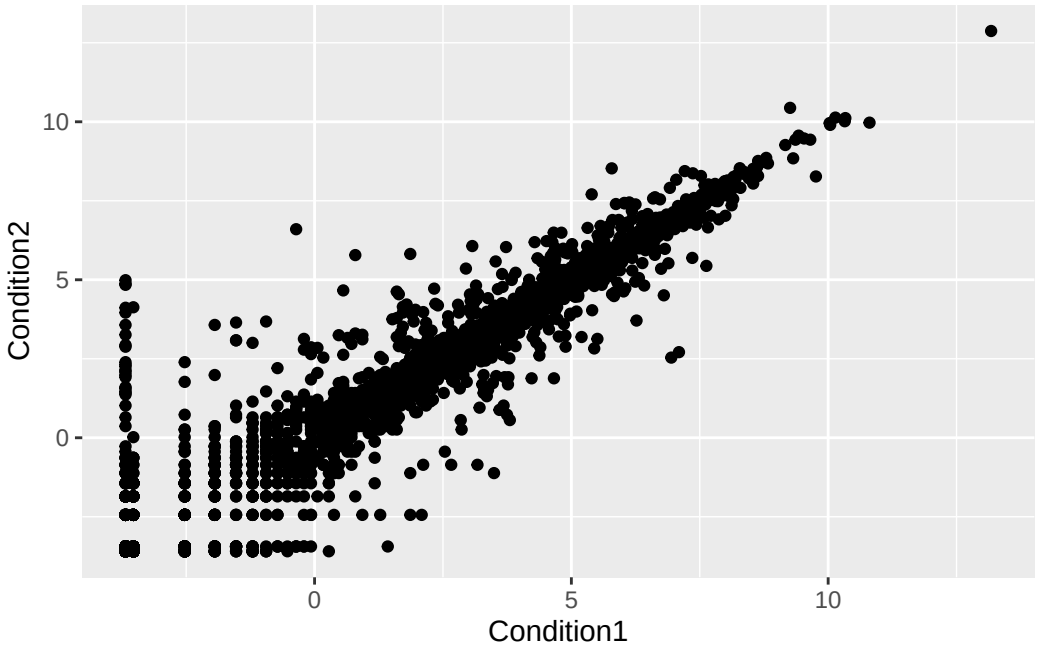
Loading the data from the URL.

```
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
```

Initial ggplot.

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



```
nrow(genes)
```

```
[1] 5196
```

```
ncol(genes)
```

```
[1] 4
```

```
colnames(genes)
```

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

```
table(genes[,'State'])
```

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

```
(table(genes[,'State']) / nrow(genes)) * 100
```

```
      down unchanging         up
  1.385681  96.170131   2.444188
```

Q9. 5196

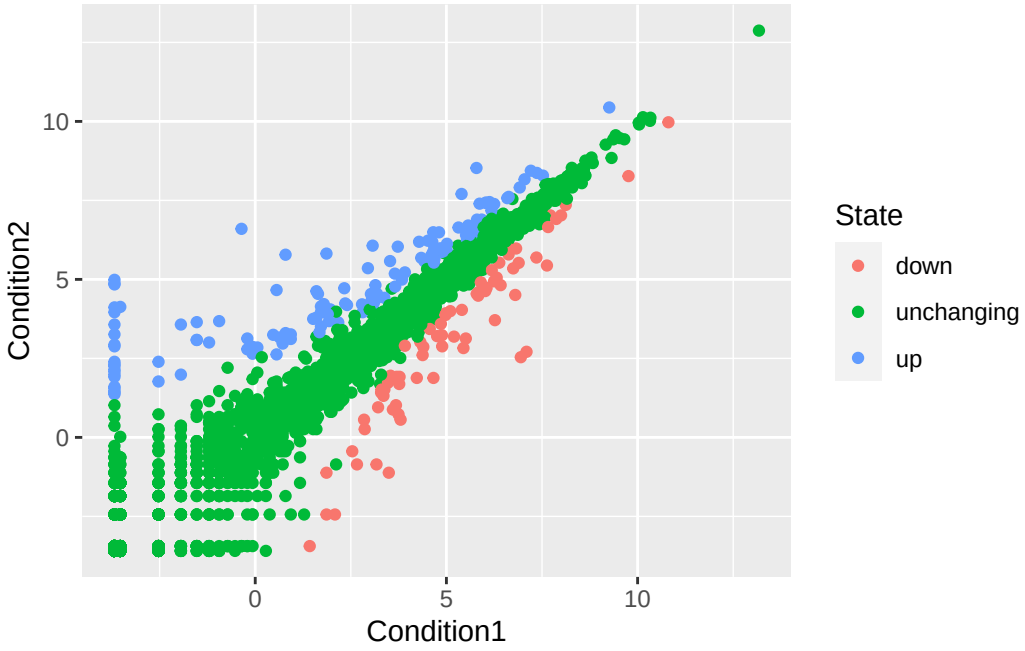
Q10. 4

Q11. 127

Q12. 2.44%

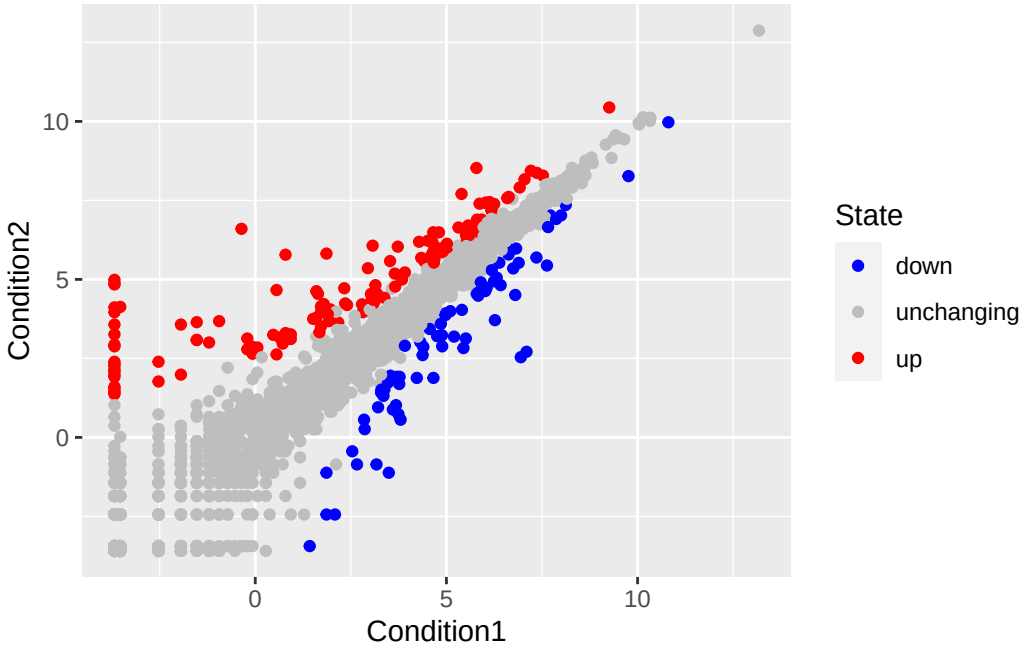
Adding color to the plot.

```
p1 <- ggplot(data = genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point()
p1
```



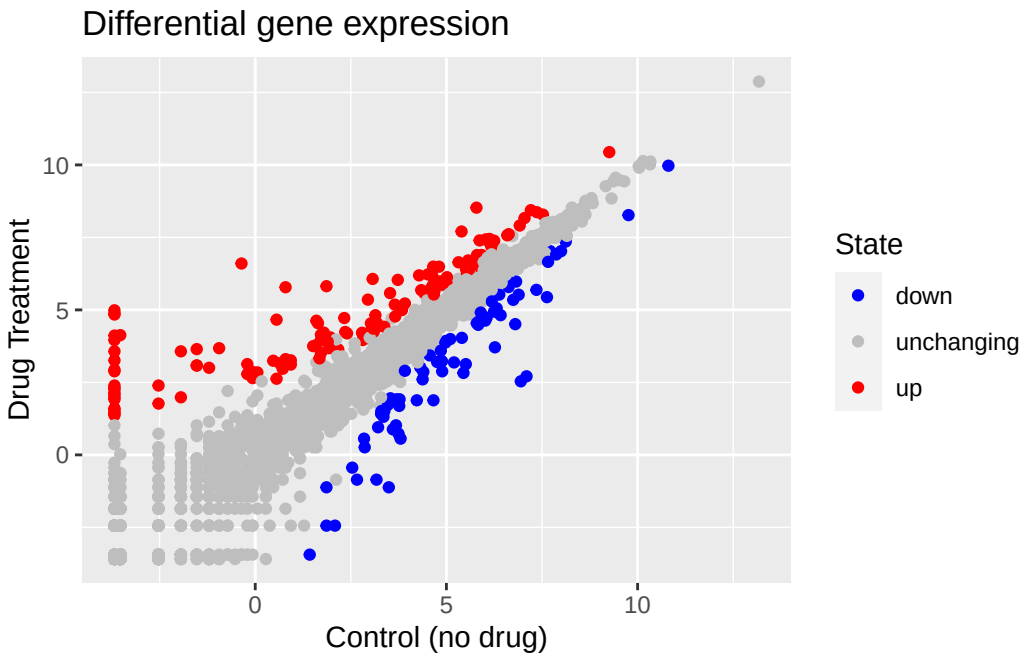
Let's change the color theme

```
p2 <- p1 + scale_color_manual(values = c("blue", "grey", "red"))
p2
```



Let's add some labels.

```
p2 + labs(title = 'Differential gene expression', x = 'Control (no drug)', y = 'Drug Treat
```



Optional extensions

Loading the dataset gapmider from the URL

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

Install package dplyr. Focus in on a single year, 2007.

```
# install.packages("dplyr")  ## un-comment to install if needed
library(dplyr)
```

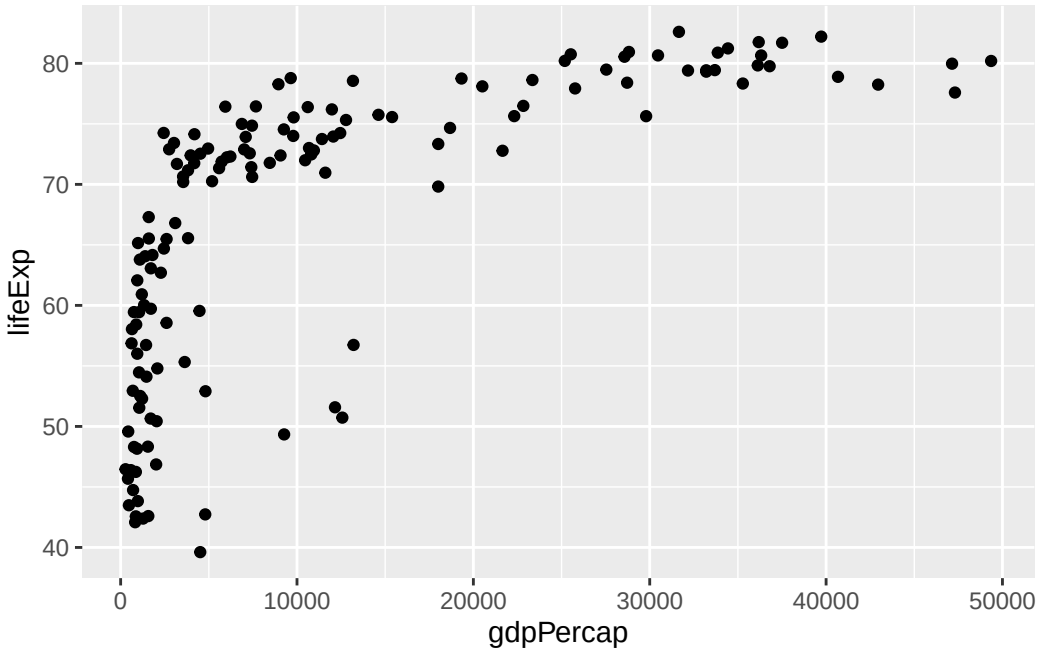
```
Attaching package: 'dplyr'

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)
```

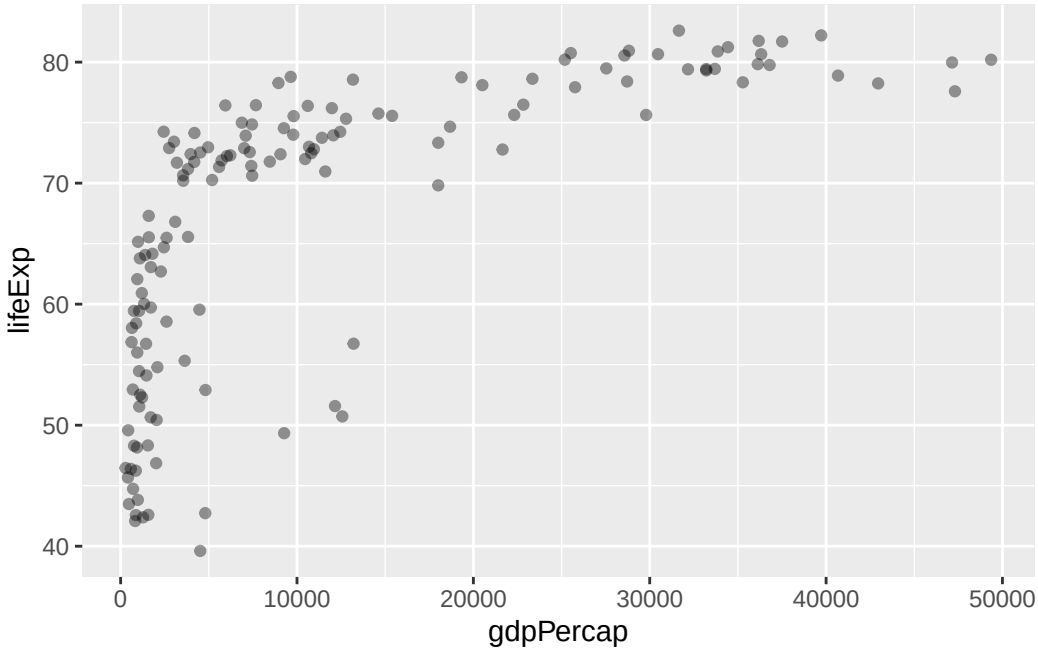
Let's consider the `gapminder_2007` dataset which contains the variables GDP per capita `gdpPercap` and life expectancy `lifeExp` for 142 countries in the year 2007

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



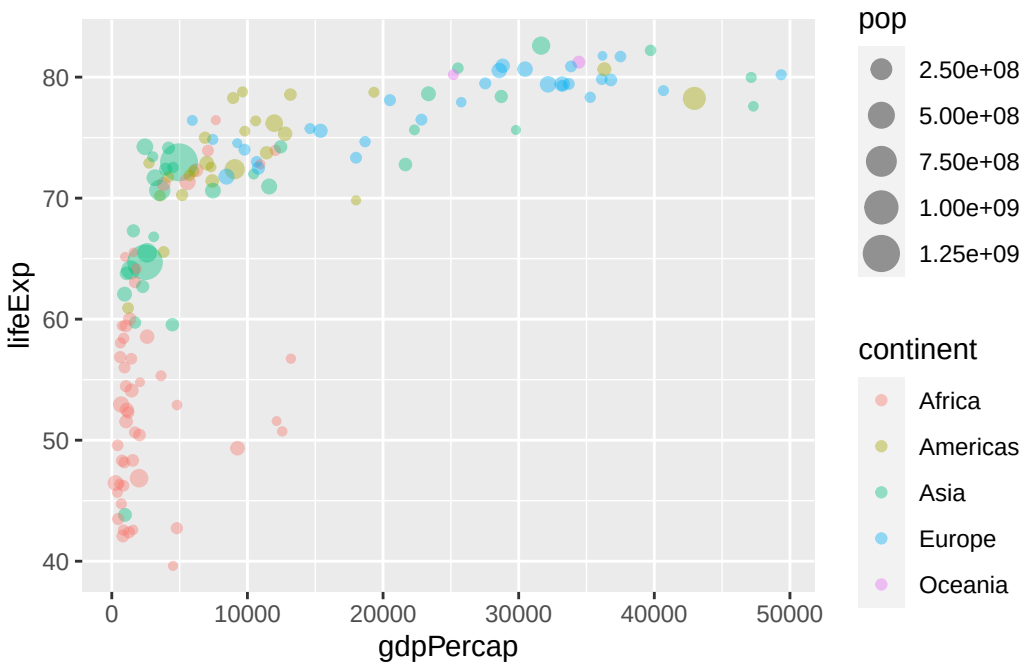
Make the points slightly transparent

```
ggplot(gapminder_2007) + aes(x=gdpPercap, y=lifeExp) + geom_point(alpha=0.4)
```



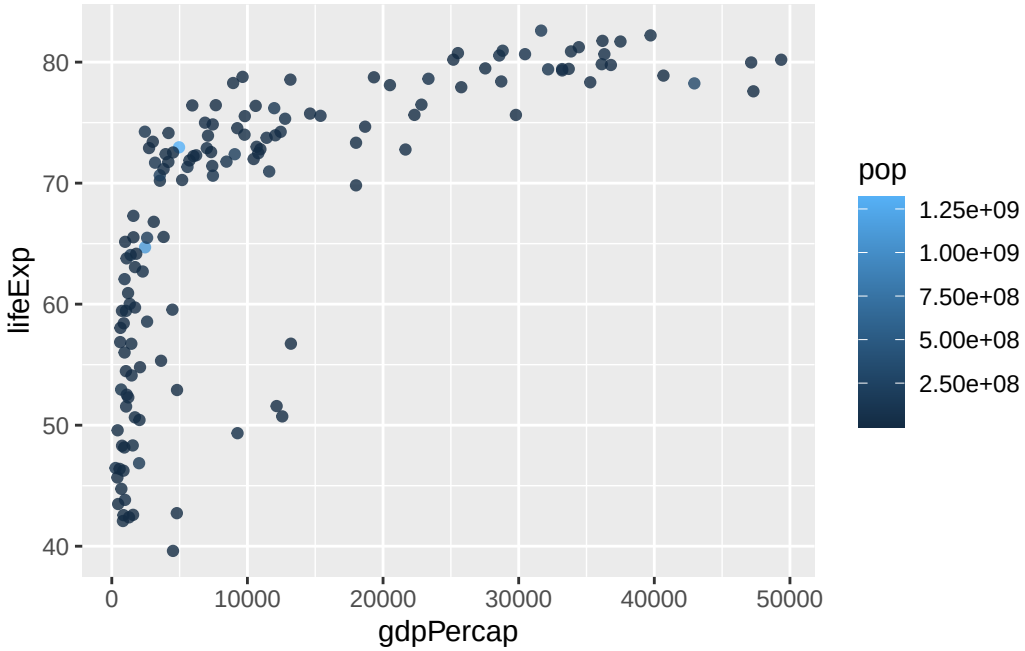
Add more variables like continent and population (pop)

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



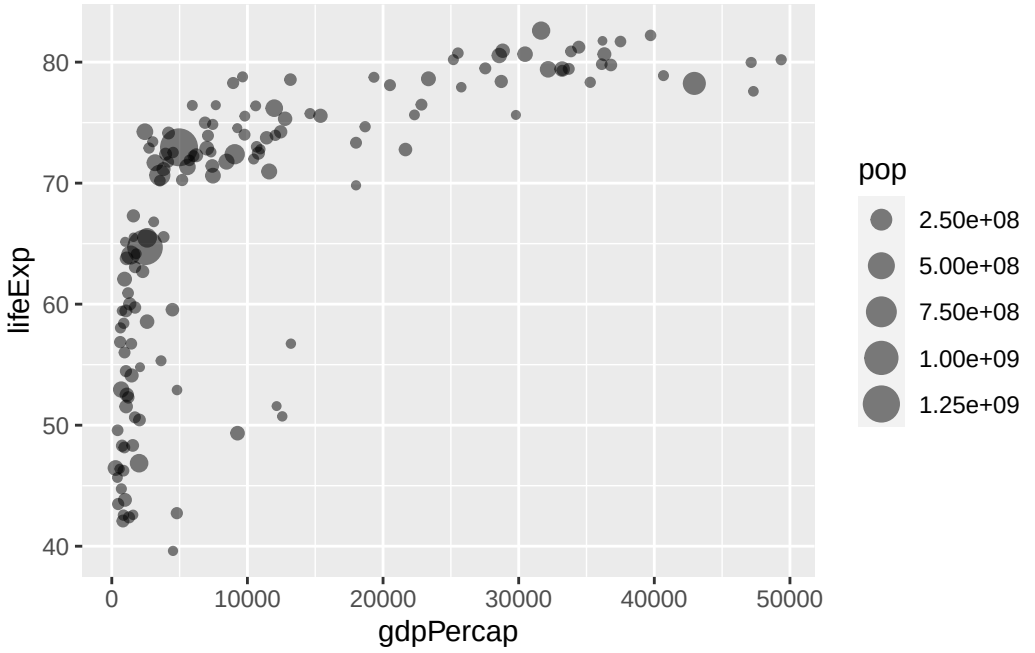
Let's see how the plot looks like if we color the points by the numeric variable population pop:

```
ggplot(gapminder_2007) + aes(x=gdpPercap, y=lifeExp, color=pop) + geom_point(alpha=0.8)
```



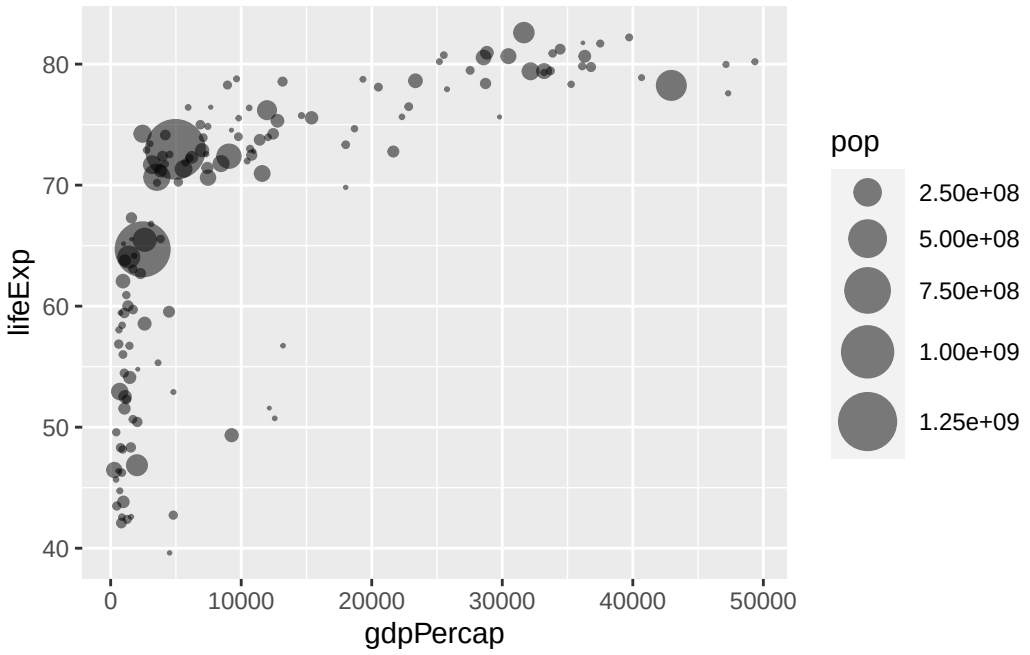
Adjust point size

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



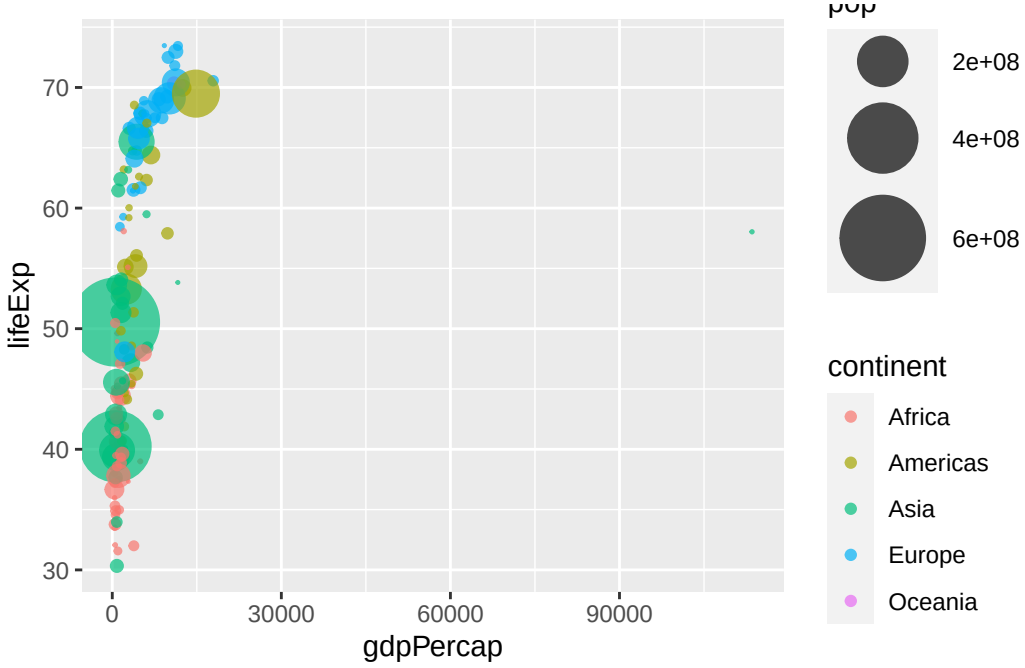
To reflect the actual population differences by the point size, we can use the scale_size_area() function.

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



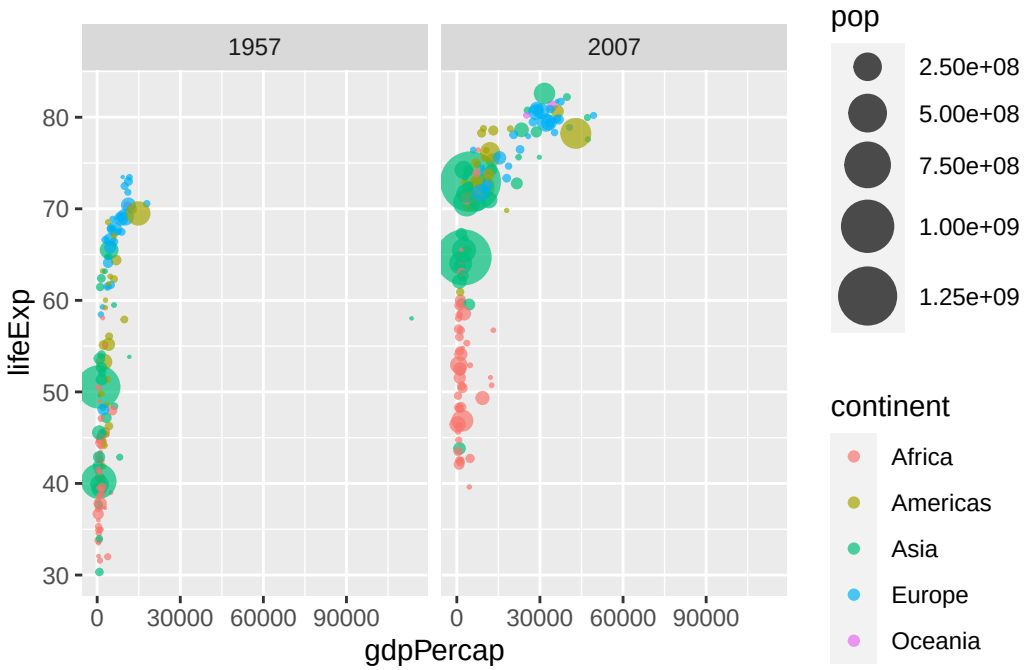
Produce my 1957 plot

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

# Filter the gapminder to include only the year 1957 and save the result as gapminder_1957
library(dplyr)
gapminder_1957 <- gapminder %>% filter(year==1957)

# Make a plot
# Create a scatter plot
# Use the color aesthetic to indicate each continent by a different color
# Use the size aesthetic to adjust the point size by the population pop
# Use scale_size_area() so that the point sizes reflect the actual population differences
ggplot(gapminder_1957) + aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) + geom_poi
```



Include 1957 and 2007 in the plot

```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)
ggplot(gapminder_1957) + geom_point(aes(x=gdpPercap, y=lifeExp, color=continent, size=pop,
```



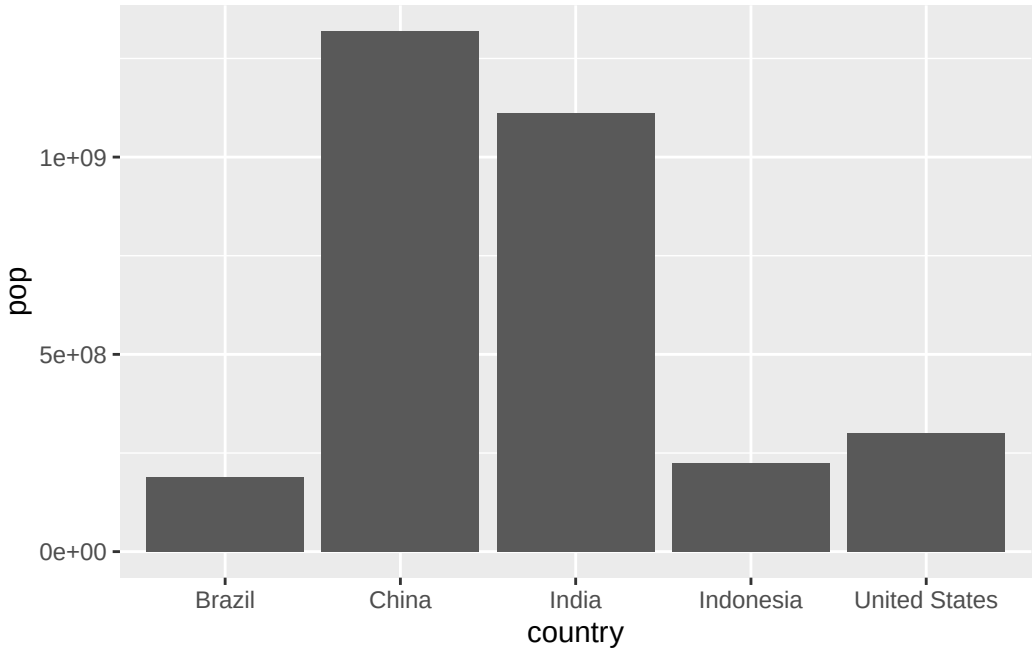
Bar Chart

Creat a bar chart with the gapminder_top5. It contains population (in millions) and life expectancy data for the biggest countries by population in 2007.

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

# Filter the gapminder to include only the year 1957 and save the result as gapminder_1957
library(dplyr)
gapminder_top5 <- gapminder %>% filter(year==2007) %>% arrange(desc(pop)) %>% top_n(5, pop
gapminder_top5
```

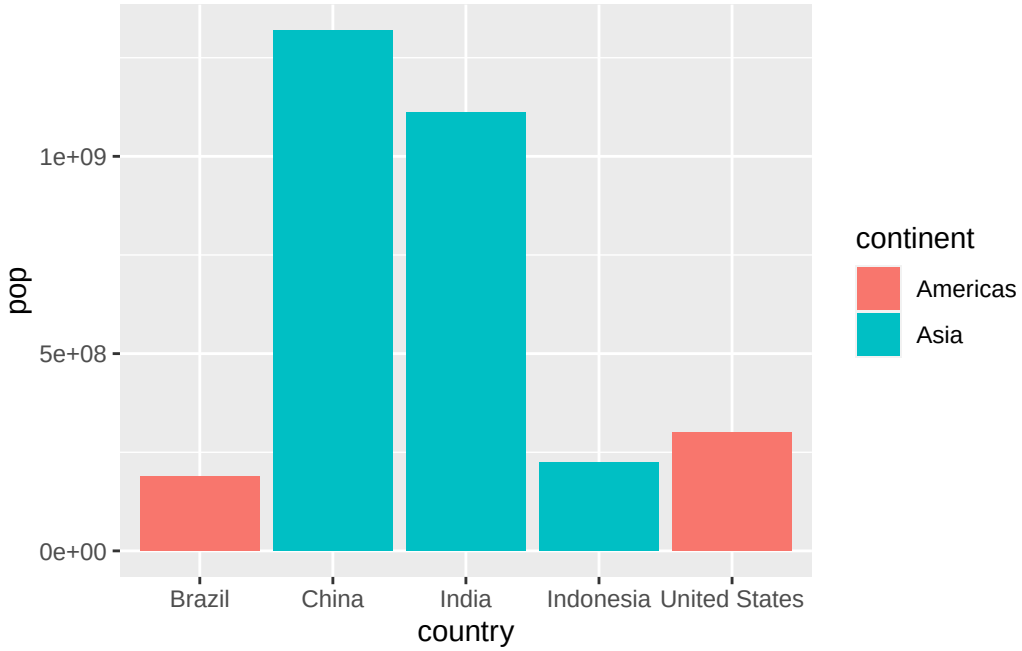
```
        country continent year lifeExp        pop gdpPercap
1         China      Asia 2007  72.961 1318683096  4959.115
2         India      Asia 2007  64.698 1110396331  2452.210
3 United States  Americas 2007  78.242  301139947 42951.653
4     Indonesia      Asia 2007  70.650  223547000  3540.652
5        Brazil  Americas 2007  72.390  190010647  9065.801
```

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



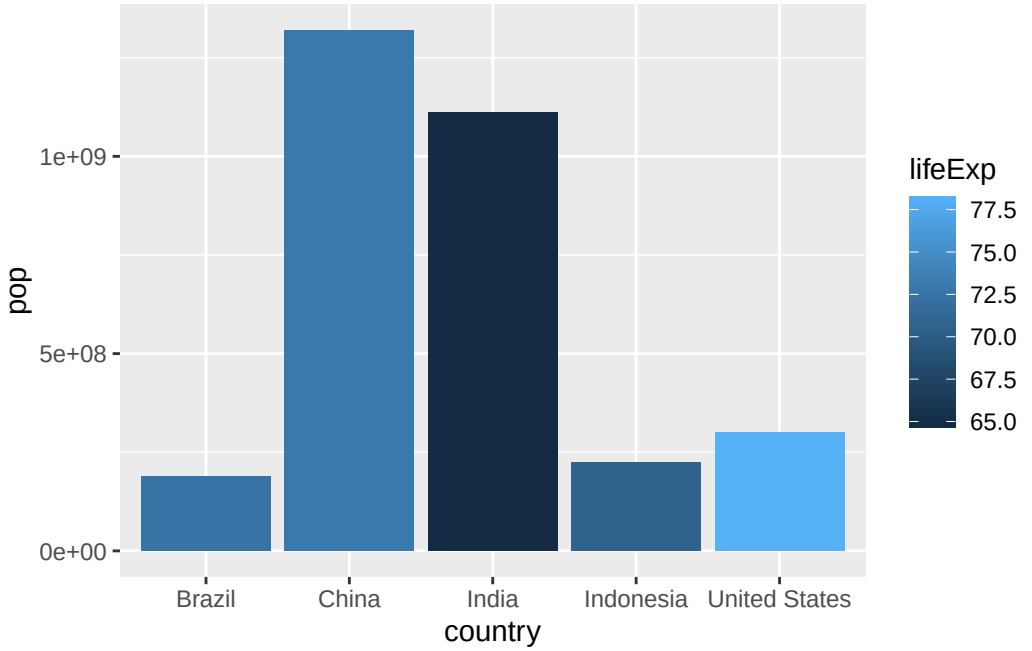
Fill bars with color

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



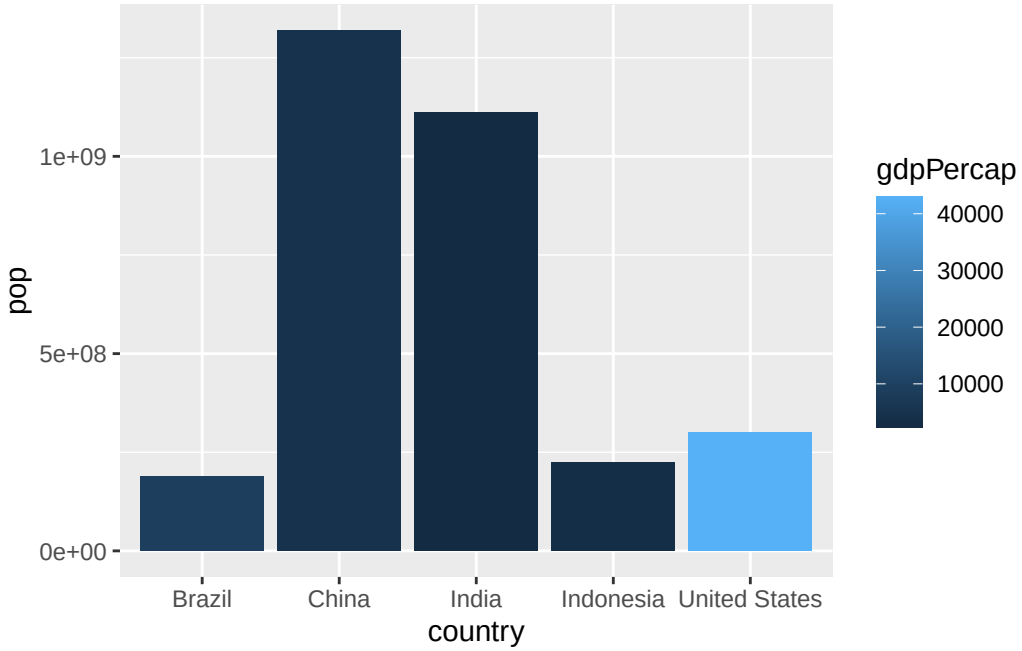
See what happens if we use a numeric variable like life expectancy lifeExp instead of the categorical variable continent.

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



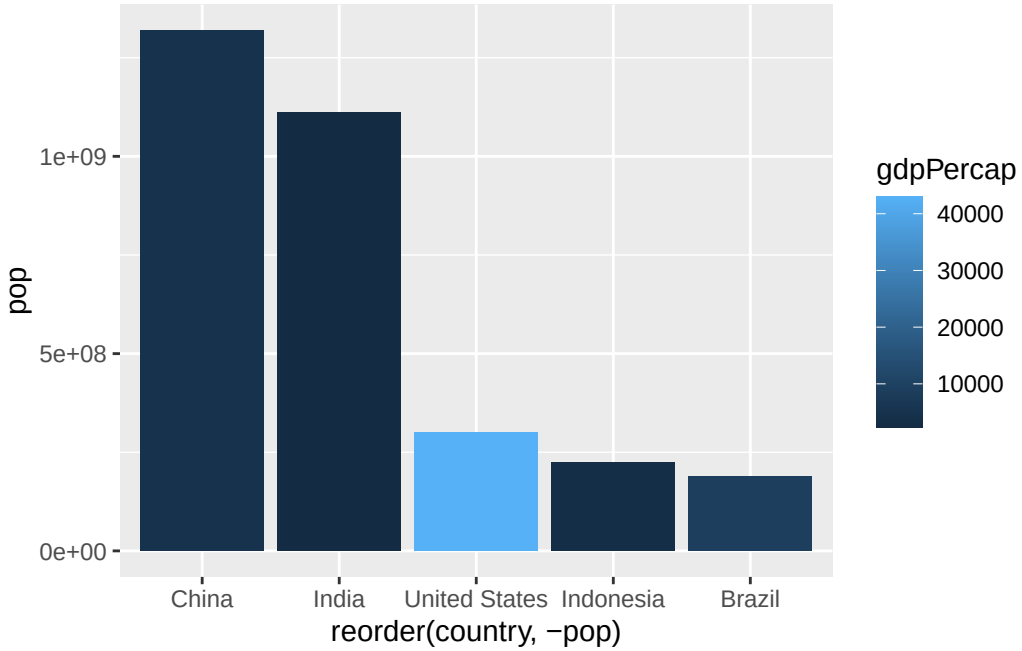
Plot population size by country. Use the GDP per capita gdpPercap as fill aesthetic

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



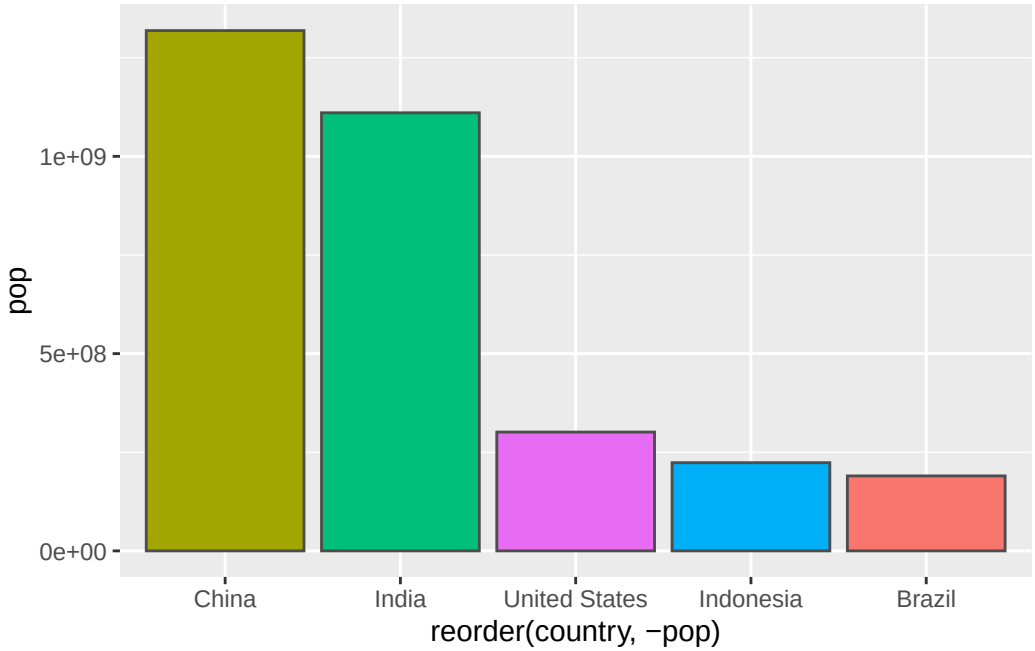
Change the order of the bars

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



Fill by counrty

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


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