

Class 5: Data Viz with ggplot

Yaniv Iny (PID:A18090586)

intro to ggplot

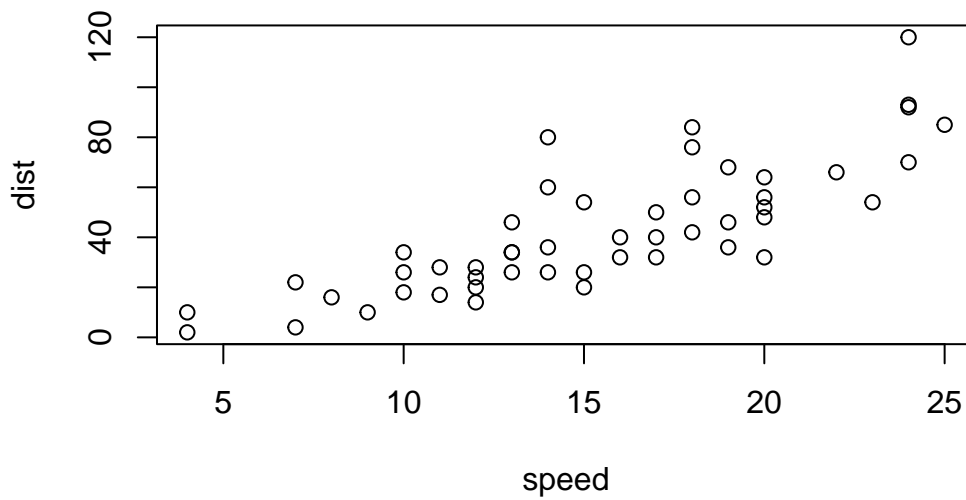
There are many graphic systems in R (ways to make plots and figures). These include “base” R plots. Today we will focus mostly on the **ggplot2** package

Lets start with a plot of a simple built in dataset called **cars**.

```
head(cars)
```

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

```
plot(cars)
```



Let's see how we can make this figure using **ggplot**. First I need to install this package on my computer. To install any R package I use the function `install.packages()`

I will run `install.packages("ggplot2")` in my R console not this quarto document so that it doesn't reinstall every time I render.

Before I can use any functions from add on packages I need to load the package from my "library()" with the `library(ggplot2)`

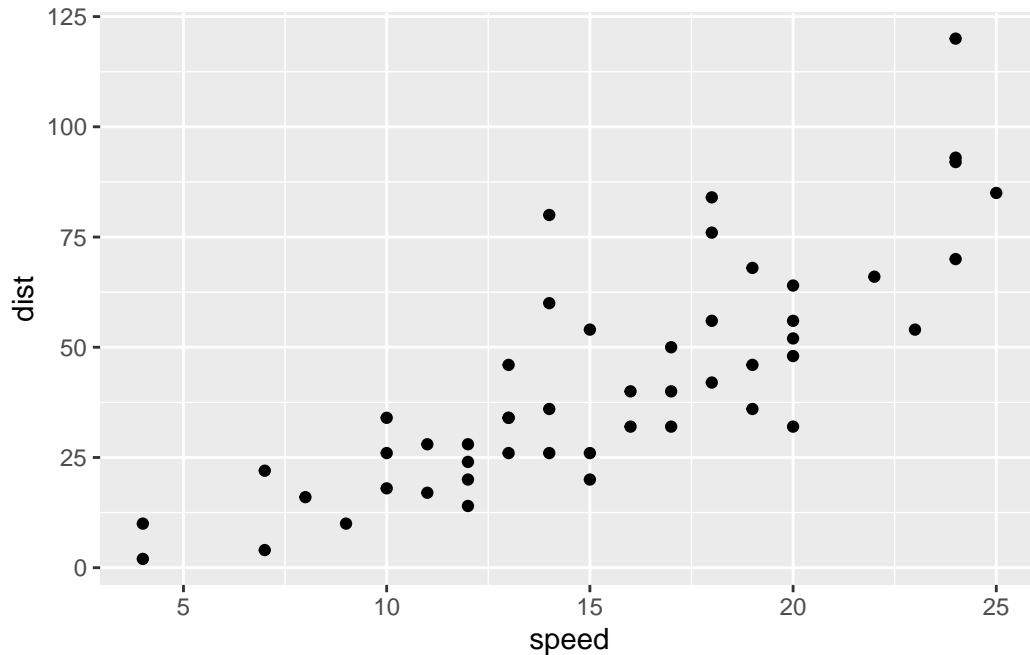
```
library(ggplot2)
ggplot(cars)
```



All ggplot figures have at least 3 things (called layers). These include:

- **Data** (the input dataset I want to plot from),
- **aes** (the aesthetic mapping of the data to my plot),
- **geoms** (the `geom_point()`, `geom_line()` etc, that I want to draw)

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



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

Network graphs

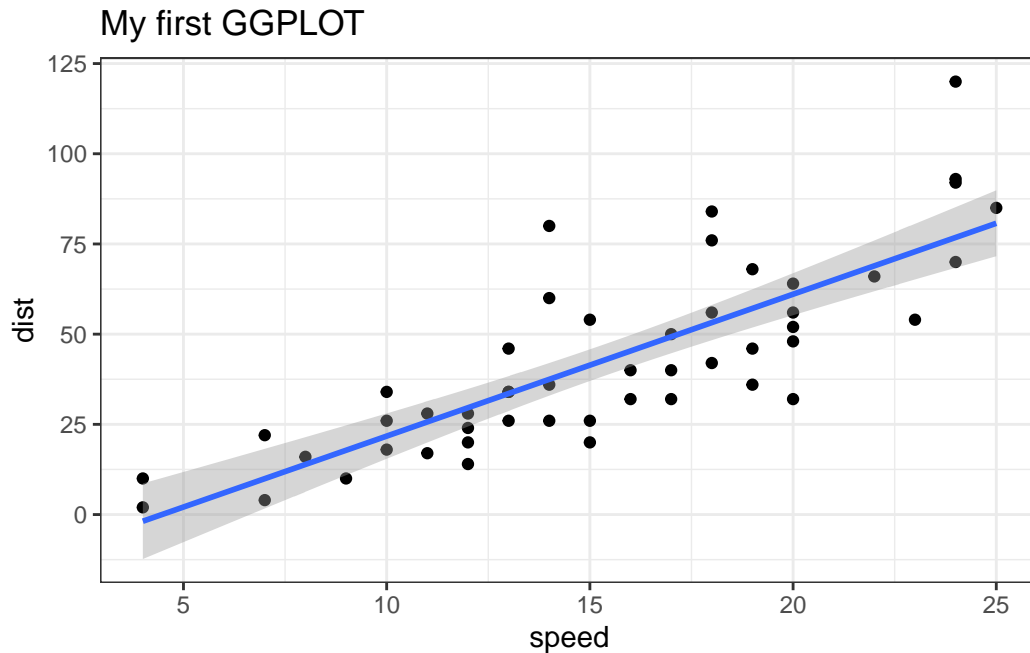
Q. Which statement about data visualization with ggplot2 is incorrect? **ggplot2 is the only way to create plots in R**

Q. Which geometric layer should be used to create scatter plots in ggplot2? **geom_point()**

Lets add a line to show the relationship here:

```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()+
  geom_smooth(method="lm") + theme_bw()+
  labs(title= "My first GGPlot")
```

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



Q1 which geometric layer should be used to create scatter plots in ggplot2?

`geom_point`

The code to read the dataset

```
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

Q. Use the `nrow()` function to find out how many genes are in this dataset. What is your answer? **5196**

Q. Use the `colnames()` function and the `ncol()` function on the genes data frame to find out what the column names are (we will need these later) and how many columns there are. How many columns did you find? **4**

Q. Use the `table()` function on the `State` column of this `data.frame` to find out how many 'up' regulated genes there are. What is your answer? **127**

Q. Using your values above and 2 significant figures. What fraction of total genes is up-regulated in this dataset? **2.44**

how many genes are in this dataset?

```
nrow(genes)
```

```
[1] 5196
```

```
ncol(genes)
```

```
[1] 4
```

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

down	unchanging	up
72	4997	127

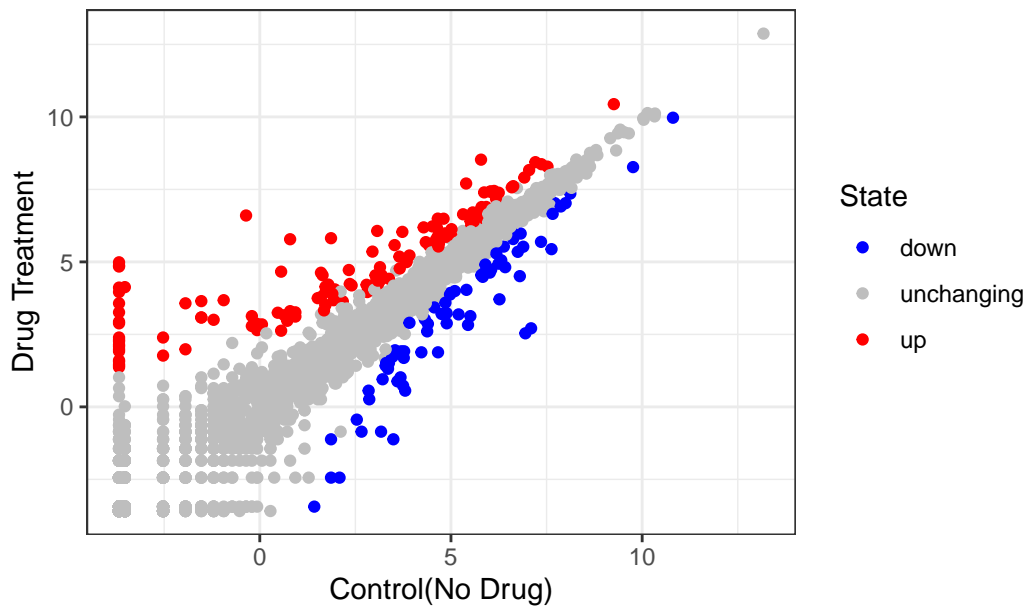
```
round( table(genes$State)/nrow(genes) * 100, 2 )
```

down	unchanging	up
1.39	96.17	2.44

A first plot of this dataset

```
ggplot(genes)+  
  aes(x=Condition1, y=Condition2, col=State) +  
  geom_point()+  
  labs(title="Gene Expresssion Changes Upon Drug Treatment",  
        x="Control(No Drug)",  
        y="Drug Treatment") +  
  theme_bw()+  
  scale_colour_manual(values=c("blue","gray","red"))
```

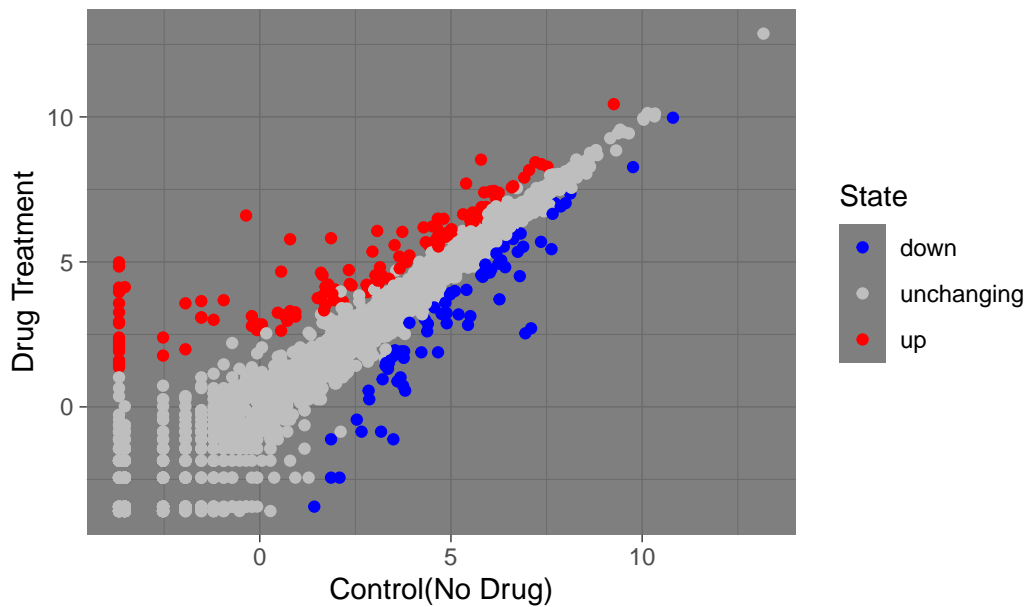
Gene Expressionssion Changes Upon Drug Treatment



```
p <- ggplot(genes)+  
  aes(x=Condition1, y=Condition2, col=State) +  
  geom_point()+  
  labs(title="Gene Expresssion Changes Upon Drug Treatment",  
        x="Control(No Drug)",  
        y="Drug Treatment") +  
  theme_bw()+  
  scale_colour_manual(values=c("blue","gray","red"))
```

```
p + theme_dark()
```

Gene Expressionssion Changes Upon Drug Treatment



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

gapminder <- read.delim(url)

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

Attaching package: 'dplyr'

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

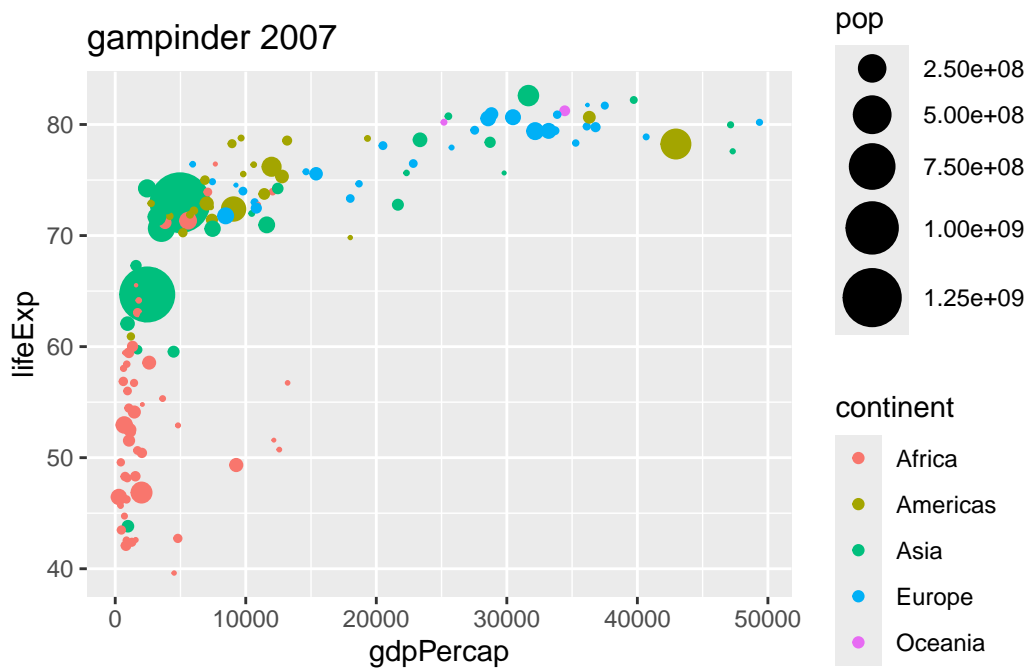
filter, lag

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

intersect, setdiff, setequal, union


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

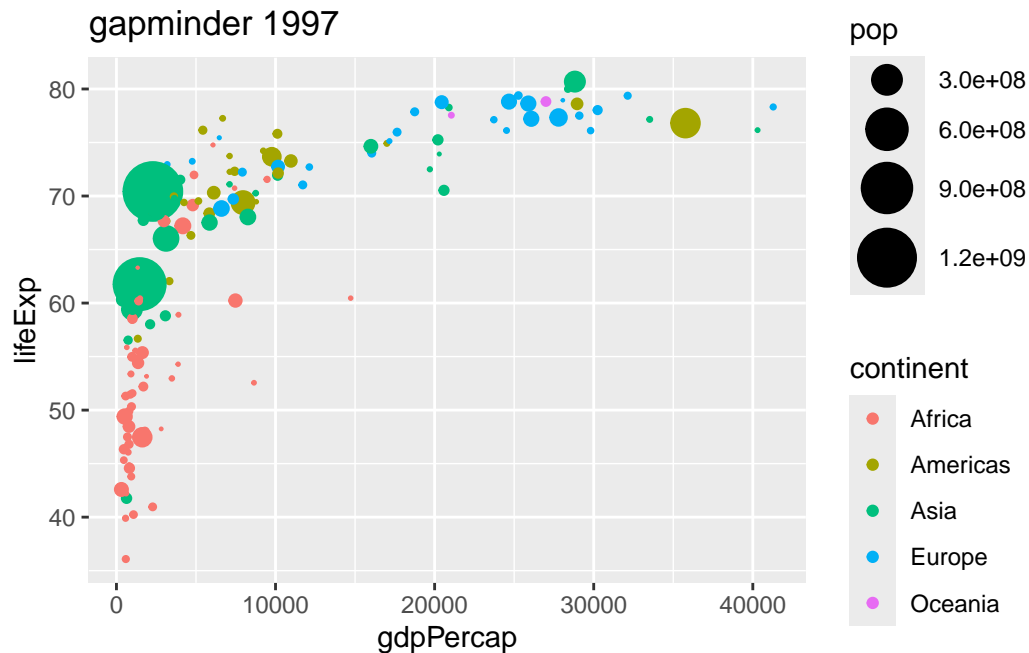
```
ggplot(gapminder_2007) +  
  aes(x=gdpPercap, y=lifeExp,color=continent, size=pop) +  
  geom_point(alpha=1.0)+  
  scale_size_area(max_size = 10)+ labs(title= "gampinder 2007")
```



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

```
gapminder_1997 <- gapminder %>% filter(year==1997)
```

```
ggplot(gapminder_1997) +  
  aes(x=gdpPercap, y=lifeExp,color=continent, size=pop) +  
  geom_point(alpha=1.0)+  
  scale_size_area(max_size = 10)+ labs(title="gapminder 1997")
```

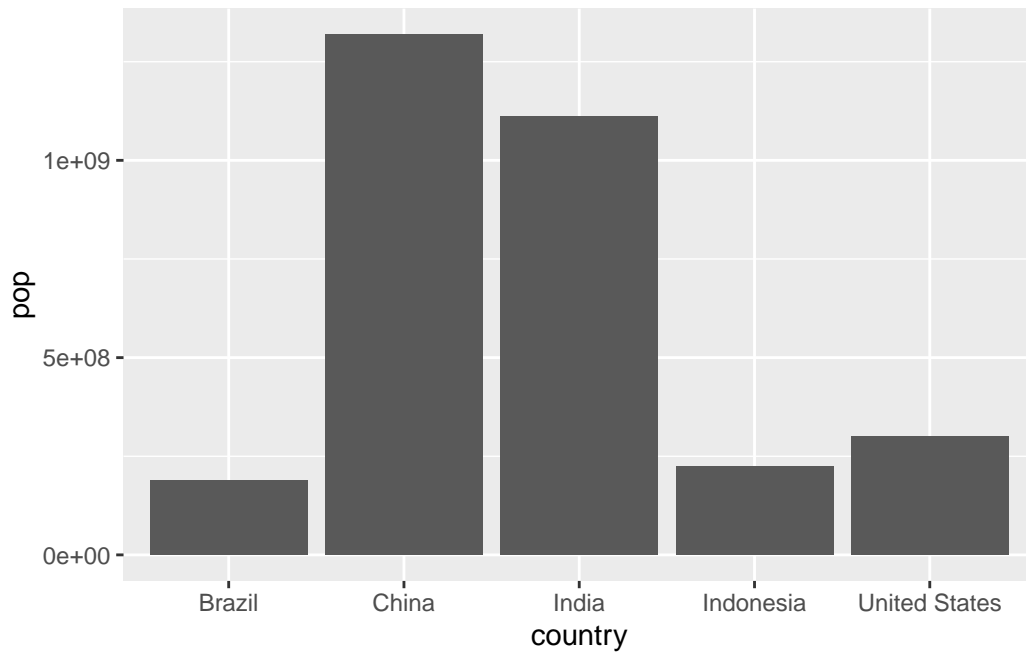


```
gapminder_top5 <- gapminder %>%
  filter(year==2007) %>%
  arrange(desc(pop)) %>%
  top_n(5, pop)

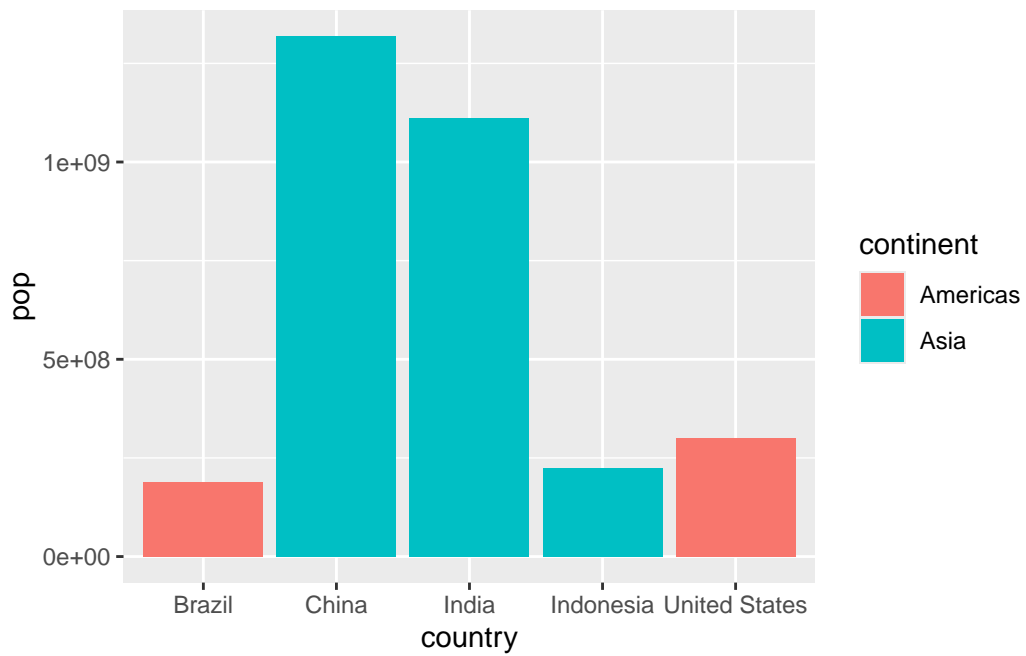
gapminder_top5
```

	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

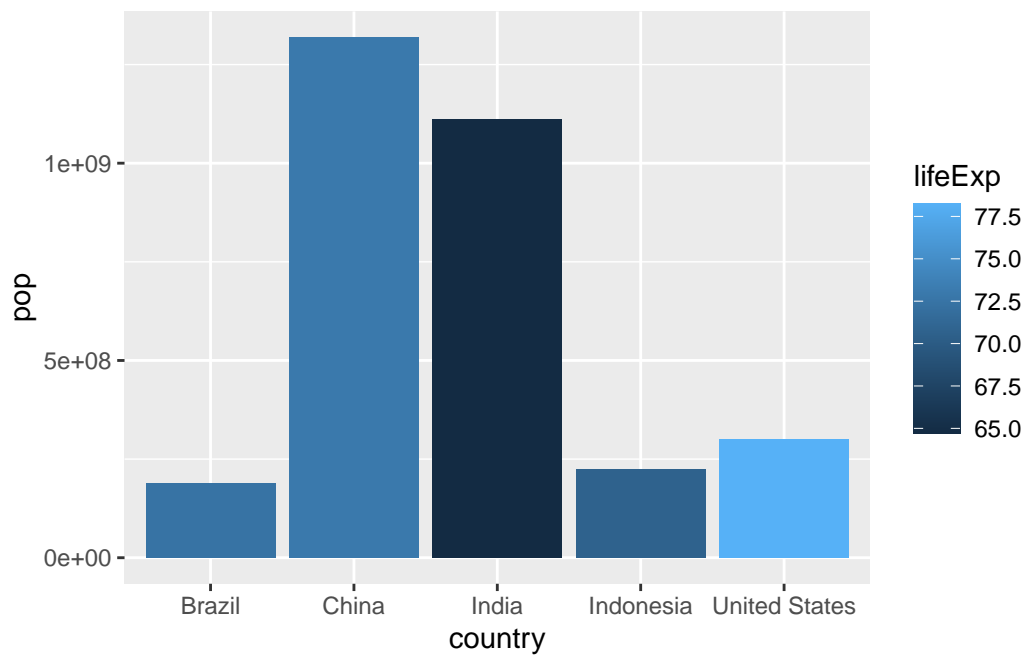
```
ggplot(gapminder_top5) +
  geom_col(aes(x = country, y = pop))
```



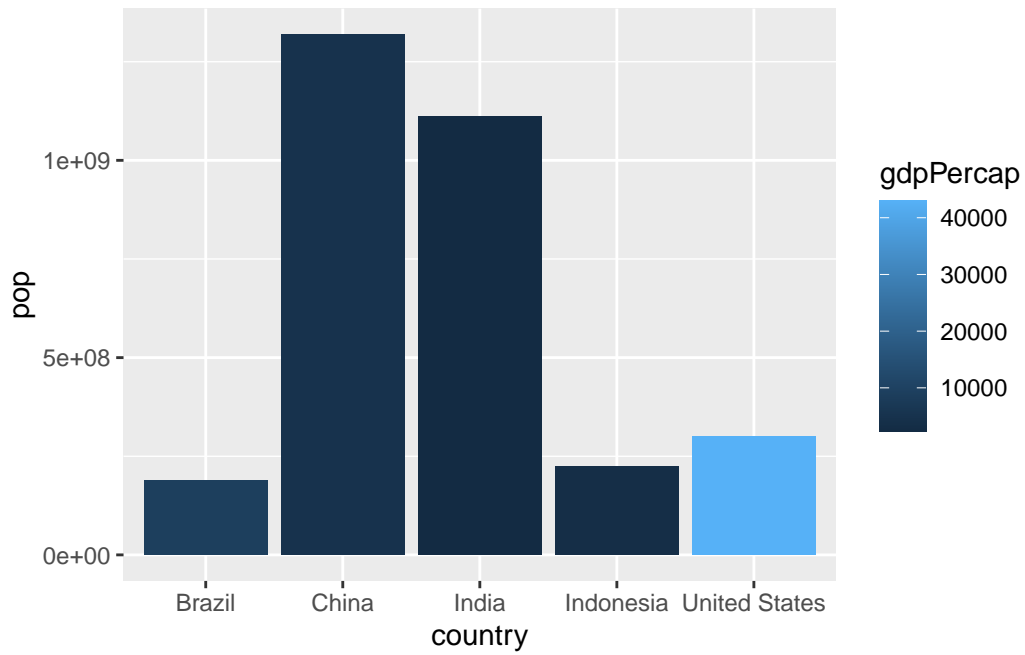
```
ggplot(gapminder_top5) +  
  geom_col(aes(x = country, y = pop, fill = continent))
```



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



```
ggplot(gapminder_top5) +  
  aes(x=country, 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")
```

