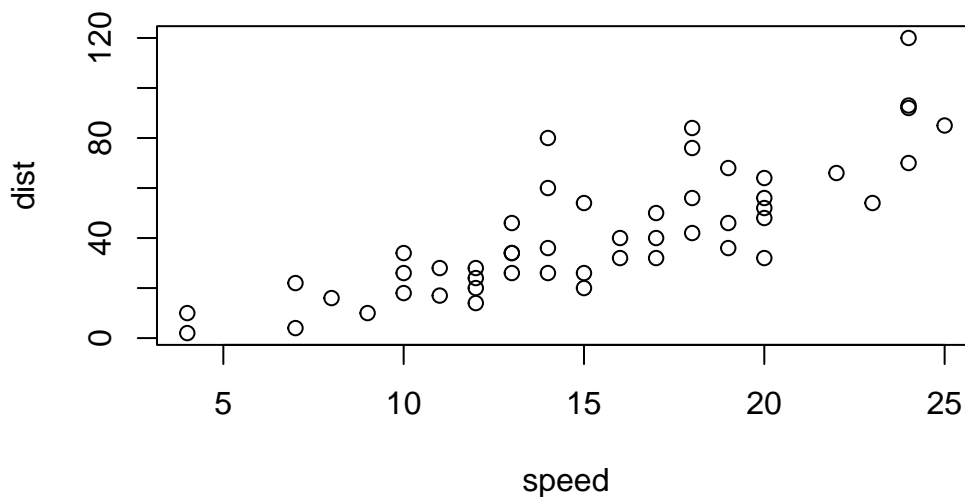


# Class 5: Data Visual with ggplot

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Ways to make figures in R: One of them that **comes with R** is the `plot()` function.

```
plot(cars)
```



A popular package for plots and figures is called **ggplot2**.

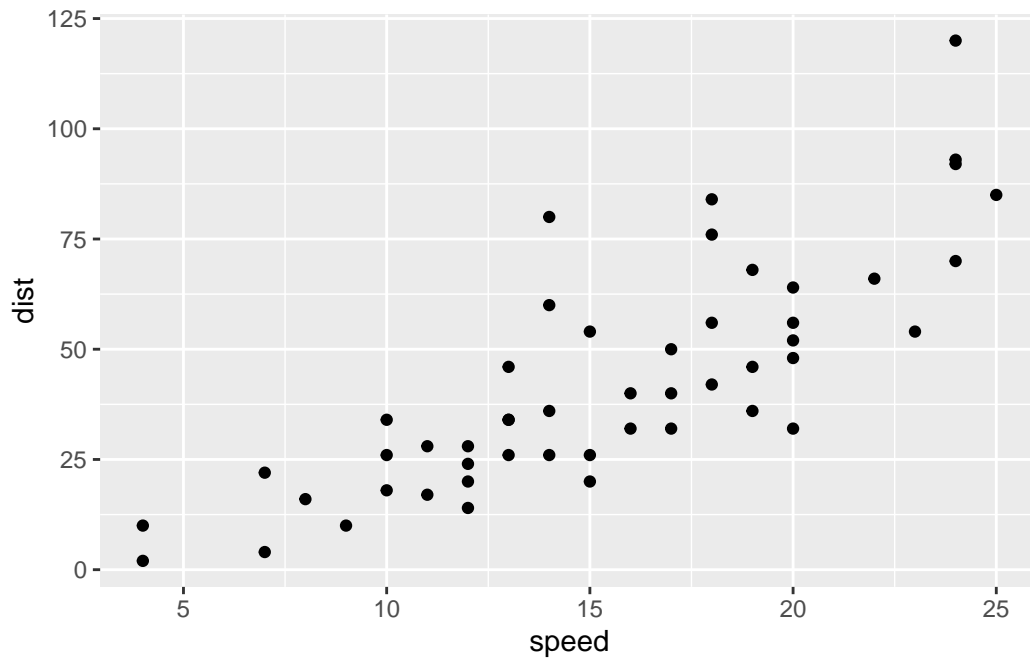
Before I can use an add on package, I must install with the `install.packages()` function. The package name should be in quotes in this command.

To use the package I need to load it with the `library()` function.

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

```
library("ggplot2")
```

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

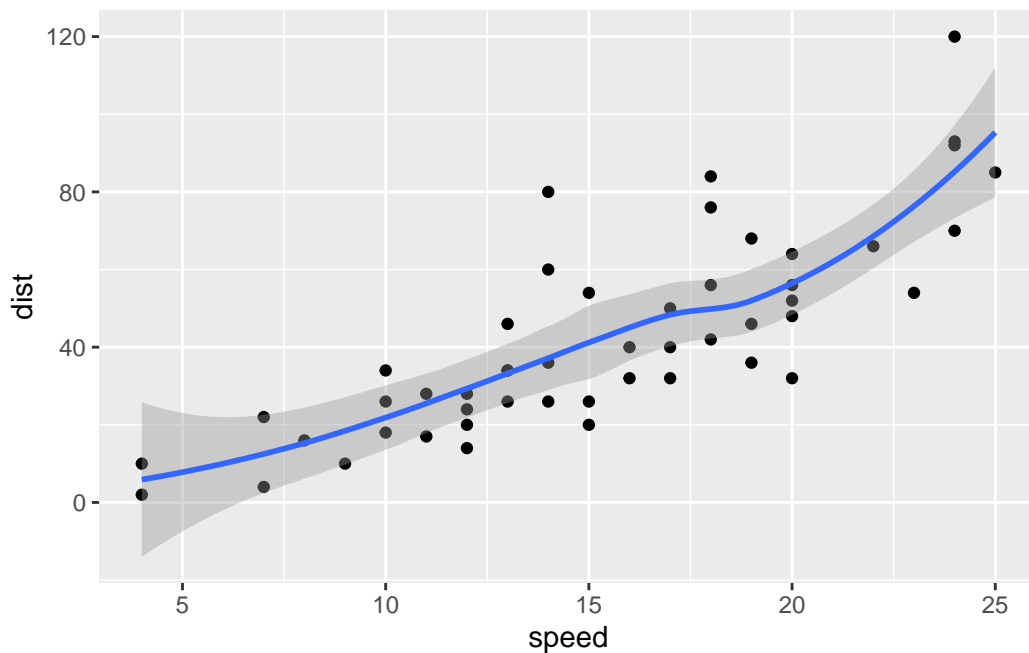


For “simple” graphs like this one, base R code is shorter than ggplot code.

Let’s fit a model and show it on the plot.

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

`geom\_smooth()` using method = 'loess' and formula = 'y ~ x'



Every ggplot has at least 3 layers.

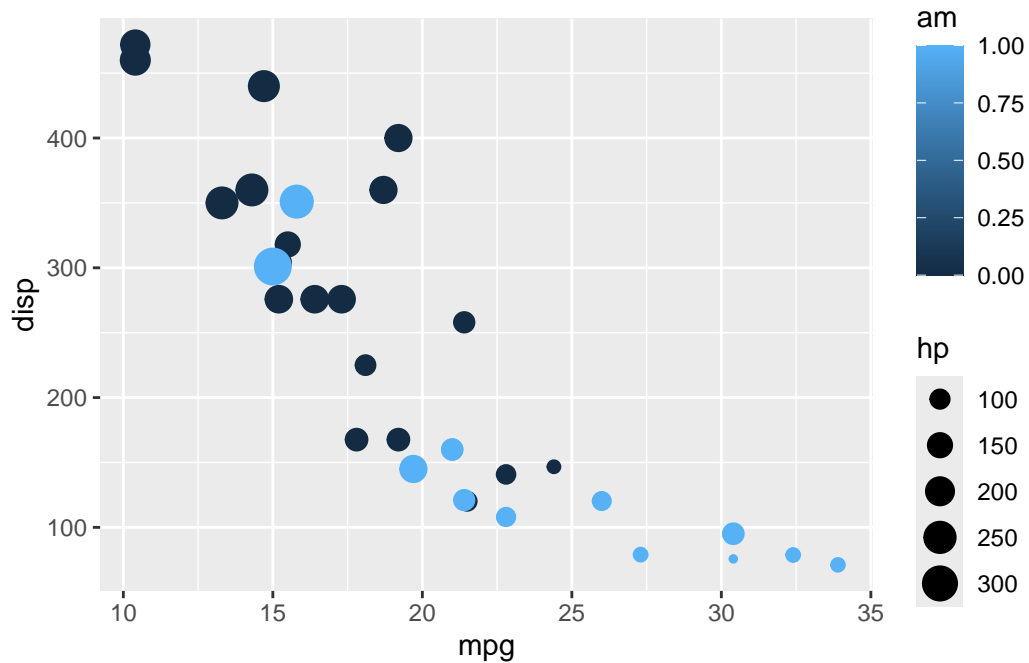
- **data:** data.frame with the numbers you want to plot
- **aesthetics:** mapping of the columns in your data frame to your plot
  - e.g. size of points, position, line type, line width, color, shape of points
- **geoms:** there are many of these, but the basics are `geom_point()`, `geom_line()` and `geom_col()`

```
head(mtcars)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	1

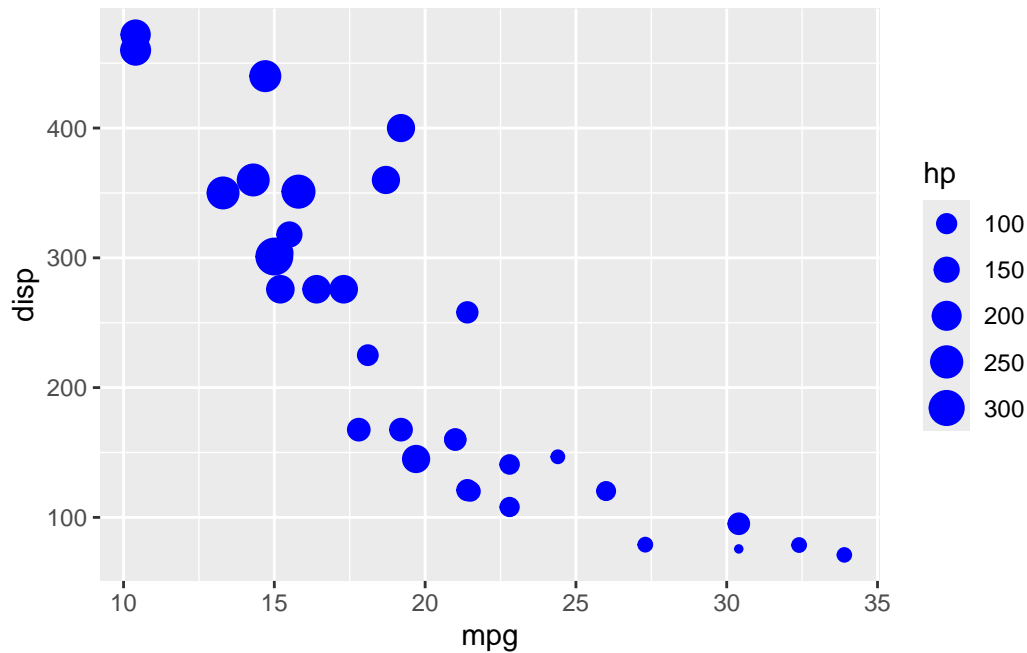
Make a ggplot of the `mtcars` data using `mpg` vs `disp` and set the size of the points to the `hp` and set the color to `am`.

```
ggplot(mtcars) +
  aes(x=mpg, y=disp, size=hp, col= am) +
  geom_point()
```



Now, color all the points blue.

```
ggplot(mtcars) +
  aes(x=mpg, y=disp, size=hp) +
  geom_point(colour="blue")
```



Make a gene expression plot that colors gene expression changes.

```
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

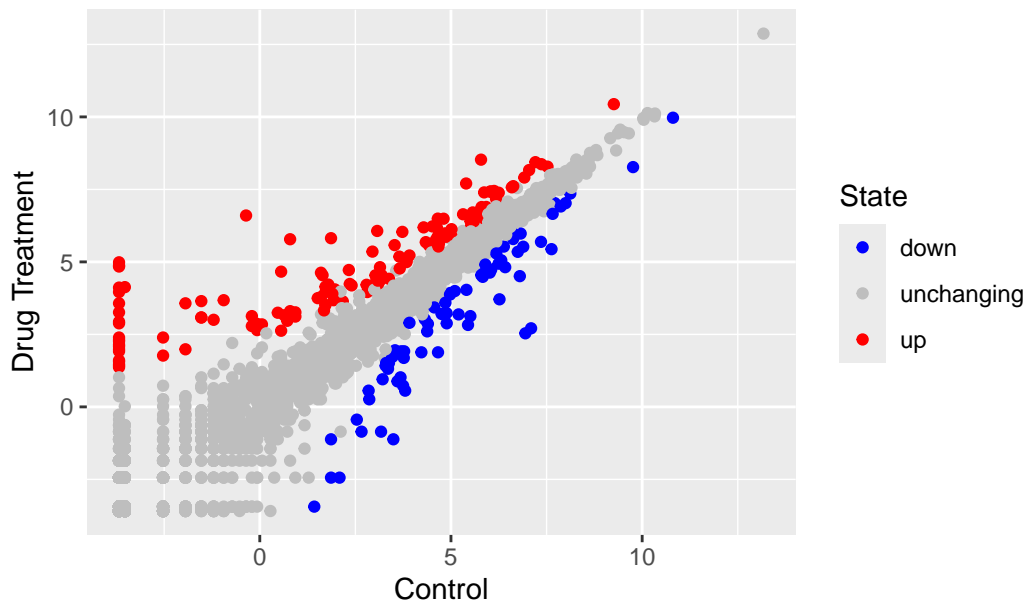
```
table(genes$State)/nrow(genes) *100
```

down	unchanging	up
1.385681	96.170131	2.444188

The functions `nrow()`, `ncol()`, and `table()` are helpful for summarizing large data frames.

```
ggplot(genes) +  
  aes(x=Condition1, y=Condition2, col=State) +  
  geom_point() +  
  scale_color_manual(values=c("blue", "grey", "red")) +  
  labs(title="Gene Expression Changes Upon Drug Treatment", x="Control", y="Drug Treatment")
```

## Gene Expression Changes Upon Drug Treatment



```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.tsv"
gapminder <- read.delim(url)
head(gapminder)
```

	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
4	Afghanistan	Asia	1967	34.020	11537966	836.1971
5	Afghanistan	Asia	1972	36.088	13079460	739.9811
6	Afghanistan	Asia	1977	38.438	14880372	786.1134

```
library(dplyr)
```

Attaching package: 'dplyr'

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

filter, lag

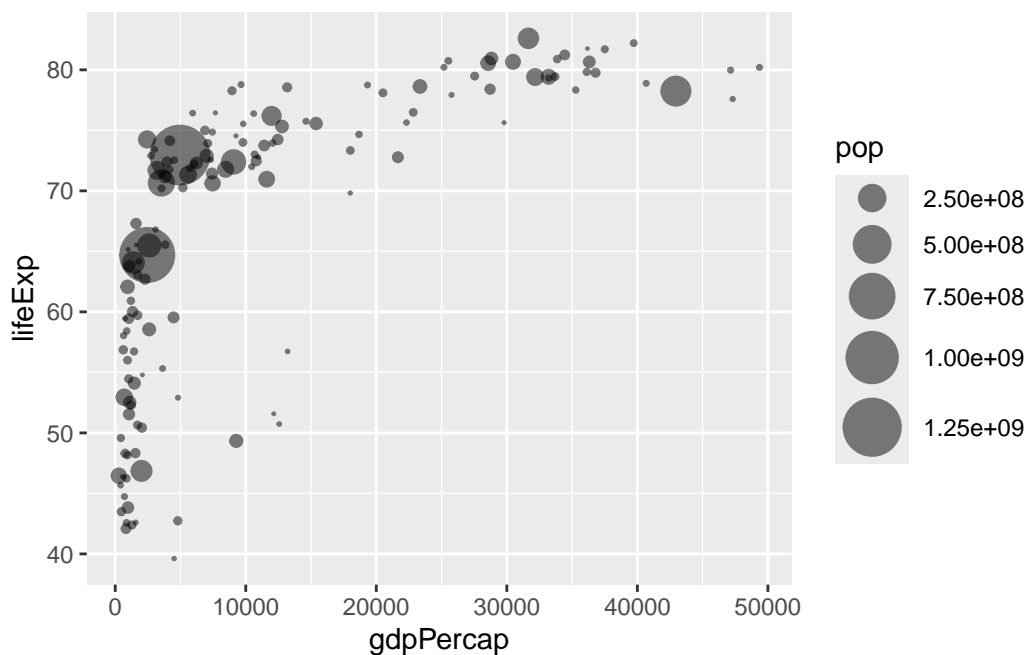
The following objects are masked from 'package:base':

```
intersect, setdiff, setequal, union
```

```
gapminder_2007 <- gapminder %>% filter(year==2007)
gapminder_1957 <- gapminder %>% filter(year==1957)
```

Make a plot of the 2007 data.

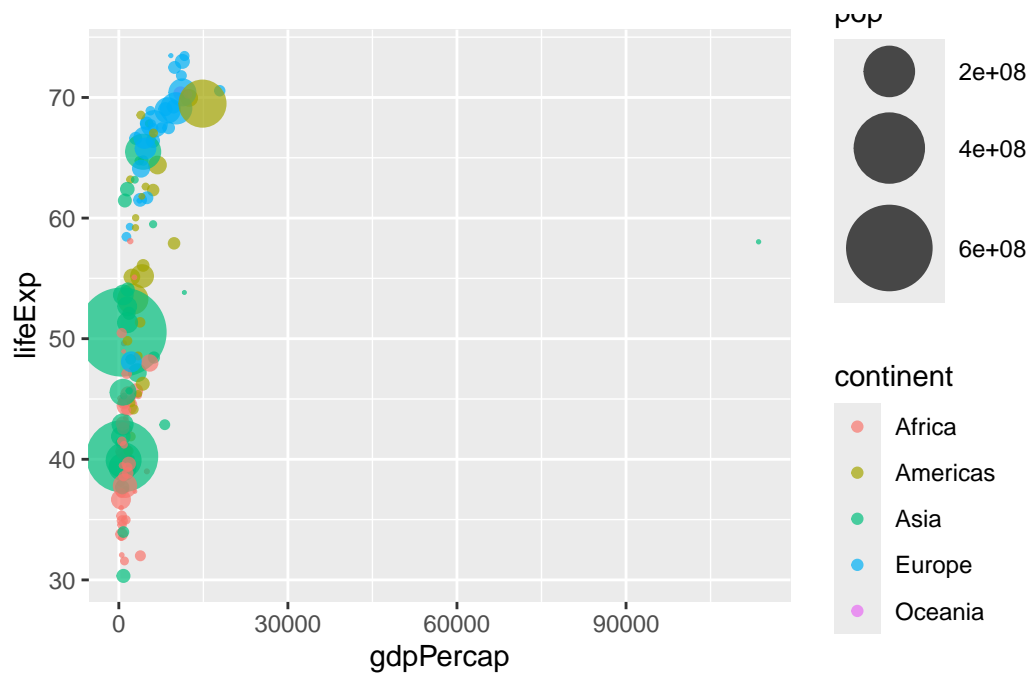
```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, size= pop) +
  geom_point(alpha=0.5) +
  scale_size_area(max_size=10)
```



Make a plot of the 1957 data.

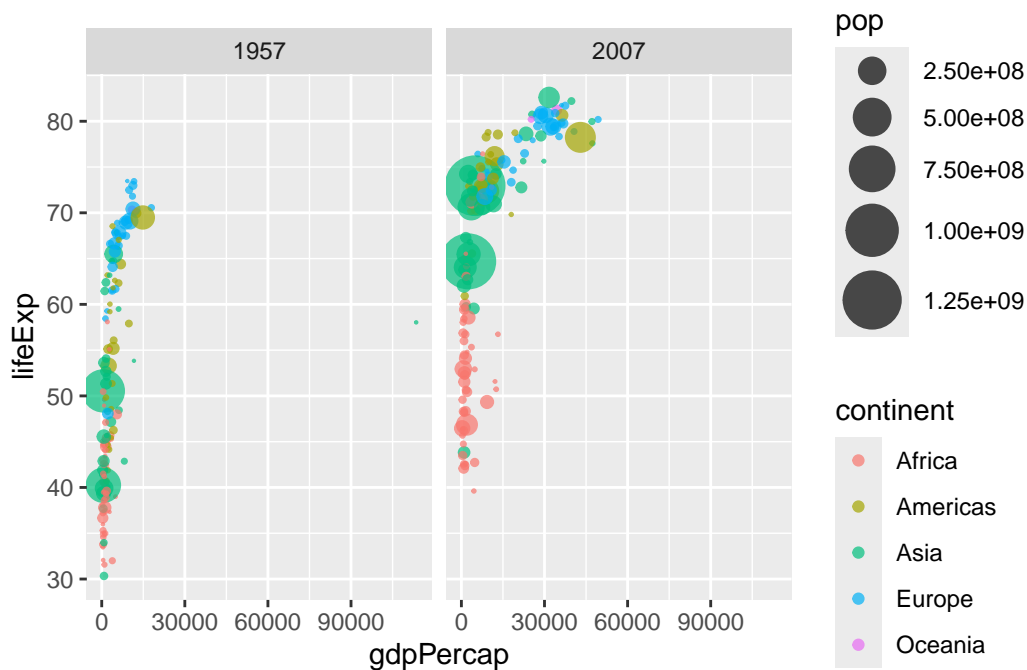
```
ggplot(gapminder_1957) +
  aes(x=gdpPercap, y=lifeExp, size= pop, col= continent) +
  geom_point(alpha=0.7) +
  scale_size_area(max_size=15)
```





Make a plot of both 2007 and 1957 data.

```
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)
```



You can use `geom_col()` to create bar charts.

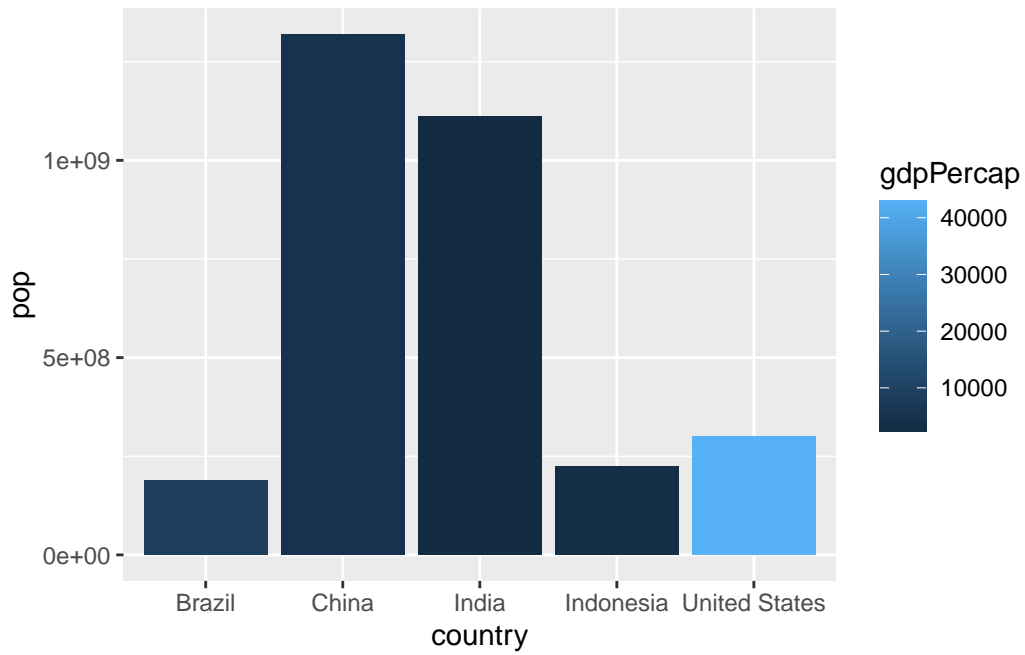
```
gapminder_top5 <- gapminder %>%
  filter(year==2007) %>%
  arrange(desc(pop)) %>%
  top_n(5, pop)

gapminder_top5
```

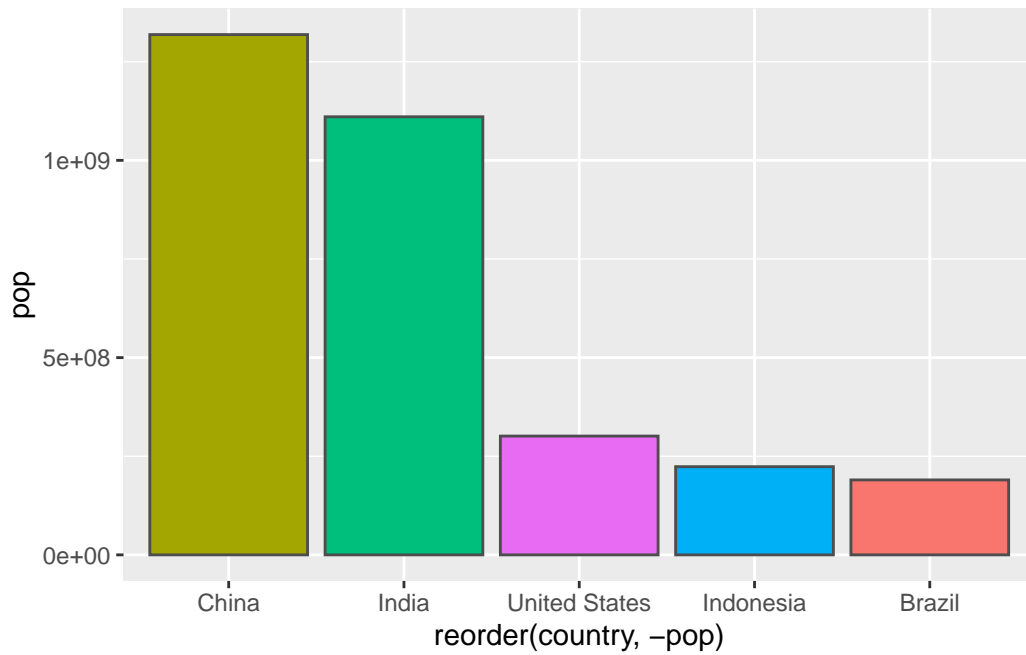
	country	continent	year	lifeExp	pop	gdpPercap
1	China	Asia	2007	72.961	1318683096	4959.115
2	India	Asia	2007	64.698	1110396331	2452.210
3	United States	Americas	2007	78.242	301139947	42951.653
4	Indonesia	Asia	2007	70.650	223547000	3540.652
5	Brazil	Americas	2007	72.390	190010647	9065.801

You can color by numeric values and get a gradient or categorical and get different colors for each category.

```
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="grey30") +  
  guides(fill="none")
```



```
ggsave("top5countrygraph.pdf")
```

Saving 5.5 x 3.5 in image

Can save plots from ggplot to the computer using `ggsave("")`.