

class05

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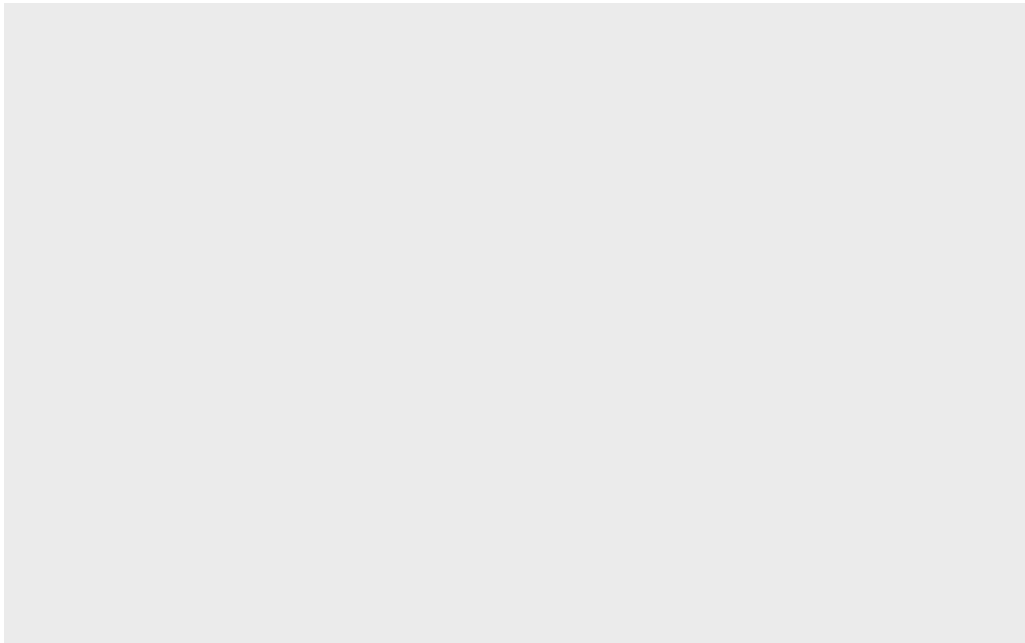
Using GGPLOT

The ggplot2 package needs to be installed as it doesn't not come with R “out of the box”

We use the ‘install.packages()’ function to do this

To use ggplot, I need to load it up using ‘library(ggplot2)’

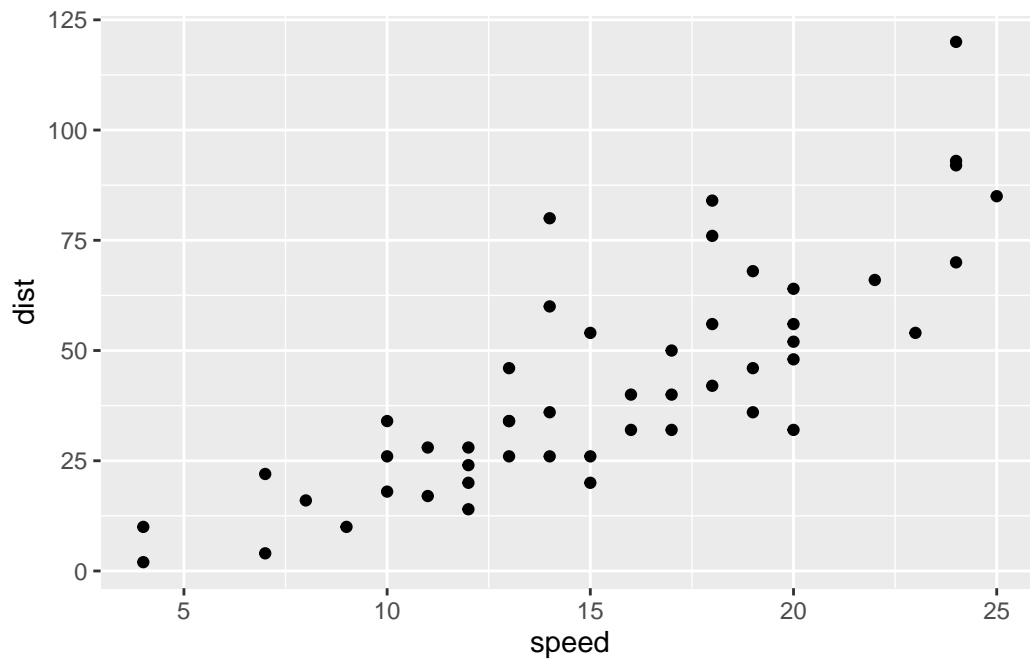
```
#install.packages (ggplot2)
library(ggplot2)
ggplot()
```



ALL ggplot figures have at least three things:

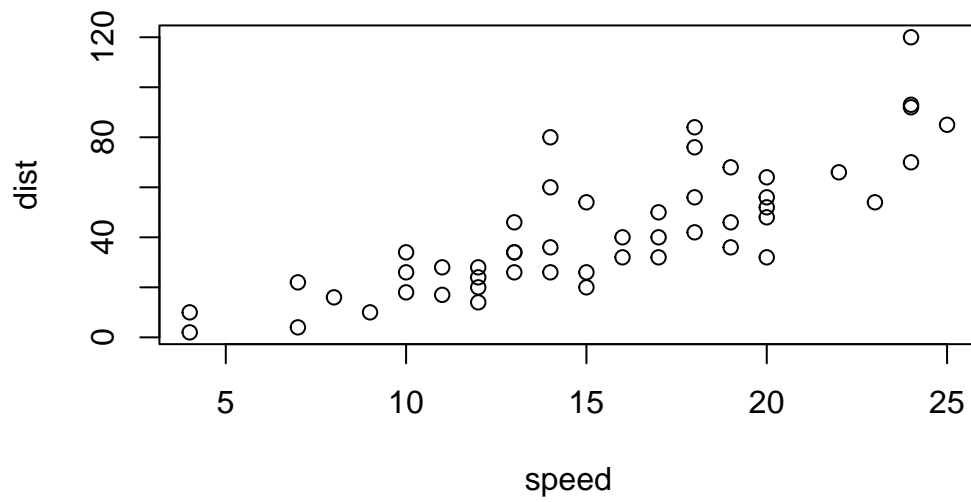
- data (the stuff we want to plot)
- aesthetic mapping (x,y)
- geoms

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



ggplot is not the only graphing system in R. There are lots of others. There is even “base R” graphics.

```
plot(cars)
```

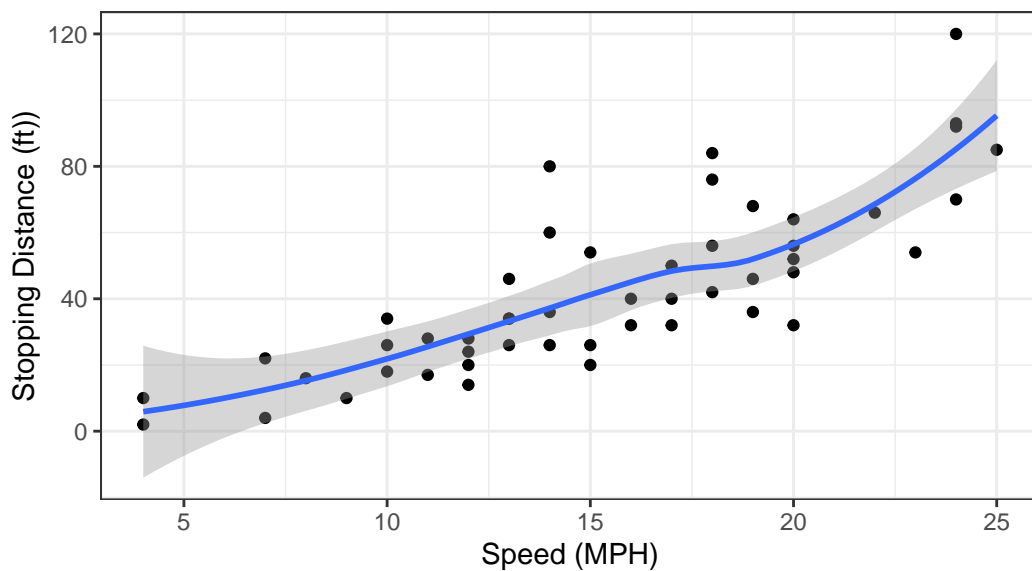


Creating Scatter Plots

```
ggplot(cars) +  
  aes(x=speed, y=dist) +geom_point() +geom_smooth() +  
  labs(title = "Speed vs. Stopping Distances of Cars", x= "Speed (MPH)", y = "Stopping Dis
```

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

Speed vs. Stopping Distances of Cars



Dataset: 'cars'

Adding More Plot Aesthetics using aes()

```
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)
```

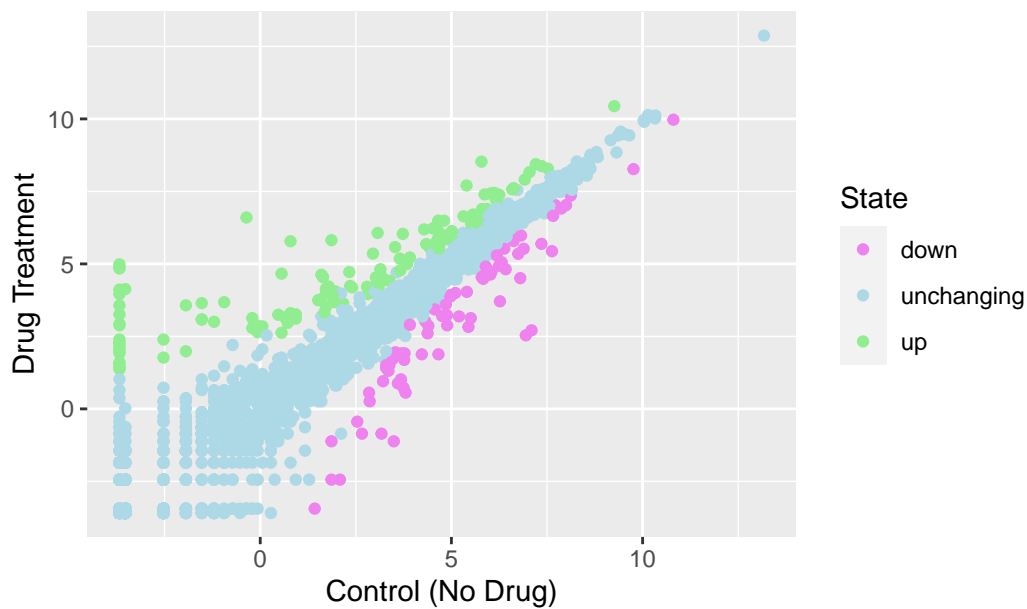
down	unchanging	up
72	4997	127

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

down	unchanging	up
1.39	96.17	2.44

```
p <- ggplot (genes) + aes(x= Condition1, y = Condition2, col=State) + geom_point()
p + scale_colour_manual( values = c("violet", "lightblue", "lightgreen"))+
  labs(title = "Gene Expression Changes upon Drug Treatment", x= "Control (No Drug)", y= "
```

Gene Expression Changes upon Drug Treatment



Going Further

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

Attaching package: 'dplyr'

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

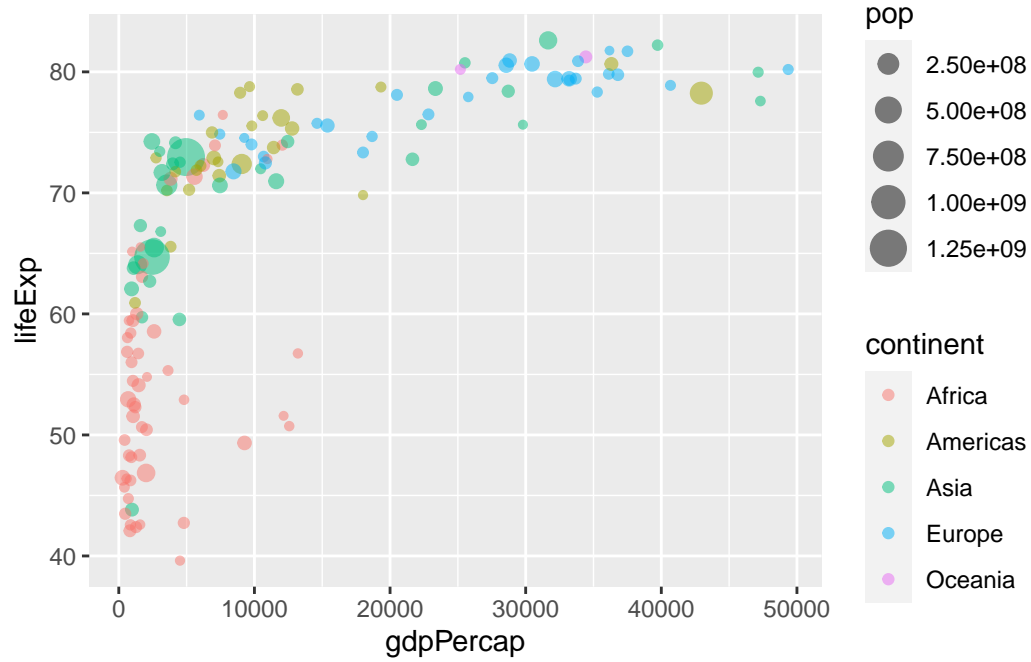
filter, lag

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

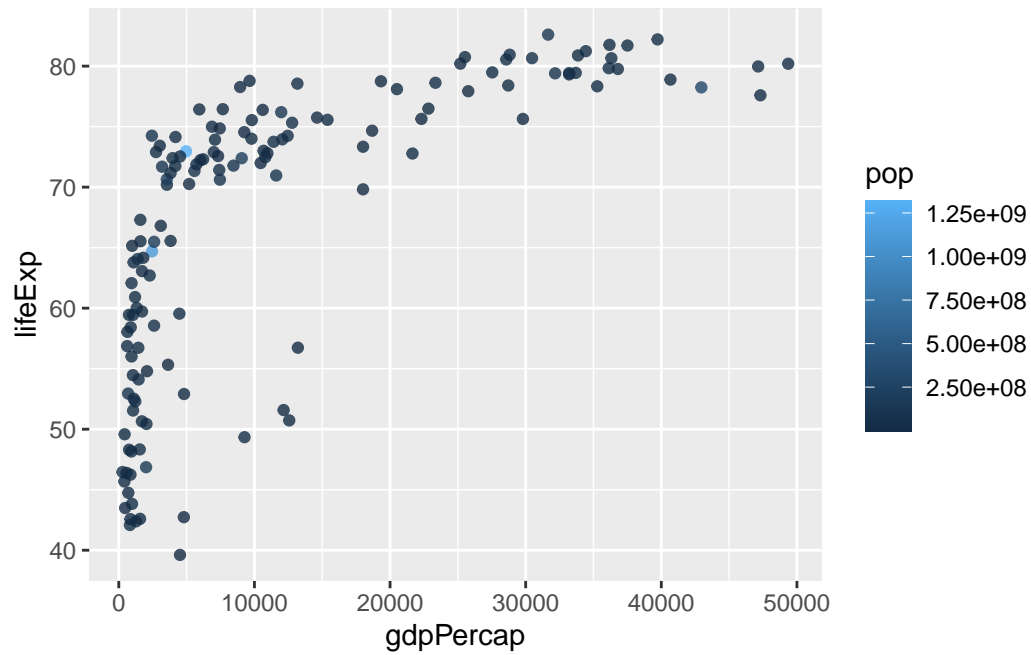
intersect, setdiff, setequal, union

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

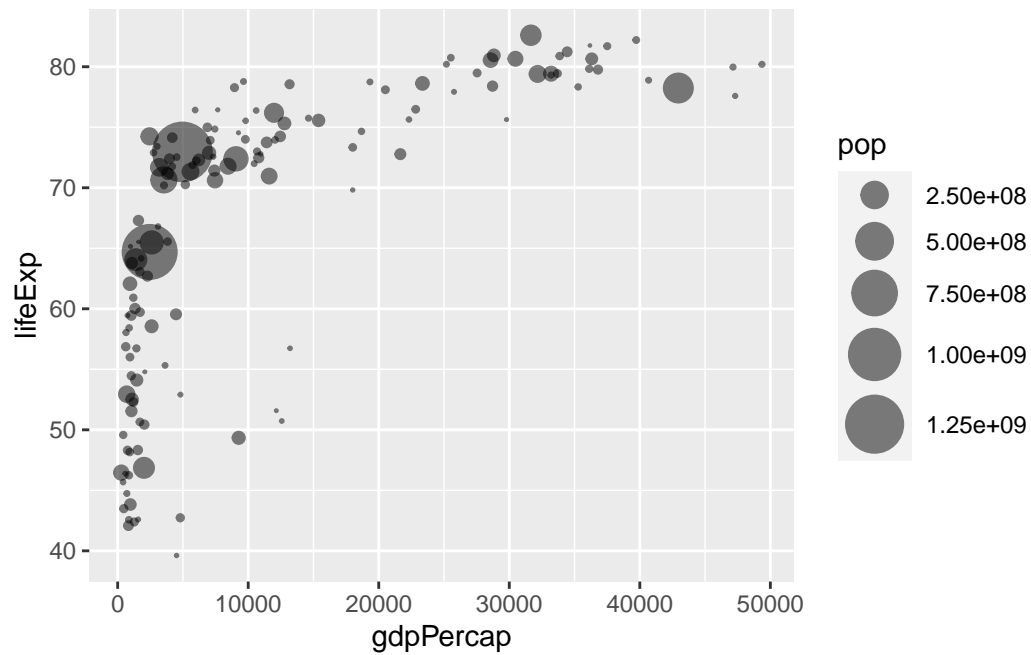
```
geom_point(alpha=0.5)
```



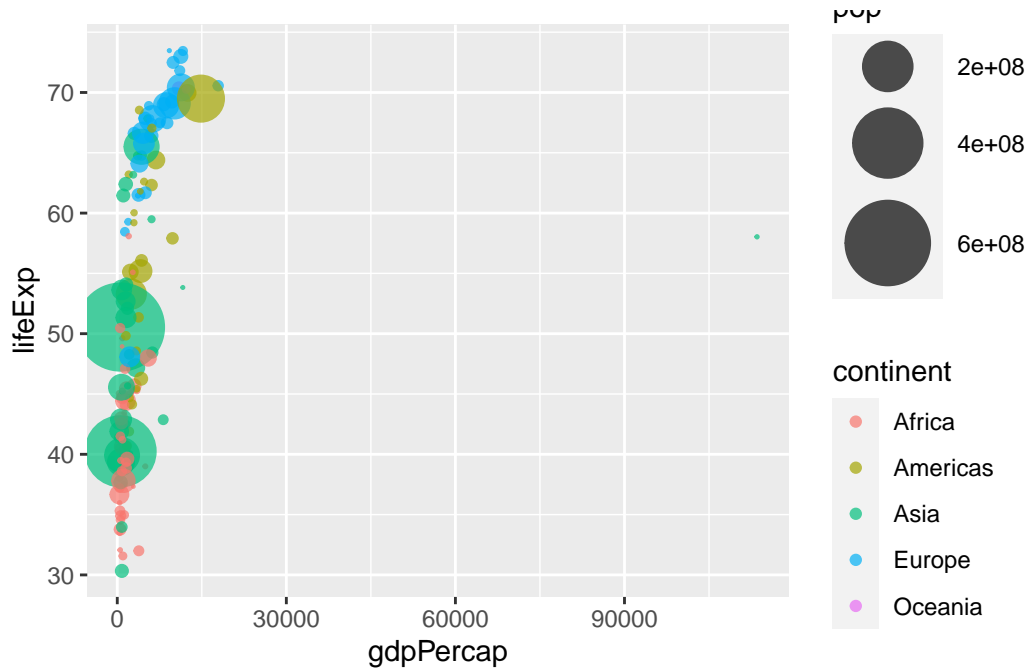
```
ggplot(gapminder_2007)+ aes(x=gdpPerCap, y=lifeExp, color = pop) +  
geom_point(alpha=0.8)
```



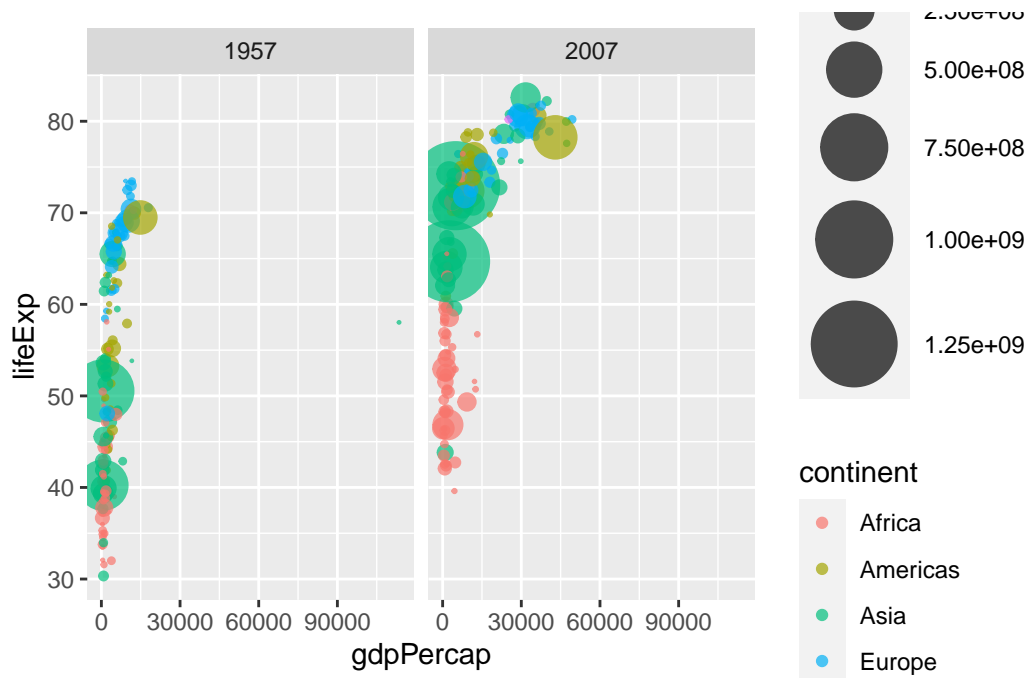
```
ggplot(gapminder_2007) + geom_point(aes(x = gdpPercap, y = lifeExp, size = pop),
alpha=0.5) + scale_size_area(max_size = 10)
```




```
gapminder_1957 <- gapminder %>% filter(year==1957)
ggplot(gapminder_1957)+
aes(x=gdpPercap, y=lifeExp, color =continent, size =pop) +geom_point(alpha=0.7) + scale_size
```



```
gapminder_1957 <- gapminder %>% filter(year==2007| year == 1957)
ggplot(gapminder_1957)+
aes(x=gdpPercap, y=lifeExp, color =continent, size =pop) +geom_point(alpha=0.7)+ scale_size
```



Bar Charts

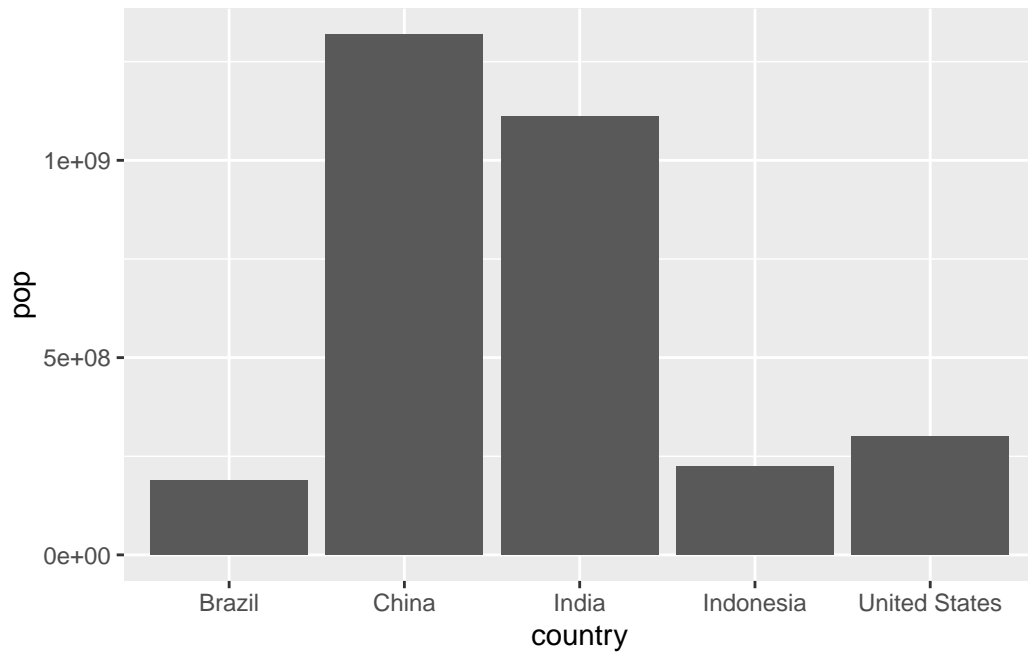
```
gapminder_top5 <- gapminder %>%
  filter(year==2007) %>%
  arrange(desc(pop)) %>%
  top_n(5, pop)
```

```
gapminder_top5
```

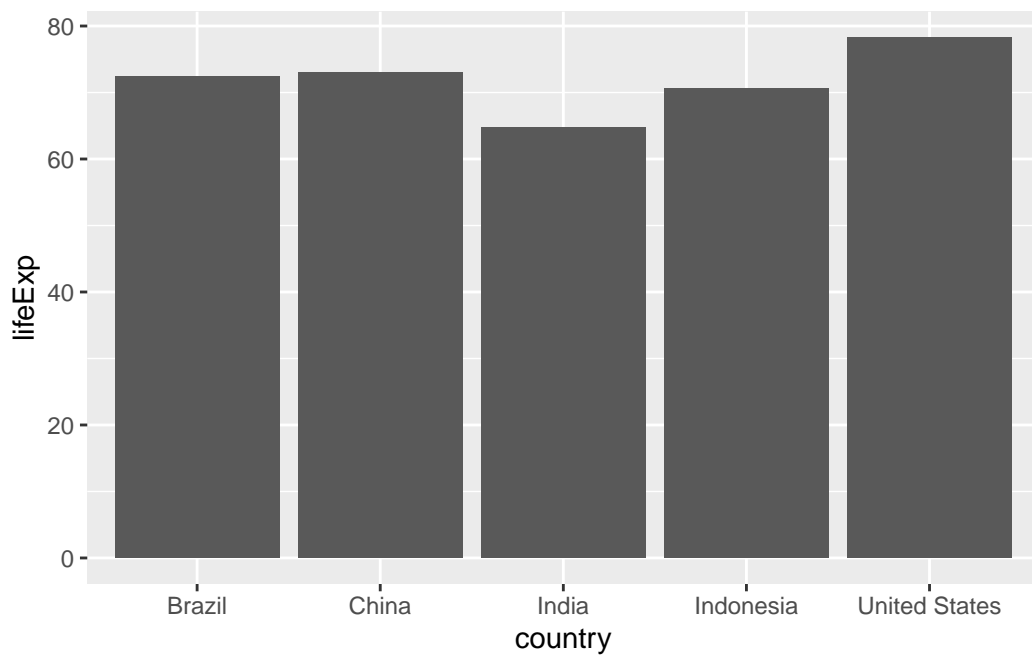
A tibble: 5 x 6

	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.

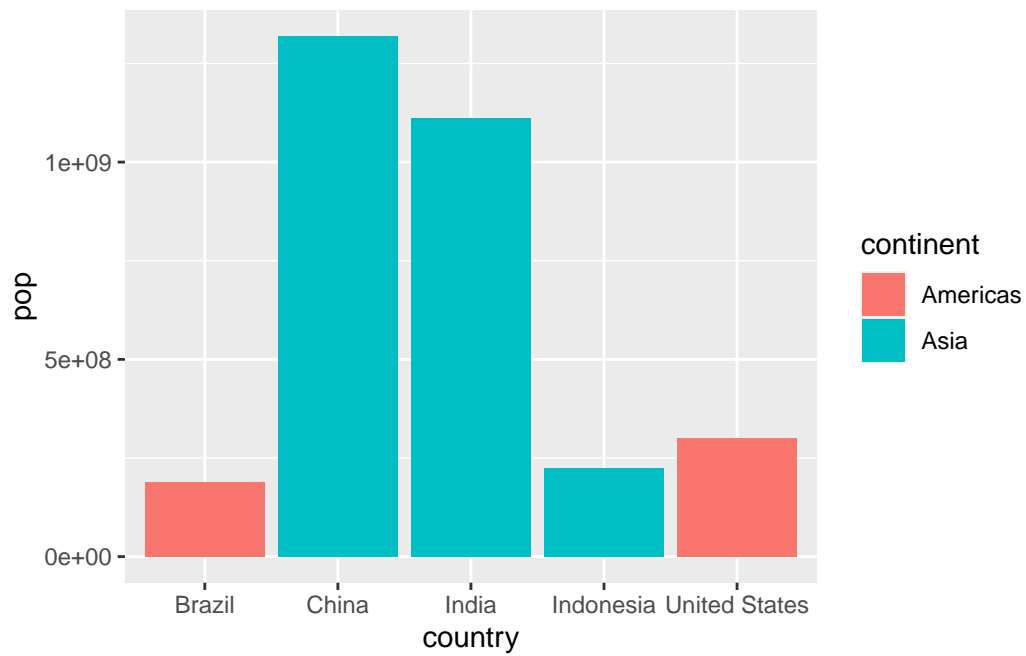
```
ggplot(gapminder_top5)+ aes(x= country, y=pop) + geom_col()
```



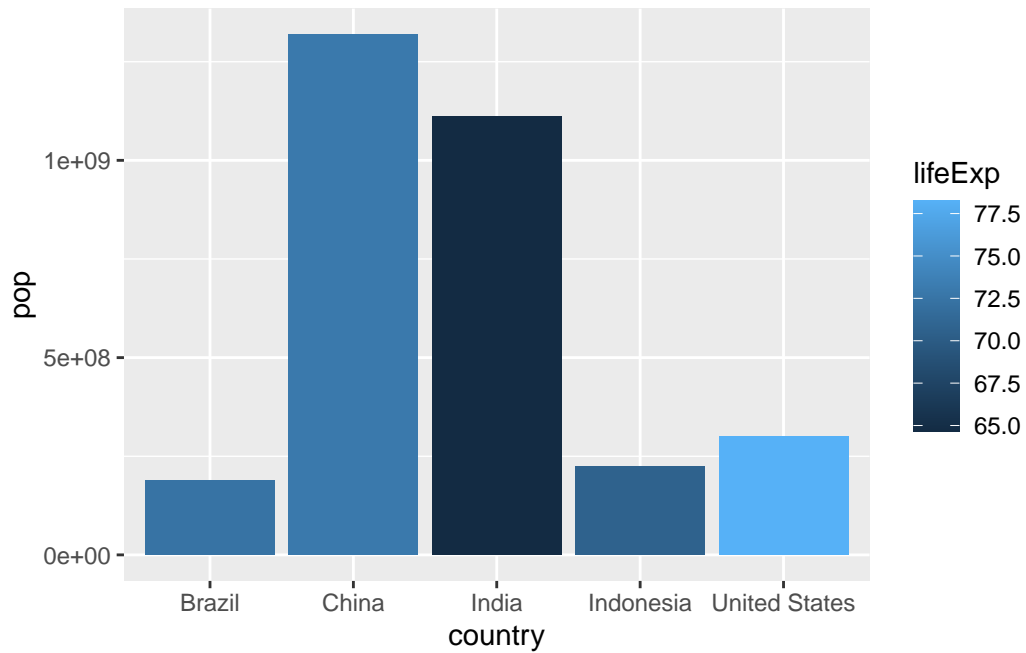
```
ggplot(gapminder_top5)+ aes(x= country, y=lifeExp) + geom_col()
```



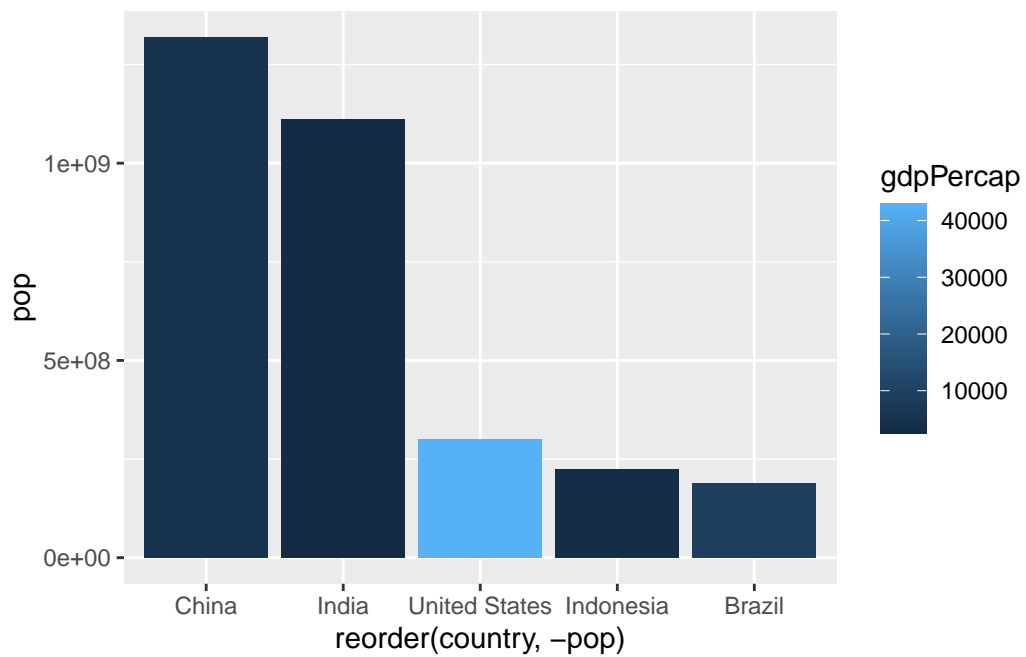
```
ggplot(gapminder_top5)+ aes(x= country, y=pop, fill = continent) + geom_col()
```



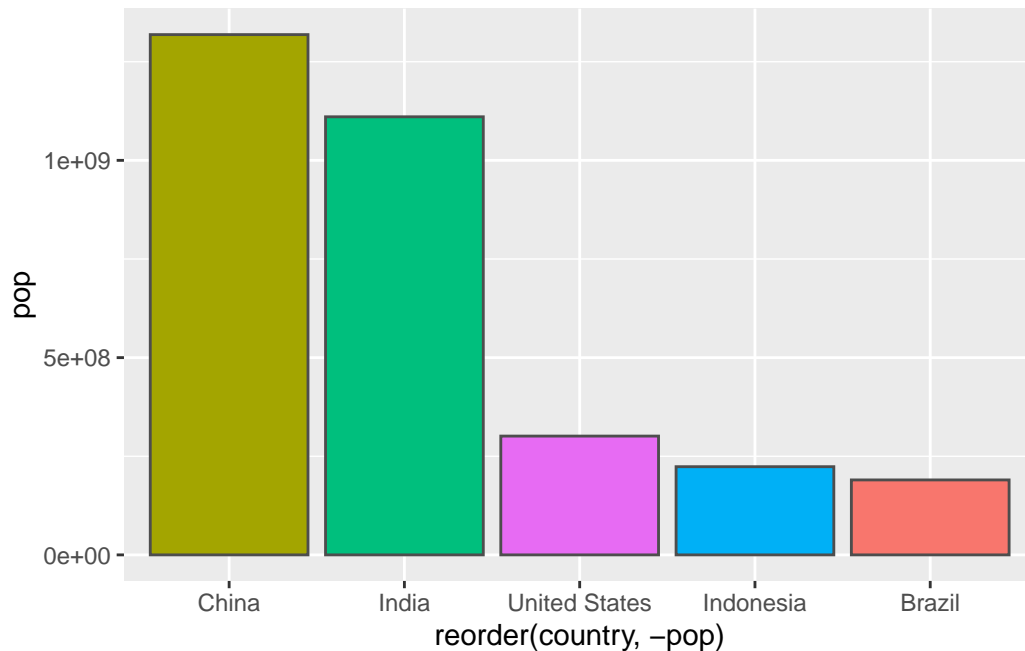
```
ggplot(gapminder_top5)+ aes(x= country, y=pop, fill = lifeExp) + geom_col()
```



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



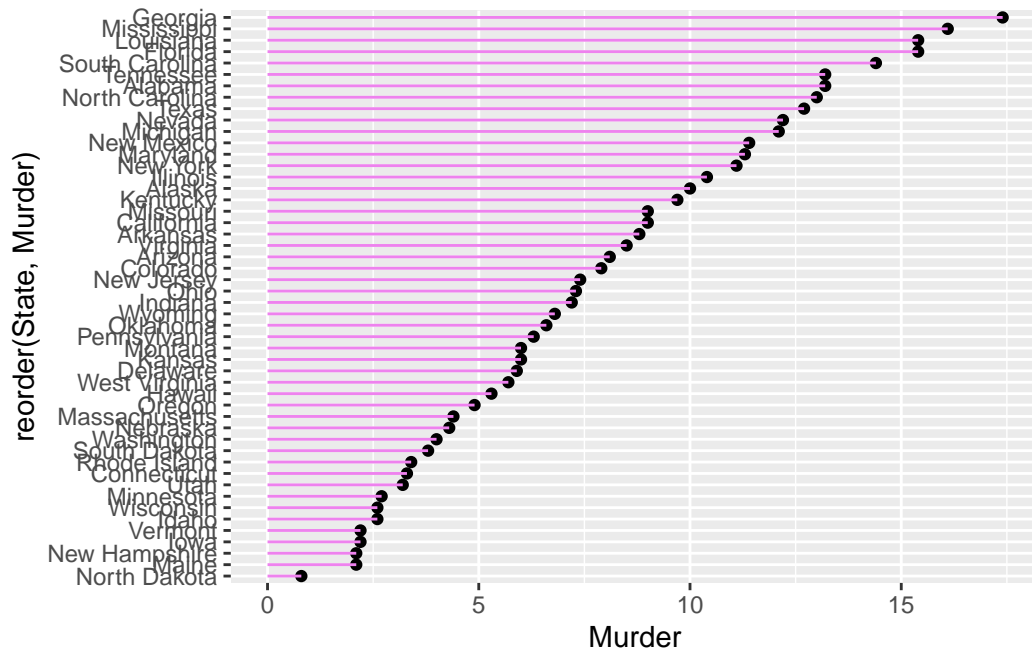
```
ggplot(gapminder_top5)+
  aes(x= reorder(country, -pop), y=pop, fill = country) +
  geom_col(col = "gray30") +guides(fill = "none")
```



```
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

```
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="violet")+
coord_flip()
```



Combining Plots

```
# install.packages ("patchwork")
library(patchwork)
p1 <- ggplot(gapminder_top5)+
  aes(x= reorder(country, -pop), y=pop, fill = gdpPercap) + geom_col()

p2 <- ggplot(gapminder_top5)+ aes(x= reorder(country, -pop), y=pop, fill = country) + geom_col()

(p1 | p2)
```

