

Class_05 Data Visualization with ggplot2

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Using GGPLOT

The ggplot2 package needs to be installed as it does not come with R naturally.

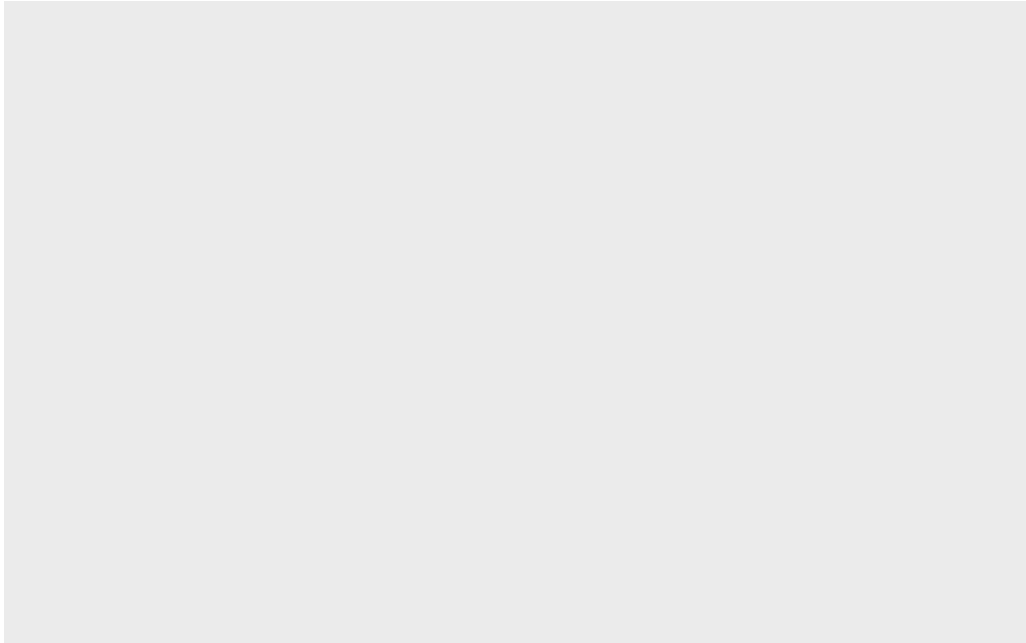
We use the `install.packages()` function to install ggplot2

```
head(cars)
```

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

To use ggplot I need to load it up before I can call any of the functions in the package. I do this with the `library()` function.

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



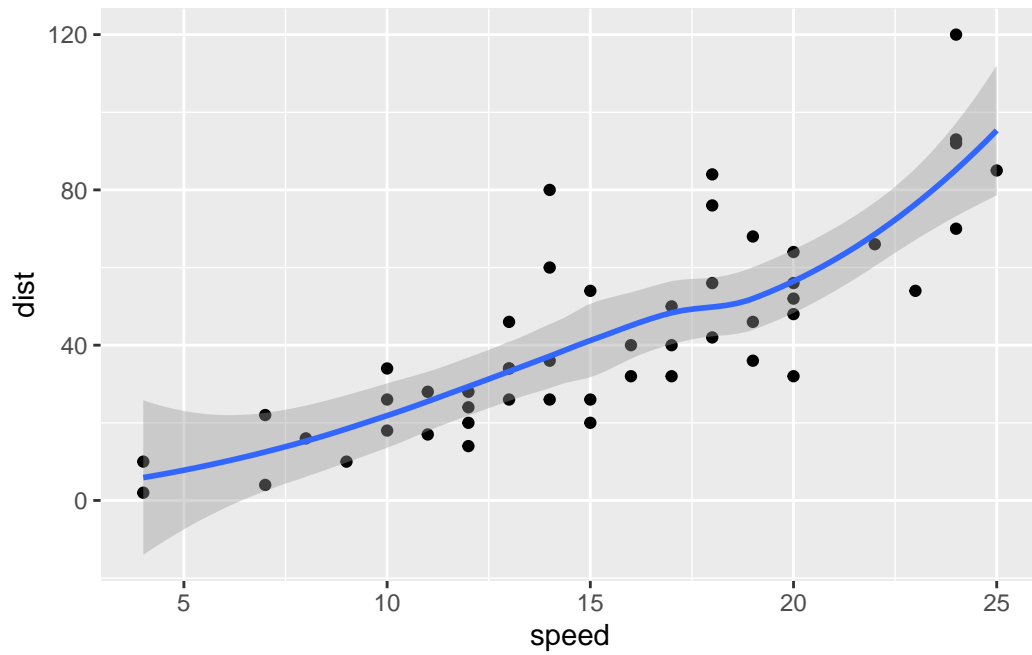
All ggplot figures have at least 3 things: -Data (the stuff we want to plot) -aesthetic mapping (aes vales) -geometries (geoms)

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



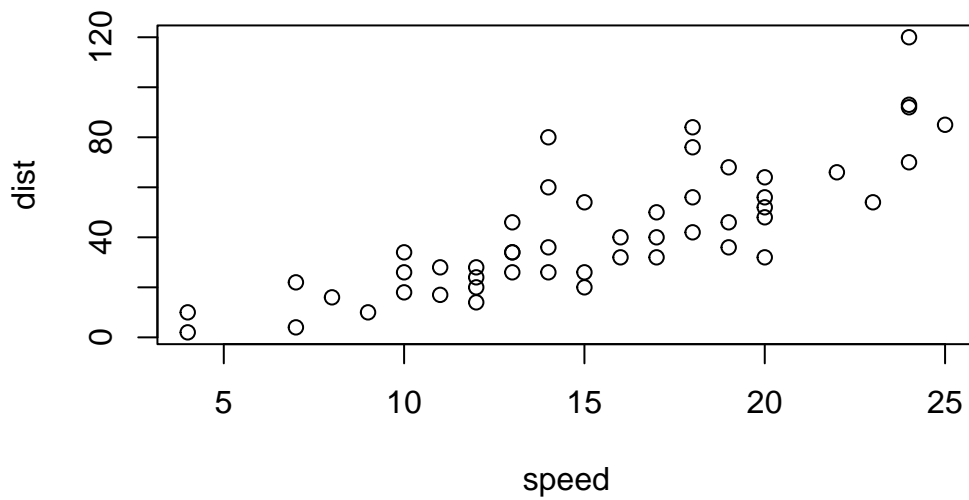
```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth()
```

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



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

```
plot(cars)
```



```
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"
```

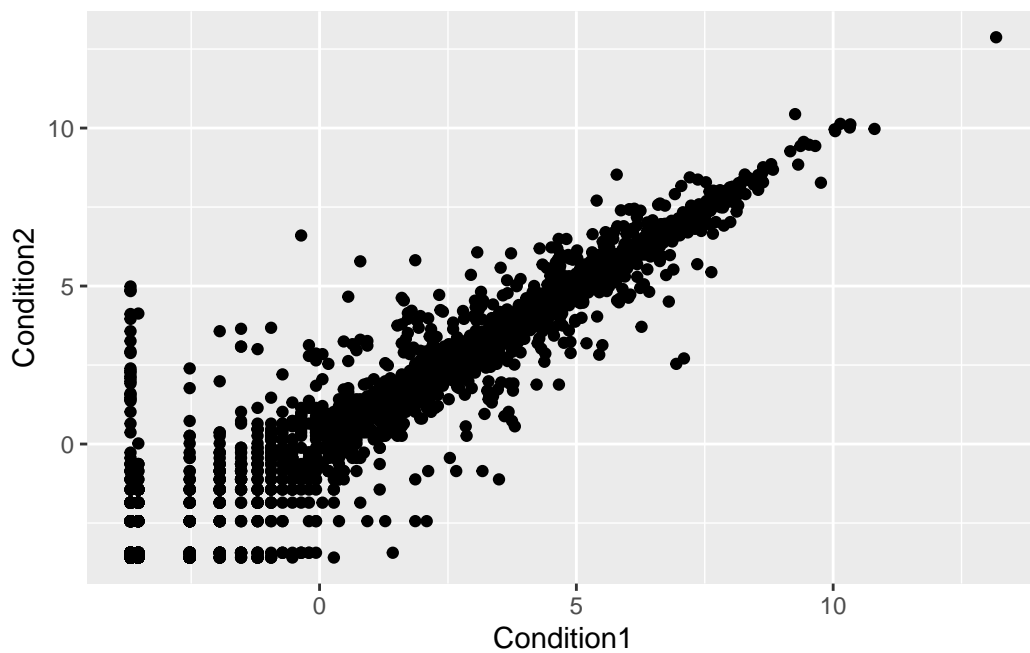
```
table(genes$State)
```

down	unchanging	up
72	4997	127

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

down	unchanging	up
1.39	96.17	2.44

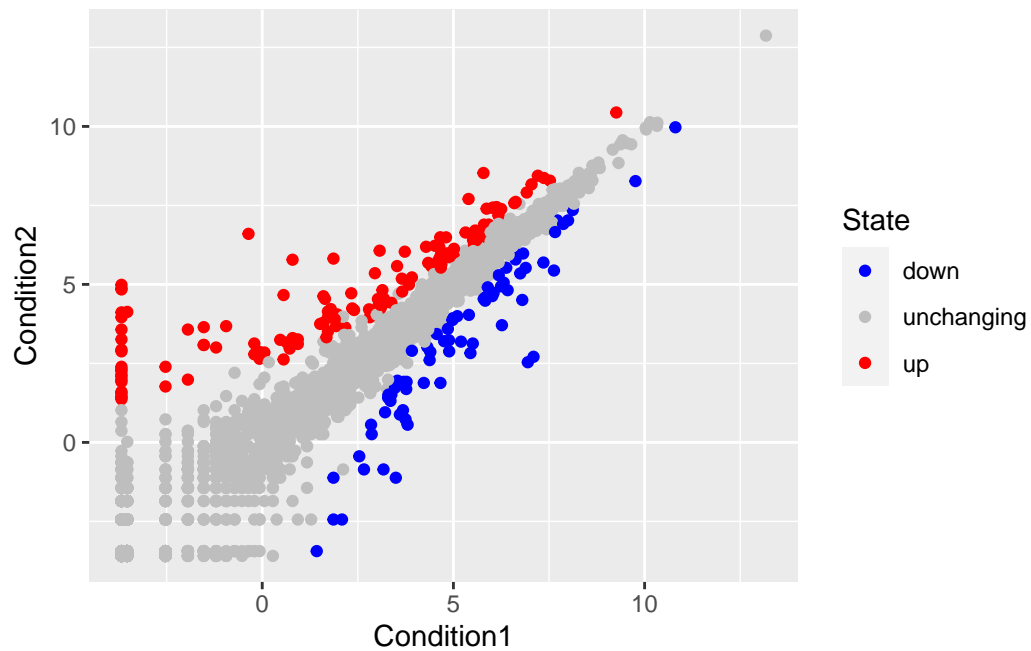
```
ggplot(genes) +  
  aes(x=Condition1, y=Condition2) +  
  geom_point()
```



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

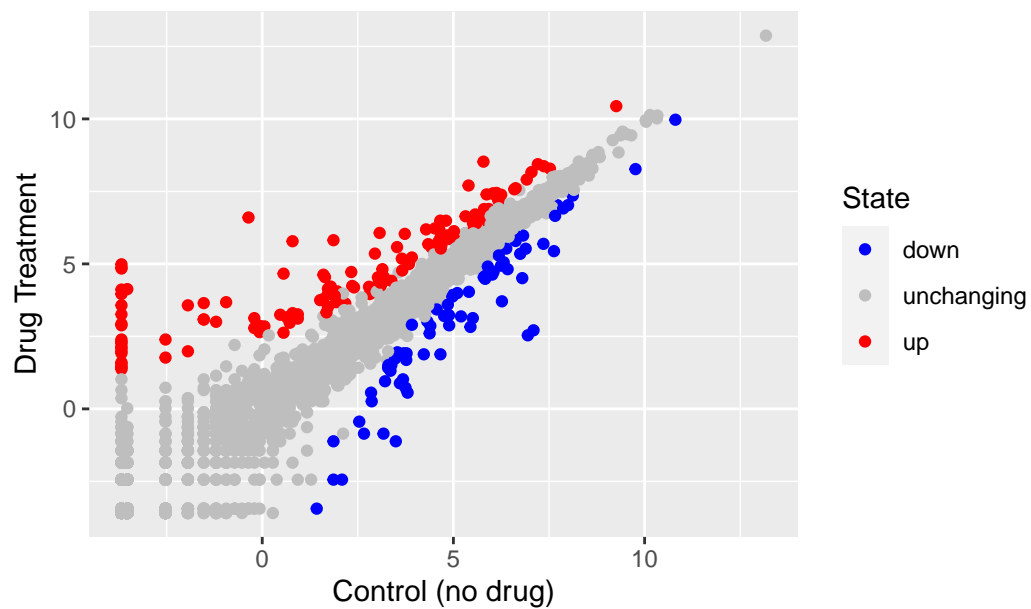
```
geom_point()
```

```
p + scale_colour_manual (values=c("blue", "grey", "red"))
```



```
p + scale_colour_manual (values=c("blue","grey","red")) +  
  labs(title="Gene Expression Changes Due to Drug Treatment",  
        x="Control (no drug)",  
        y= "Drug Treatment")
```

Gene Expression Changes Due to Drug Treatment



Section 7:

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

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

Attaching package: 'dplyr'

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

filter, lag

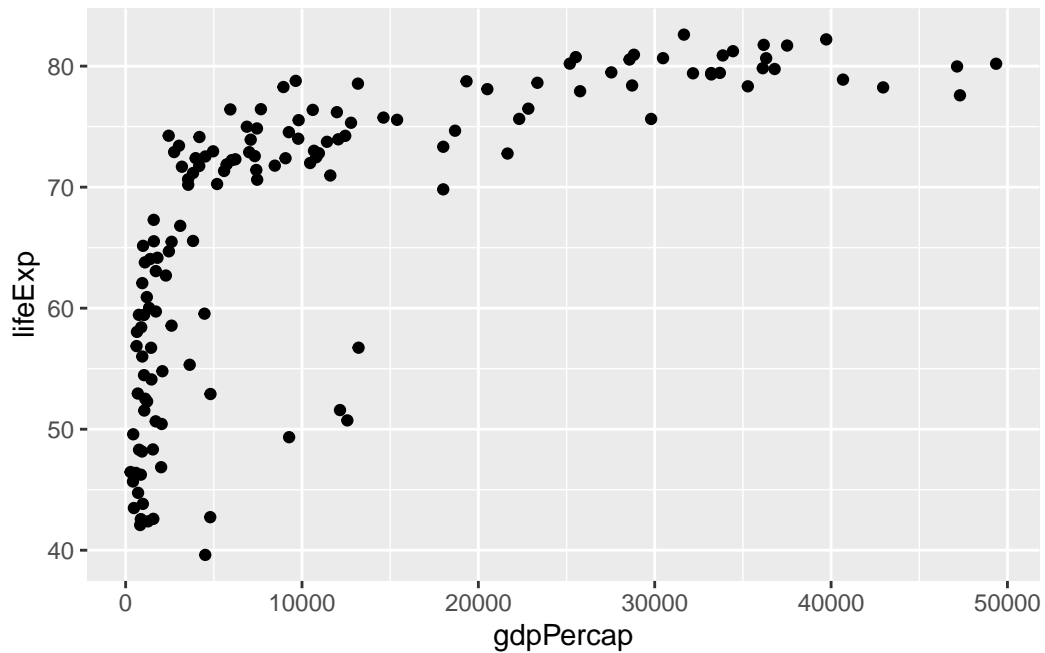
The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

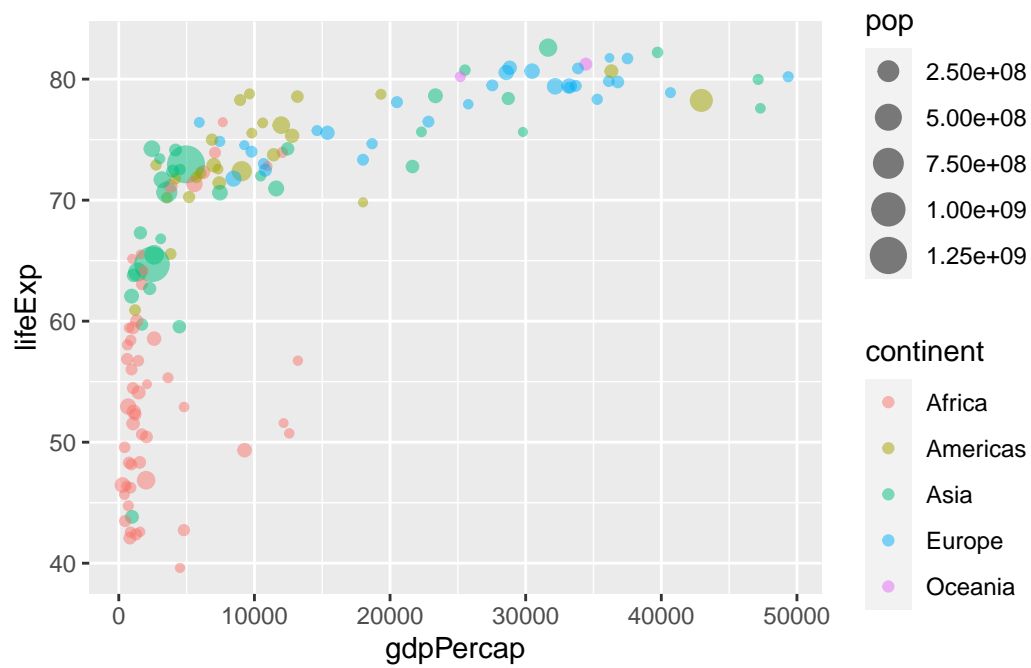
```
gapminder_2007 <- gapminder %>% filter(year==2007)
```



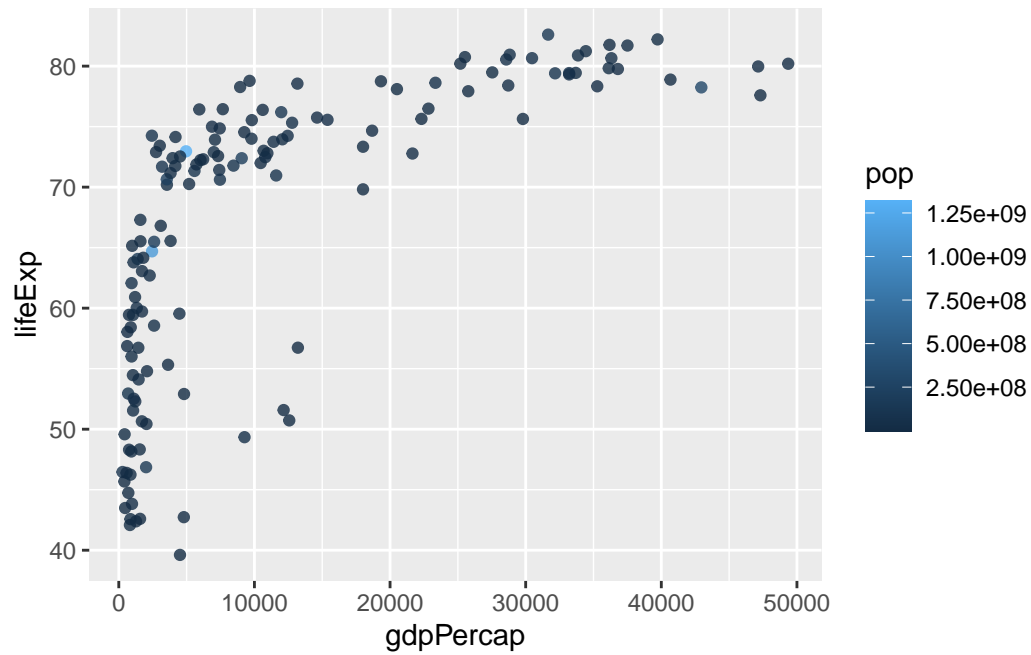
```
ggplot(gapminder_2007)+
  aes(x=gdpPerCap, y =lifeExp)+
  geom_point()
```



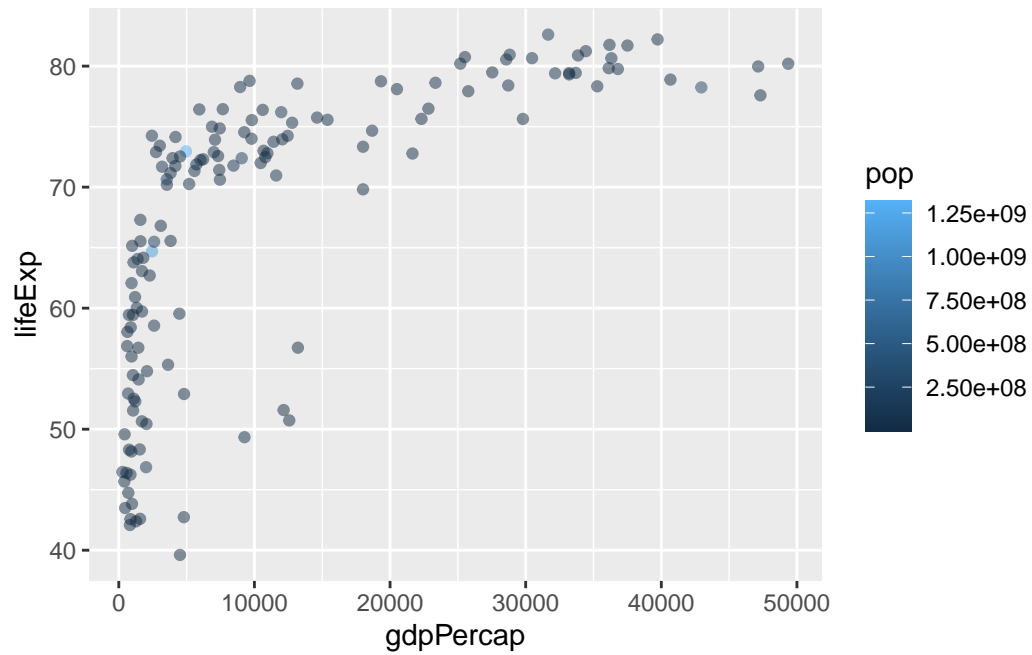
```
ggplot(gapminder_2007)+
  aes(x=gdpPerCap, y =lifeExp, color=continent, size=pop)+
  geom_point(alpha=0.5)
```



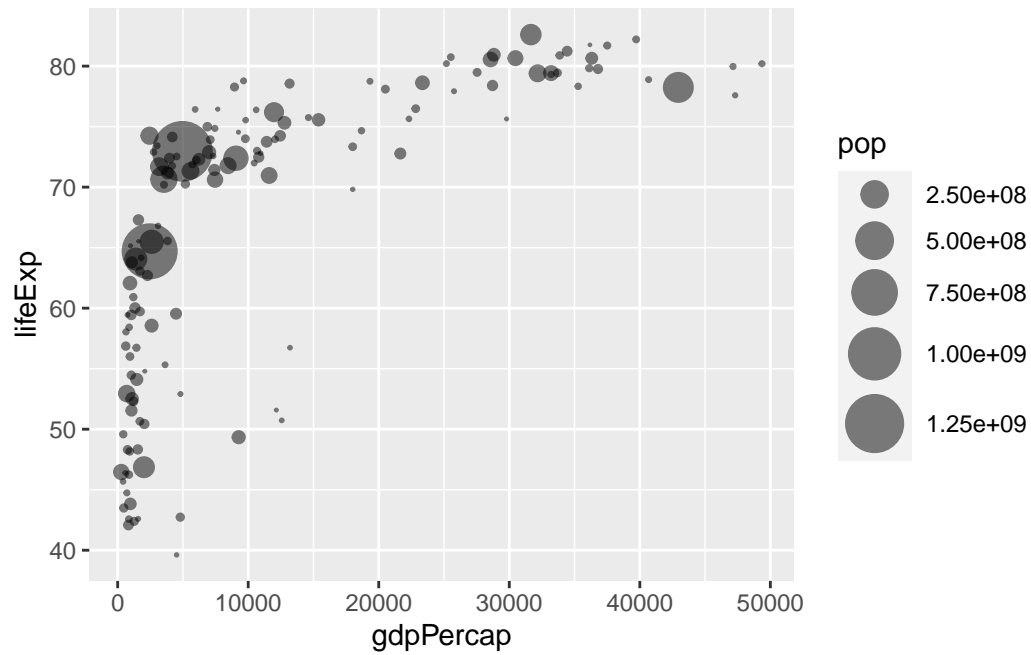
```
ggplot(gapminder_2007)+  
  aes(x=gdpPerCap, y =lifeExp, color=pop)+  
  geom_point(alpha=0.8)
```



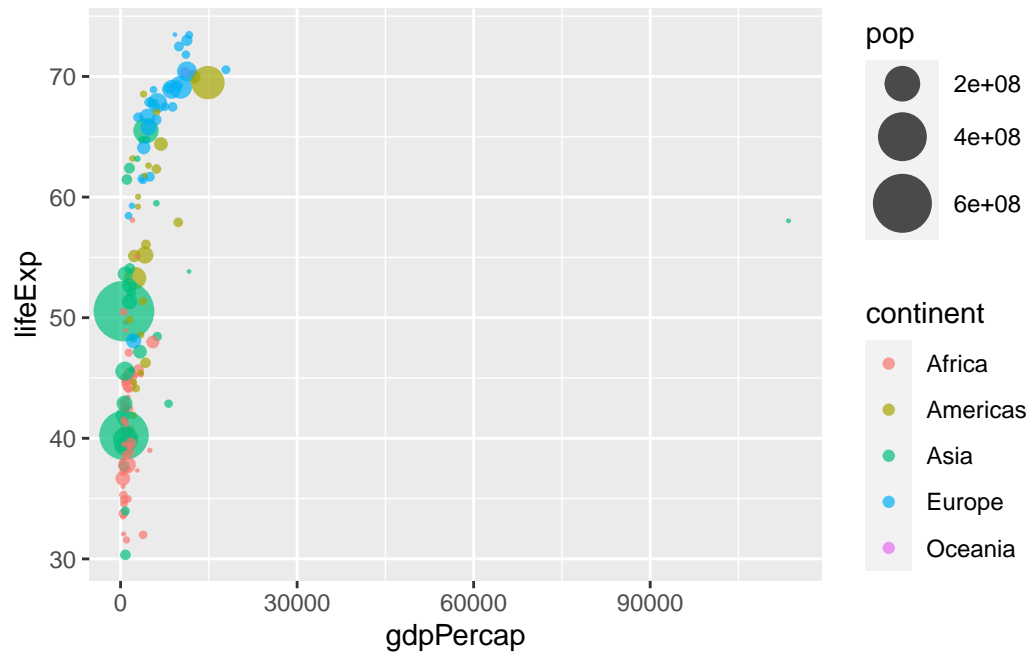
```
ggplot(gapminder_2007)+  
  aes(x=gdpPercap, y =lifeExp, color=pop)+  
  geom_point(alpha=0.5)
```



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

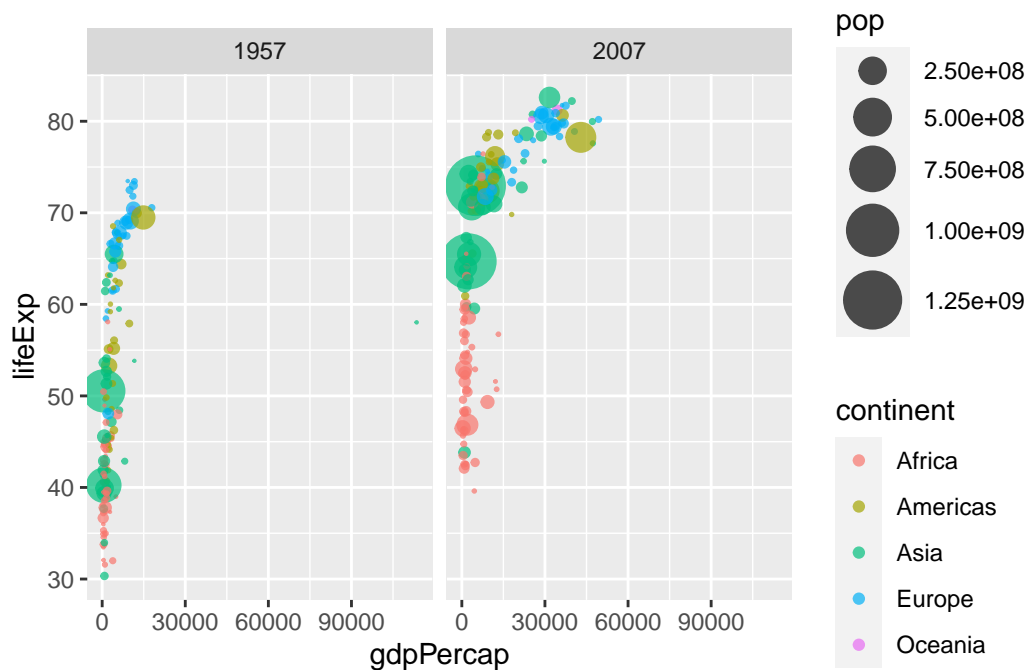


```
gapminder_1957 <- gapminder %>% filter(year==1957)
ggplot(gapminder_1957) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.7) +
  scale_size_area (max_size = 10)
```



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

ggplot(gapminder_1957) +
  geom_point(aes(x = gdpPercap, y = lifeExp, color=continent,
                 size = pop), alpha=0.7) +
  scale_size_area(max_size = 10) +
  facet_wrap(~year)
```



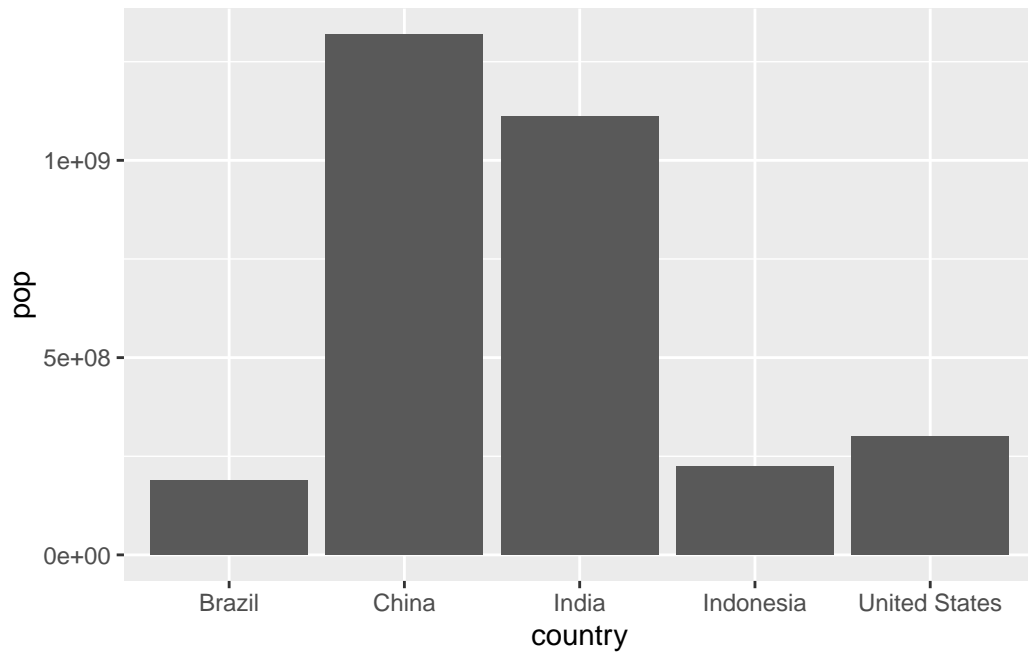
Section 8

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

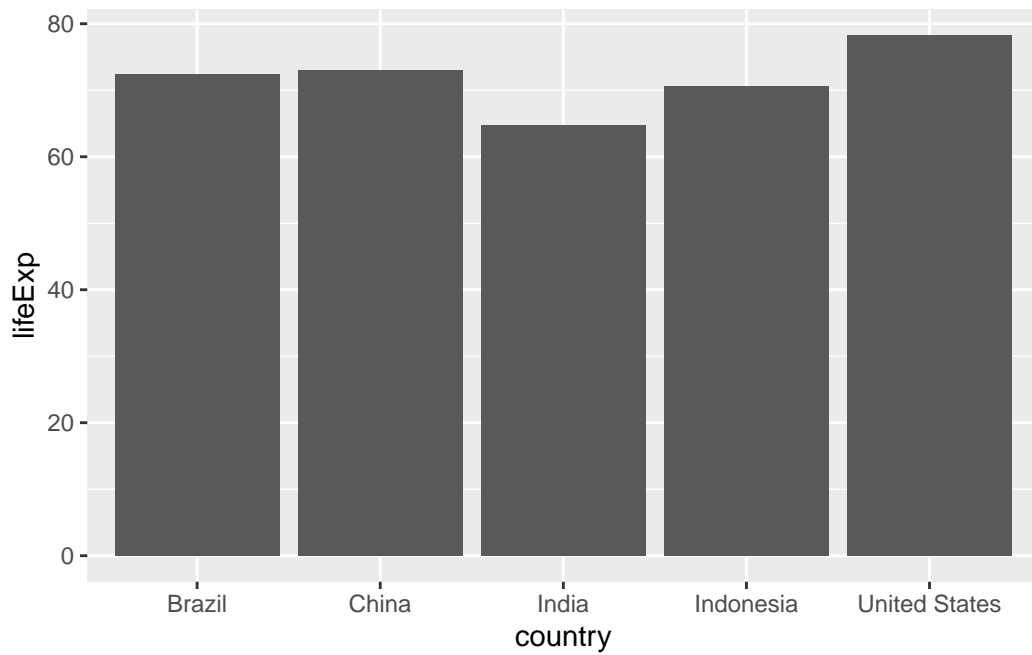
A tibble: 5 x 6

	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.

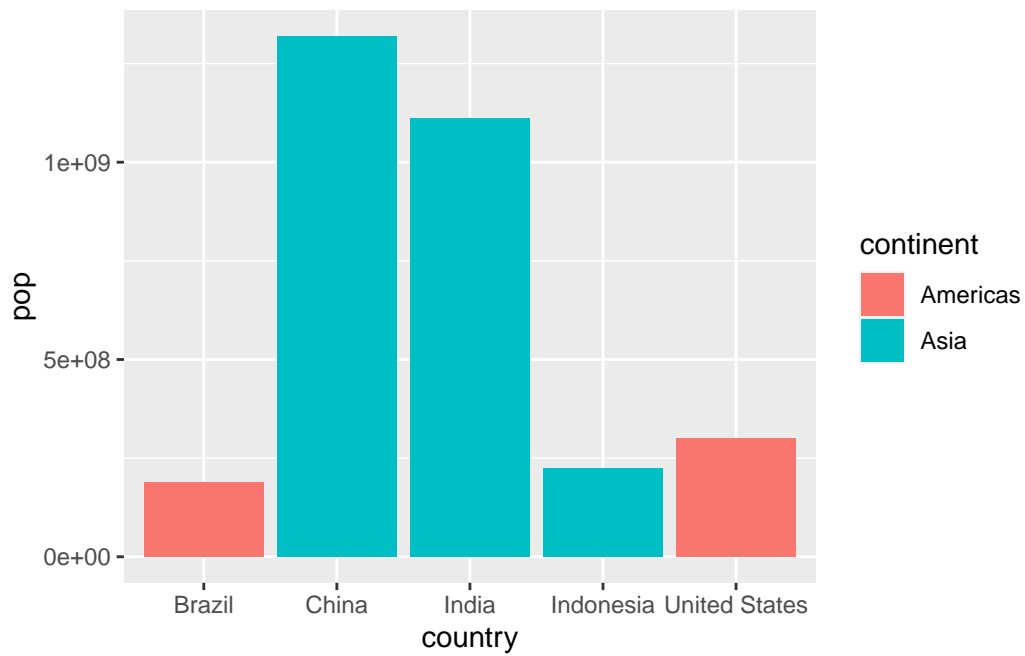
```
ggplot(gapminder_top5)+
  geom_col(aes(x=country, y=pop))
```



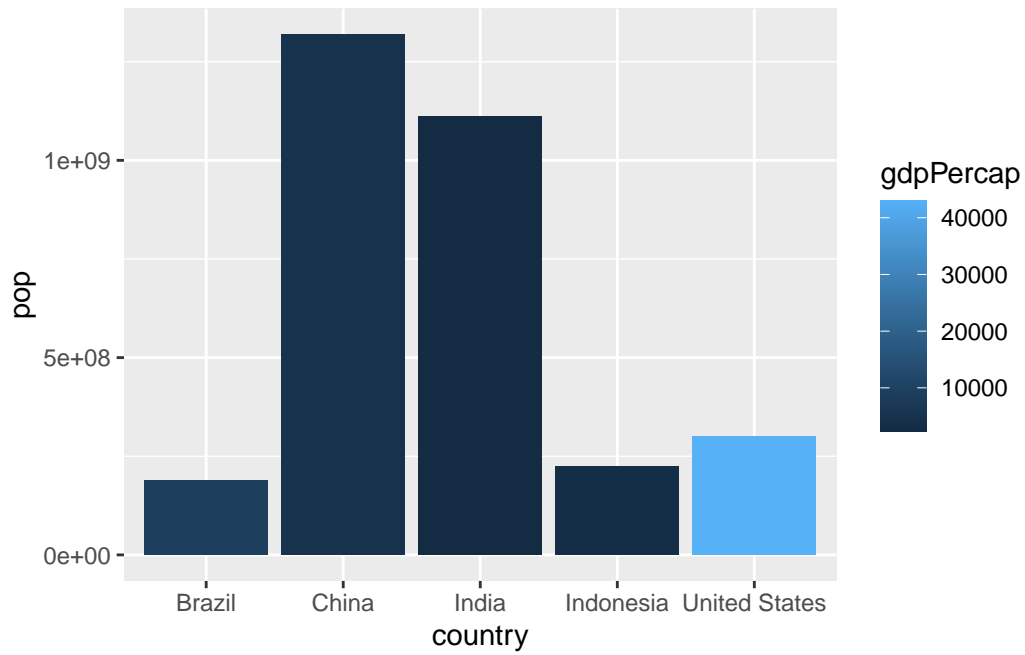
```
ggplot(gapminder_top5)+  
  geom_col(aes(x=country, y=lifeExp))
```



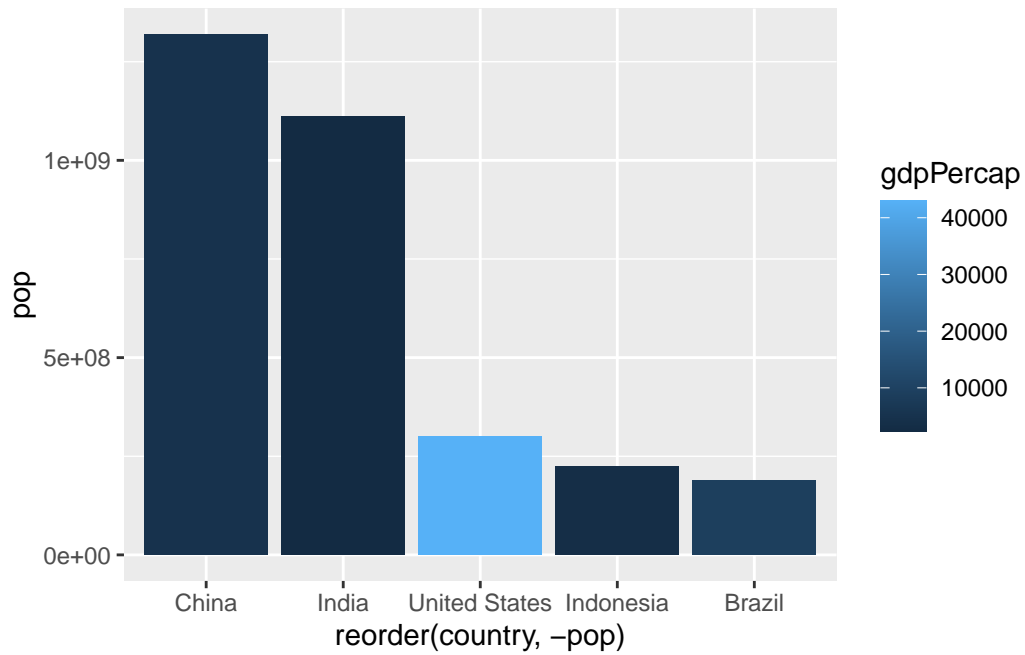

```
ggplot(gapminder_top5)+
  geom_col(aes(x=country, y=pop, fill=continent))
```



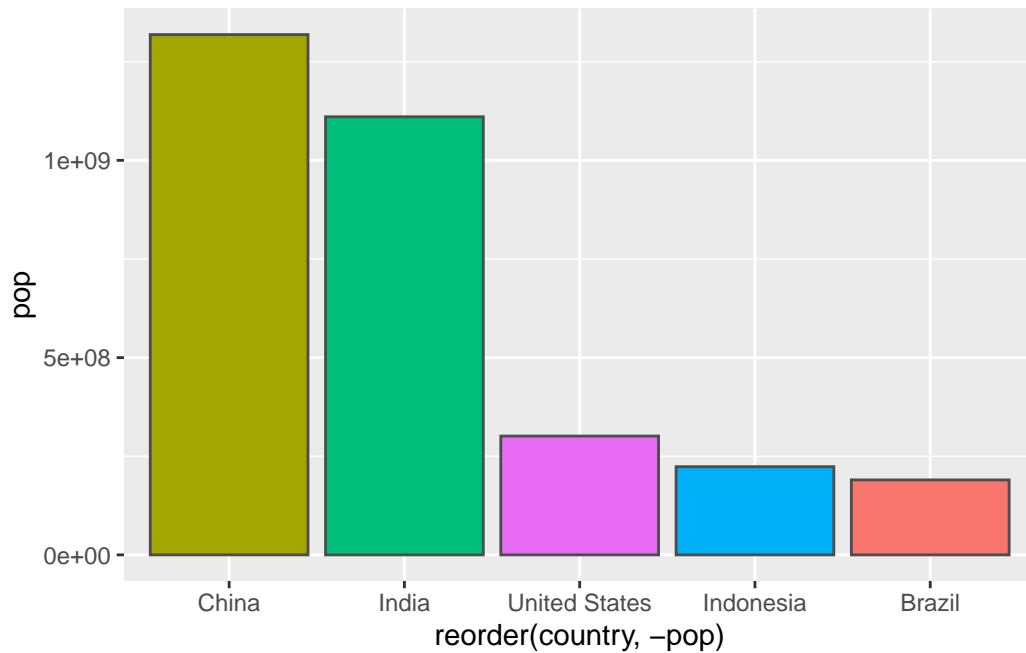
```
ggplot(gapminder_top5)+
  aes(x=country, y=pop, fill=gdpPercap) +
  geom_col()
```



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



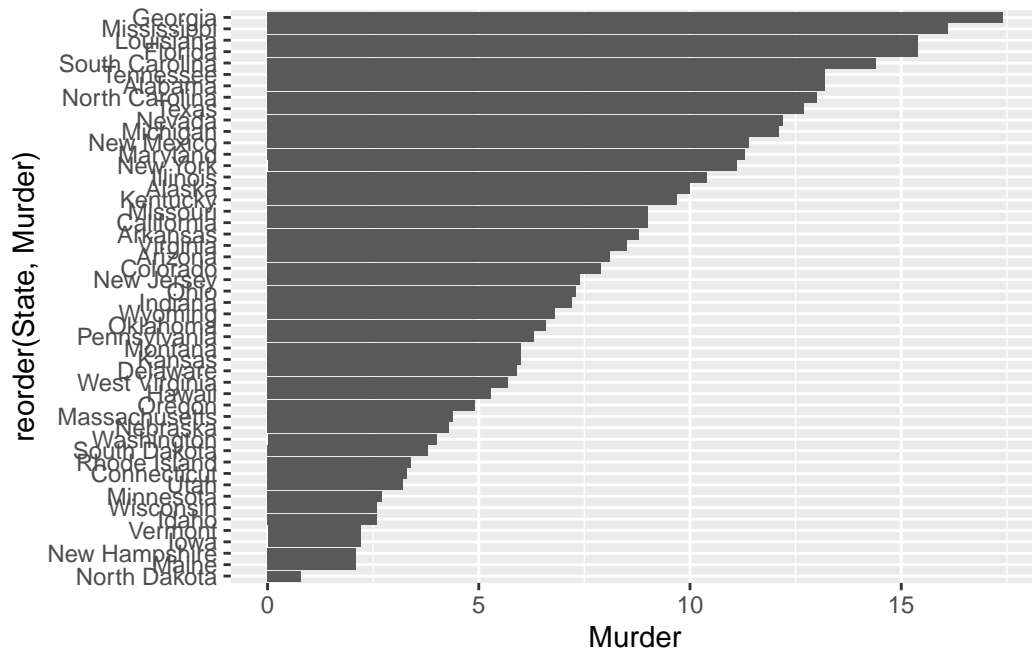
```
ggplot(gapminder_top5) +  
  aes(x=reorder(country, -pop), y=pop, fill=country) +  
  geom_col(col="gray30") +  
  guides(fill="none")
```



```
head(USArrests)
```

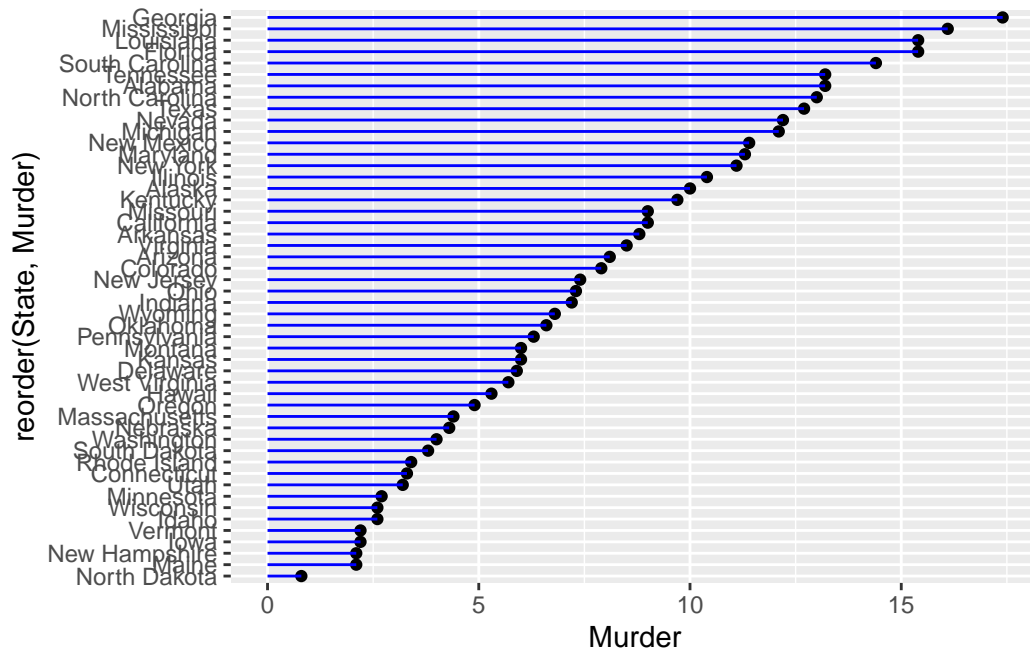
	Murder	Assault	UrbanPop	Rape
Alabama	13.2	236	58	21.2
Alaska	10.0	263	48	44.5
Arizona	8.1	294	80	31.0
Arkansas	8.8	190	50	19.5
California	9.0	276	91	40.6
Colorado	7.9	204	78	38.7

```
USArrests$State <- rownames(USArrests)
ggplot(USArrests) +
  aes(x=reorder(State,Murder), y=Murder) +
  geom_col() +
  coord_flip()
```



Combination

```
ggplot(USArrests) +
  aes(x=reorder(State,Murder), y=Murder) +
  geom_point() +
  geom_segment(aes(x=State,
                   xend=State,
                   y=0,
                   yend=Murder), color="blue") +
  coord_flip()
```



Section 9:

```
library(gapminder)
library(gganimate)

ggplot(gapminder, aes(gdpPercap, lifeExp, size = pop, colour = country)) +
  geom_point(alpha = 0.7, show.legend = FALSE) +
  scale_colour_manual(values = country_colors) +
  scale_size(range = c(2, 12)) +
  scale_x_log10() +
  facet_wrap(~continent) +
  labs(title = 'Year: {frame_time}', x = 'GDP per capita', y = 'life expectancy') +
  transition_time(year) +
  shadow_wake(wake_length = 0.1, alpha = FALSE)
```

Section 10 Combining Plots:

```
library(patchwork)

# Setup some example plots
p1 <- ggplot(mtcars) + geom_point(aes(mpg, disp))
```

```

p2 <- ggplot(mtcars) + geom_boxplot(aes(gear, disp, group = gear))
p3 <- ggplot(mtcars) + geom_smooth(aes(dis, qsec))
p4 <- ggplot(mtcars) + geom_bar(aes(carb))

# Use patchwork to combine them here:
(p1 | p2 | p3) /
  p4

```

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

