Class 05: Data Visualization with GGPLOT

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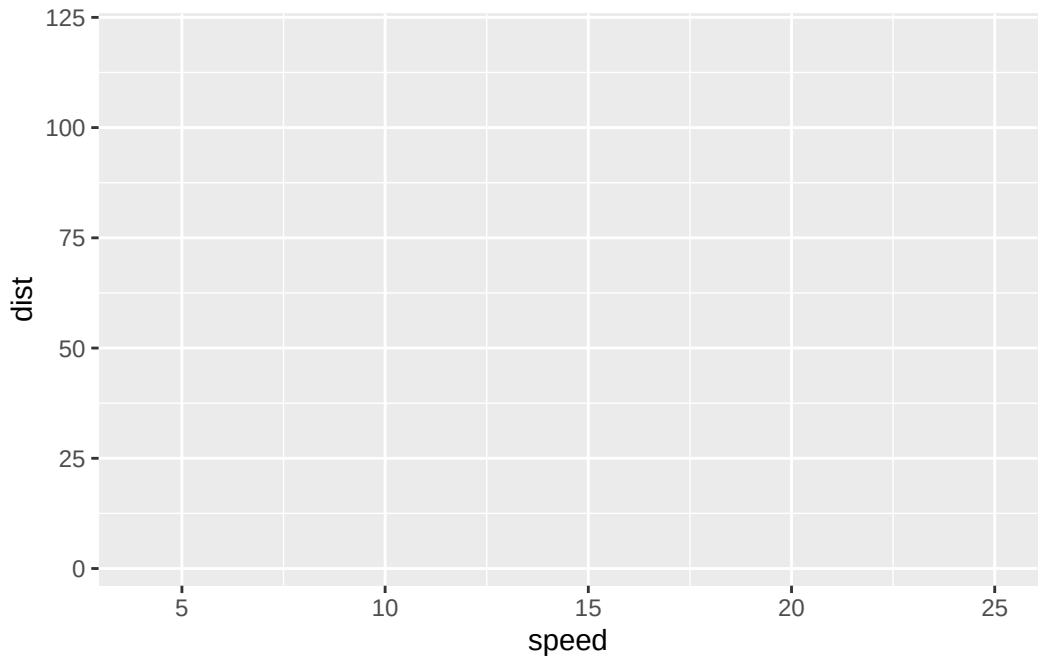
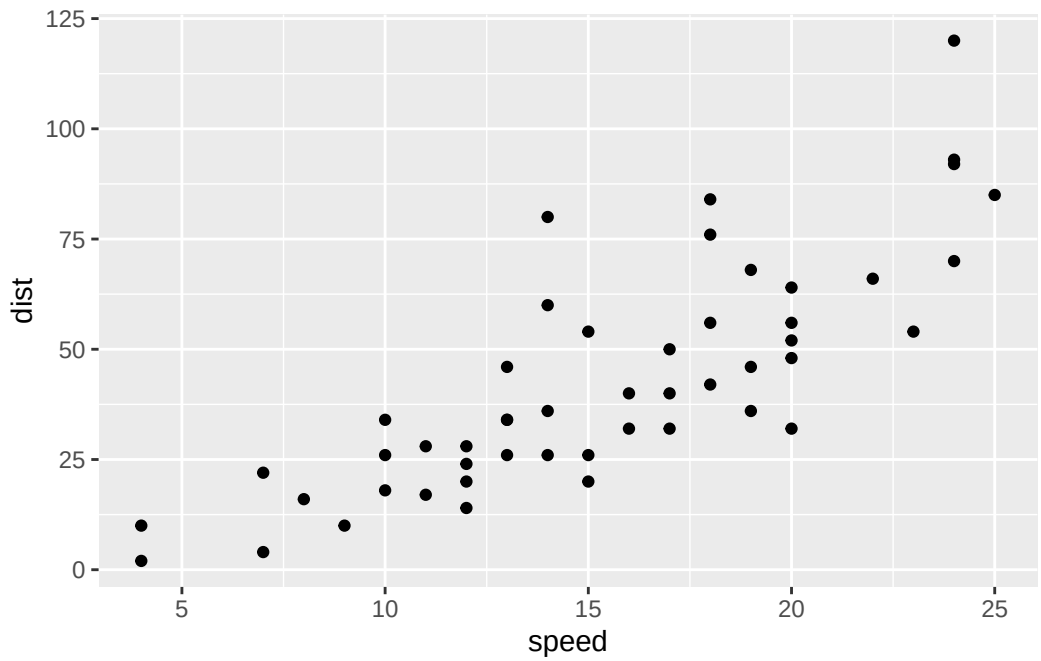
0.1 Cars data ggplot

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

ggplot(cars)
```

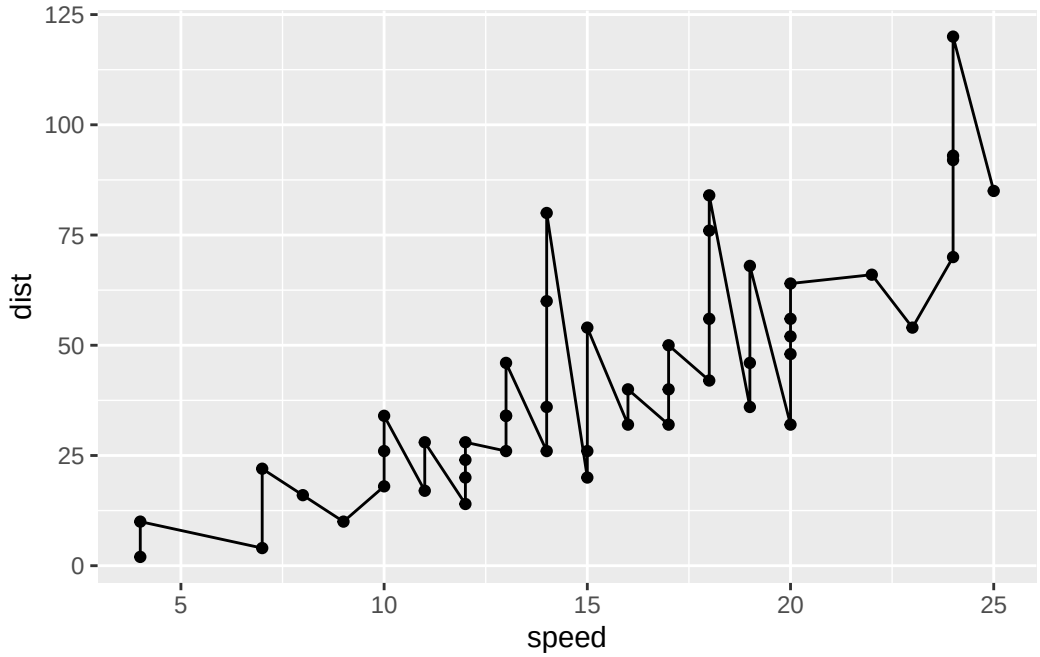
```
ggplot(cars) +
  aes(x=speed, y=dist)
```



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

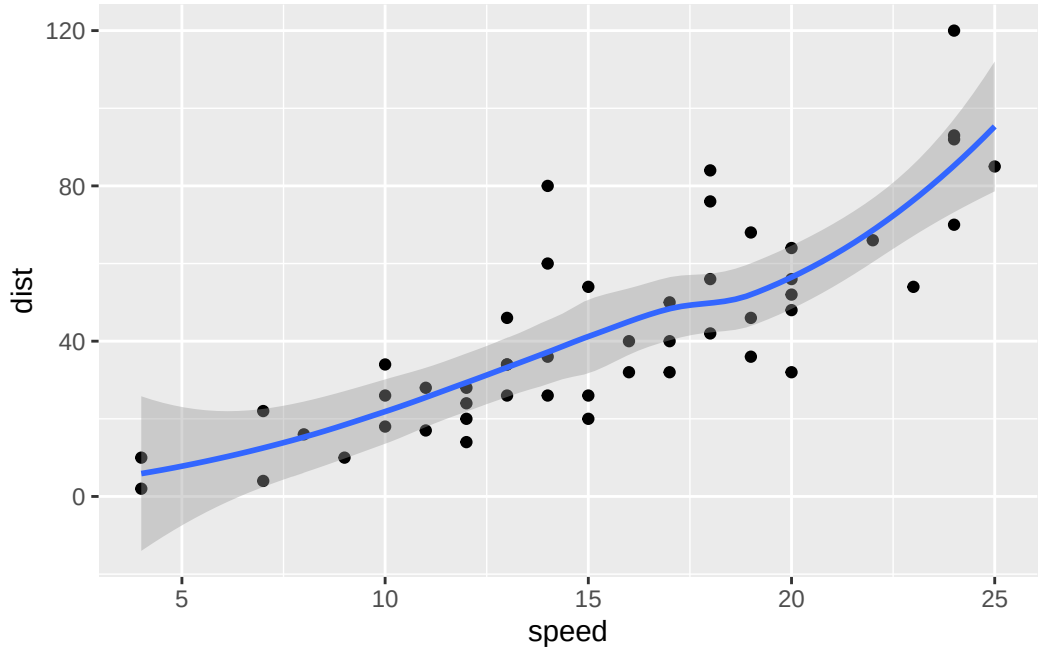



```
x <- ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()

x + geom_line()
```



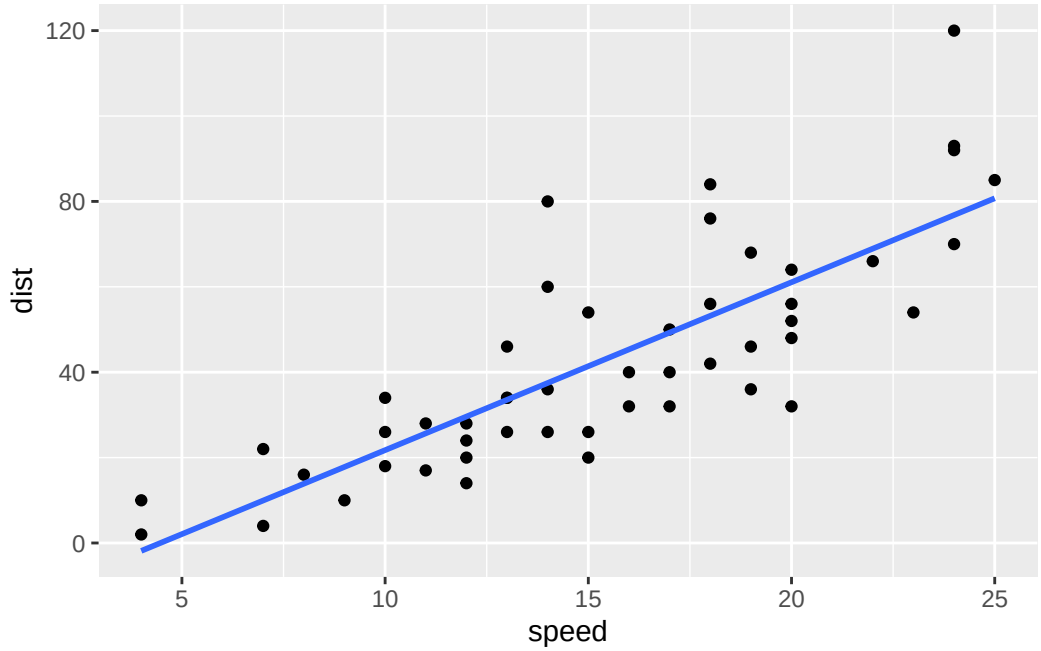

```
x + geom_smooth()
```

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



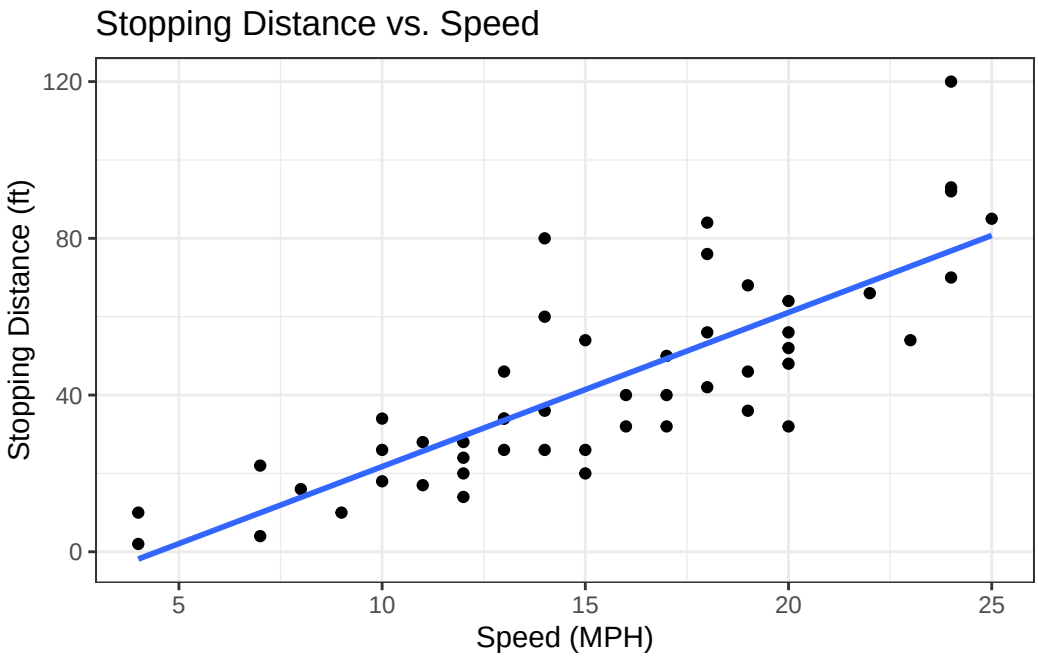

```
x + geom_smooth(method = "lm", se = FALSE)
```

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




```
x + geom_smooth(method = "lm", se = FALSE) +
  labs (title = "Stopping Distance vs. Speed",
          x = "Speed (MPH)",
          y = "Stopping Distance (ft)") +
  theme_bw()
```

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



0.2 Anti-viral drug data analysis

```
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)
```

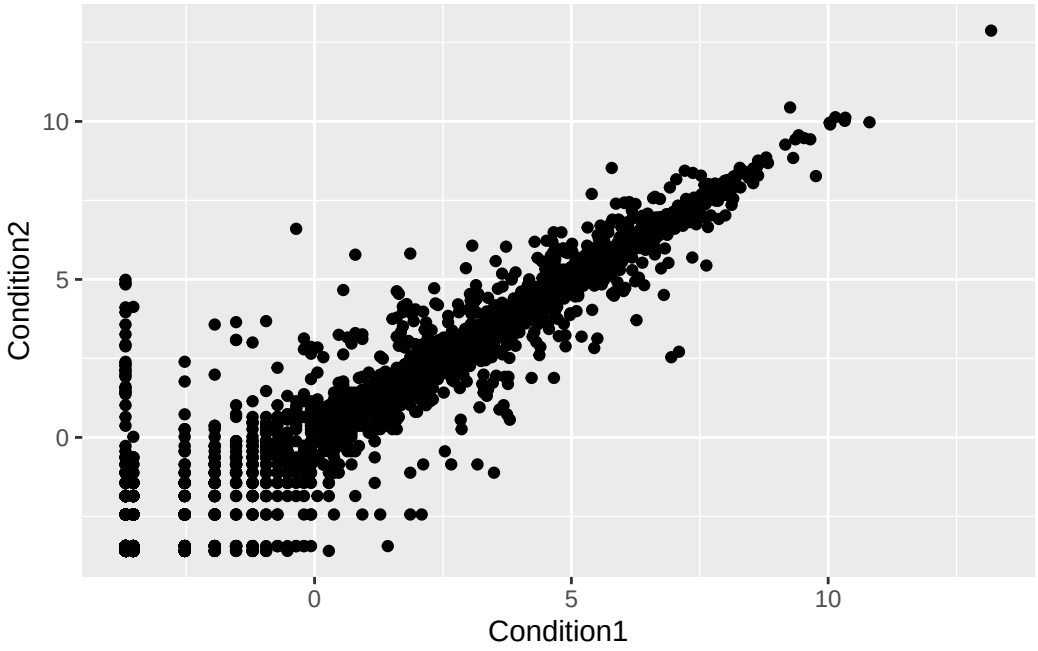
```
      down unchanging         up
        72       4997        127
```

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

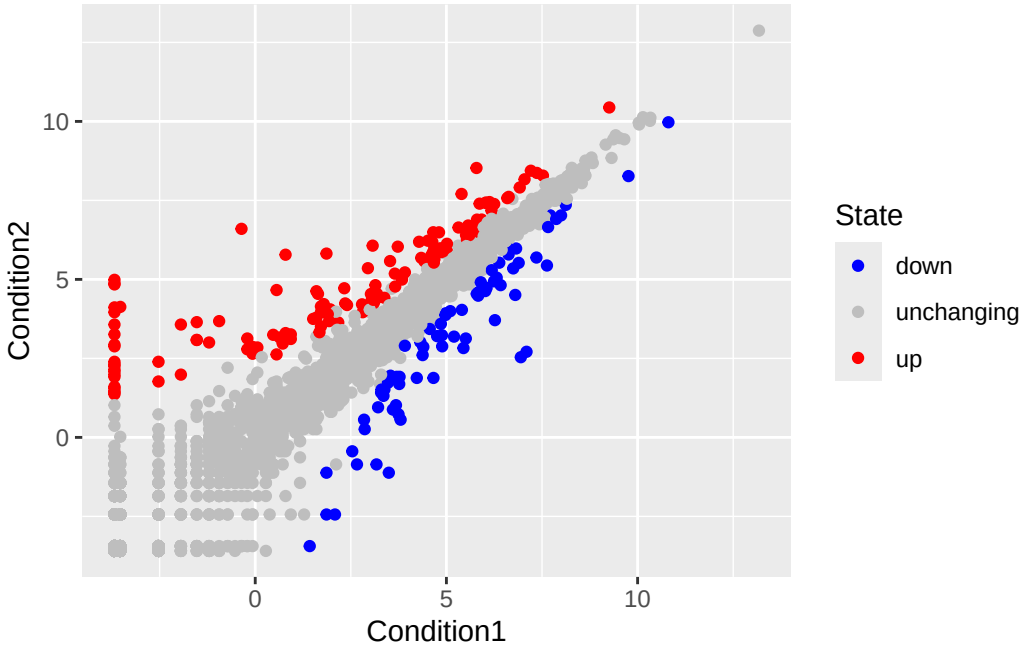
```
      down unchanging         up
      1.39      96.17       2.44
```

0.3 Anti-viral drug data ggplot

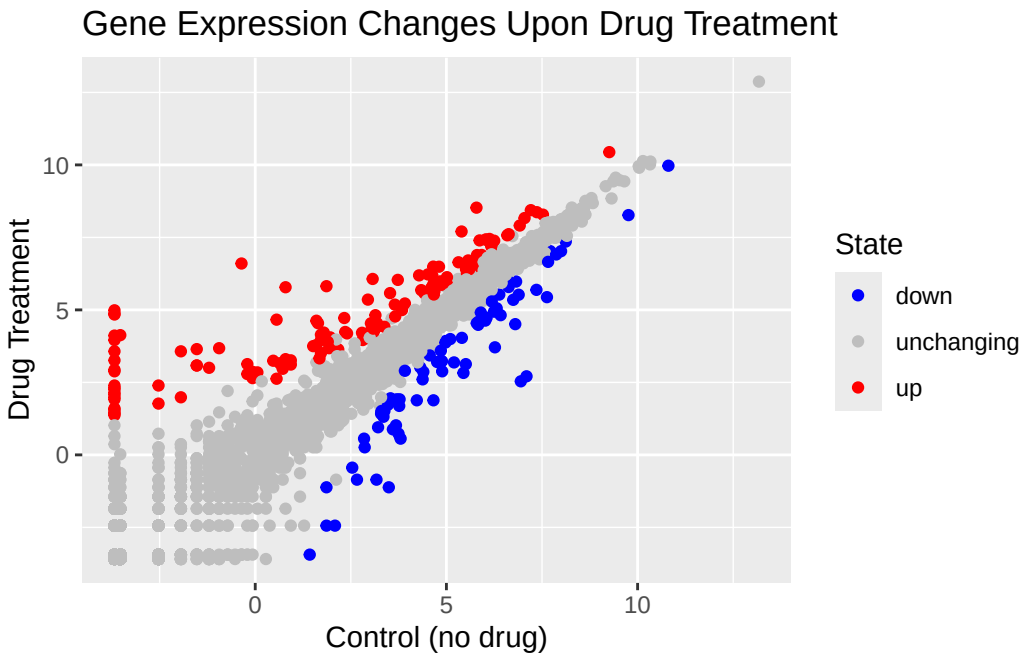
```
ggplot(genes) +
    aes(x=Condition1, y=Condition2) +
    geom_point()
```




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

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




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

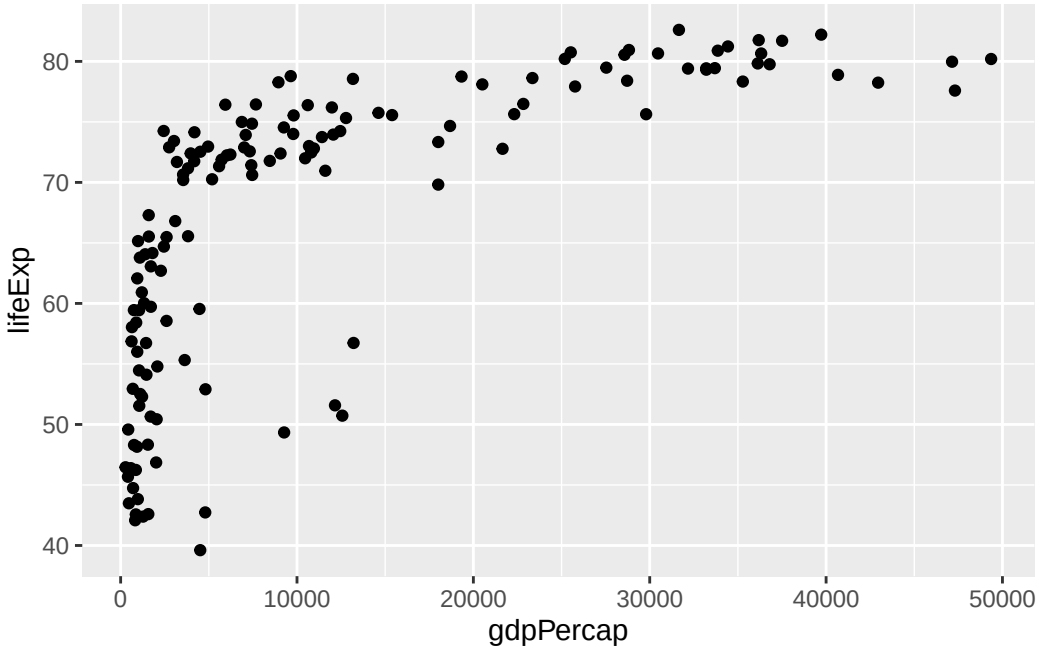


0.4 Economic and demographic data

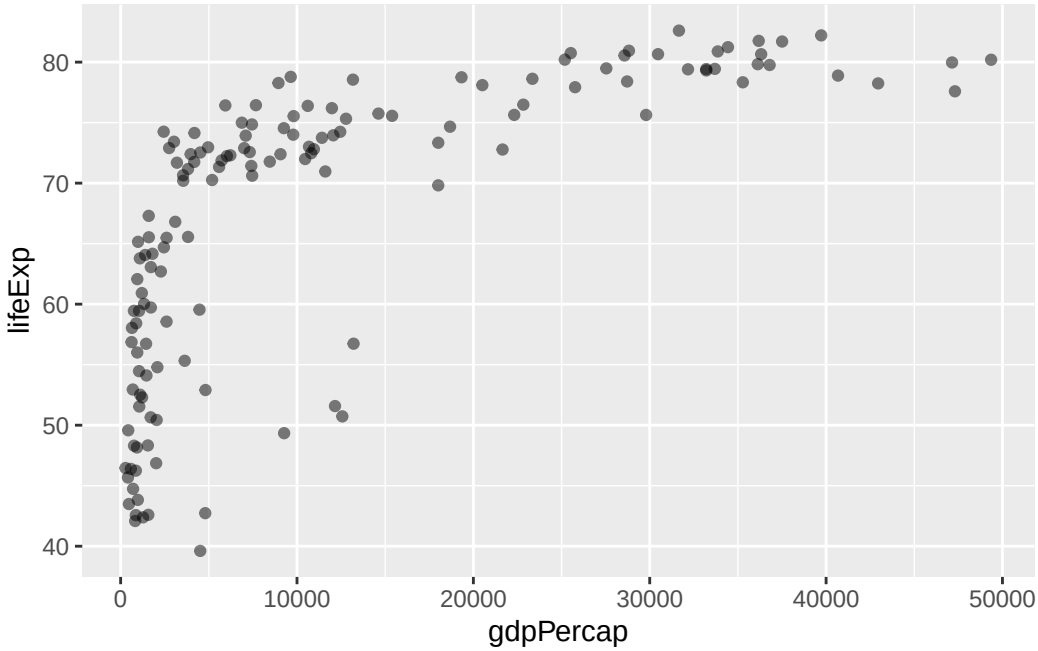
```
##install.packages("gapminder")
library(gapminder)

##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
```

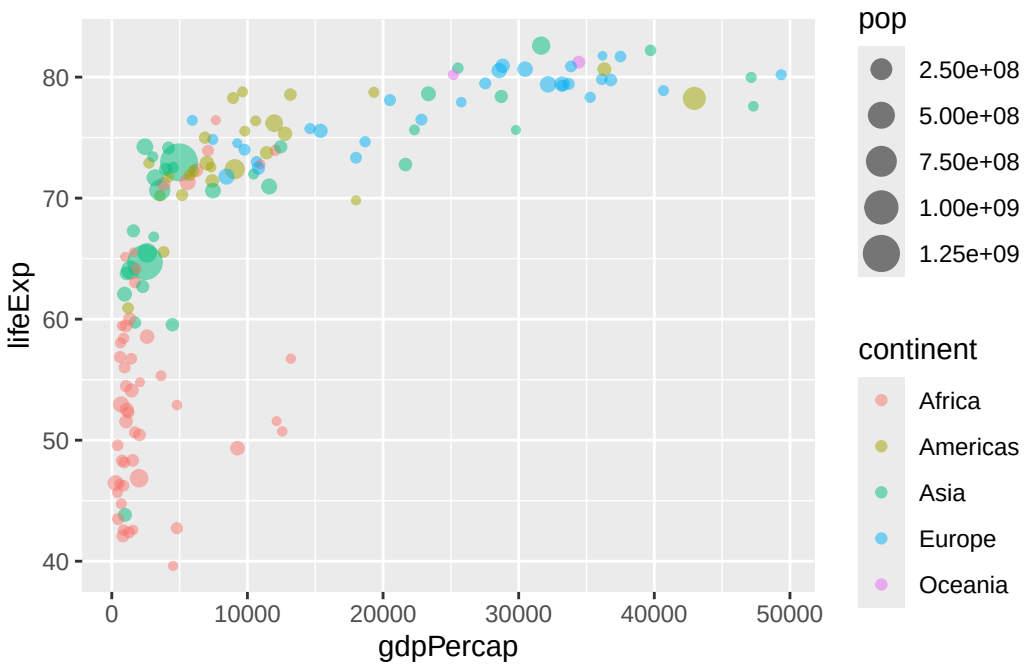
```r
gapminder_2007 <- gapminder %>% filter(year==2007)

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



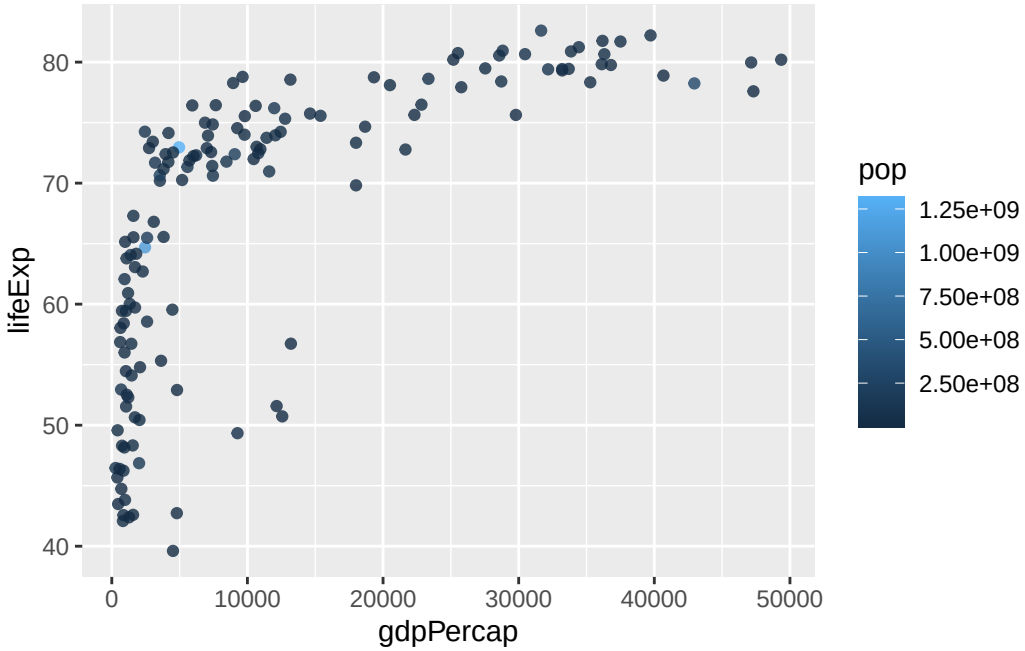

```r
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.5)
```



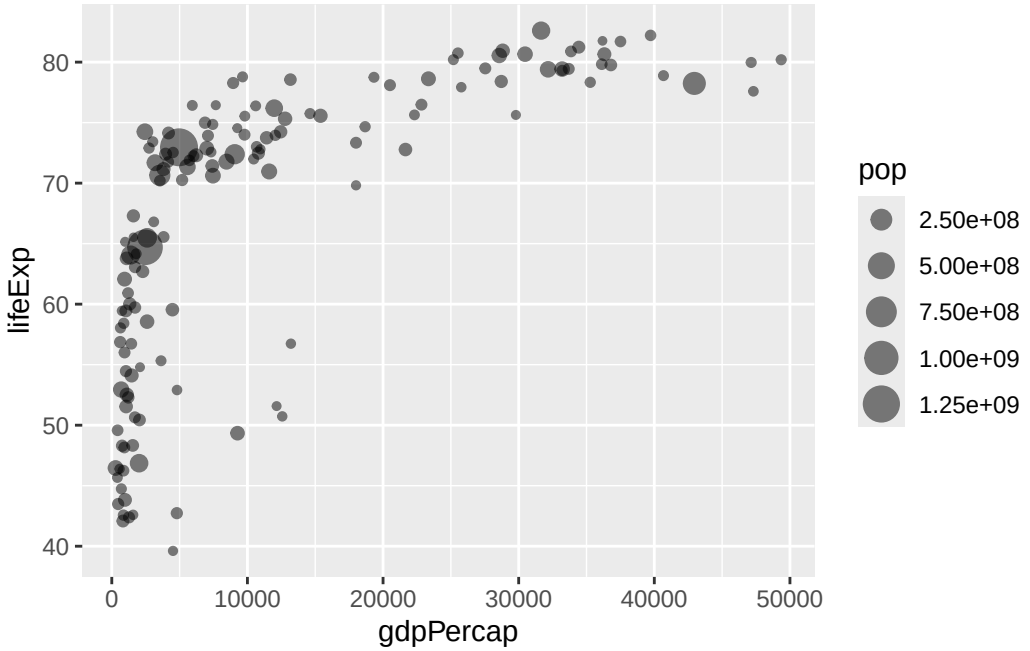

```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)
```



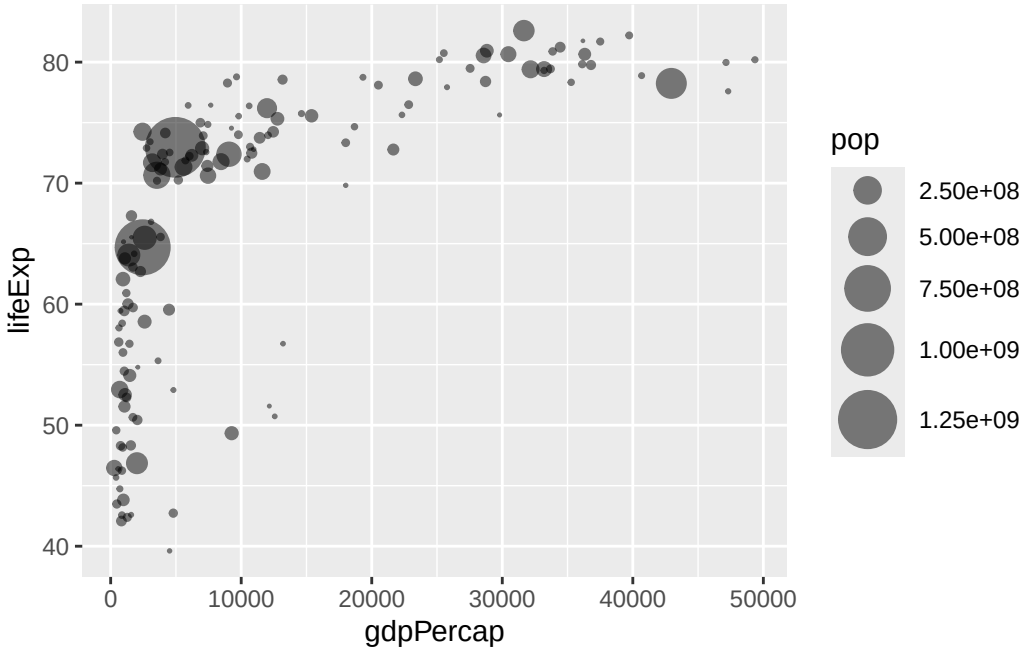

```
ggplot(gapminder_2007) +
  aes(x = gdpPercap, y = lifeExp, color = pop) +
  geom_point(alpha=0.8)
```



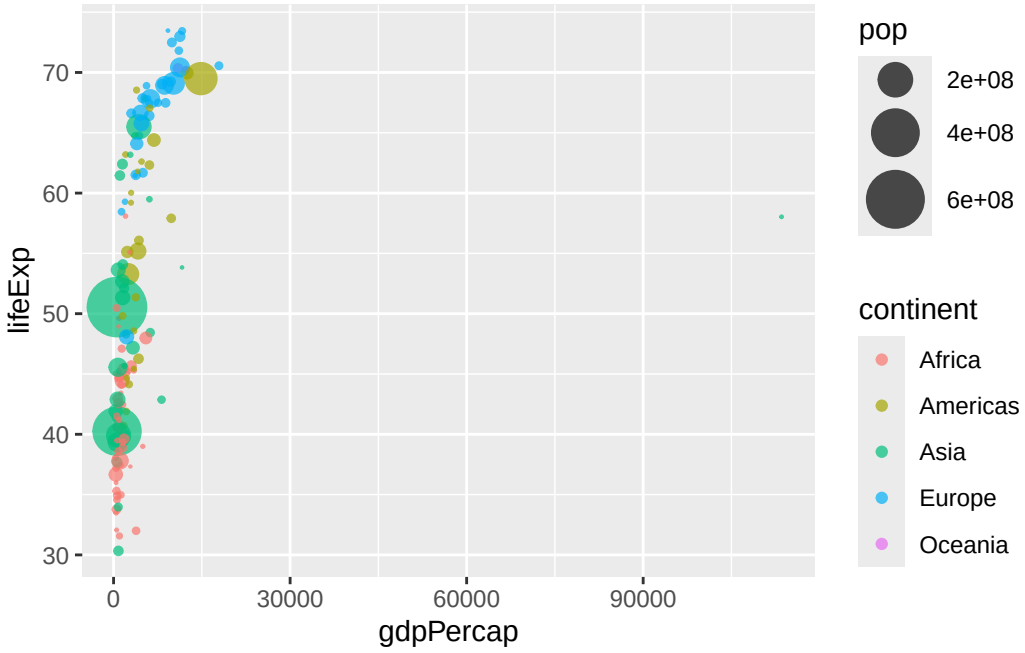

```
ggplot(gapminder_2007) +
  aes(x = gdpPercap, y = lifeExp, size = pop) +
  geom_point(alpha=0.5)
```



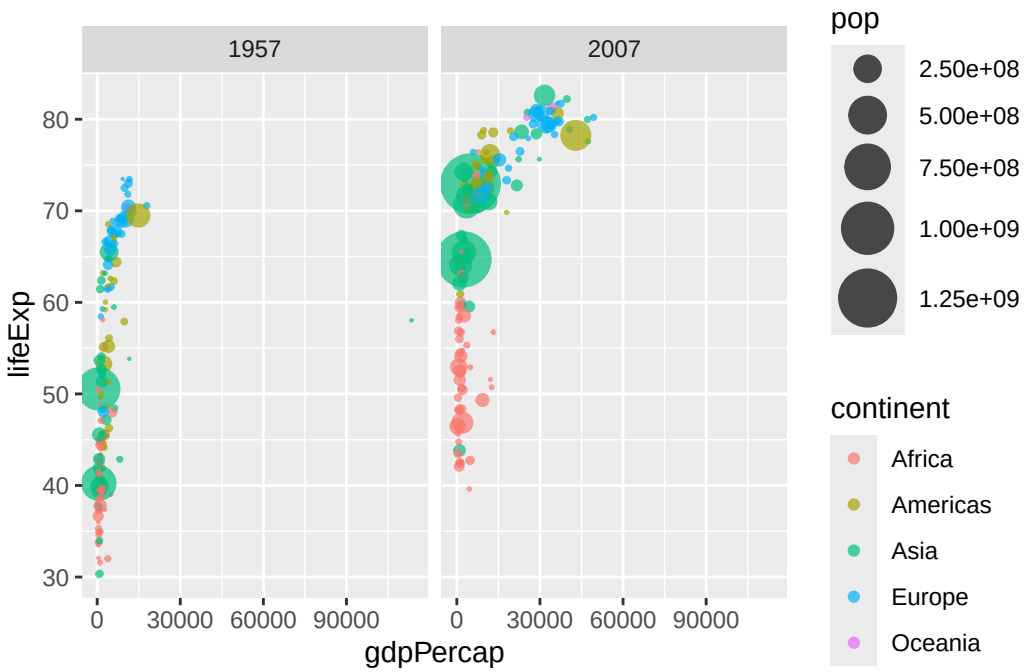

```
ggplot(gapminder_2007) +
  geom_point(aes(x = gdpPercap, y = lifeExp,
                 size = pop), alpha=0.5) +
  scale_size_area(max_size = 10)
```




```
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)
```

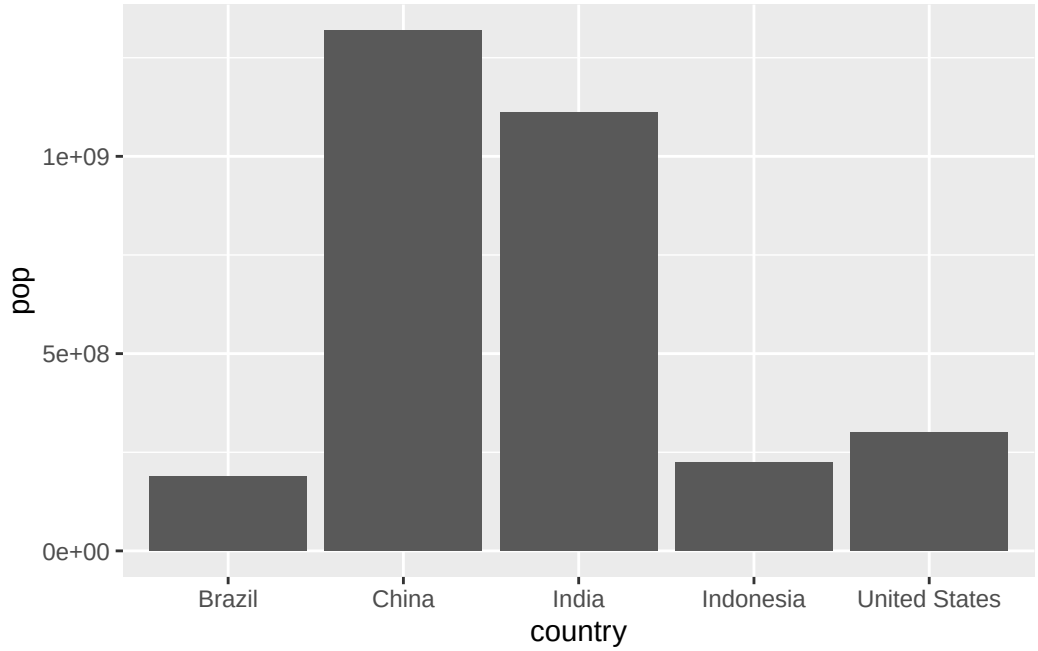


0.5 OPTIONAL

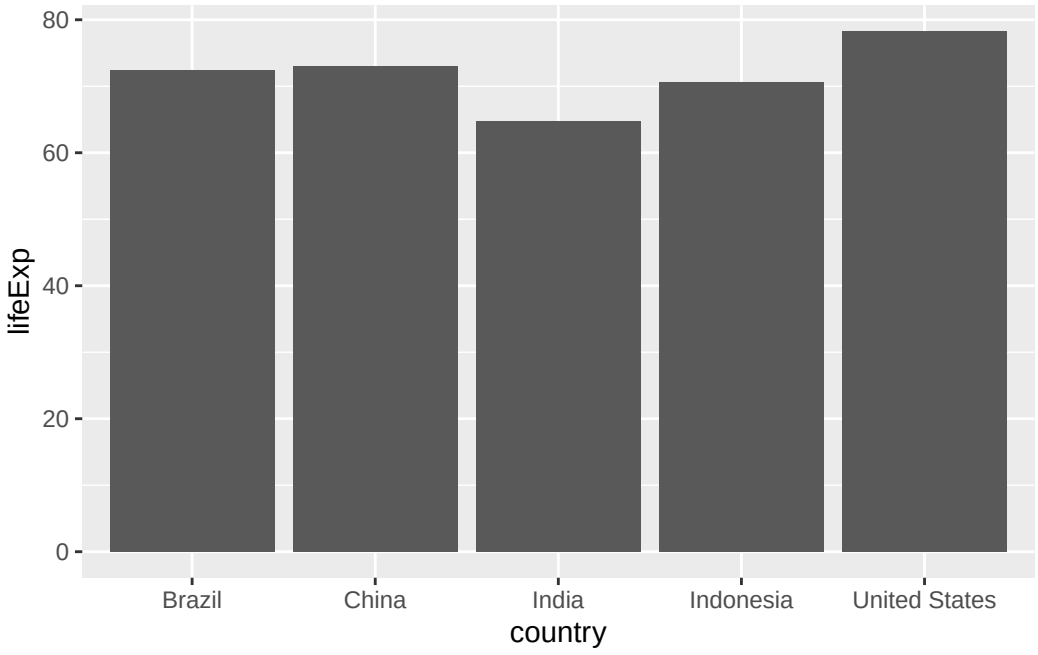
```
gapminder_top5 <- gapminder %>%
  filter(year==2007) %>%
  arrange(desc(pop)) %>%
  top_n(5, pop)

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.
```

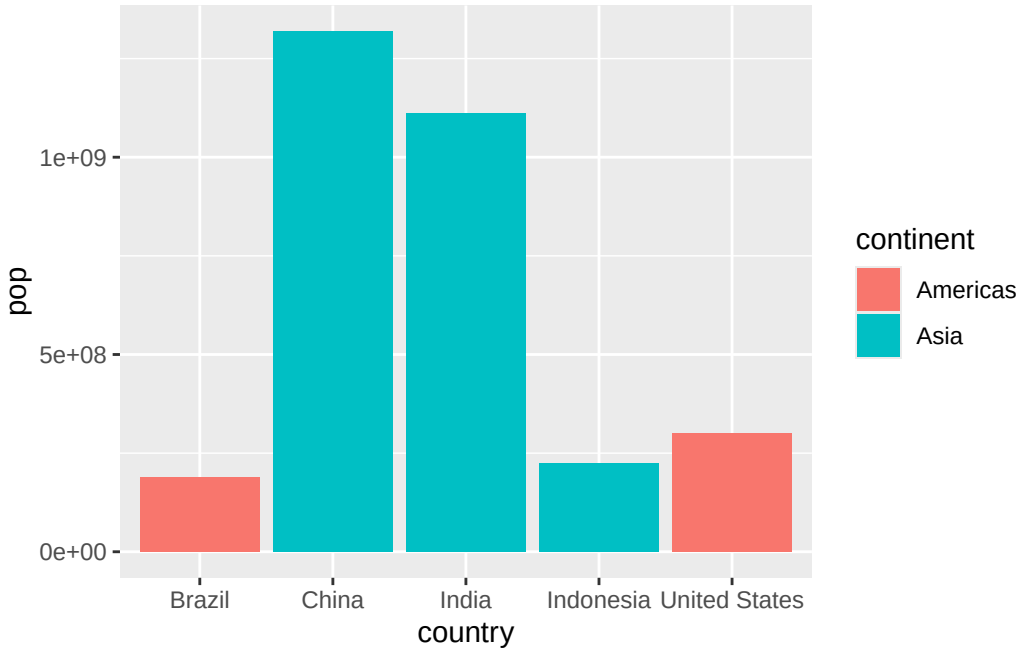
```
ggplot(gapminder_top5) +
  geom_col(aes(x = country, y = pop))
```



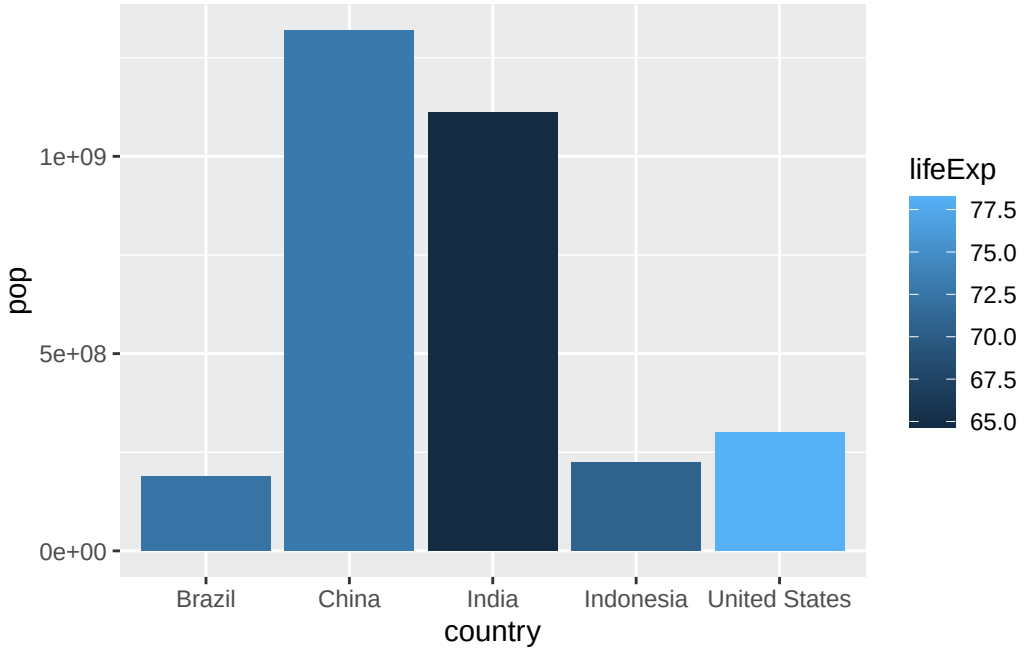

```
ggplot(gapminder_top5) +
  geom_col(aes(x = country, y = lifeExp))
```



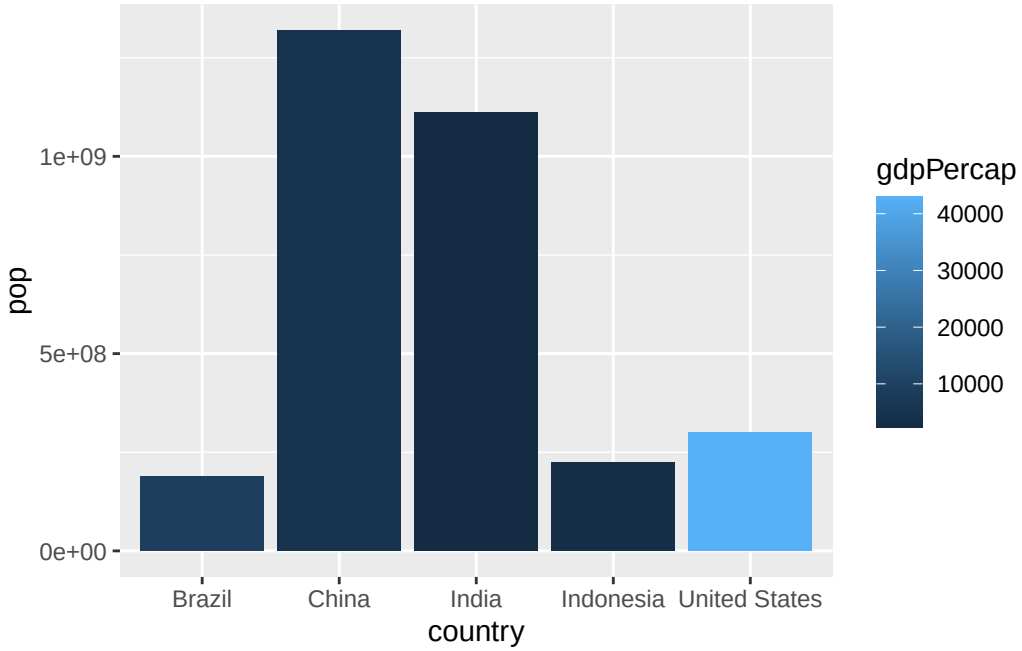
```
ggplot(gapminder_top5) +
  geom_col(aes(x = country, y = pop, fill = continent))
```



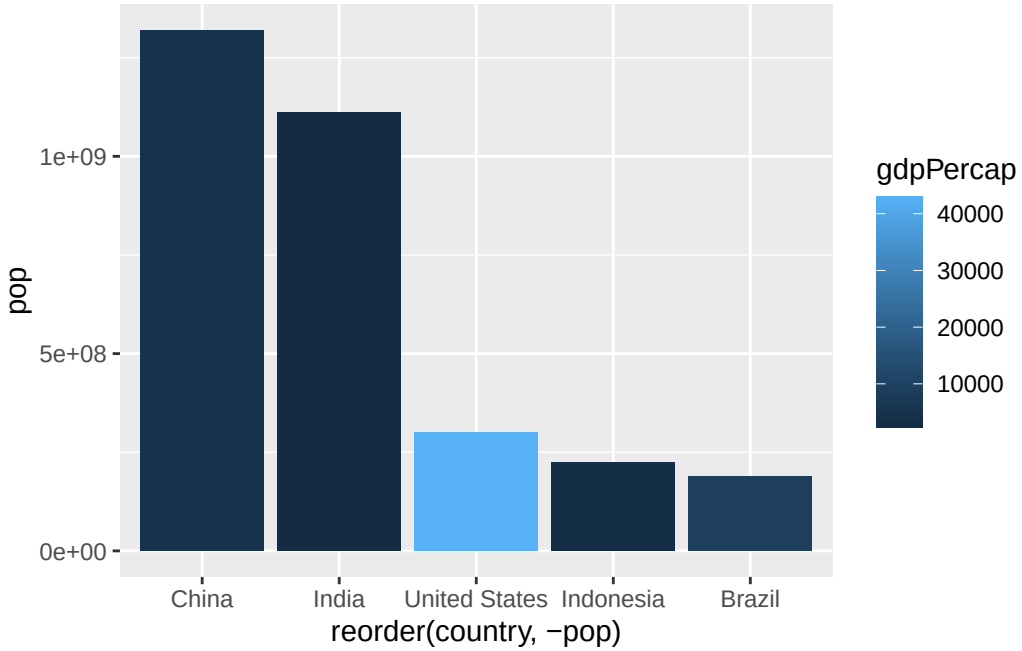

```
ggplot(gapminder_top5) +
  geom_col(aes(x = country, y = pop, fill = lifeExp))
```



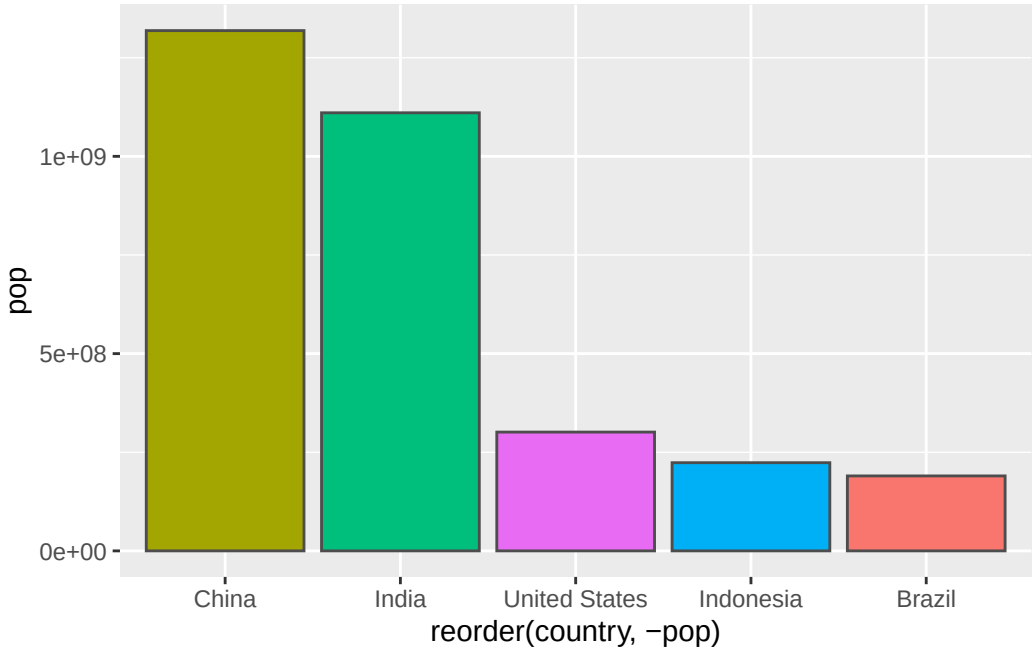

```
ggplot(gapminder_top5) +
  aes(x=country, y=pop, fill=gdpPercap) +
  geom_col()
```




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



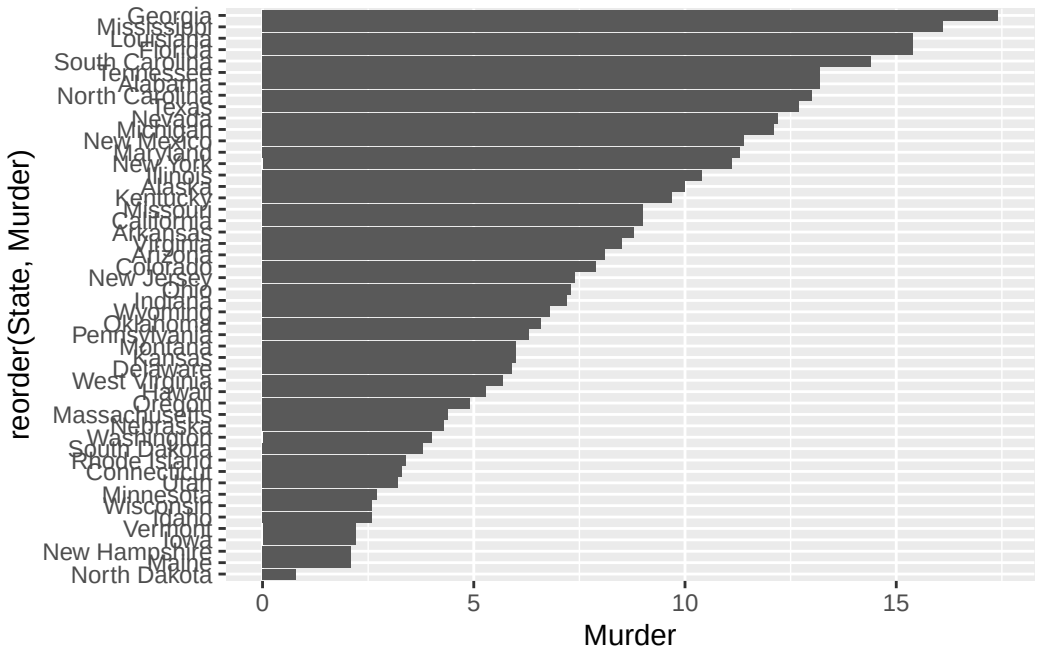

```
ggplot(gapminder_top5) +
  aes(x=reorder(country, -pop), y=pop, fill=country) +
  geom_col(col="gray30") +
  guides(fill="none")
```



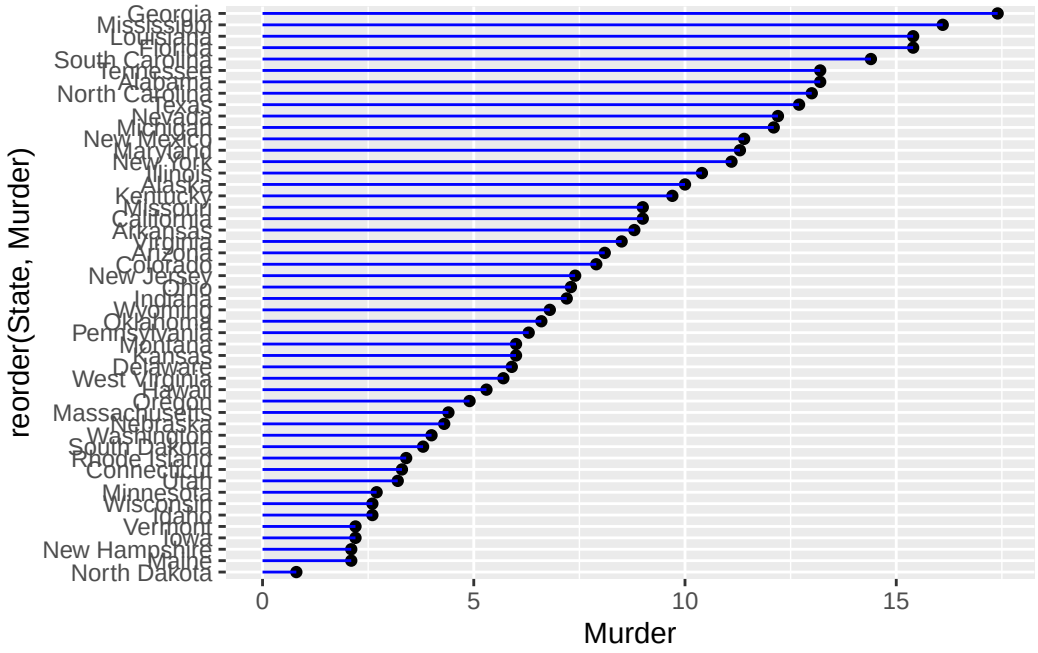

```
head(USArrests)
```

```
           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()
```




```
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()
```


reorder(State, Murder)
Georgia
Mississippi
Louisiana
Florida
South Carolina
Tennessee
Alabama
North Carolina
Texas
Nevada
Michigan
New Mexico
Maryland
New York
Illinois
Alaska
Kentucky
Missouri
California
Arkansas
Virginia
Arizona
Colorado
New Jersey
Ohio
Indiana
Wyoming
Oklahoma
Pennsylvania
Montana
Kansas
Delaware
West Virginia
Hawaii
Oregon
Massachusetts
Nebraska
Washington
South Dakota
Rhode Island
Connecticut
Utah
Minnesota
Wisconsin
Idaho
Vermont
Iowa
New Hampshire
Maine
North Dakota
0
5
10
15
Murder