Class 5 Data Visualization with ggplot2

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Using GGPLOT

The ggplot2 package needs to be installed as it does not come with R "out of the box."

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

```
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.

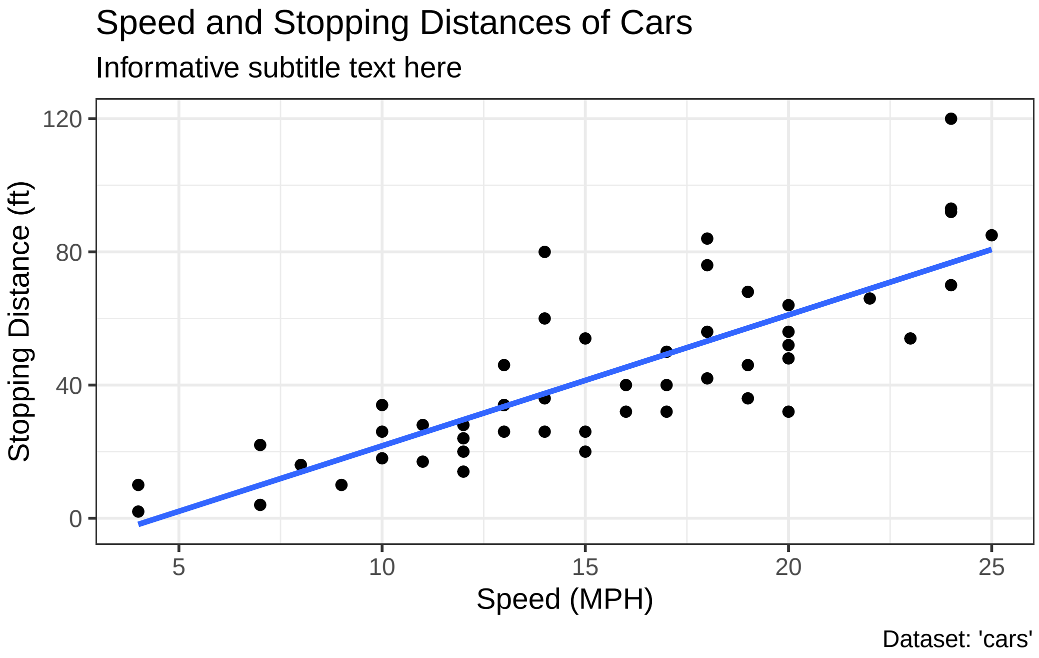
```
library(ggplot2)
```

All ggplot figures have at least 3 things: - data (the stuff we want to plot) - aesthetic mapping (aed values) - geoms

```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  labs(title="Speed and Stopping Distances of Cars",
       x="Speed (MPH)",
       y="Stopping Distance (ft)",
       subtitle="Informative subtitle text here",
```

```r
       caption="Dataset: 'cars'") +
  geom_smooth(method="lm", se=FALSE) +
  theme_bw()
```

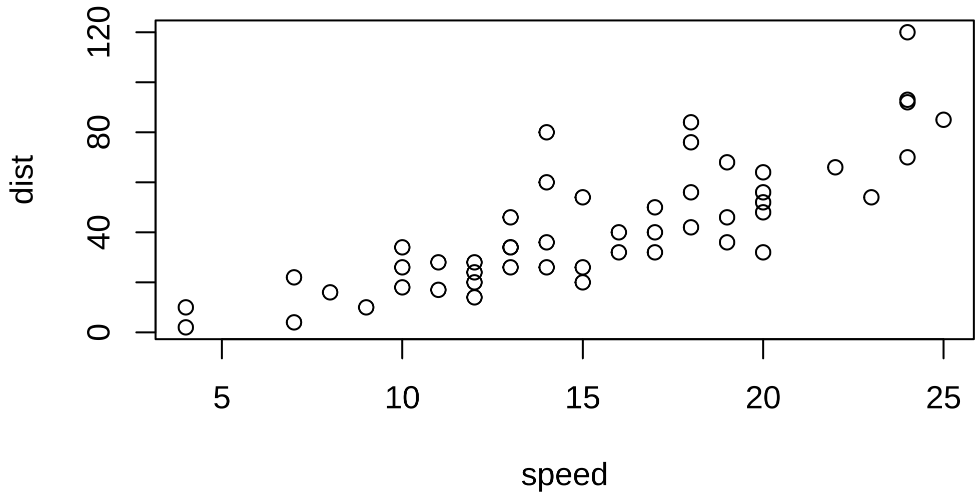
```
`geom_smooth()` using formula = 'y ~ x'
```



To figure out what parameters are able to be manipulated, hover over the function and press ‘F1’ in RStudio. - Or, type ‘?(function_name)’ into the R console.

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

```r
plot(cars)
```



6. Creating Scatter Plots

Adding more plot aesthetics through `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"])
```

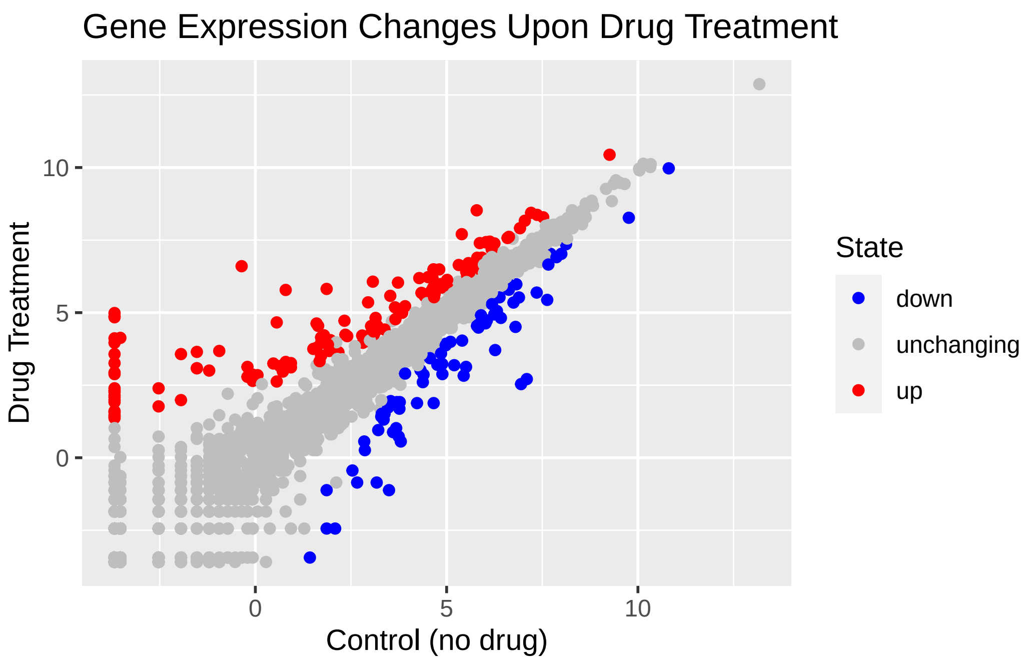
```
State
      down unchanging         up 
        72       4997        127 
```

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

```

      down unchanging         up 
      1.39      96.17       2.44 
```

- There are 5196 rows, 4 columns ("Gene", "Condition1", "Condition2", "State"), 127 'up' regulated genes, & 2.44 of the total genes are 'up' regulated.

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

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



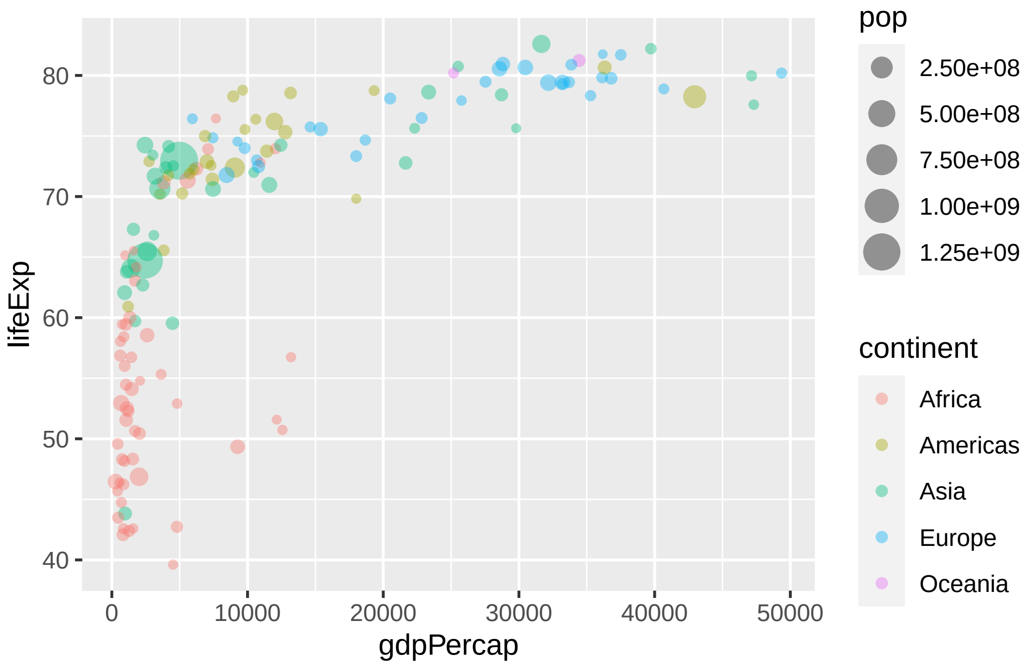
7. Going further with gapminder dataset

```
## Remove # if packages are not already installed
# install.packages("gapminder")

## Install dplyr package to focus on a single year
# install.packages("dplyr")
```

```
library(gapminder)
library(dplyr)
```

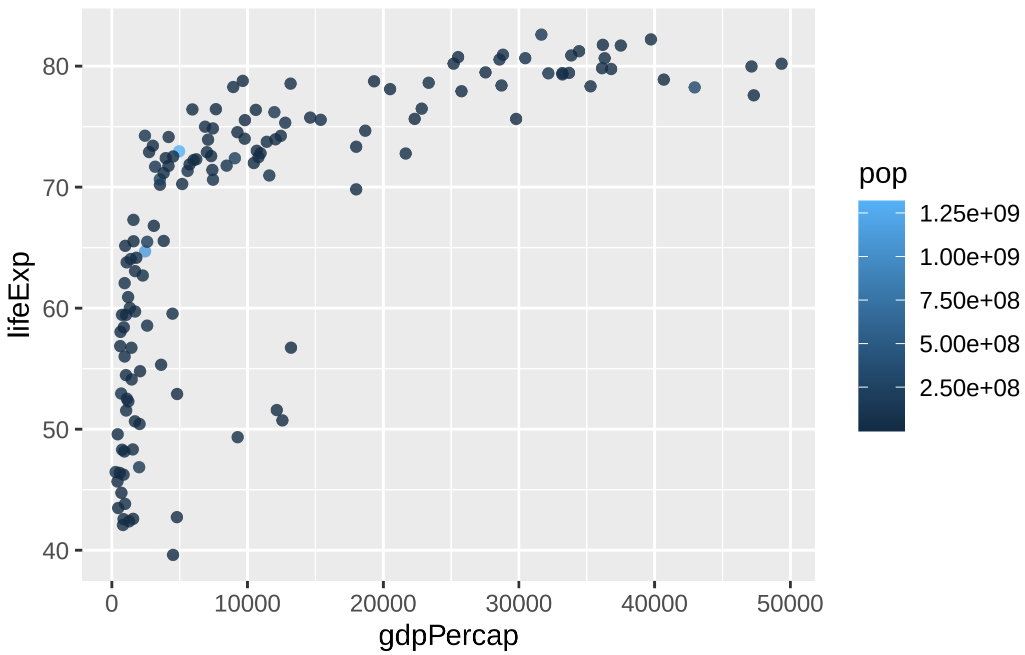
```

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=0.4)
```



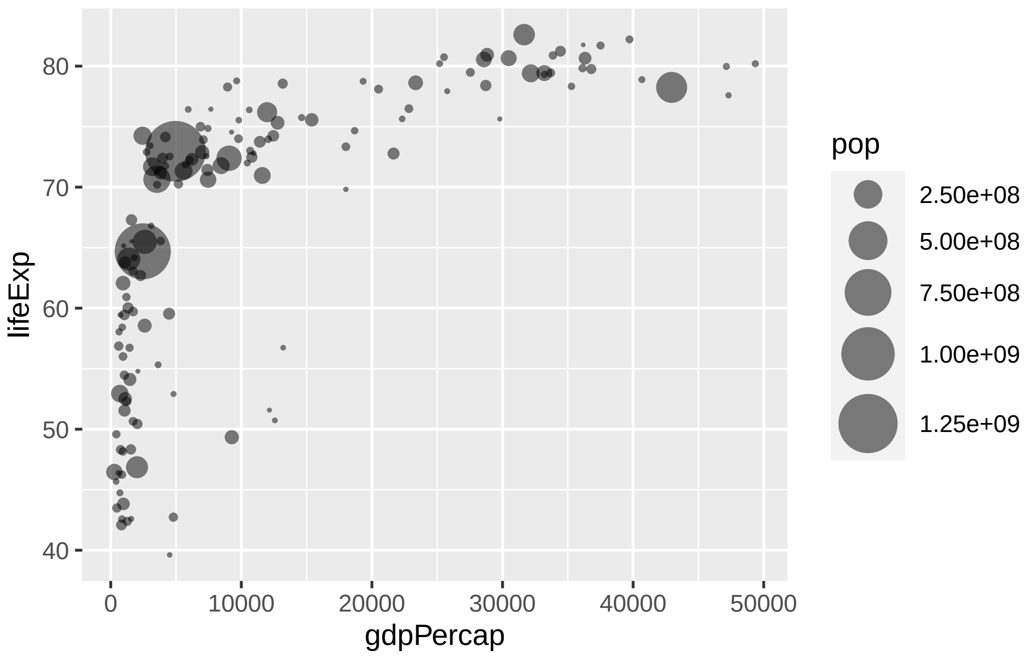
If the plot points were colored by the numeric variable population pop:

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



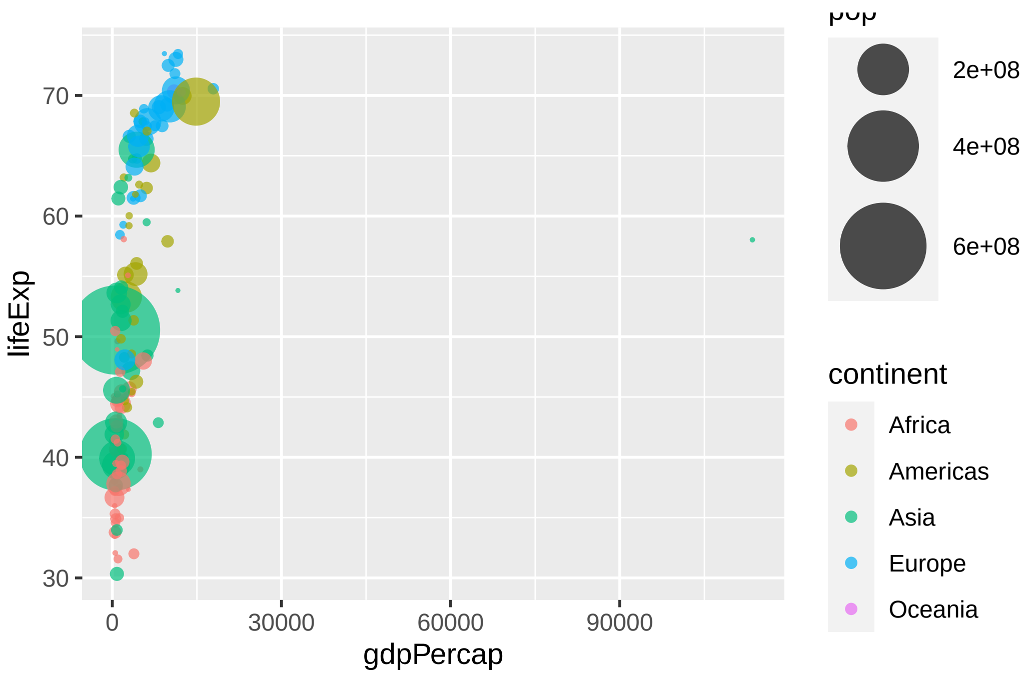
Adjusting point size based on the population (size=pop) of each country:

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



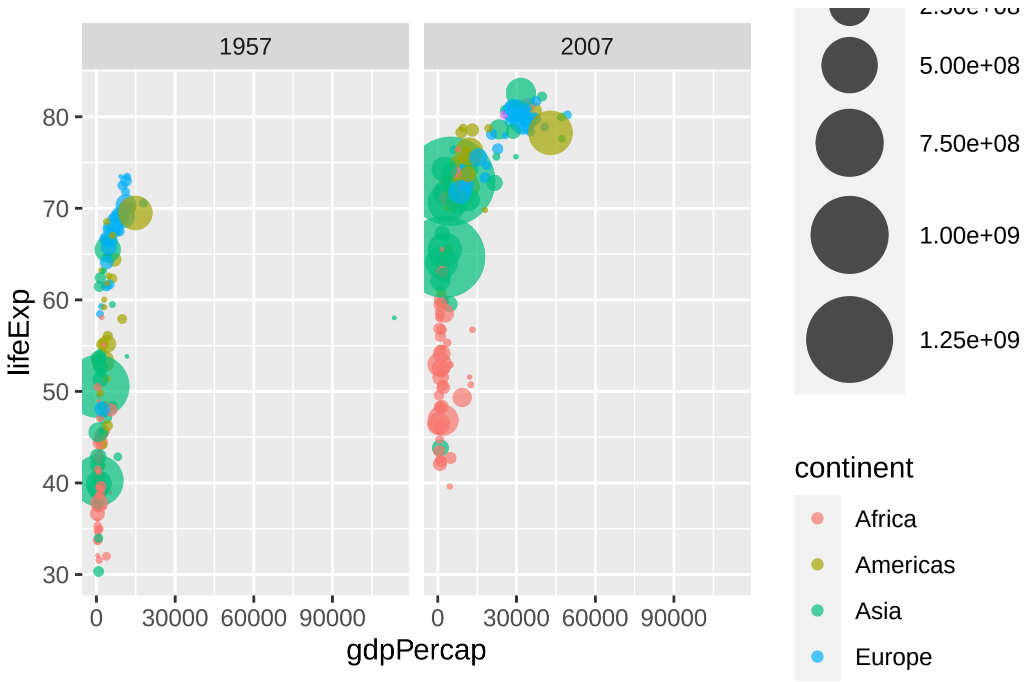
For the gapminder year 1957:

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

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



Comparing the years 1957 & 2007:

```
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 = 15) +
  facet_wrap(~year)
```



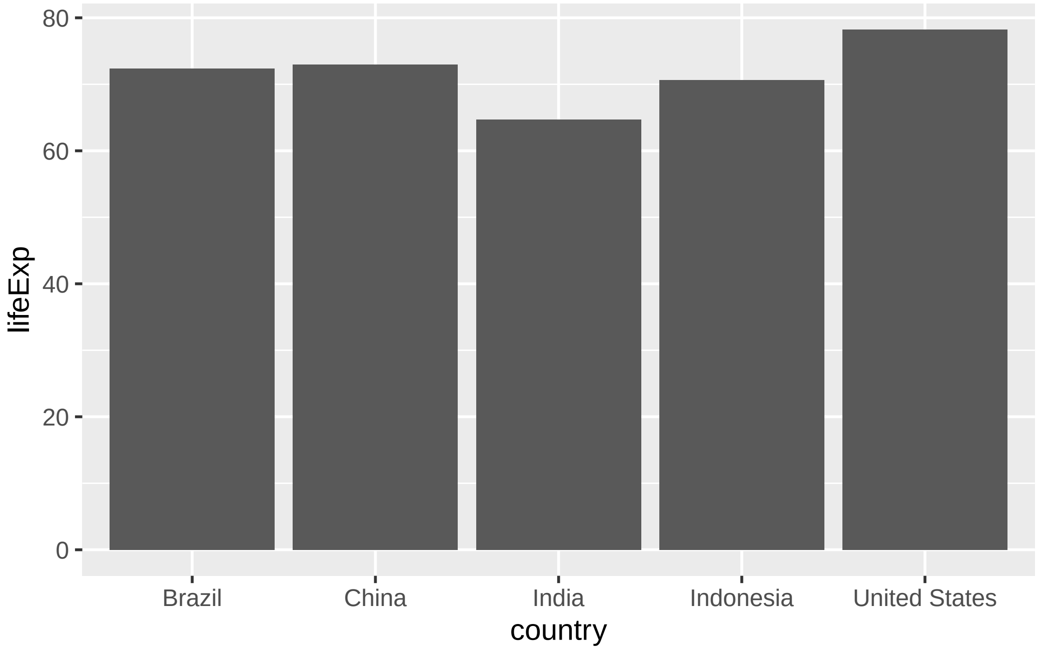
8. Bar Charts

```
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.
```

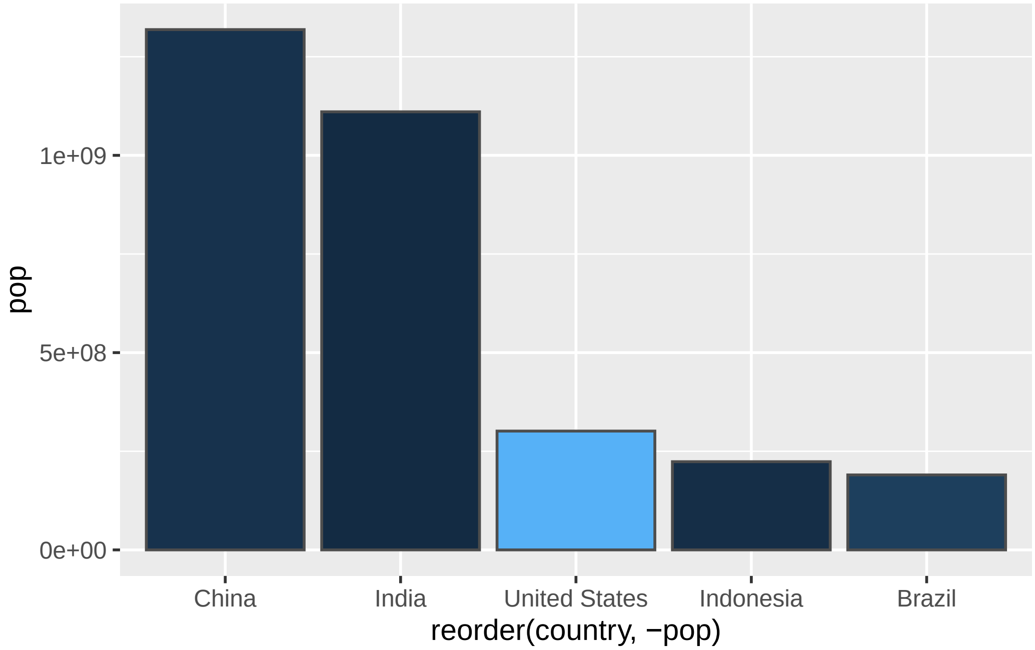
Creating a simple bar chart:

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



Filling bars with color: - `geom_col(col="gray30")` adds a grey outline to the bars. - `guides(fill="none")` will remove the legend.

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


1e+09
5e+08
0e+00
pop
China
India
United States
Indonesia
Brazil
reorder(country, −pop)