Class5.R

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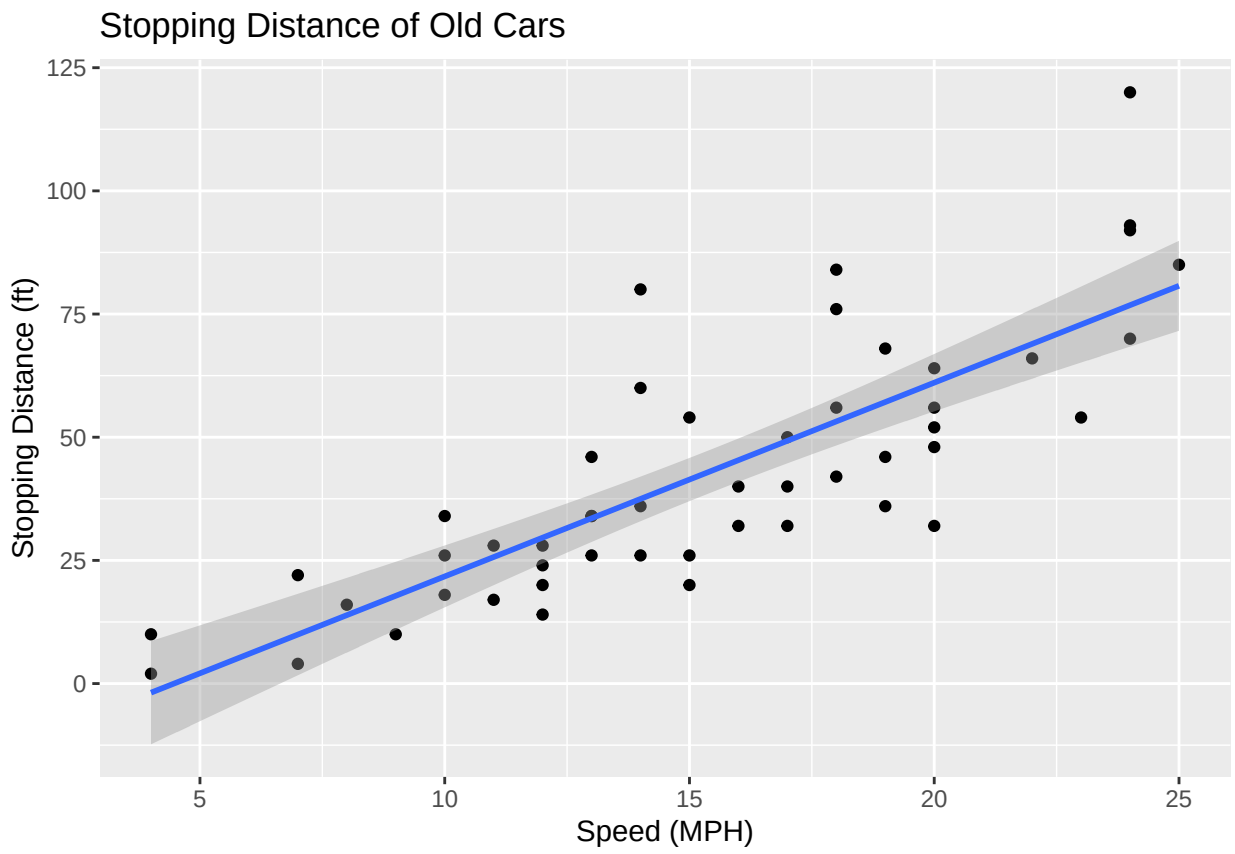
```
# Class5: Data visualization

# Today we are going to use ggplot2 packages to help us visualize data

#First we need to load the packages!
library(ggplot2)


# We will use this inbiult "cars" dataset first
head(cars)
```

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

```
# All ggplots have at least 3 layers,
# data + aes + geoms
ggplot(cars) +
  aes(x=speed, y=dist) +
  #geom_points develops scatter plot
  #do different plots with geom_(type of graph you want)
  #lm= linear model (linearizes data sets)
  #smooth adds line of best regression
  #method is used to argue what methods we want to see to visualize data
  geom_point() +
  geom_smooth(method="lm") +
  #labs= labels that we will be adding to the data set
  labs(title="Stopping Distance of Old Cars",
                      x="Speed (MPH)", y="Stopping Distance (ft)")
```

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




```
#Side-not: ggplot is not the only graphics system
#a very popular one is good old "base" R graphcs
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
```

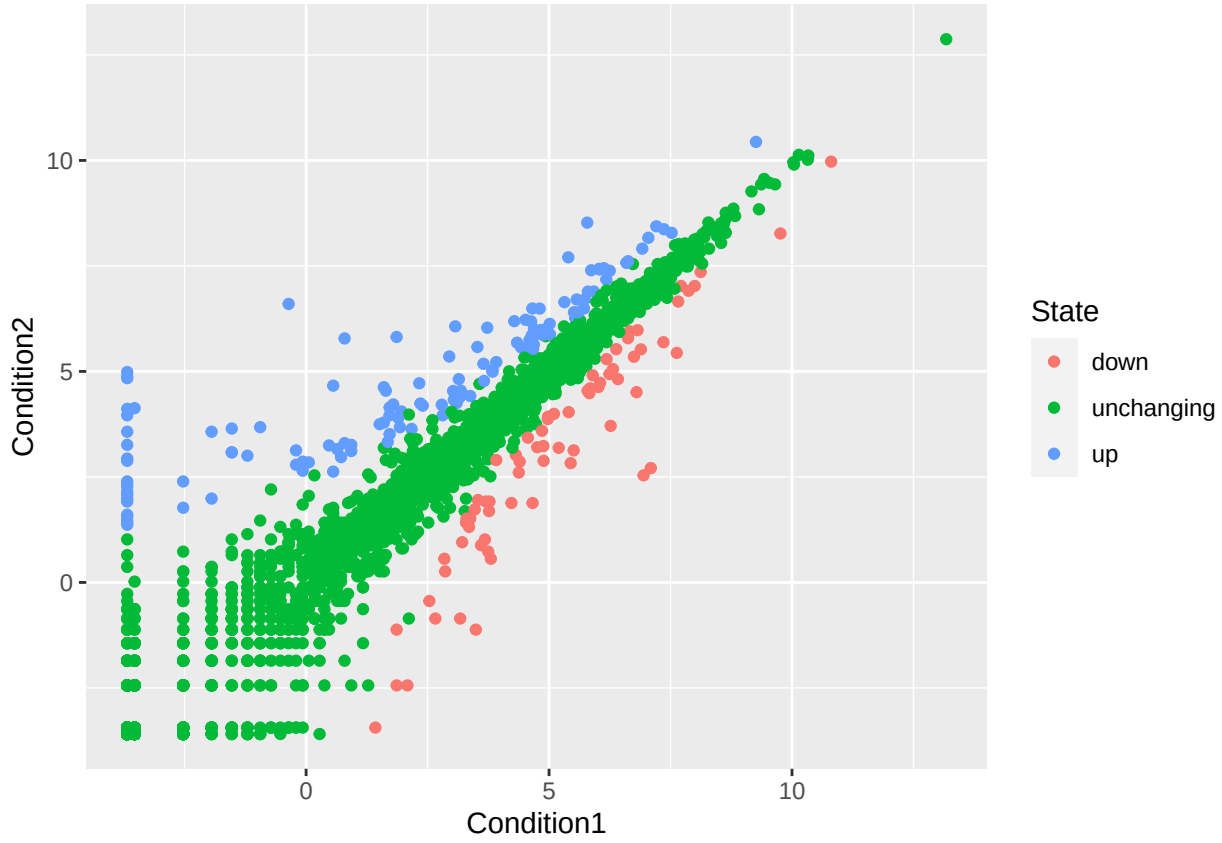
```
table(genes$State)
```

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

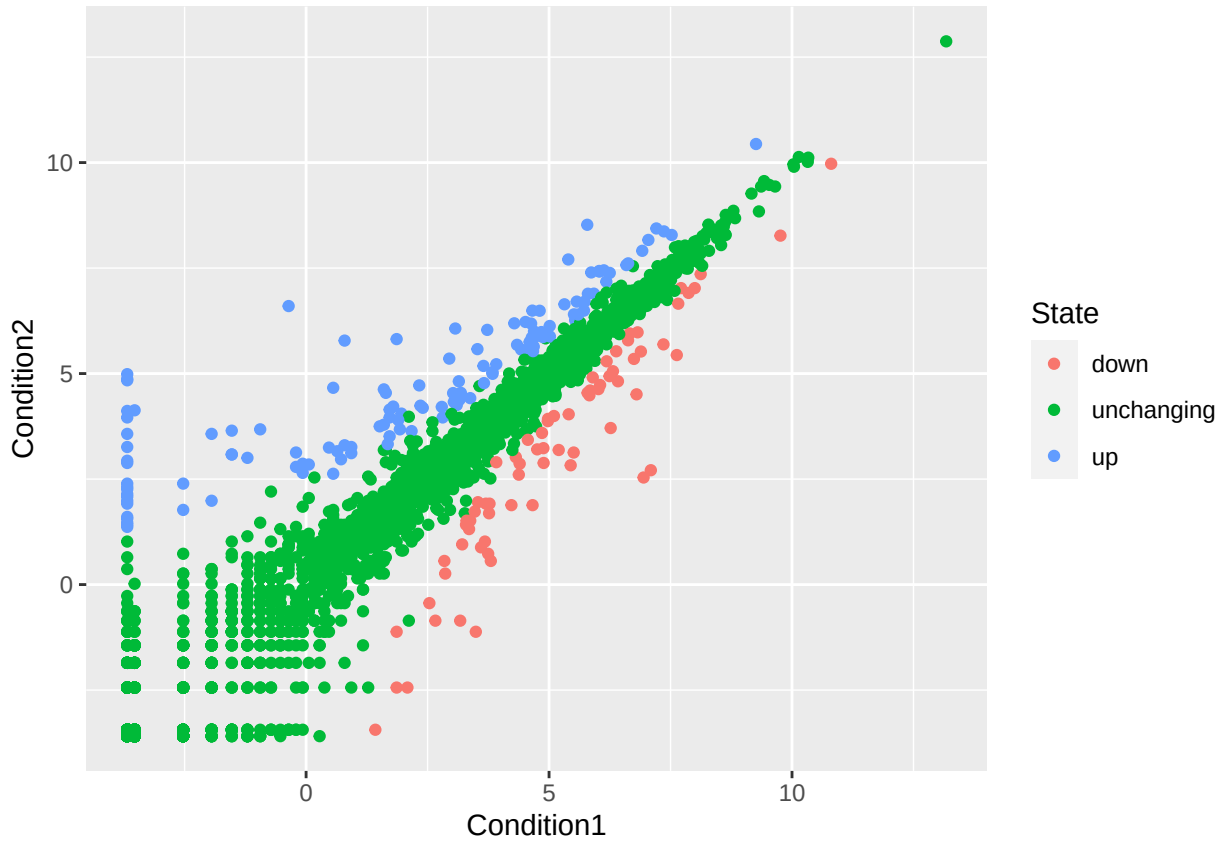
```
round(table(genes$State)/nrow(genes) * 100, 2)
```

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

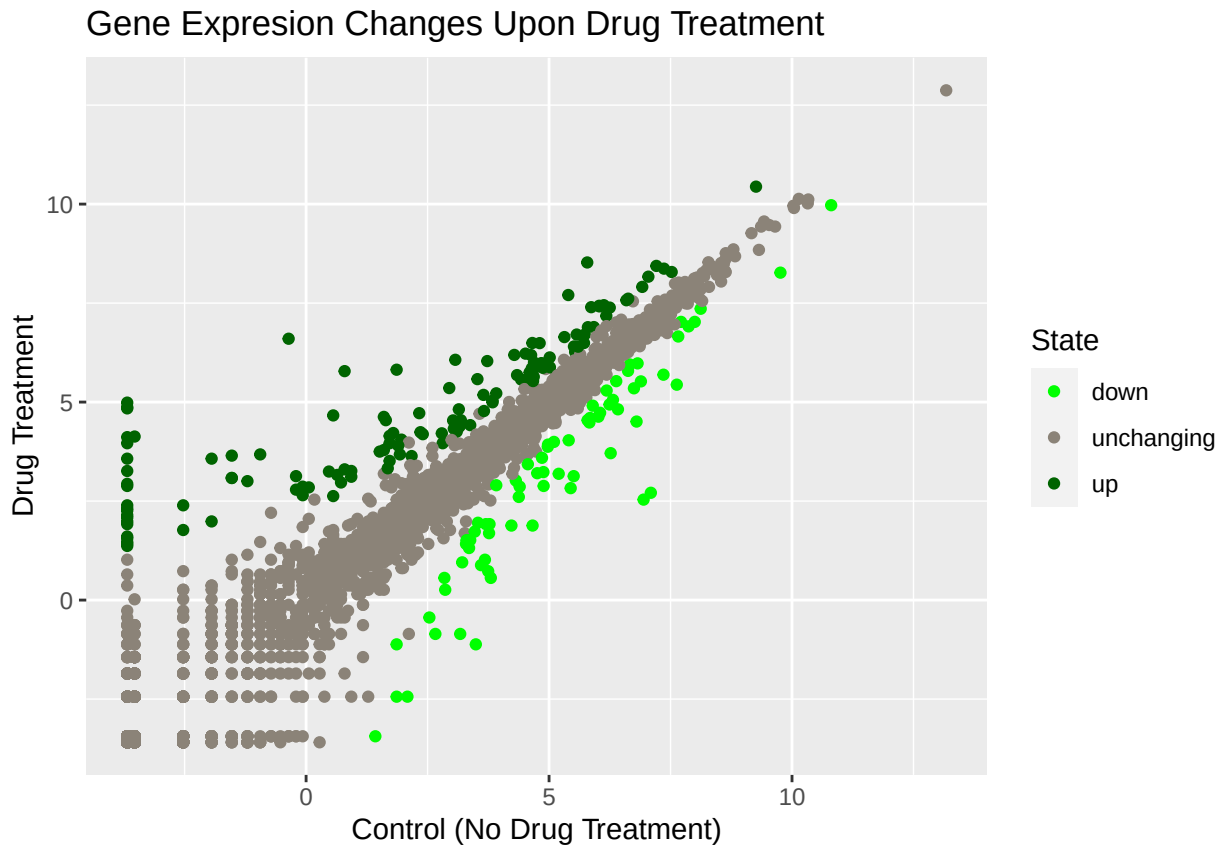
```
ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
```



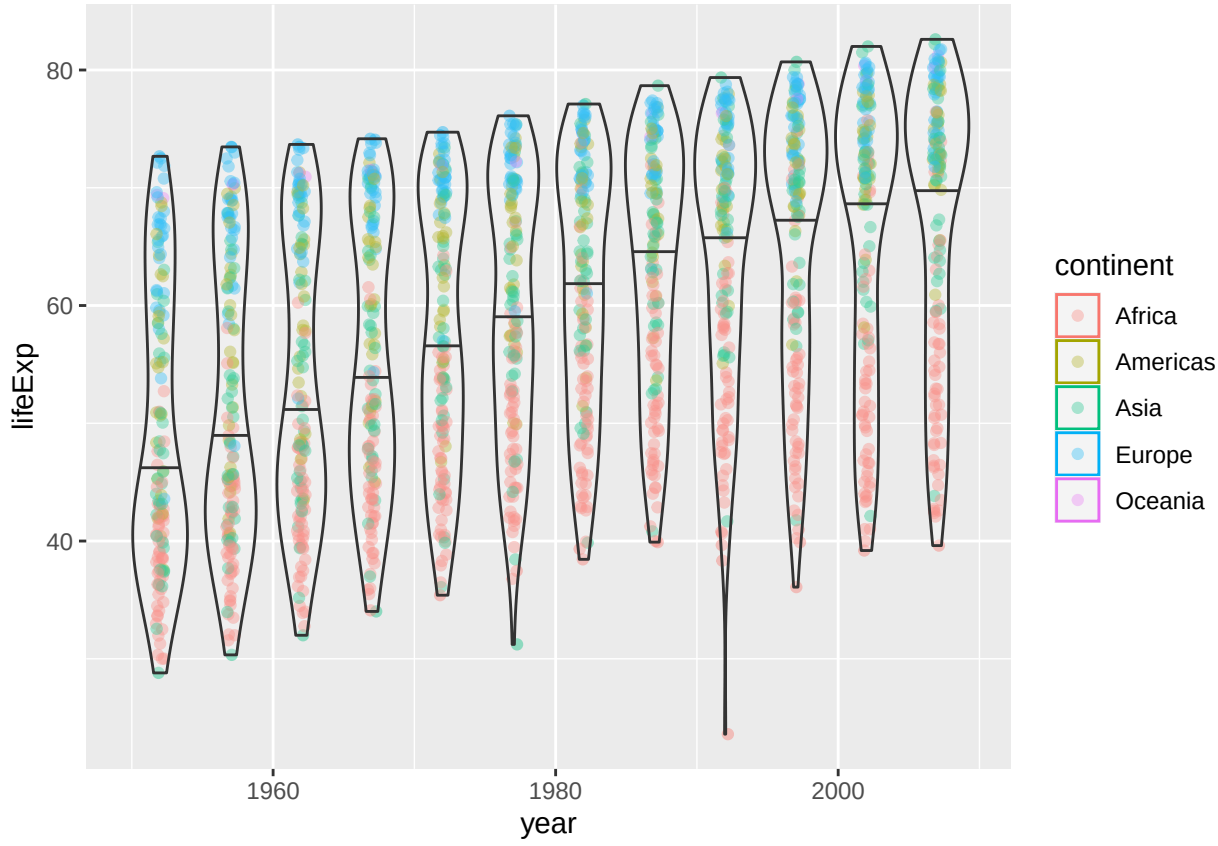

```
p <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
p
```




```
p+scale_color_manual(values = c("green", "antiquewhite4", "dark green")) +
  labs(x="Control (No Drug Treatment)", y="Drug Treatment", title="Gene Expresion Changes Upon Drug Trea
```




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


ggplot(gapminder) + aes(x=year, y=lifeExp, col=continent) + geom_jitter(width=0.3, alpha=0.4) + geom_vi
```




```
#install.packages("plotly")
#library (plotly)
#ggplotly()

# install.packages("dplyr")  ## uncoment to install if needed
#install.packages("dplyr")
library(dplyr)
```

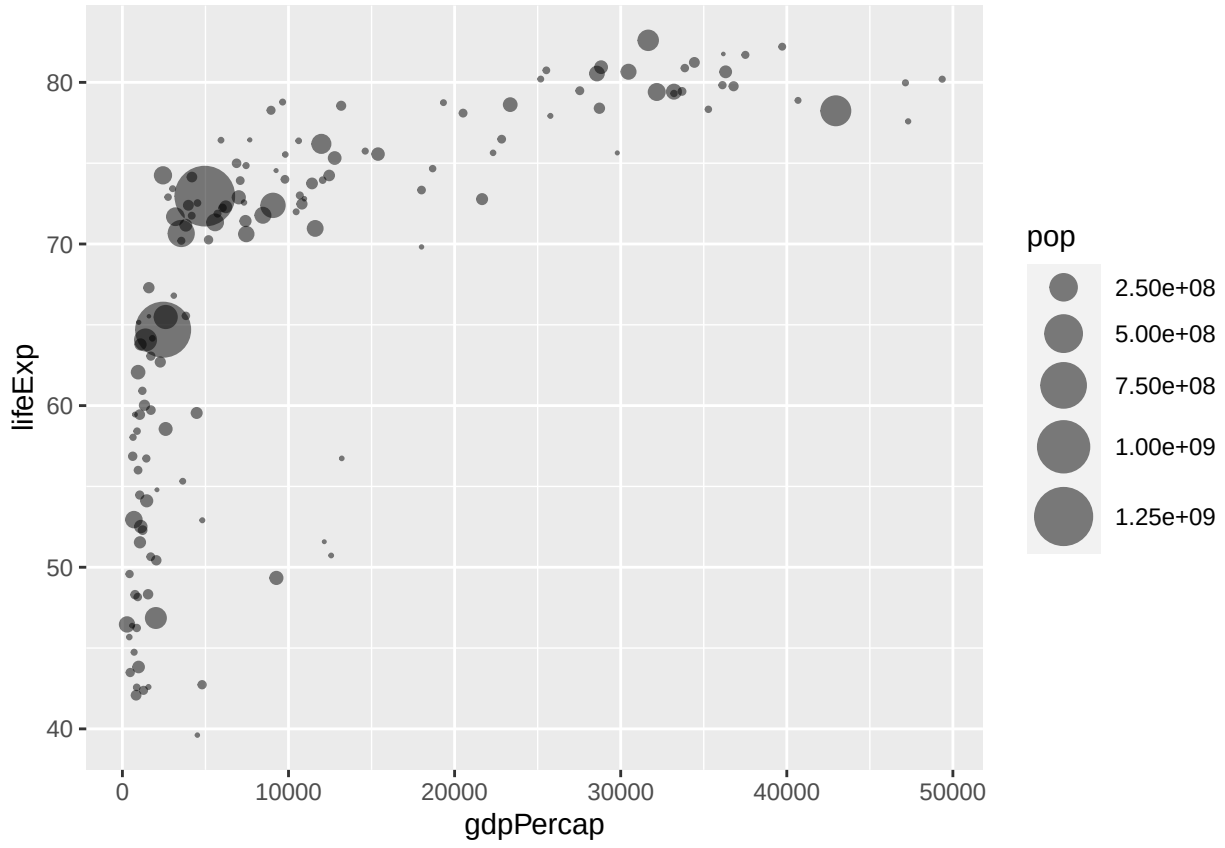
```
##
## Attaching package: 'dplyr'

## 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)
gapminder_2007
```

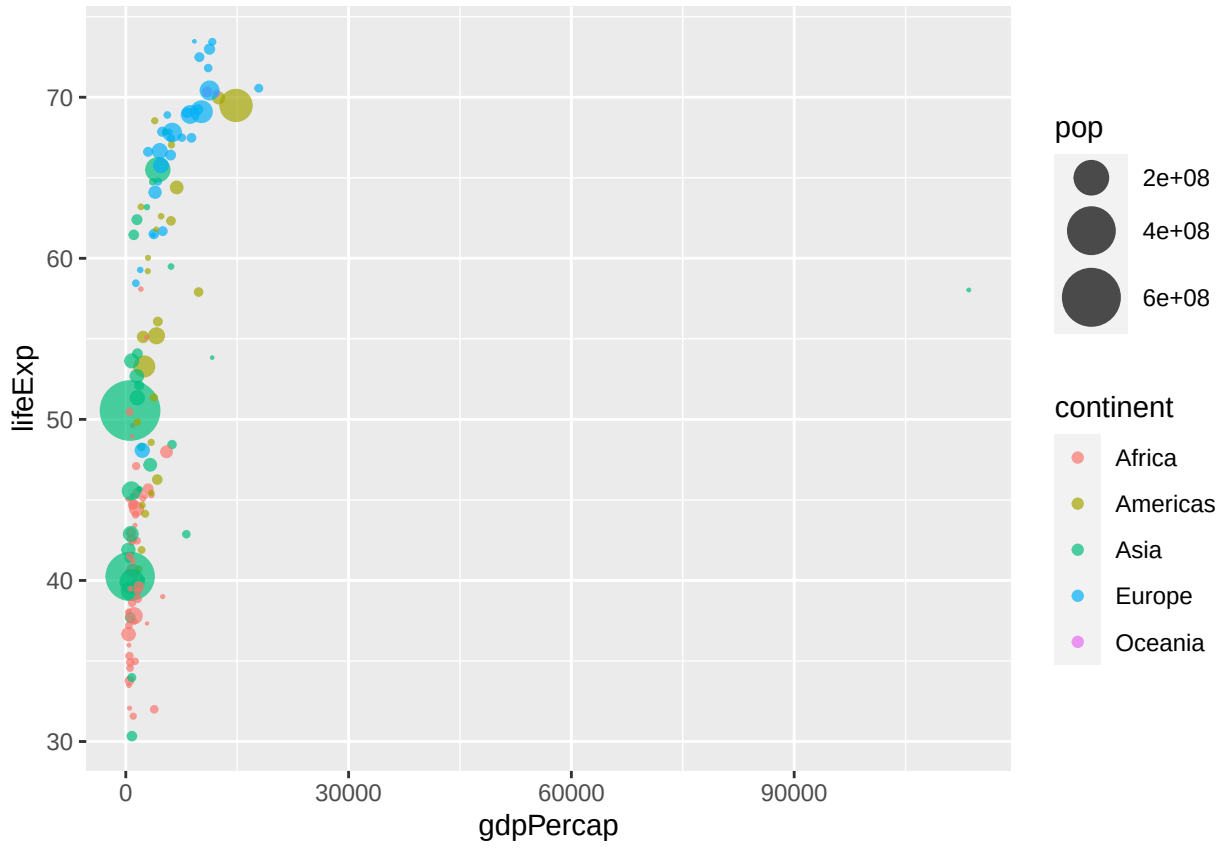
```
## # A tibble: 142 x 6
##    country     continent  year lifeExp       pop gdpPercap
```

```
##    <fct>       <fct>     <int>   <dbl>     <int>     <dbl>
##  1 Afghanistan Asia       2007    43.8  31889923      975.
##  2 Albania     Europe     2007    76.4   3600523     5937.
##  3 Algeria     Africa     2007    72.3  33333216     6223.
##  4 Angola      Africa     2007    42.7  12420476     4797.
##  5 Argentina   Americas   2007    75.3  40301927    12779.
##  6 Australia   Oceania    2007    81.2  20434176    34435.
##  7 Austria     Europe     2007    79.8   8199783    36126.
##  8 Bahrain     Asia       2007    75.6    708573    29796.
##  9 Bangladesh  Asia       2007    64.1 150448339     1391.
## 10 Belgium     Europe     2007    79.4  10392226    33693.
## # ... with 132 more rows
```

```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, size=pop) +
  #aplha makes the points transparent
  geom_point(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)
```

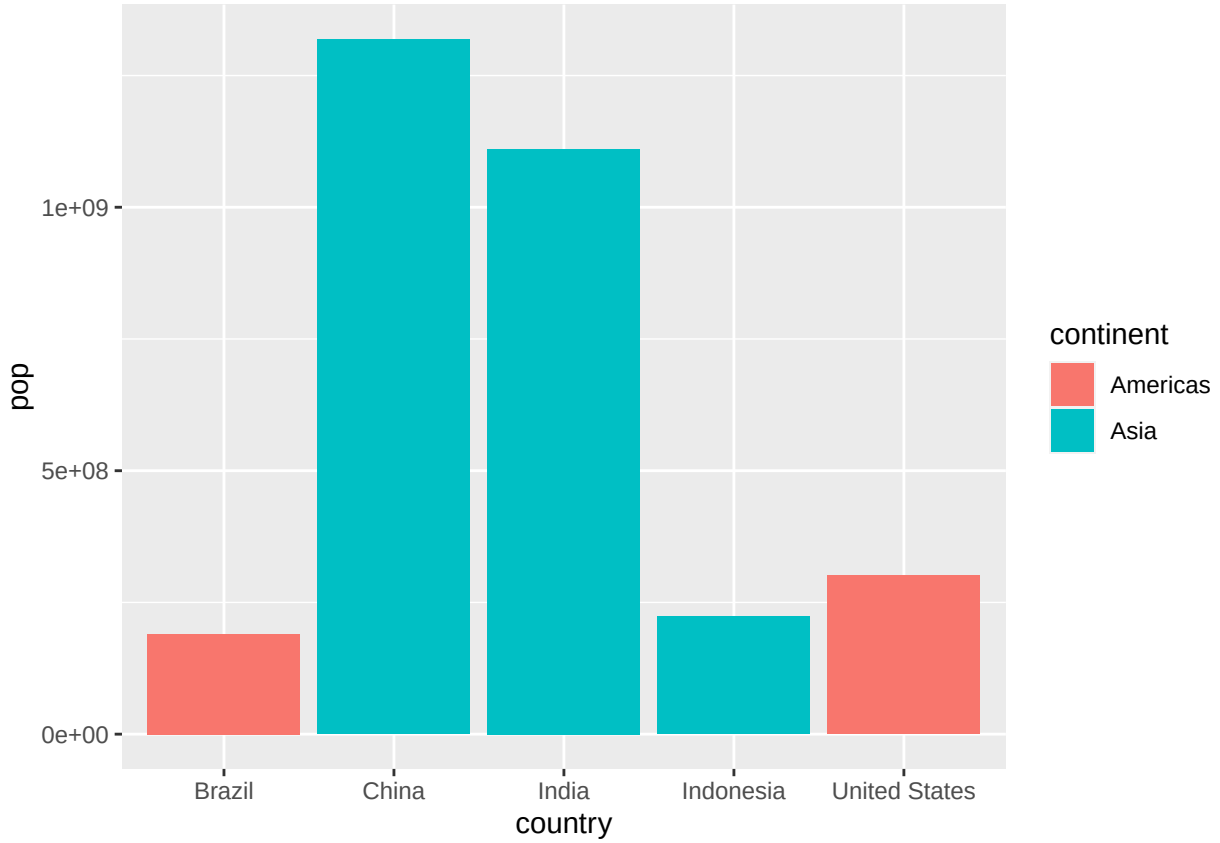



```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)
# the |year ==2007 will add the data from 2007 next to 1957 data sets
ggplot(gapminder_1957) +
  aes(x = gdpPercap, y = lifeExp, color=continent,size = pop) +
  geom_point(alpha=0.7) +
  scale_size_area(max_size = 10) +
  facet_wrap(~year)
```

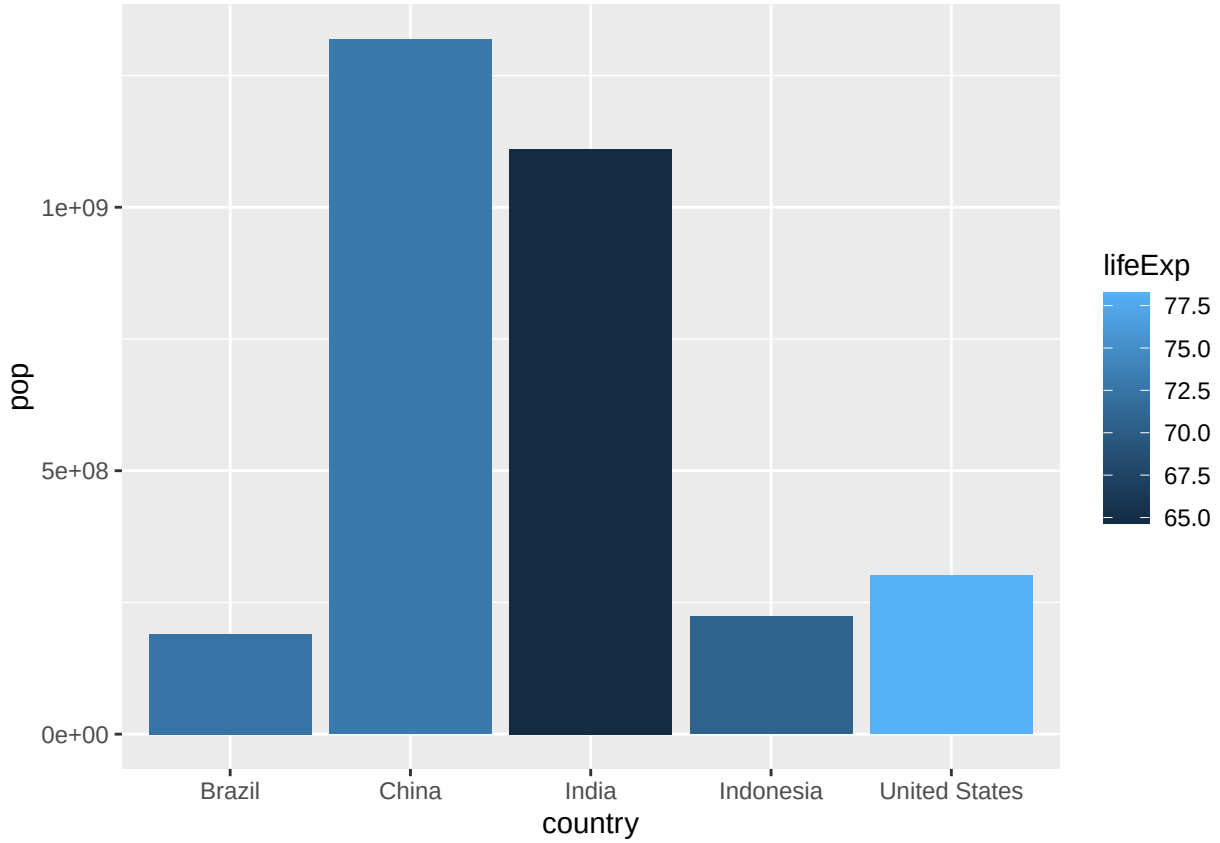

```
#You should now include the layer facet_wrap(~year) to produce the following plot:

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, fill=continent))
```

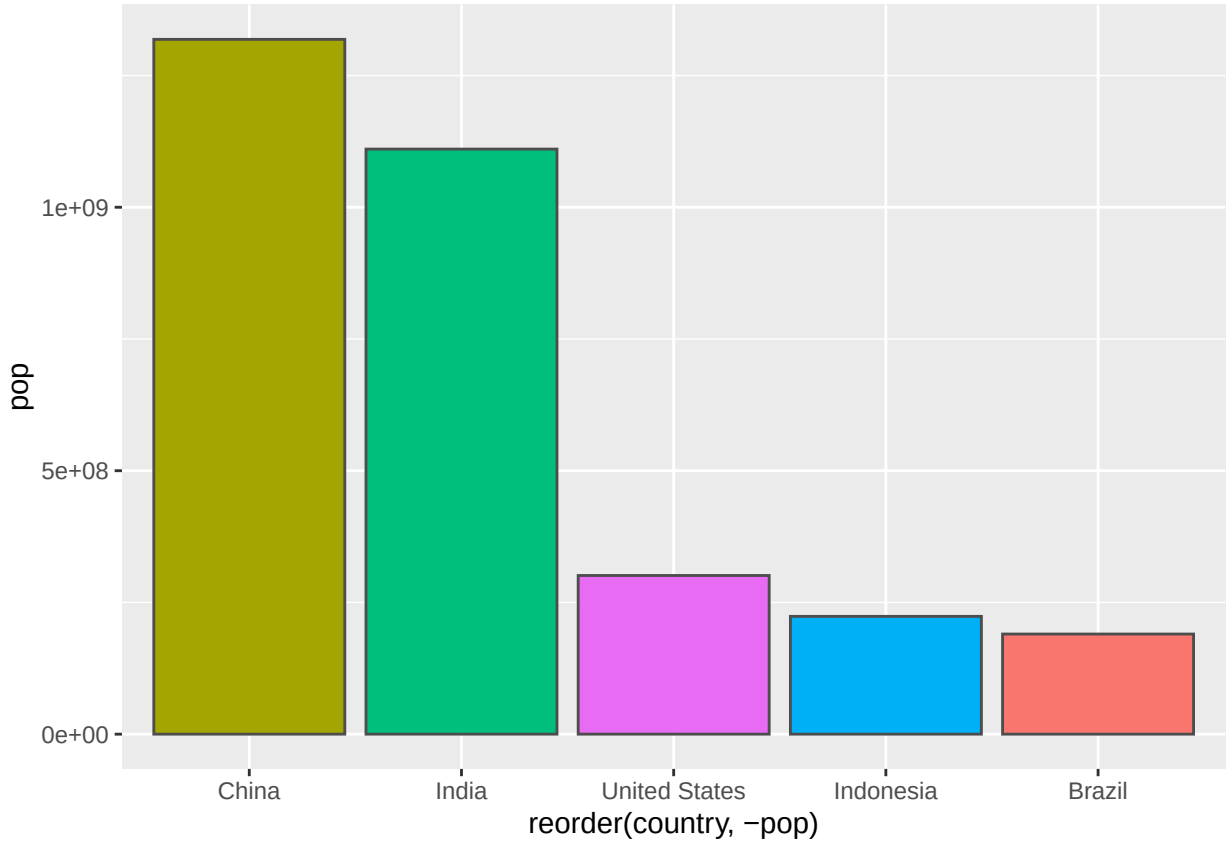



```
ggplot(gapminder_top5) +
  geom_col(aes(x = country, y = pop, fill=lifeExp))
```




```
# Plot population size by country
ggplot(gapminder_top5) +
  aes(x=reorder (country, -pop), y=pop, fill=country) +
  geom_col(col="gray30") +
  guides(fill=FALSE)
```

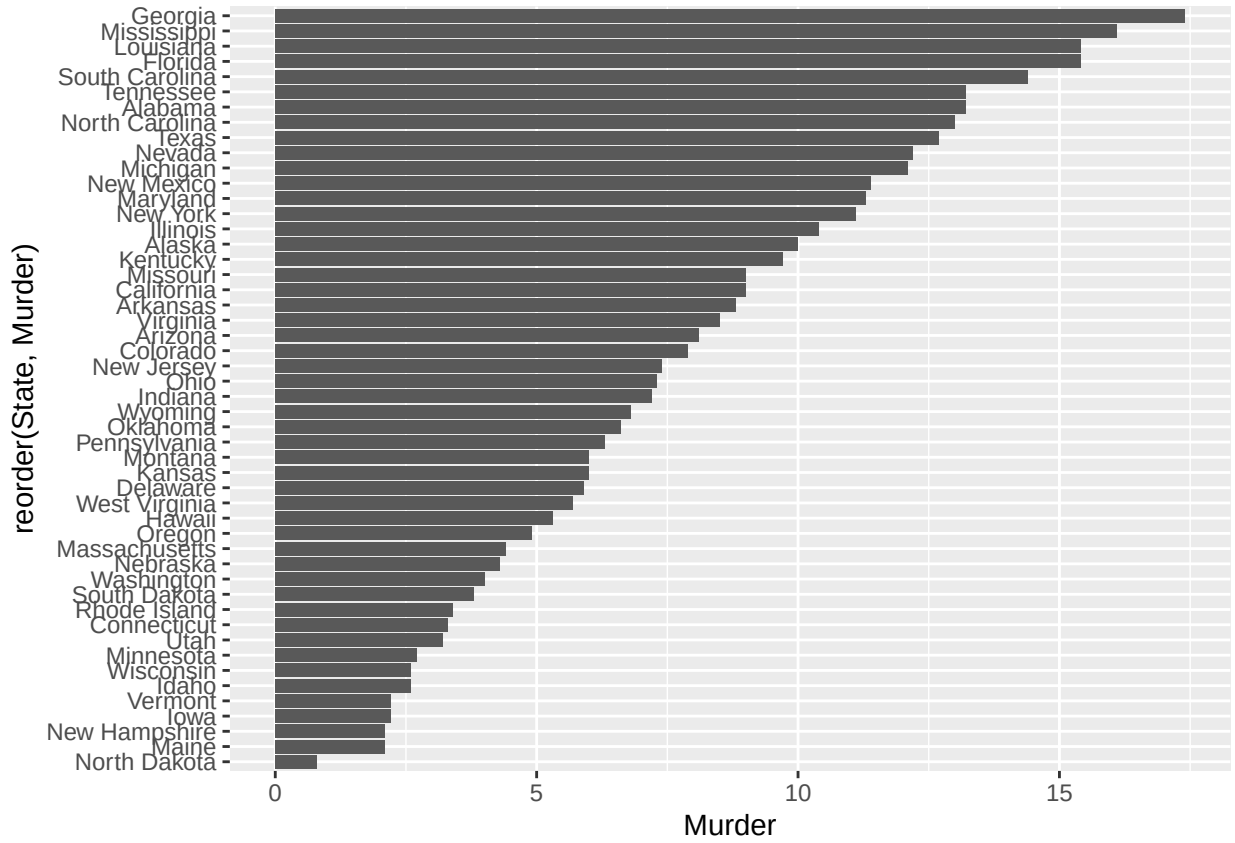
```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```



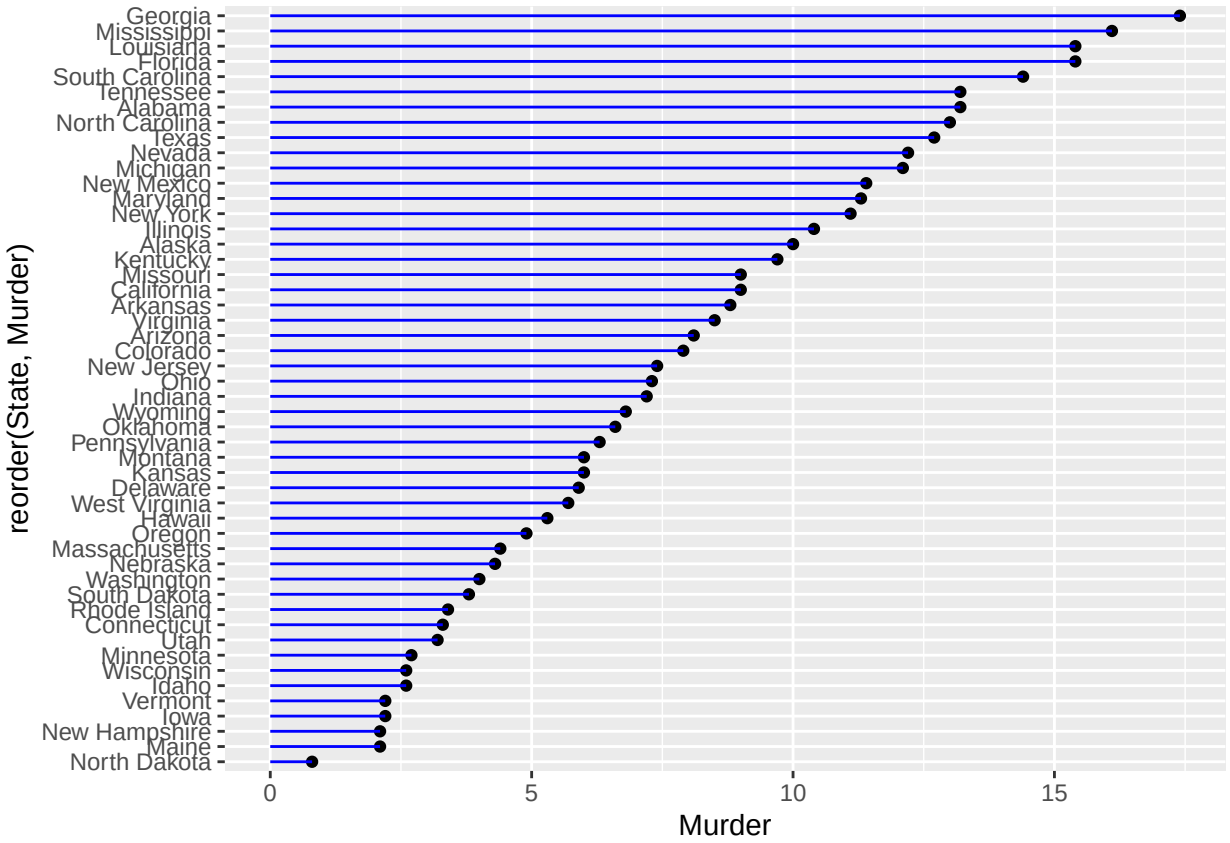

```
#FLIPPING CHARTS
head(USArrests)
```

```
##            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()
```




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

# Setup nice regular ggplot of the gapminder data
#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 by continent
  #facet_wrap(~continent) +
  # Here comes the gganimate specific bits
  #labs(title = 'Year: {frame_time}', x = 'GDP per capita', y = 'life expectancy') +
  #transition_time(year) +
  #shadow_wake(wake_length = 0.1, alpha = FALSE)


#install.packages("patchwork")
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(disp, 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'
```