Visualization

Matt Bartley

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Visualization - GG-Plot & Dplyr

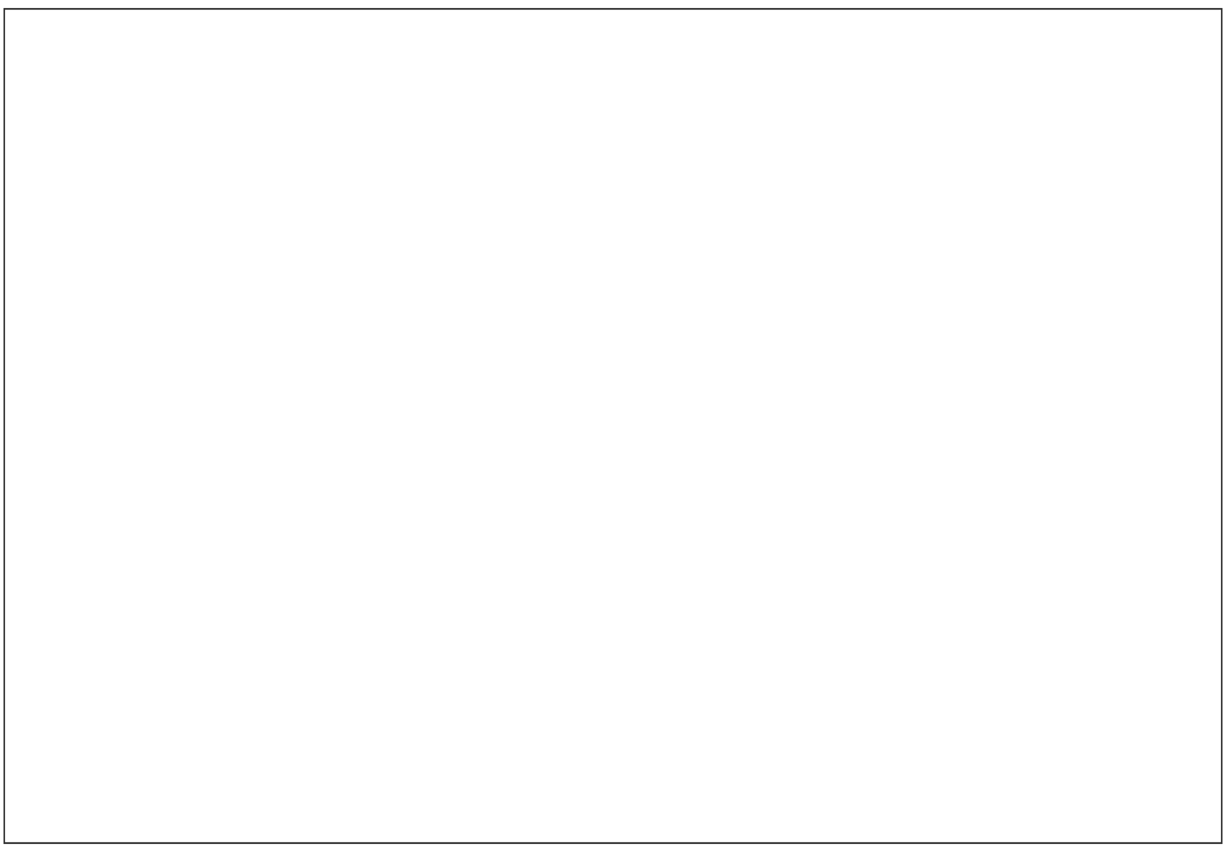
Basics

The geometry layer defines the plot type and takes the format geom_X where X is the plot type.

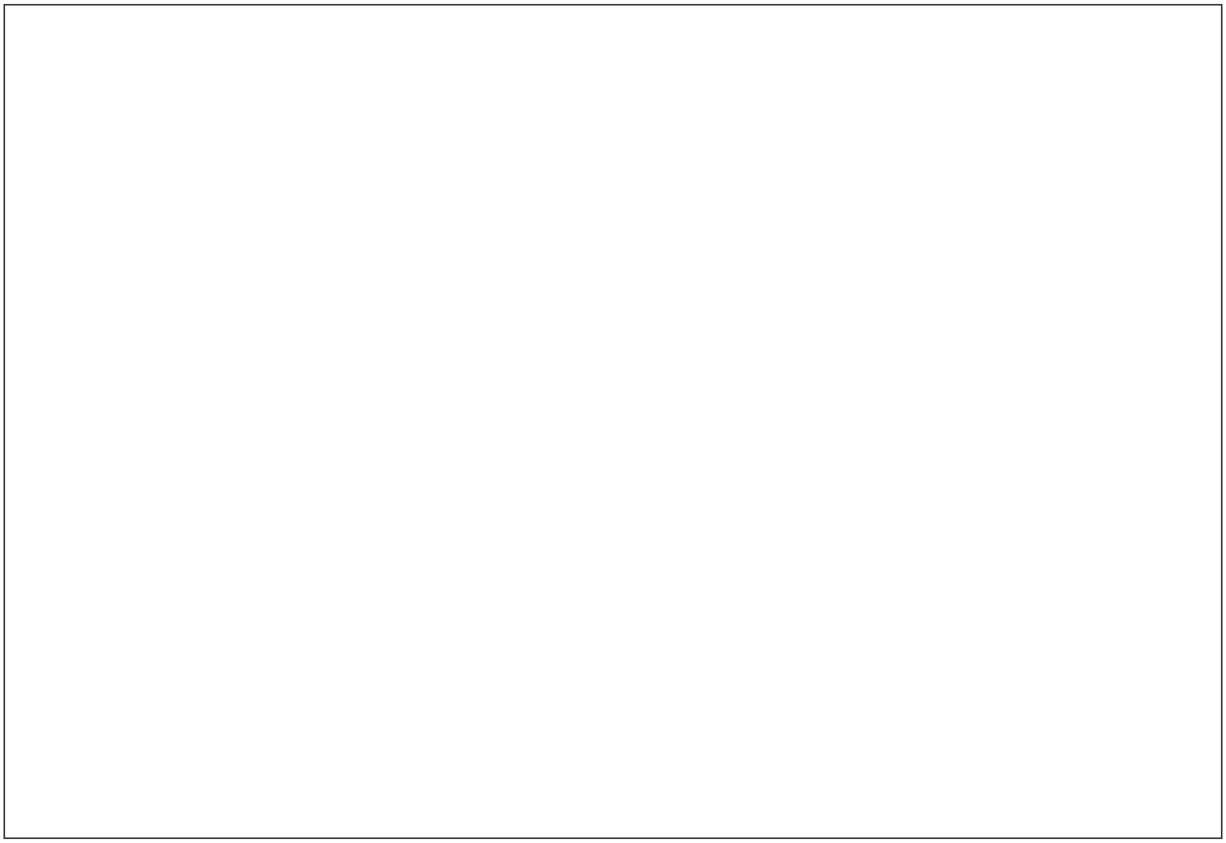
Aesthetic mappings describe how properties of the data connect with features of the graph (axis position, color, size, etc.) Define aesthetic mappings with the aes() function.

aes() uses variable names from the object component (for example, total rather than murders$total).

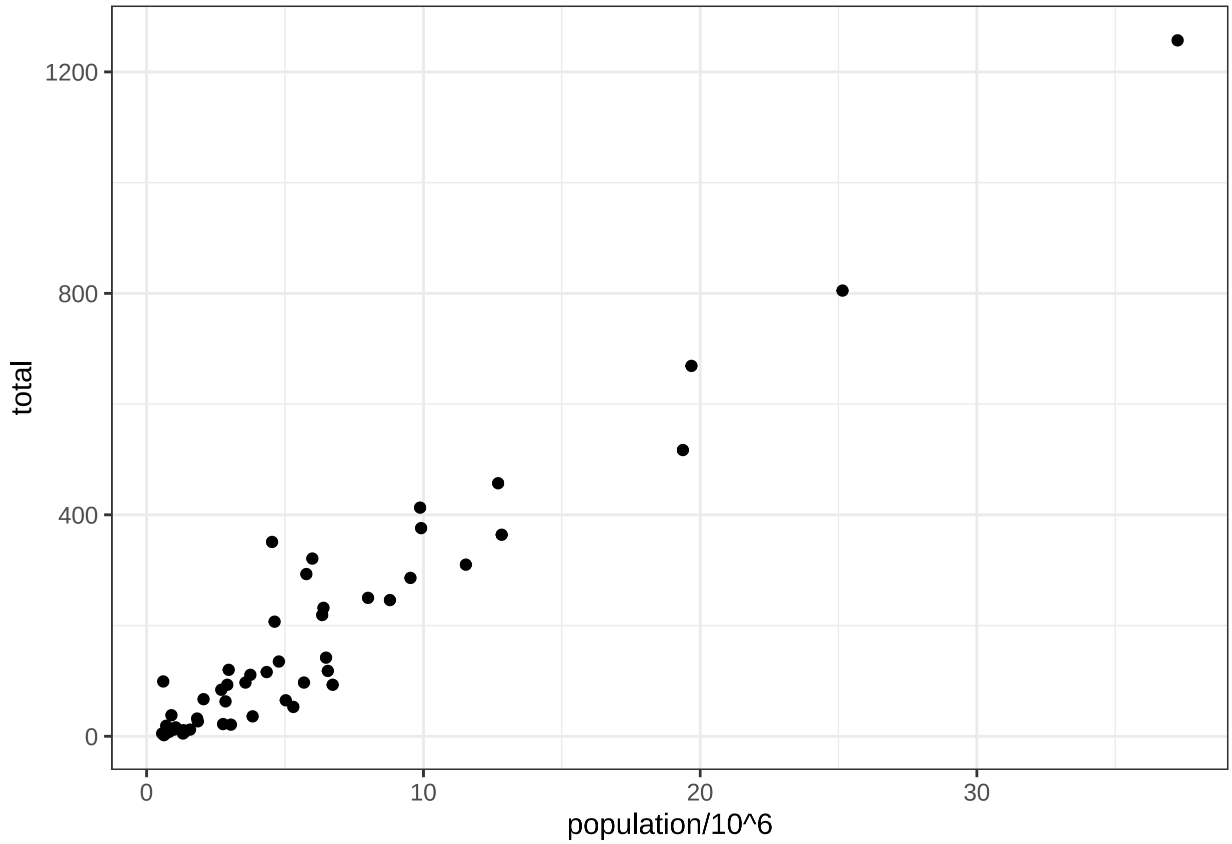
```
ggplot(data = murders)
```



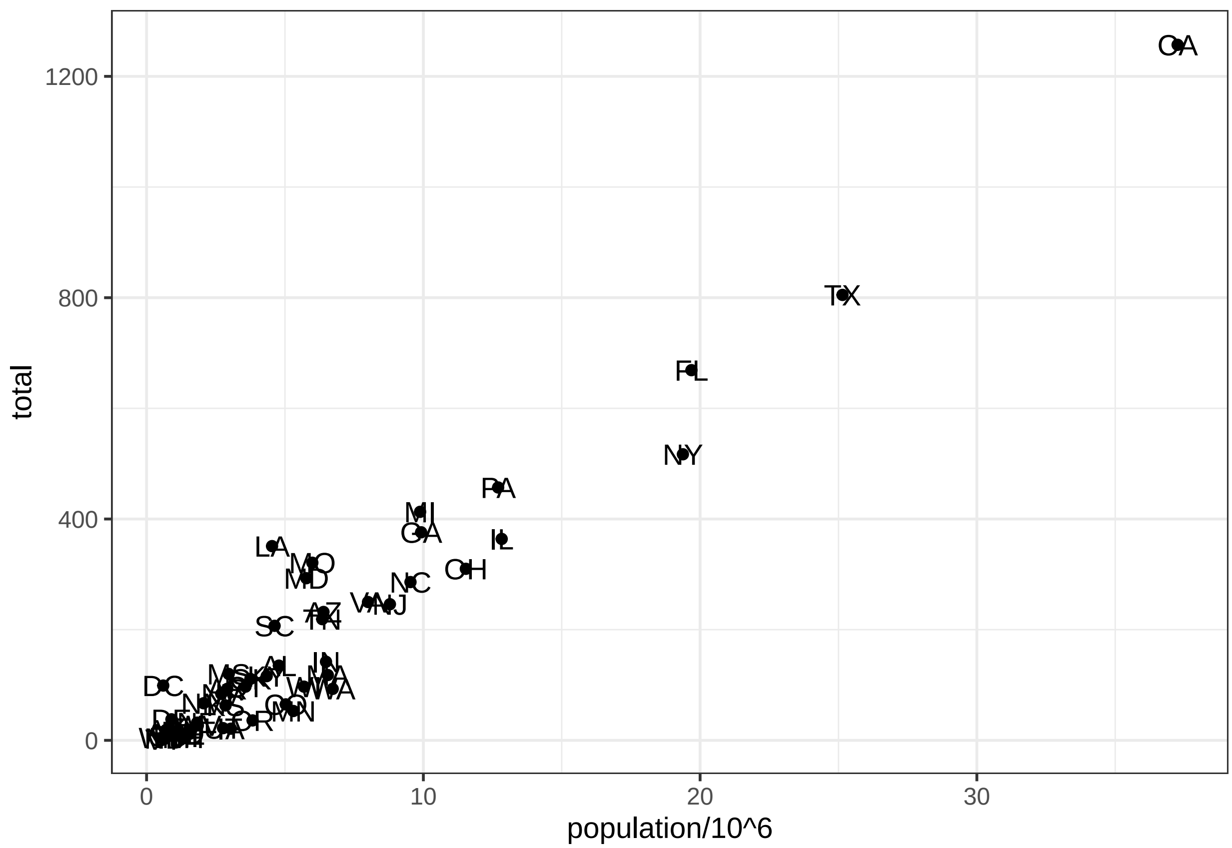
```
murders %>% ggplot()
```



```r
p <- ggplot(data = murders)

# add points layer to predefined ggplot object
p + geom_point(aes(population/10^6, total))
```

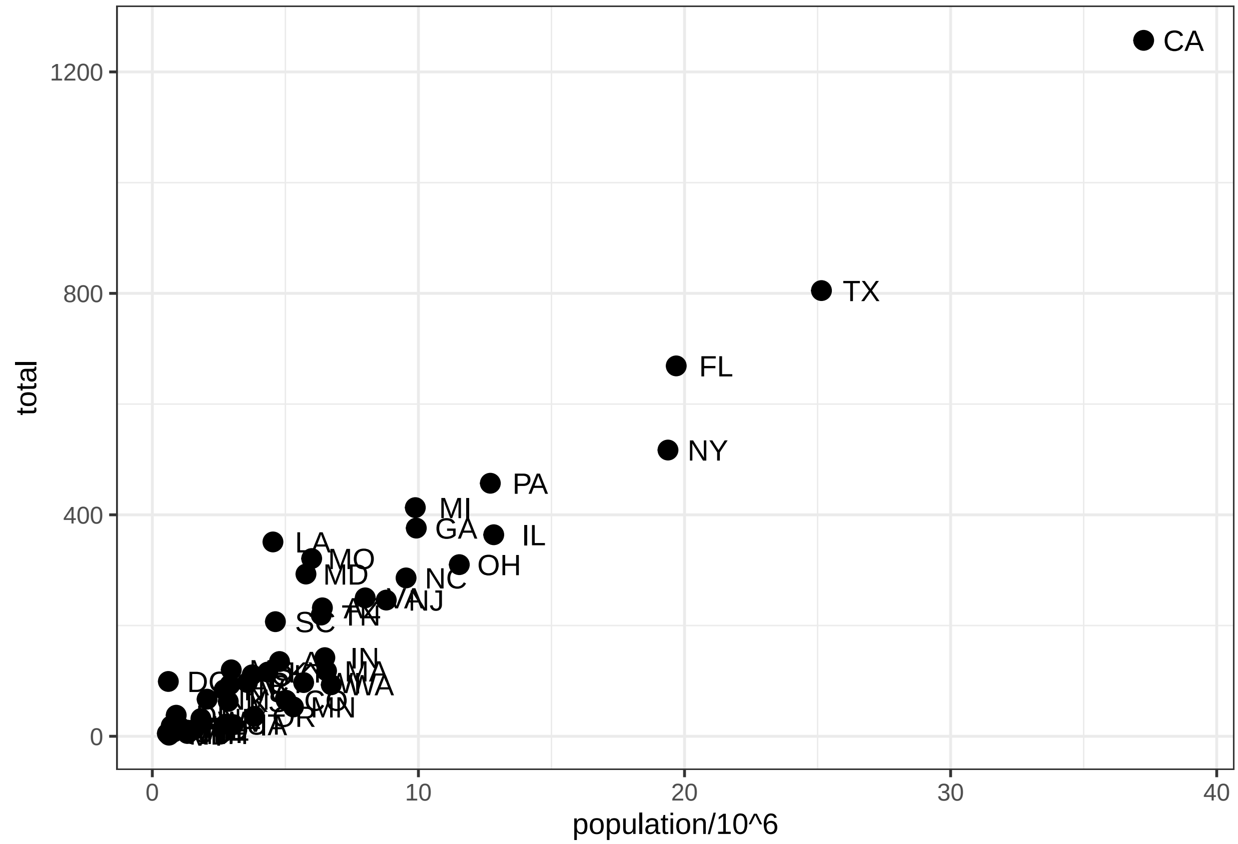



```
# add text layer to scatterplot
p + geom_point(aes(population/10^6, total)) +
    geom_text(aes(population/10^6, total, label = abb))
```

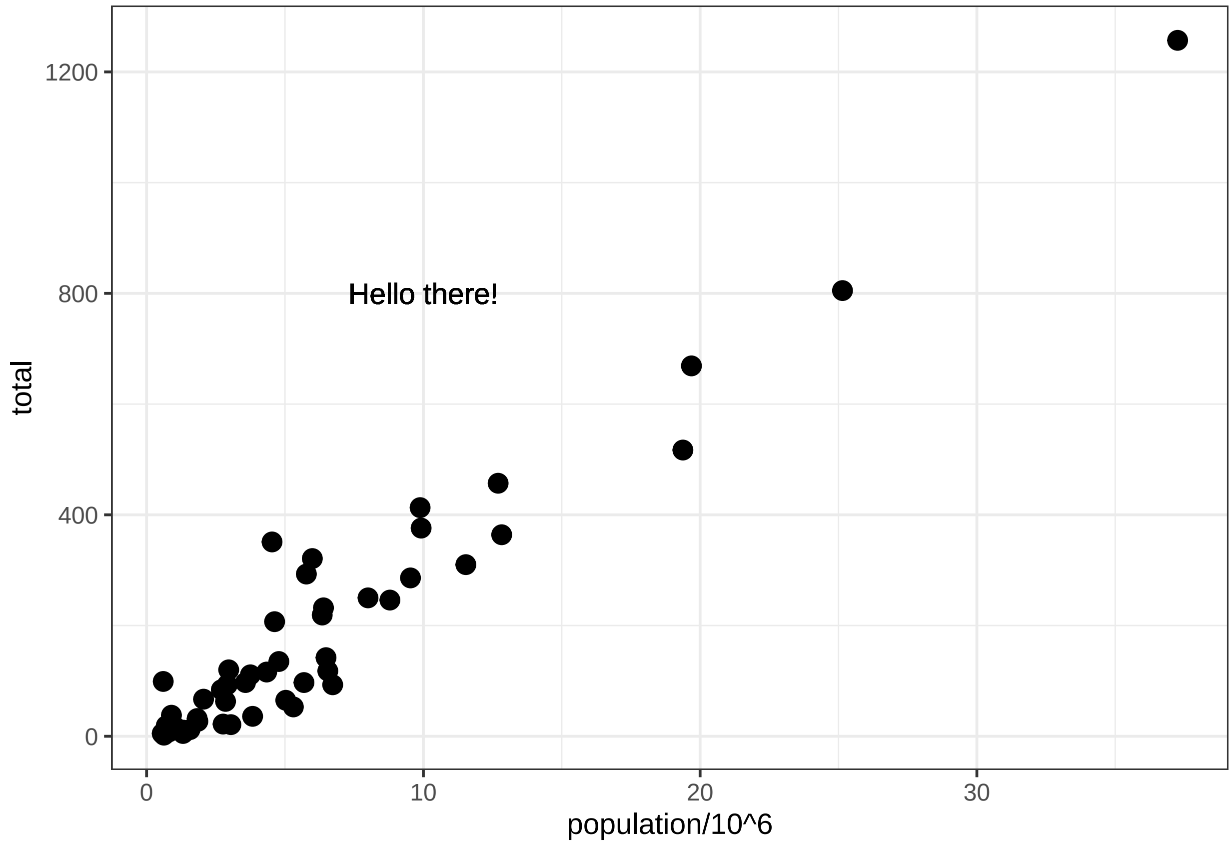


Global aesthetic mappings apply to all geometries and can be defined when you initially call ggplot(). All the geometries added as layers will default to this mapping. Local aesthetic mappings add additional information or override the default mappings.

```
# simplify code by adding global aesthetic
p <- murders %>% ggplot(aes(population/10^6, total, label = abb))
p + geom_point(size = 3) +
    geom_text(nudge_x = 1.5)
```




```r
# local aesthetics override global aesthetics
p + geom_point(size = 3) +
    geom_text(aes(x = 10, y = 800, label = "Hello there!"))
```

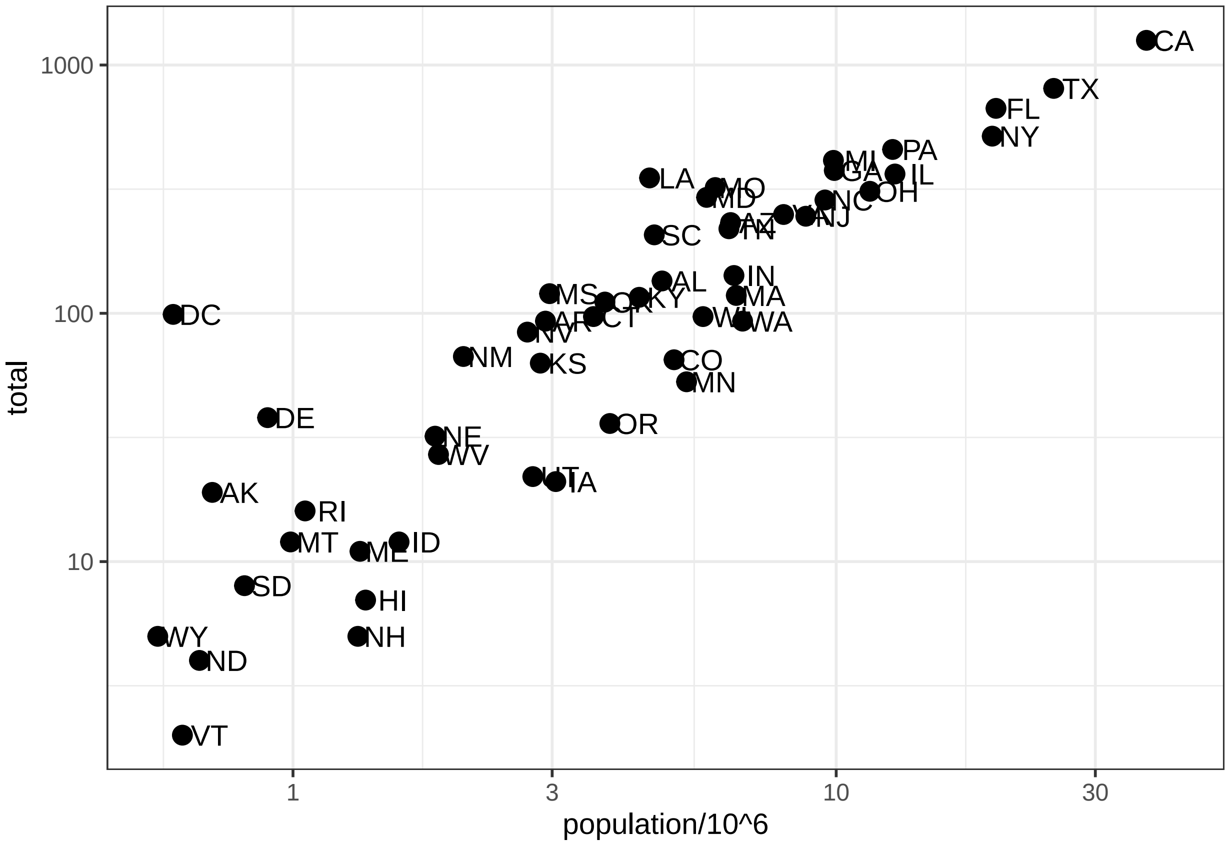


Convert the x-axis to log scale with scale_x_continuous(trans = "log10") or scale_x_log10(). Similar functions exist for the y-axis.

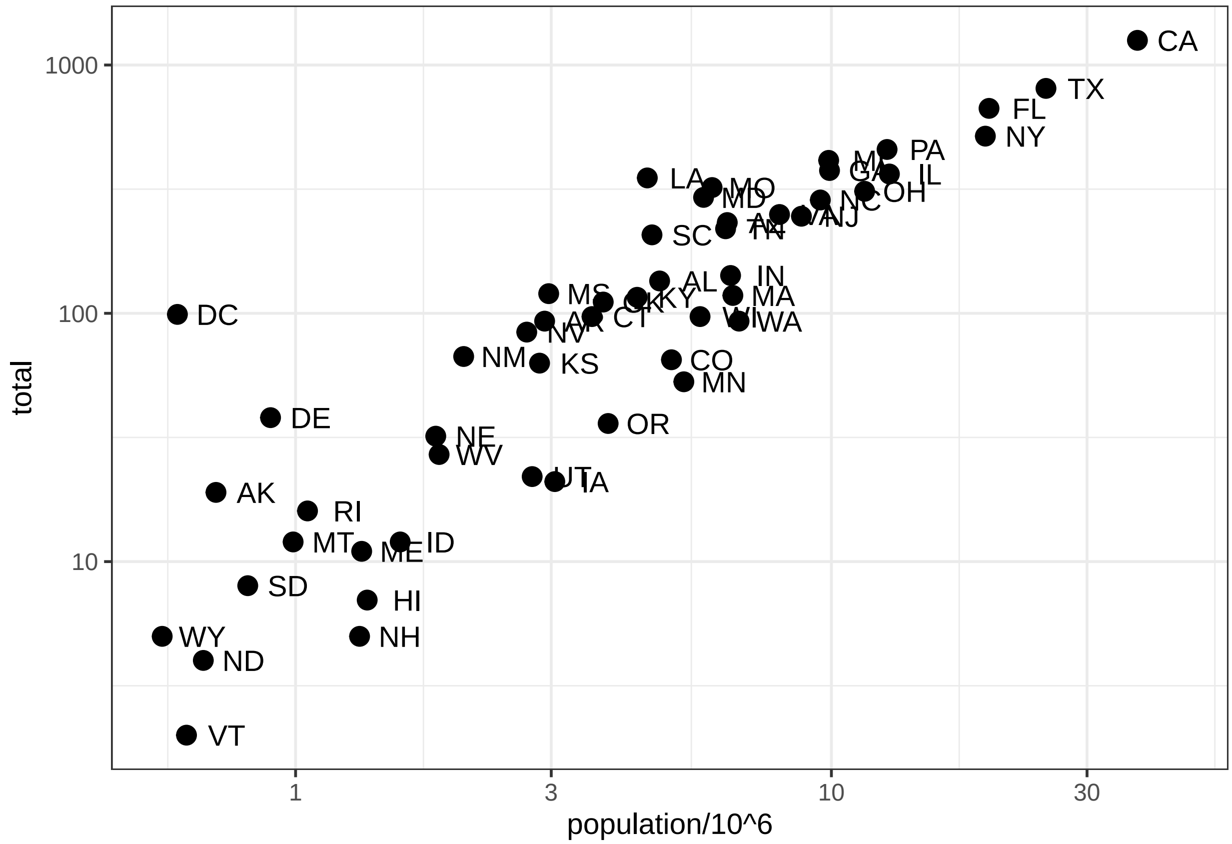
Add axis titles with xlab() and ylab() functions. Add a plot title with the ggtitle() function. Add a color mapping that colors points by a variable by defining the col argument within aes(). To color all points the same way, define col outside of aes().

Add a line with the geom_abline() geometry. geom_abline() takes arguments slope (default = 1) and intercept (default = 0). Change the color with col or color and line type with lty.

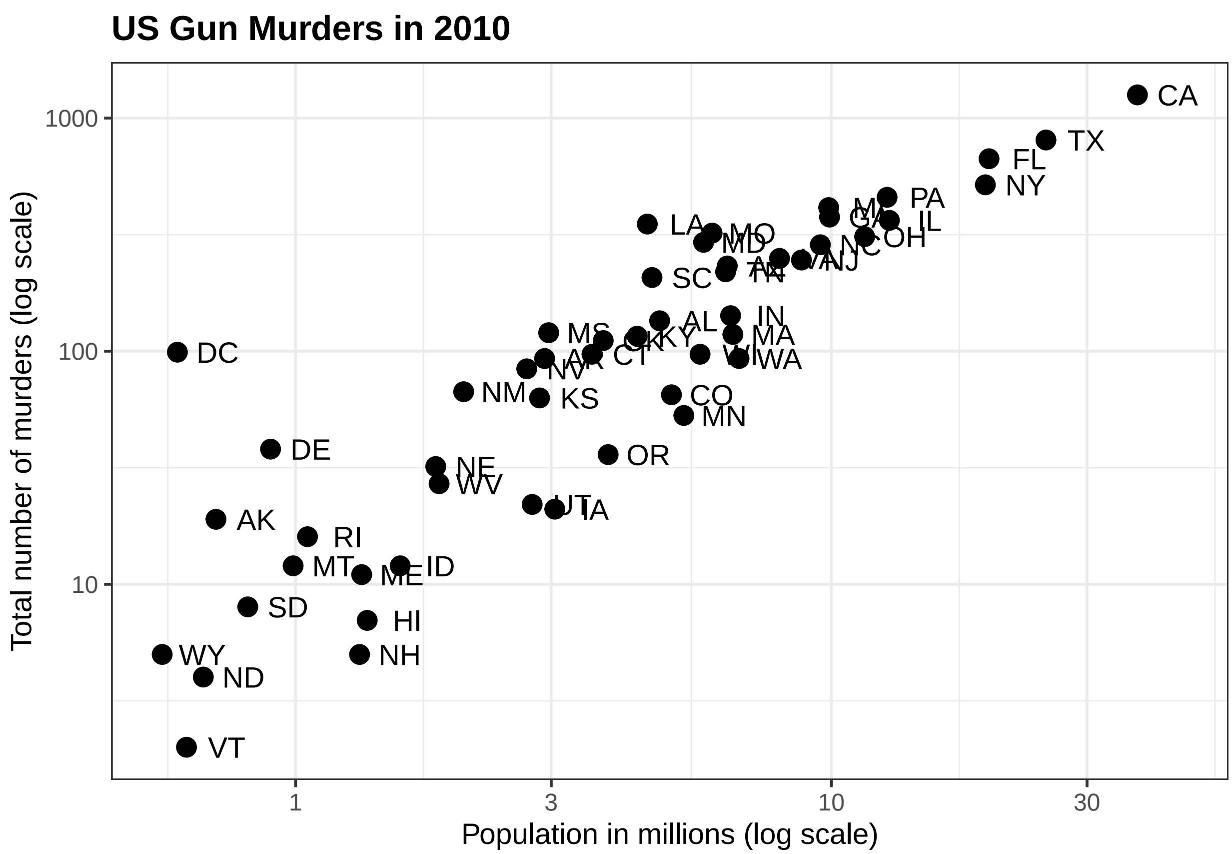
```
# log base 10 scale the x-axis and y-axis
p + geom_point(size = 3) +
    geom_text(nudge_x = 0.05) +
    scale_x_continuous(trans = "log10") +
    scale_y_continuous(trans = "log10")
```



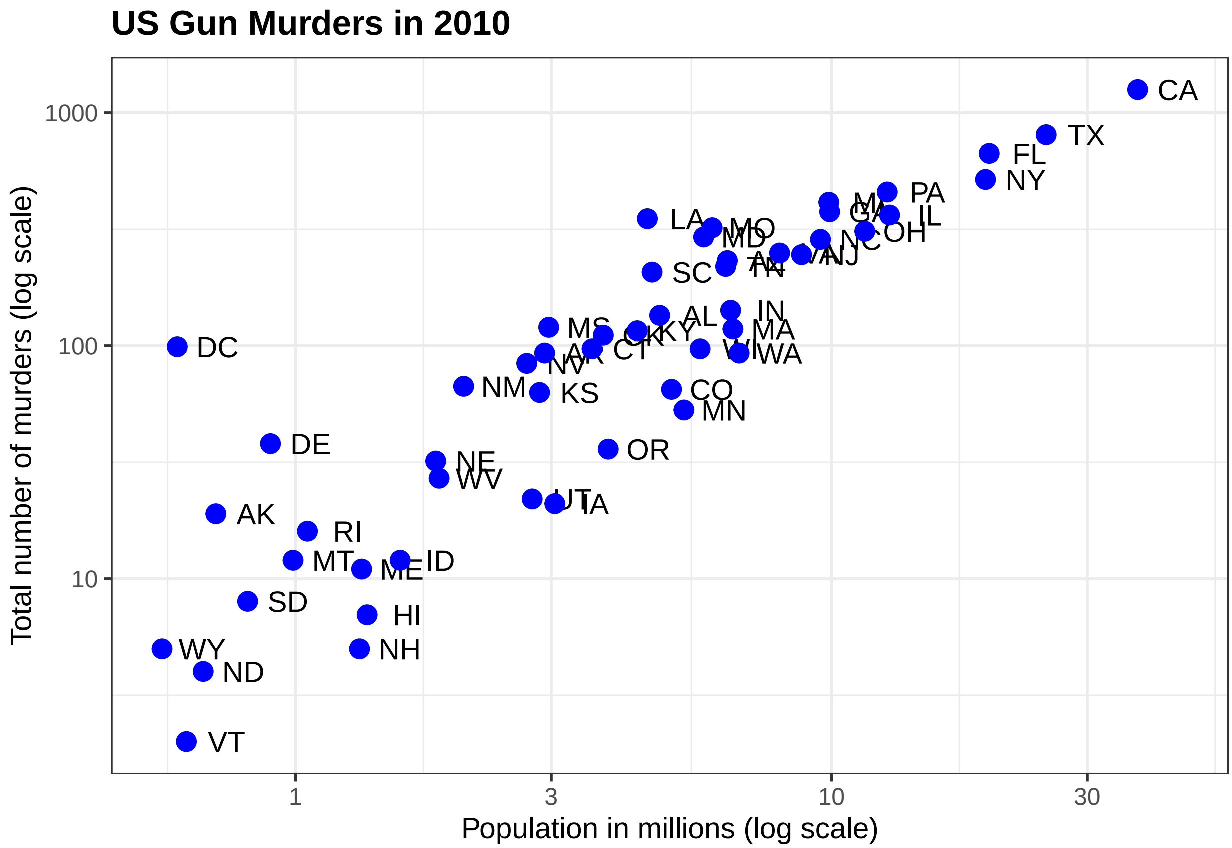

```
# efficient log scaling of the axes
p + geom_point(size = 3) +
    geom_text(nudge_x = 0.075) +
    scale_x_log10() +
    scale_y_log10()
```



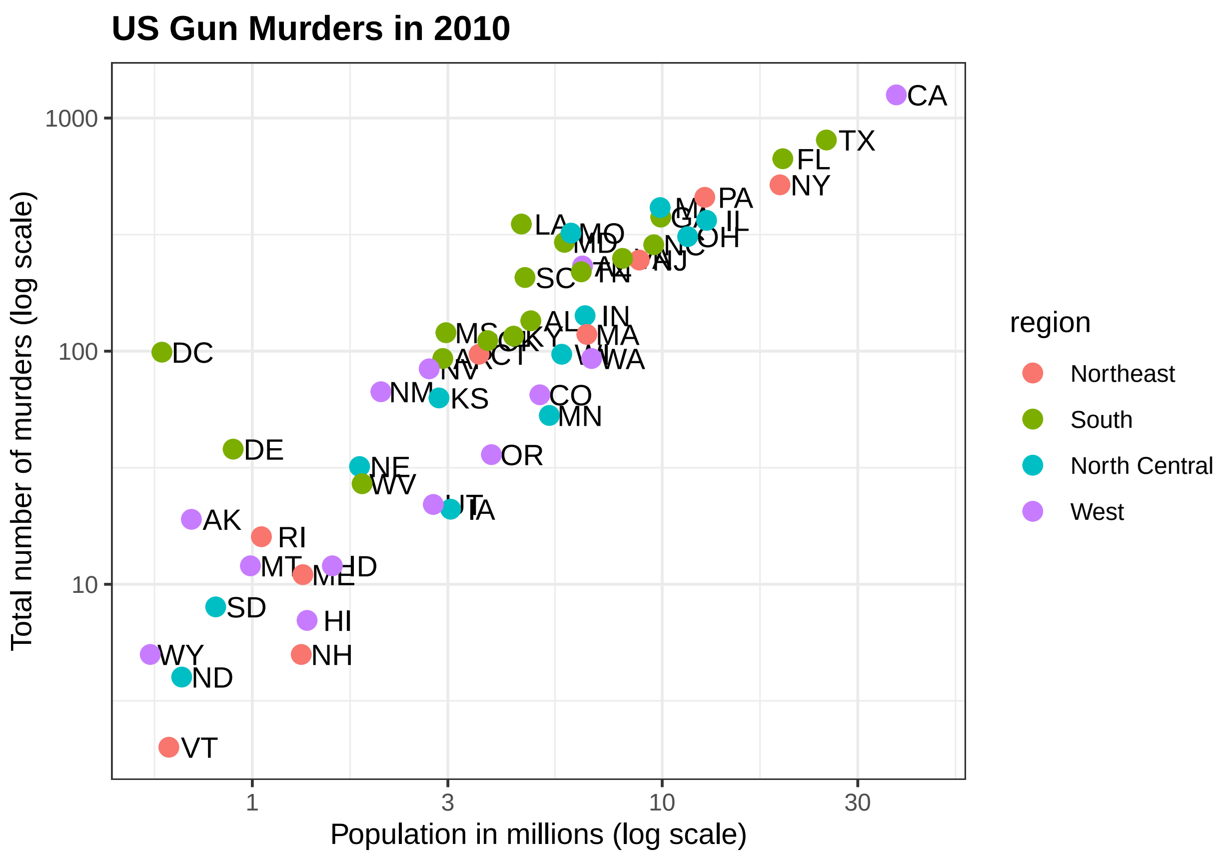

```r
# add labels and title
p + geom_point(size = 3) +
    geom_text(nudge_x = 0.075) +
    scale_x_log10() +
    scale_y_log10() +
    xlab("Population in millions (log scale)") +
    ylab("Total number of murders (log scale)") +
    ggtitle("US Gun Murders in 2010")
```




```
# redefine p to be everything except the points layer
p <- murders %>%
    ggplot(aes(population/10^6, total, label = abb)) +
    geom_text(nudge_x = 0.075) +
    scale_x_log10() +
    scale_y_log10() +
    xlab("Population in millions (log scale)") +
    ylab("Total number of murders (log scale)") +
    ggtitle("US Gun Murders in 2010")

# make all points blue
p + geom_point(size = 3, color = "blue")
```




```r
# color points by region
p + geom_point(aes(col = region), size = 3)
```



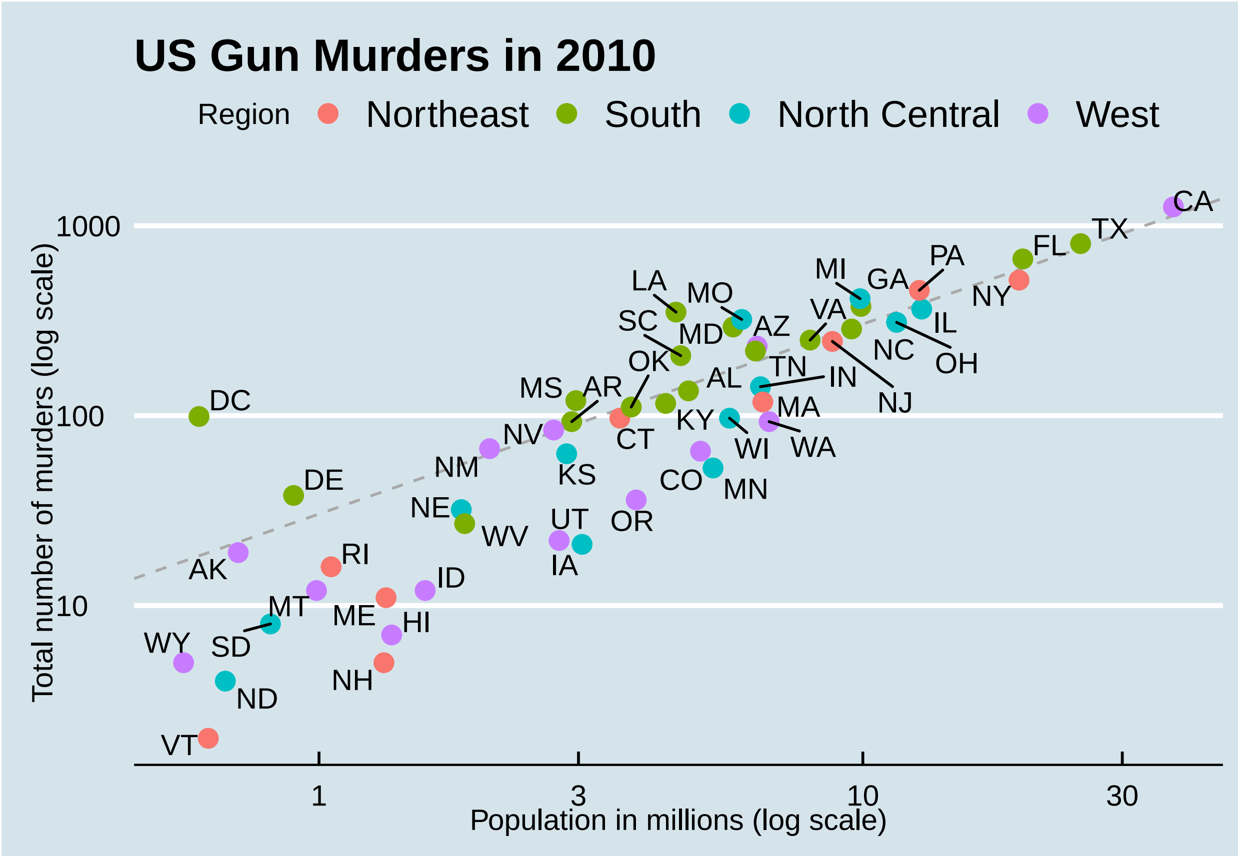
Gun Murders Scatterplot Full Example

The style of a ggplot graph can be changed using the theme() function.

The ggthemes package adds additional themes.

The ggrepel package includes a geometry that repels text labels, ensuring they do not overlap with each other: geom_text_repel().

```
# define the intercept
r <- murders %>%
    summarize(rate = sum(total) / sum(population) * 10^6) %>%
    .$rate

# make the plot, combining all elements
murders %>%
    ggplot(aes(population/10^6, total, label = abb)) +
    geom_abline(intercept = log10(r), lty = 2, color = "darkgrey") +
    geom_point(aes(col = region), size = 3) +
    geom_text_repel() +
    scale_x_log10() +
    scale_y_log10() +
    xlab("Population in millions (log scale)") +
    ylab("Total number of murders (log scale)") +
    ggtitle("US Gun Murders in 2010") +
    scale_color_discrete(name = "Region") +
    theme_economist()
```



Other Types of Plots

Histograms

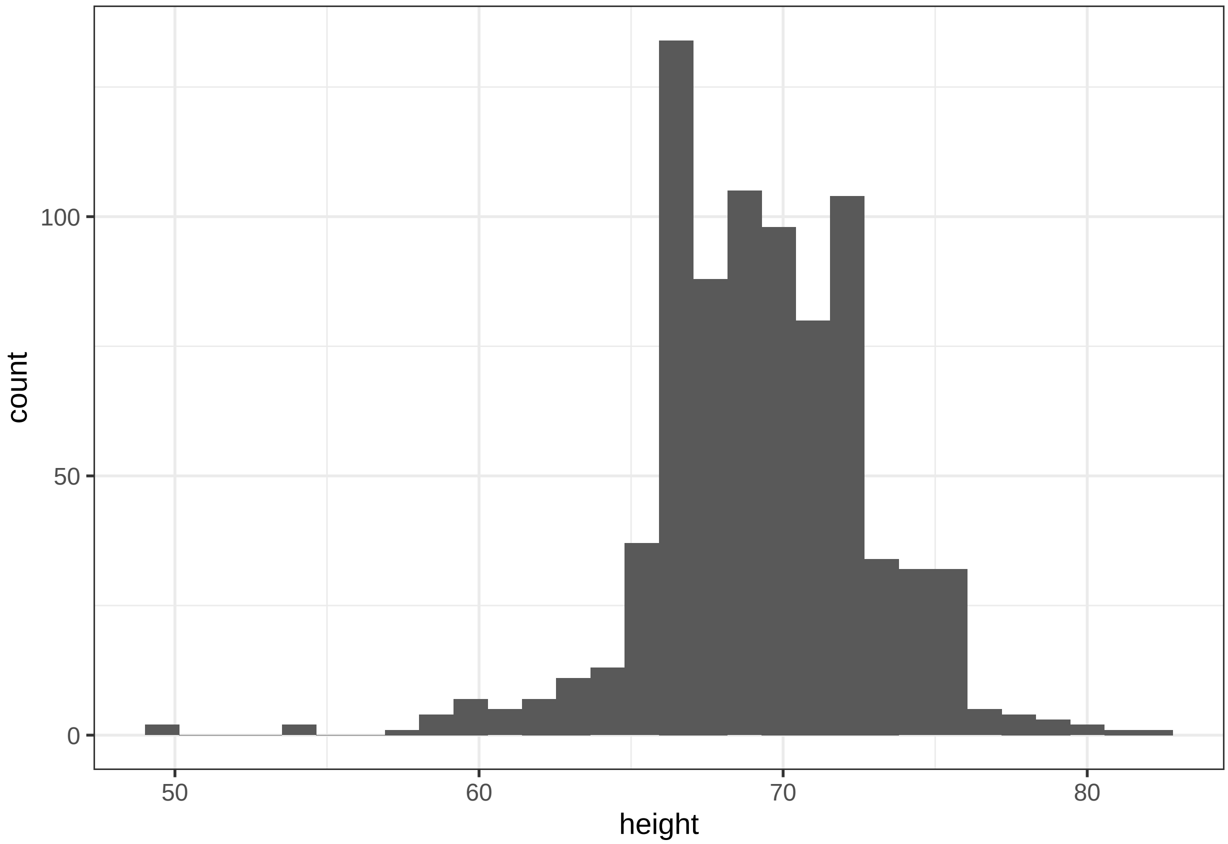
geom_histogram() creates a histogram. Use the binwidth argument to change the width of bins, the fill argument to change the bar fill color, and the col argument to change bar outline color.

geom_density() creates smooth density plots. Change the fill color of the plot with the fill argument.

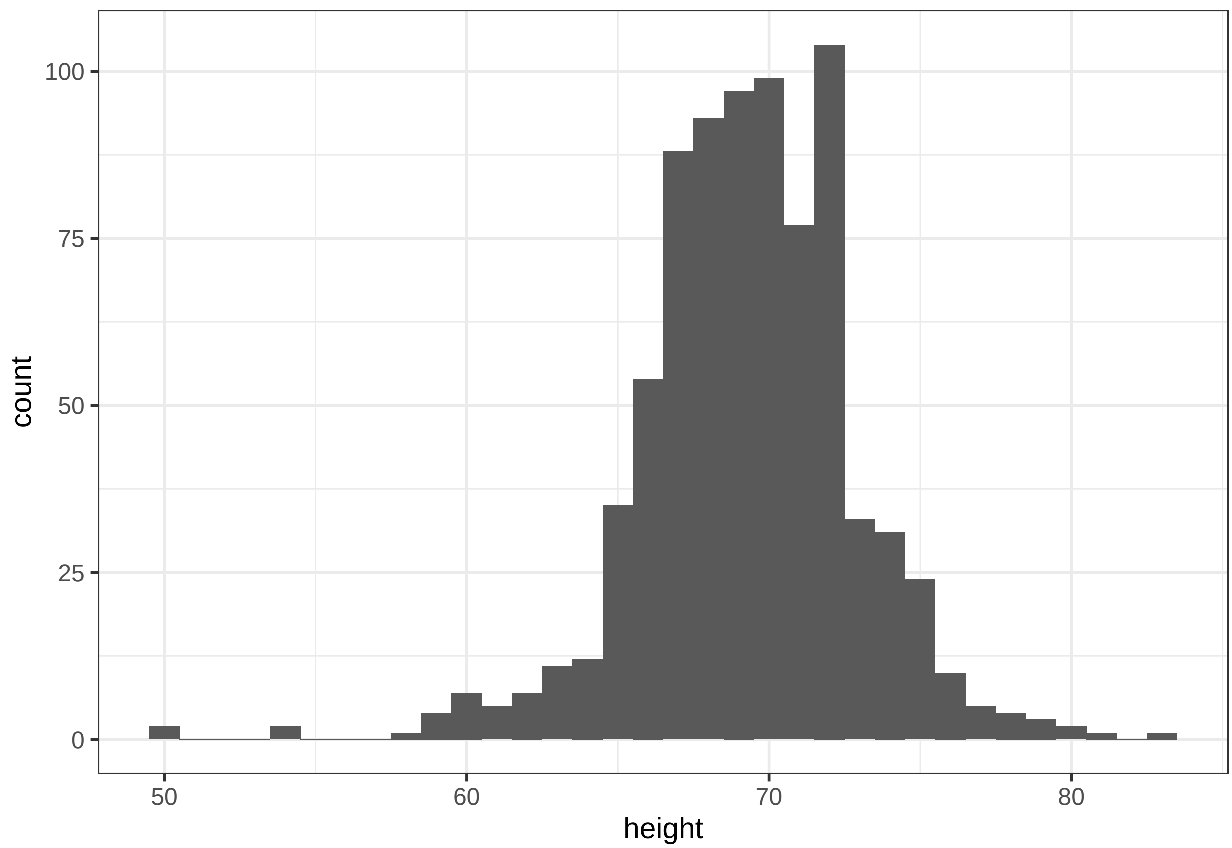
geom_qq() creates a quantile-quantile plot. This geometry requires the sample argument. By default, the data are compared to a standard normal distribution with a mean of 0 and standard deviation of 1. This can be changed with the dparams argument, or the sample data can be scaled.

```
data(heights)

p <- heights %>% filter(sex=="Male") %>% ggplot(aes(x=height))

# basic histogram
p + geom_histogram()
```

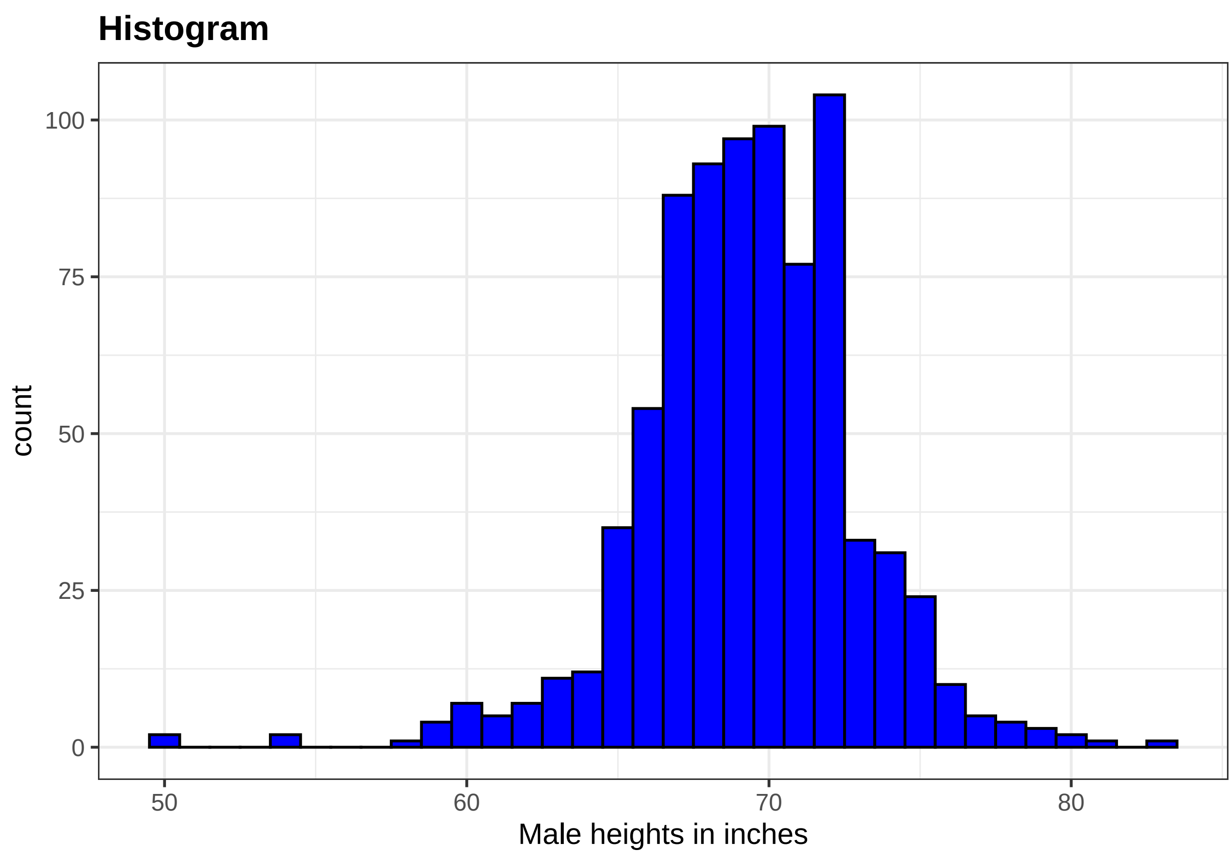
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
p + geom_histogram(binwidth=1)
```

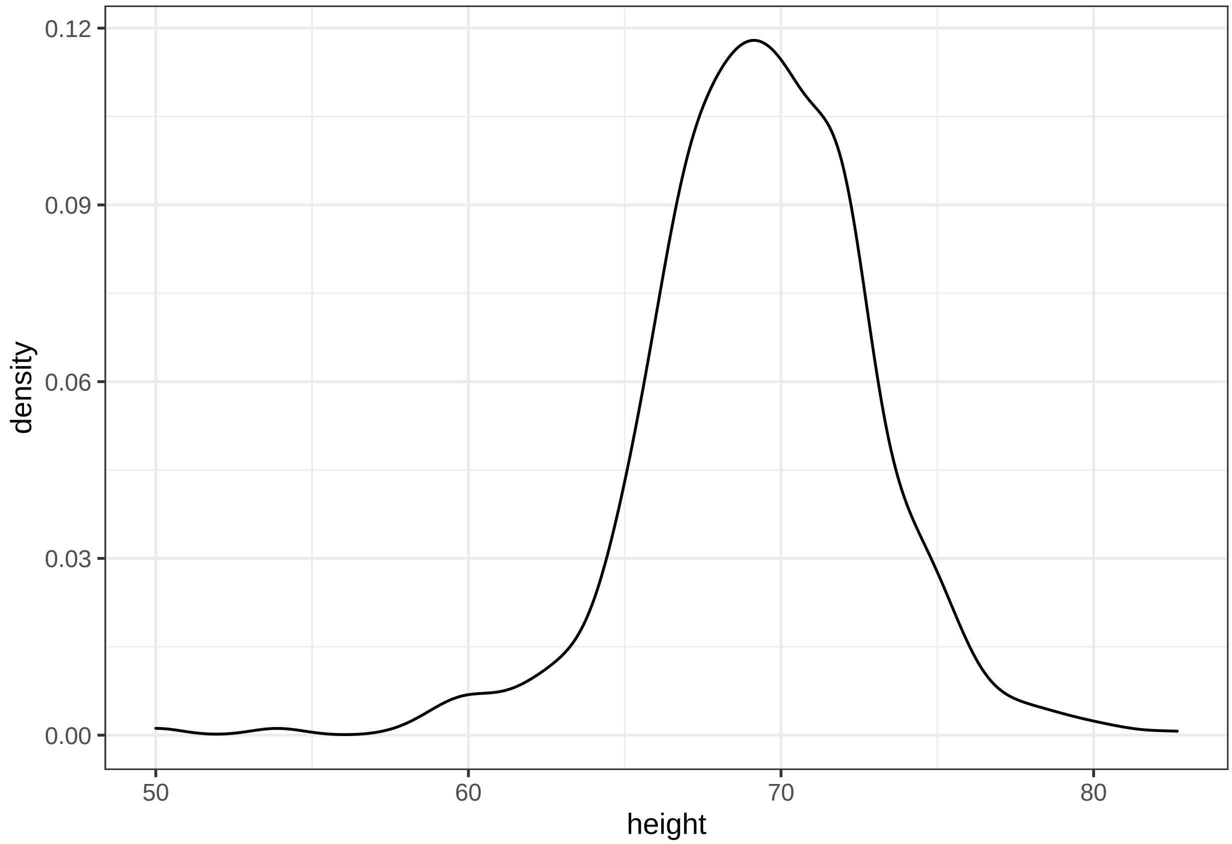



```r
# histogram with blue fill, black outline, labels and title
p + geom_histogram(binwidth=1, fill="blue", col="black") +
  xlab("Male heights in inches") +
  ggtitle("Histogram")
```

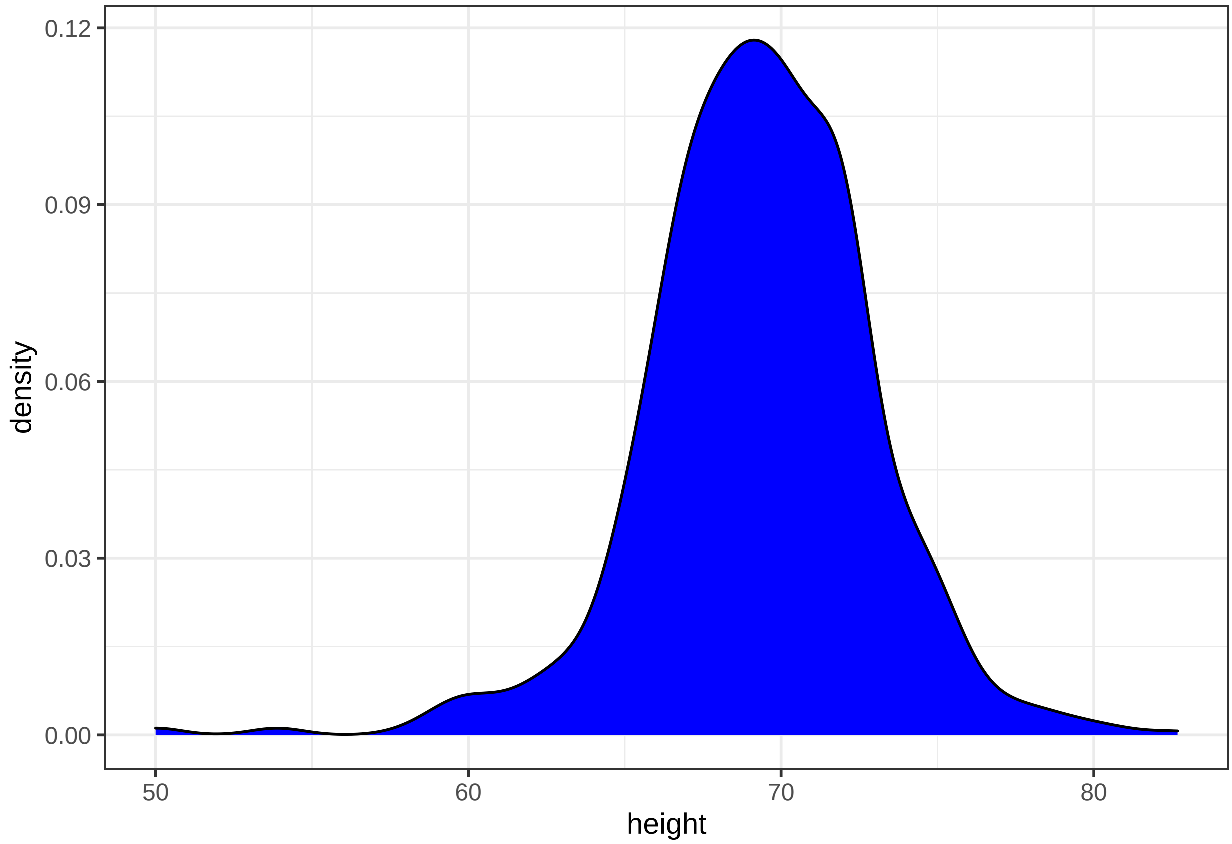


Smooth Density Plots

```
p + geom_density()
```

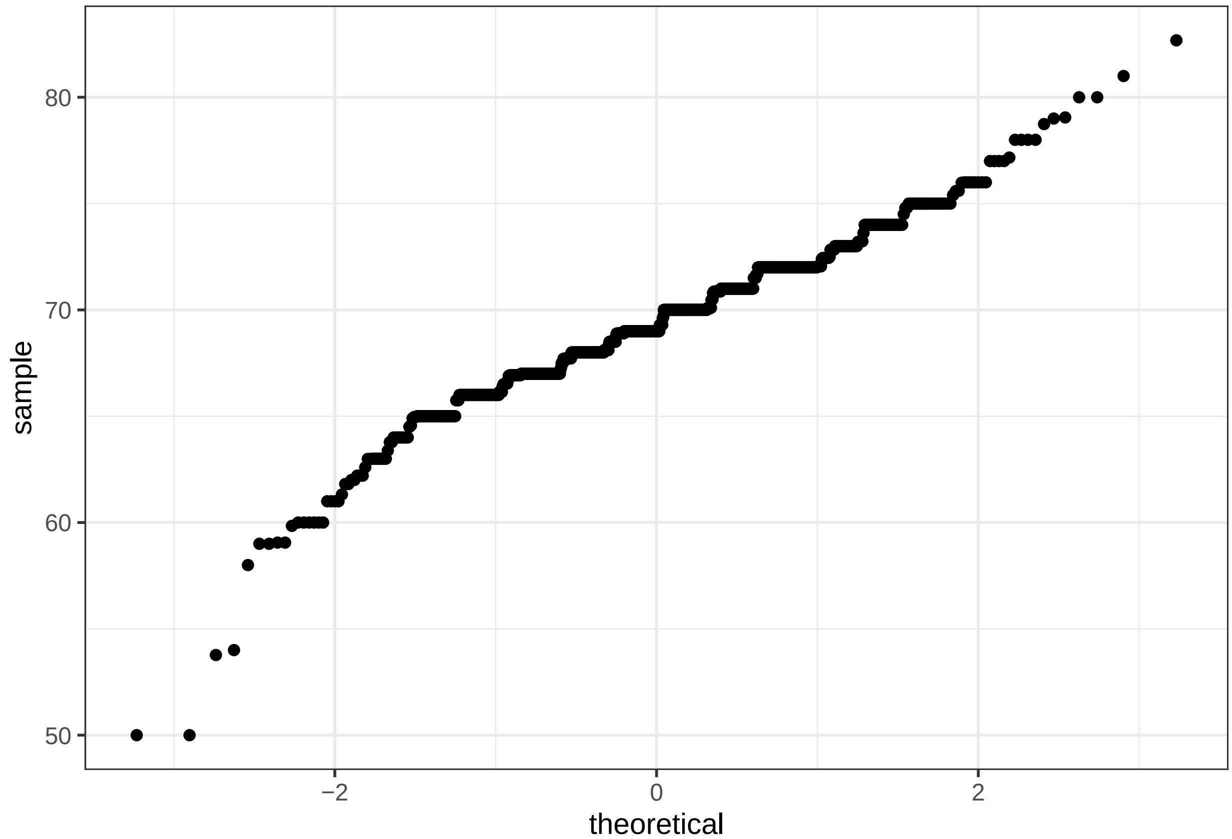



```
p + geom_density(fill = "blue")
```

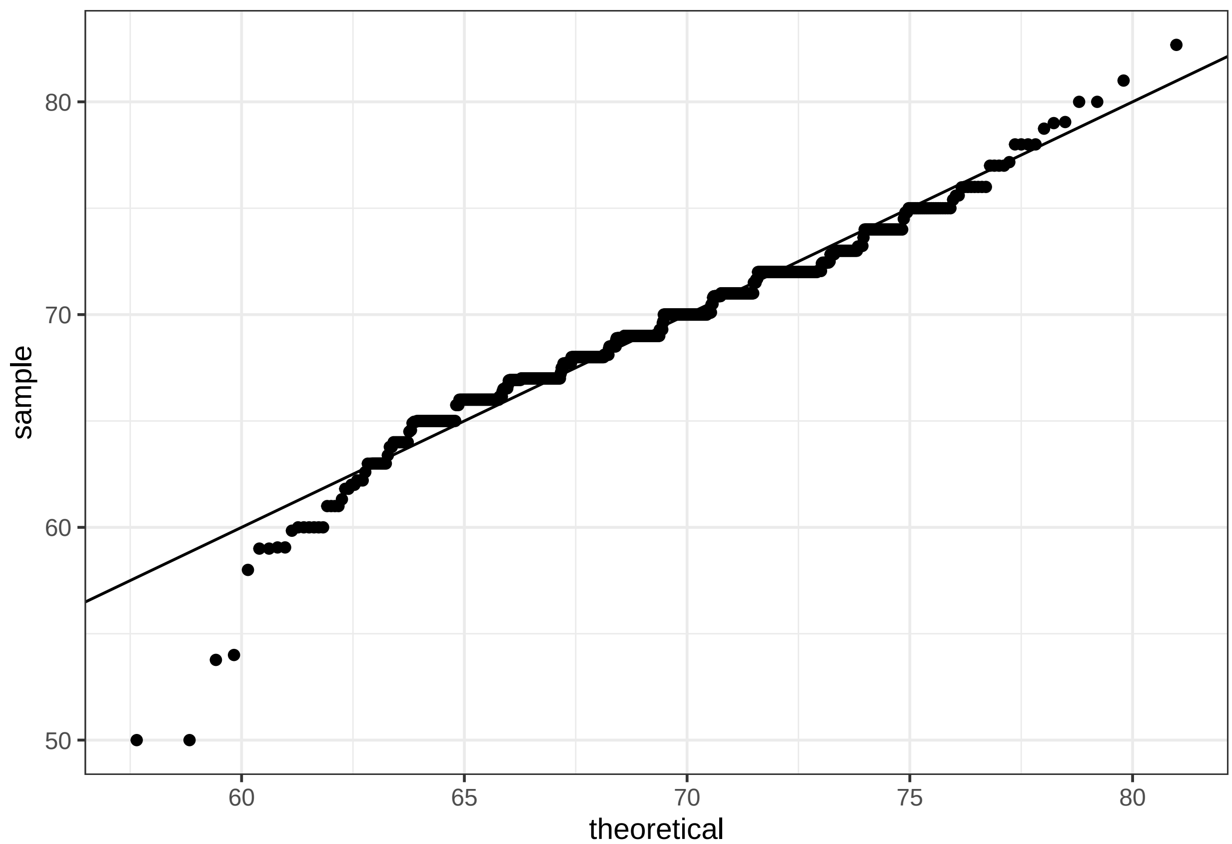


Q-Q Plots

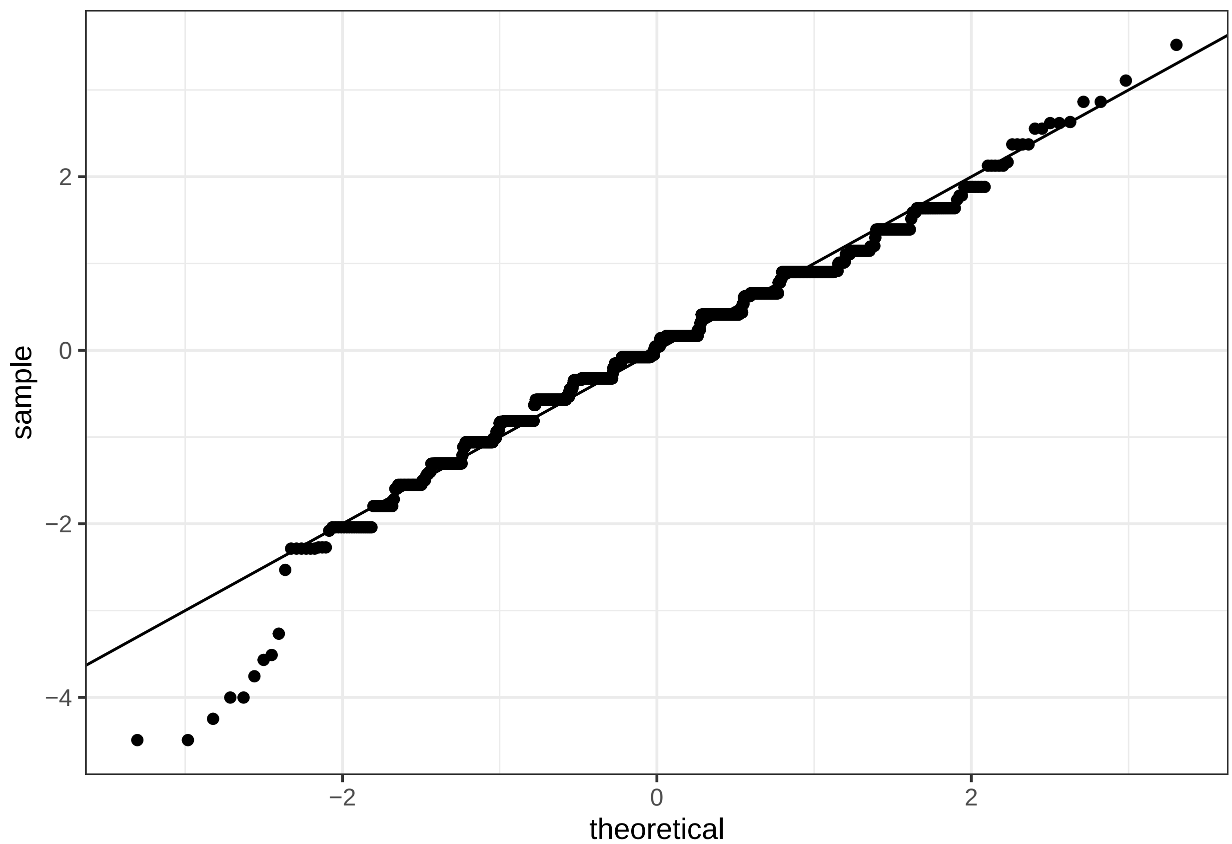
```
# basic QQ-plot
p <- heights %>% filter(sex == "Male") %>%
    ggplot(aes(sample = height))
p + geom_qq()
```




```r
# QQ-plot against a normal distribution with same mean/sd as data
params <- heights %>%
    filter(sex == "Male") %>%
    summarize(mean = mean(height), sd = sd(height))
    p + geom_qq(dparams = params) +
    geom_abline()
```




```r
# QQ-plot of scaled data against the standard normal distribution
heights %>%
    ggplot(aes(sample = scale(height))) +
    geom_qq() +
    geom_abline()
```



DPLYR Features

Summarize

```
summary(heights)
```

```
##      sex          height
##  Female:238   Min.   :50.00
##  Male  :812   1st Qu.:66.00
##               Median :68.50
##               Mean   :68.32
##               3rd Qu.:71.00
##               Max.   :82.68
```

```
s <- heights %>%
    filter(sex == "Male") %>%
    summarize(avg = mean(height),
              stdev = sd(height),
              min = min(height),
              max = max(height))

s
```

```
##        avg    stdev min      max
## 1 69.31475 3.611024  50 82.67717
```

Dot Placeholder

```r
us_murder_rate <- murders %>%
  summarize(rate = sum(total) / sum(population) * 1000000) %>%
  .$rate

us_murder_rate
```

```
## [1] 30.34555
```

Group By

```r
heights %>%
  group_by(sex) %>%
  summarize(avg = mean(height),
            stdev = sd(height))
```

```
## # A tibble: 2 x 3
##   sex      avg stdev
##   <fct>  <dbl> <dbl>
## 1 Female  64.9  3.76
## 2 Male    69.3  3.61
```

Sorting

```r
murders <- murders %>% mutate(murder_rate = total/population * 100000)
murders %>% arrange(desc(murder_rate)) %>% head()
```

```
##                  state abb        region population total murder_rate
## 1 District of Columbia  DC         South     601723    99   16.452753
## 2            Louisiana  LA         South    4533372   351    7.742581
## 3             Missouri  MO North Central    5988927   321    5.359892
## 4             Maryland  MD         South    5773552   293    5.074866
## 5       South Carolina  SC         South    4625364   207    4.475323
## 6             Delaware  DE         South     897934    38    4.231937
```

```r
murders %>% arrange(desc(murder_rate)) %>% top_n(10)
```

```
## Selecting by murder_rate
```

```
##                   state abb        region population total murder_rate
## 1  District of Columbia  DC         South     601723    99   16.452753
## 2             Louisiana  LA         South    4533372   351    7.742581
## 3              Missouri  MO North Central    5988927   321    5.359892
## 4              Maryland  MD         South    5773552   293    5.074866
## 5        South Carolina  SC         South    4625364   207    4.475323
## 6              Delaware  DE         South     897934    38    4.231937
## 7              Michigan  MI North Central    9883640   413    4.178622
## 8           Mississippi  MS         South    2967297   120    4.044085
## 9               Georgia  GA         South    9920000   376    3.790323
## 10              Arizona  AZ          West    6392017   232    3.629527
```

Case Study: Trends in World Health & Economics

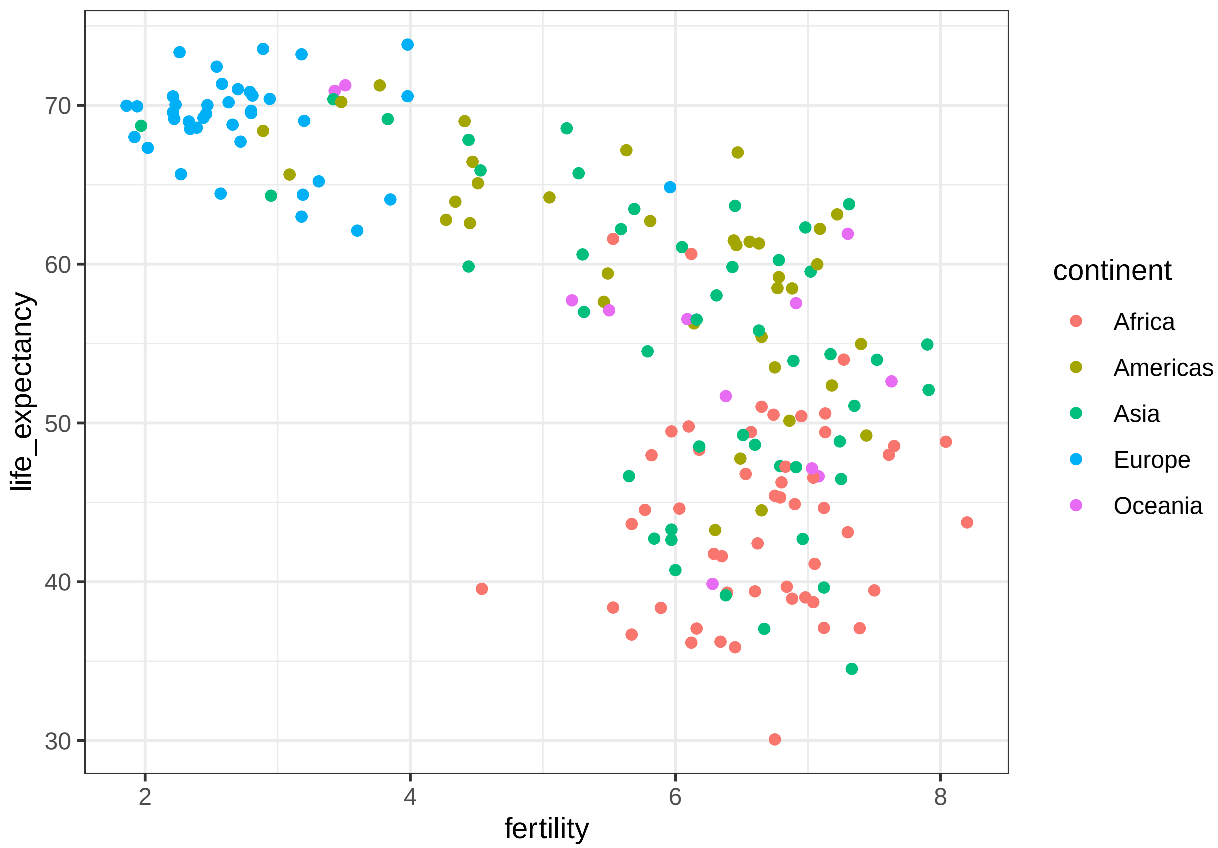
```r
head(gapminder)
```

```
##                country year infant_mortality life_expectancy fertility
## 1             Albania 1960           115.40           62.87      6.19
## 2             Algeria 1960           148.20           47.50      7.65
## 3              Angola 1960           208.00           35.98      7.32
## 4 Antigua and Barbuda 1960               NA           62.97      4.43
## 5           Argentina 1960            59.87           65.39      3.11
## 6             Armenia 1960               NA           66.86      4.55
##   population          gdp continent          region
## 1    1636054           NA    Europe Southern Europe
## 2   11124892  13828152297    Africa Northern Africa
## 3    5270844           NA    Africa   Middle Africa
## 4      54681           NA  Americas       Caribbean
## 5   20619075 108322326649  Americas   South America
## 6    1867396           NA      Asia    Western Asia
```

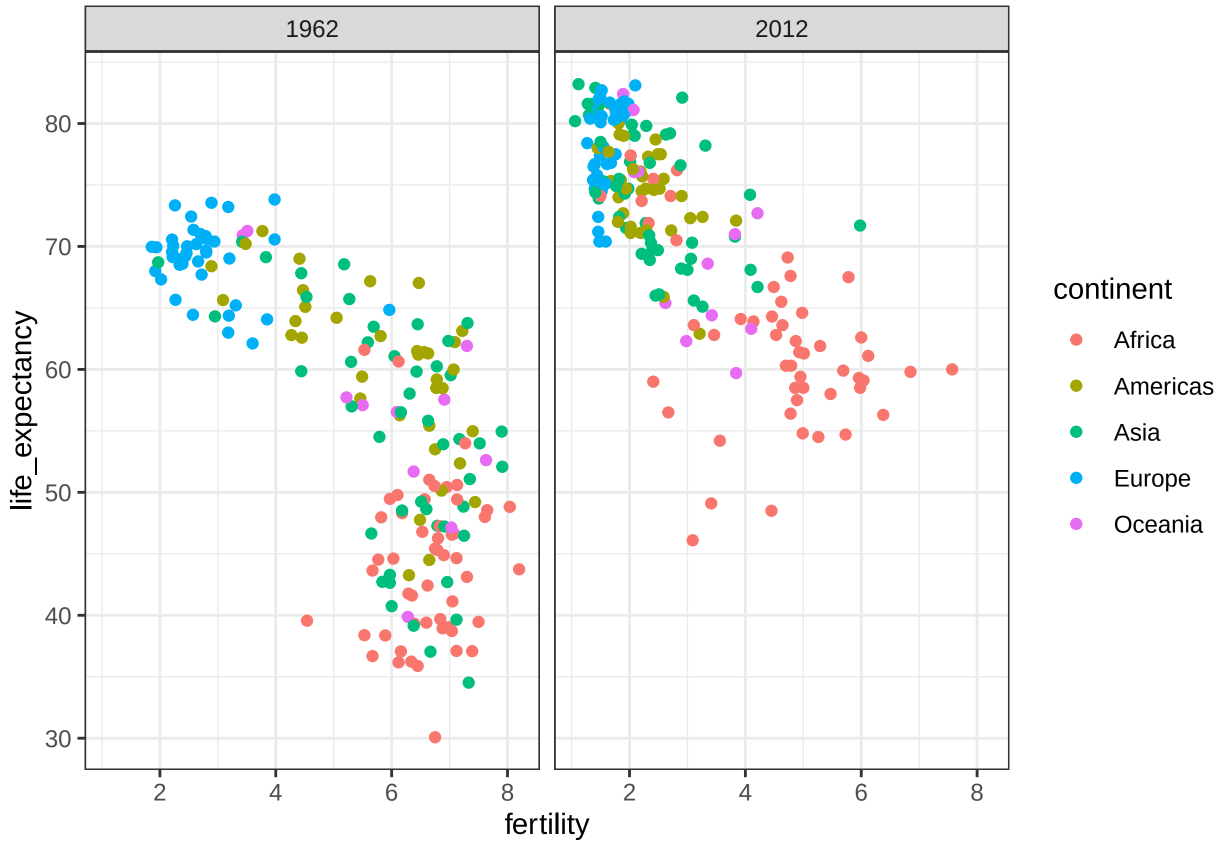
```
gapminder %>%
    filter(year == 2015 & country %in% c("Sri Lanka",
                                         "Turkey",
                                         "Poland",
                                         "South Korea",
                                         "Malaysia",
                                         "Russia",
                                         "Pakistan",
                                         "Vietnam",
                                         "Thailand",
                                         "South Africa")) %>%
  arrange(desc(infant_mortality)) %>%
  select(country, infant_mortality)
```

```
##         country infant_mortality
## 1      Pakistan             65.8
## 2  South Africa             33.6
## 3       Vietnam             17.3
## 4        Turkey             11.6
## 5      Thailand             10.5
## 6     Sri Lanka              8.4
## 7        Russia              8.2
## 8      Malaysia              6.0
## 9        Poland              4.5
## 10  South Korea              2.9
```

```
filter(gapminder, year == 1962) %>%
  ggplot( aes(fertility, life_expectancy, color = continent)) +
  geom_point()
```

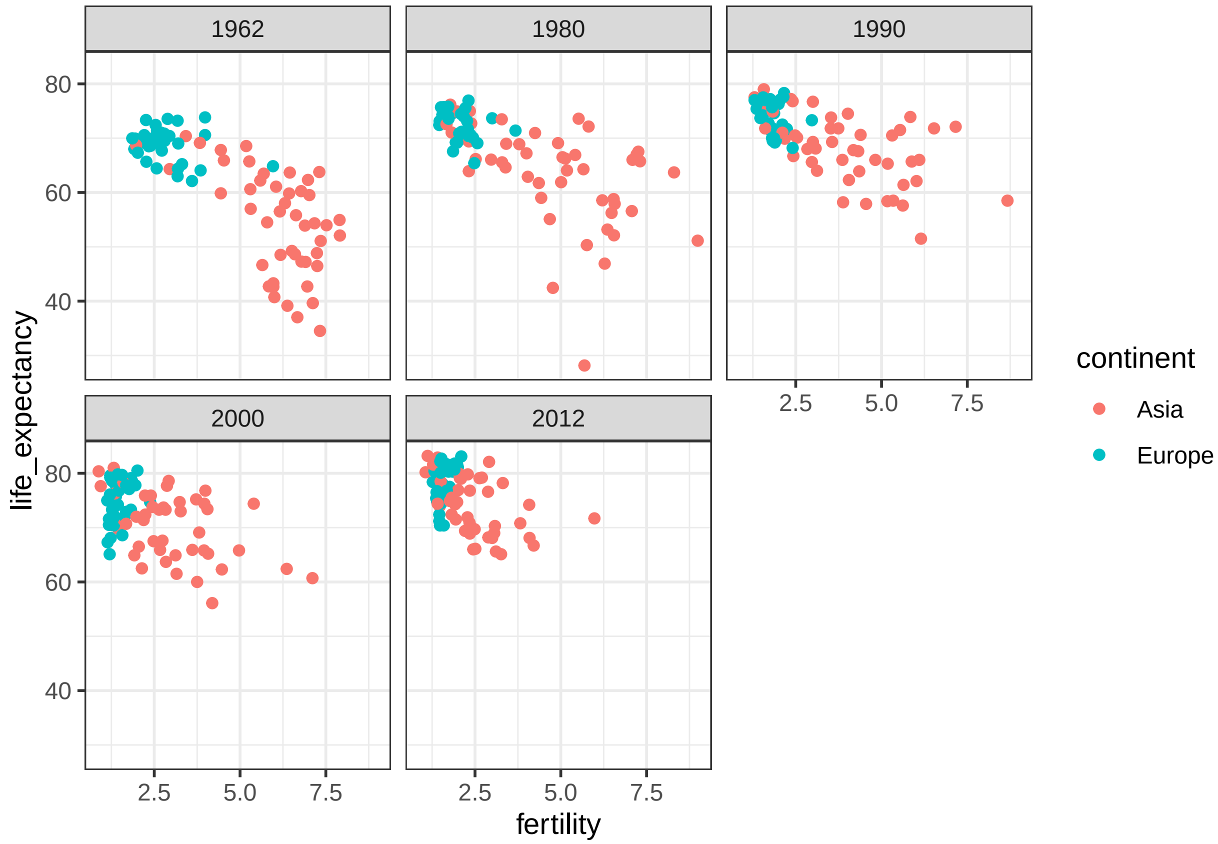



```r
filter(gapminder, year%in%c(1962, 2012)) %>%
  ggplot(aes(fertility, life_expectancy, col = continent)) +
  geom_point() +
  facet_grid(.~year)
```



Examining Life Expectancy by Year

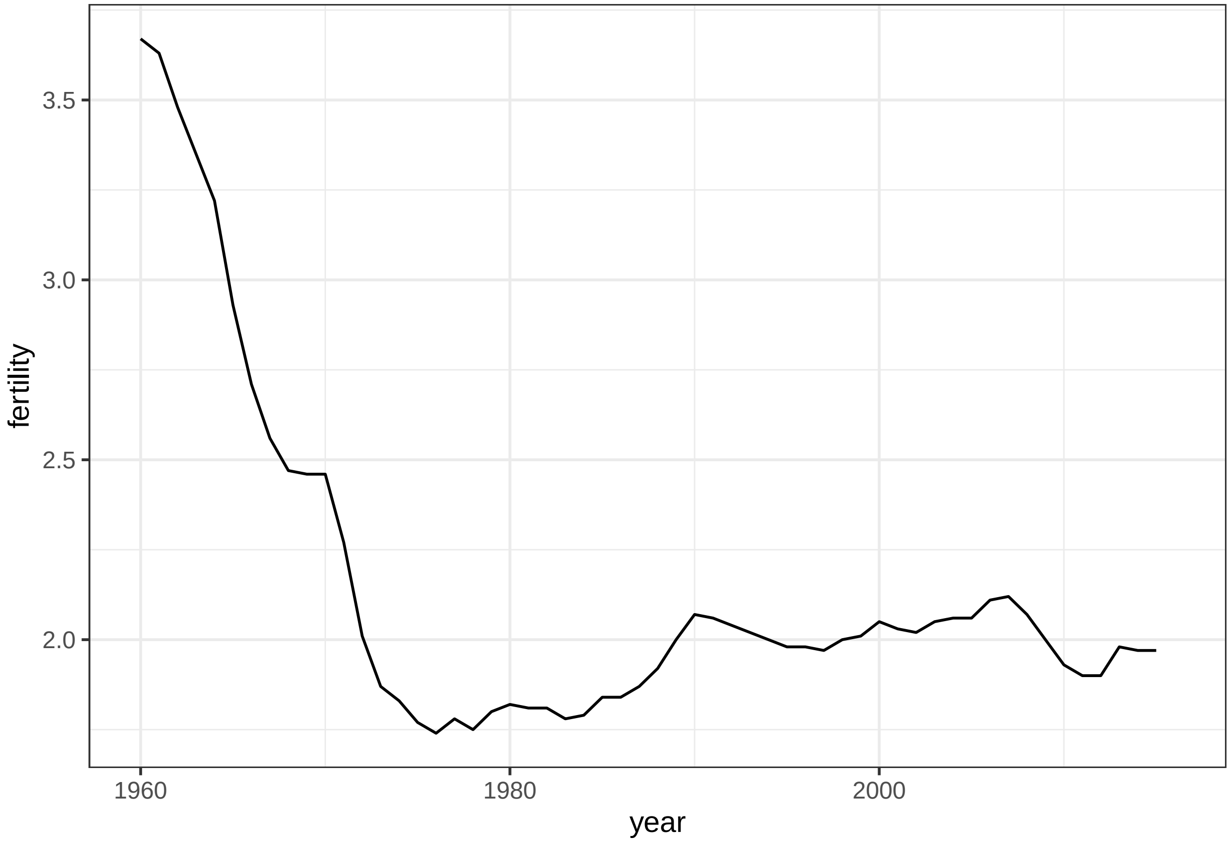
```
years <- c(1962, 1980, 1990, 2000, 2012)
continents <- c("Europe", "Asia")
gapminder %>%
  filter(year %in% years & continent %in% continents) %>%
  ggplot( aes(fertility, life_expectancy, col = continent)) +
  geom_point() +
  facet_wrap(~year)
```



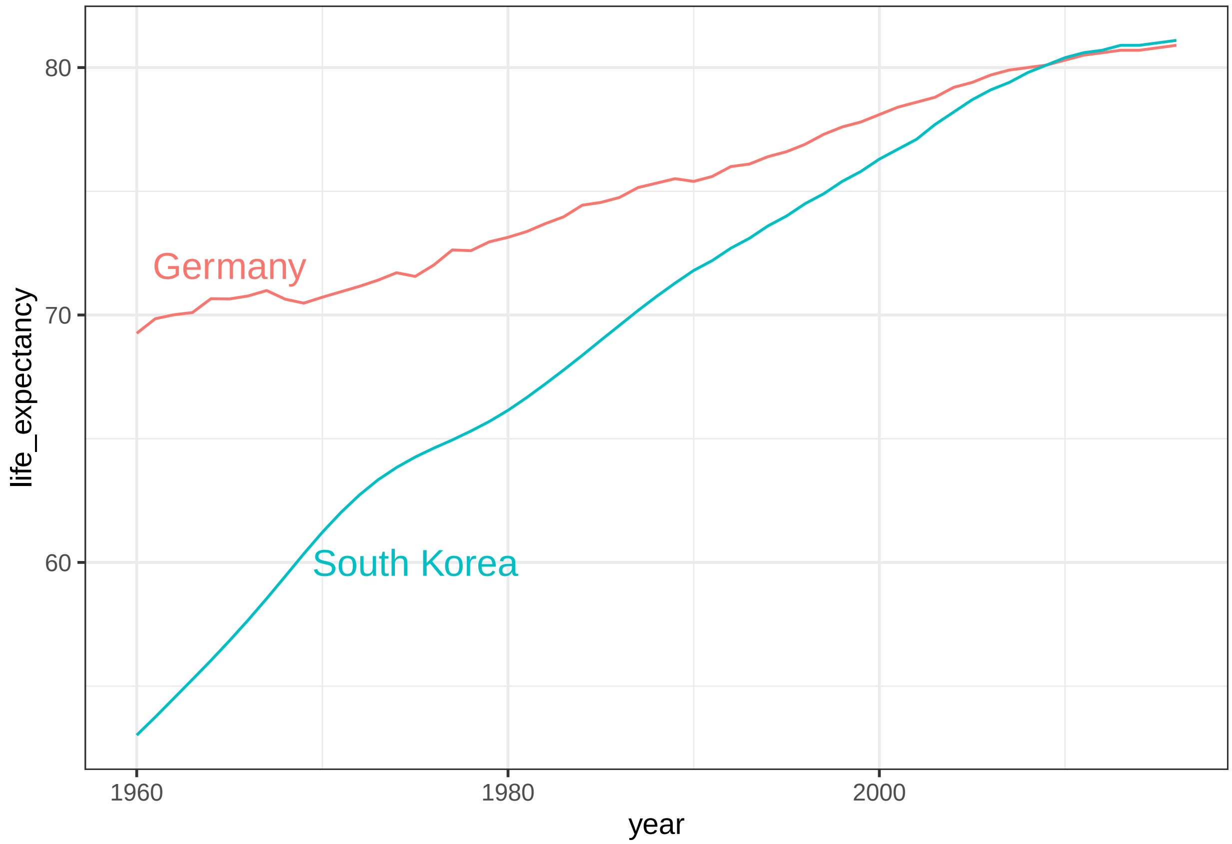
Examining Fertility and Life Expectancy through Time Series

```
gapminder %>%
  filter(country == "United States") %>%
  ggplot(aes(year, fertility)) +
  geom_line()
```

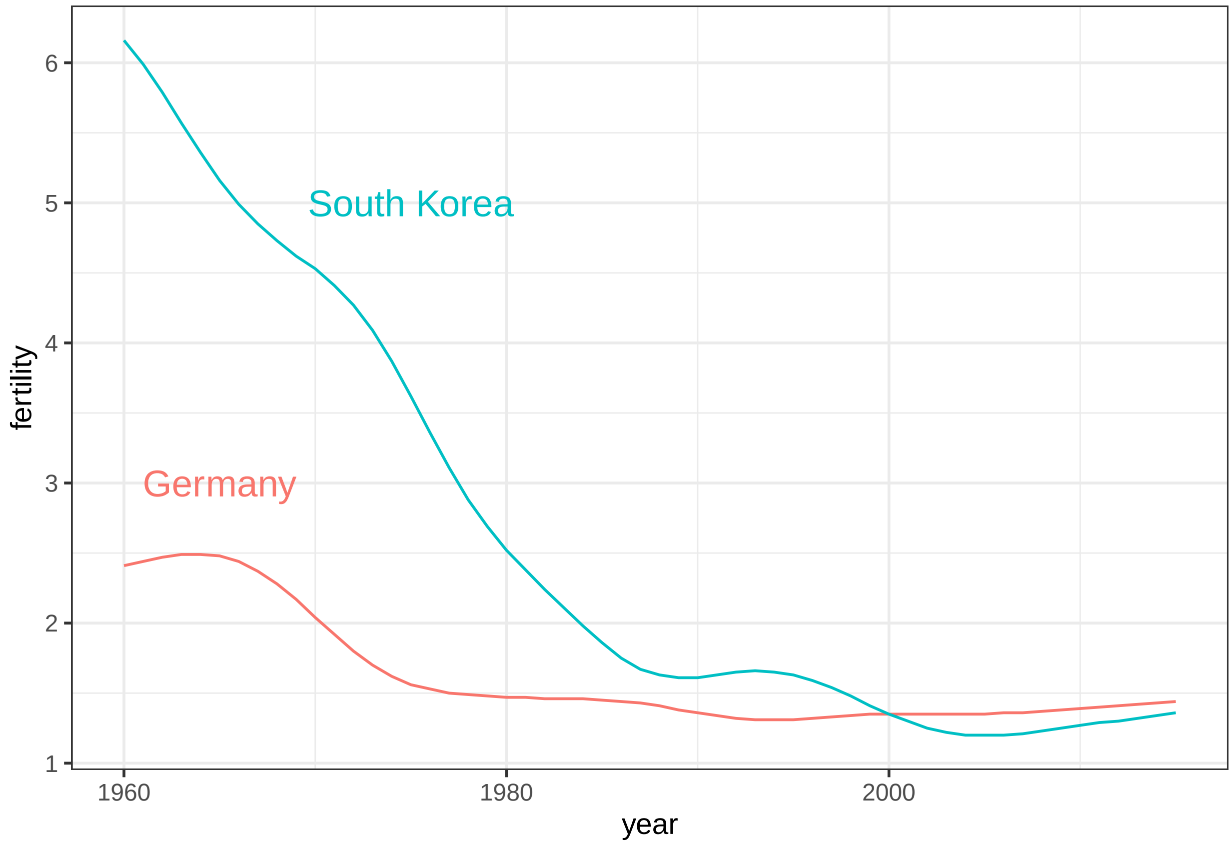
```
## Warning: Removed 1 row(s) containing missing values (geom_path).
```




```
countries <- c("South Korea","Germany")
labels <- data.frame(country = countries, x = c(1975,1965), y = c(60,72))

gapminder %>%
  filter(country %in% countries) %>%
  ggplot(aes(year, life_expectancy, col=country)) +
  geom_line() +
  geom_text(data=labels, aes(x, y, label=country), size=5) +
  theme(legend.position="none")
```




```
labels2 <- data.frame(country = countries, x = c(1975,1965), y = c(5,3))

gapminder %>%
  filter(country %in% countries & !is.na(fertility)) %>%
  ggplot(aes(year, fertility, col=country)) +
  geom_line() +
  geom_text(data=labels2, aes(x, y, label=country), size=5) +
  theme(legend.position="none")
```



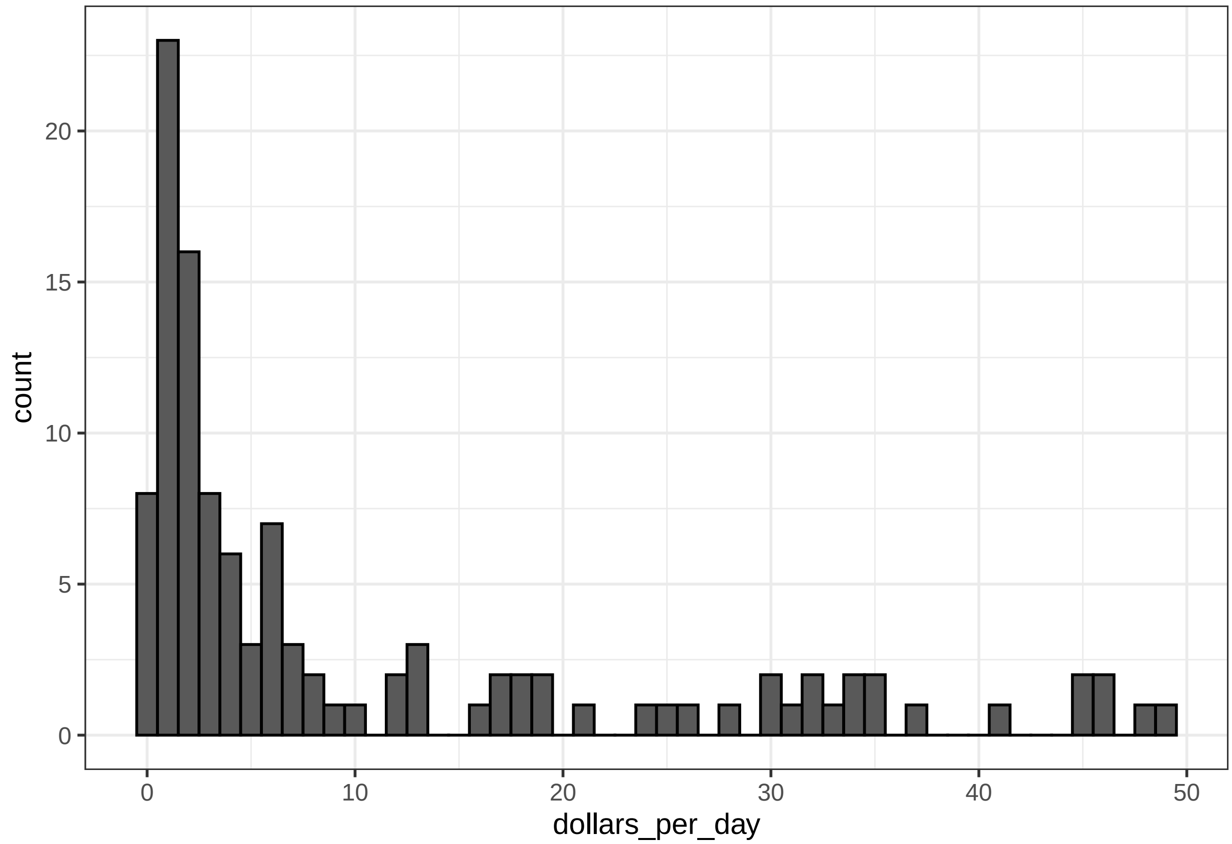
Log Transformation to Rank GDP Data

We use GDP data to compute income in US dollars per day, adjusted for inflation.

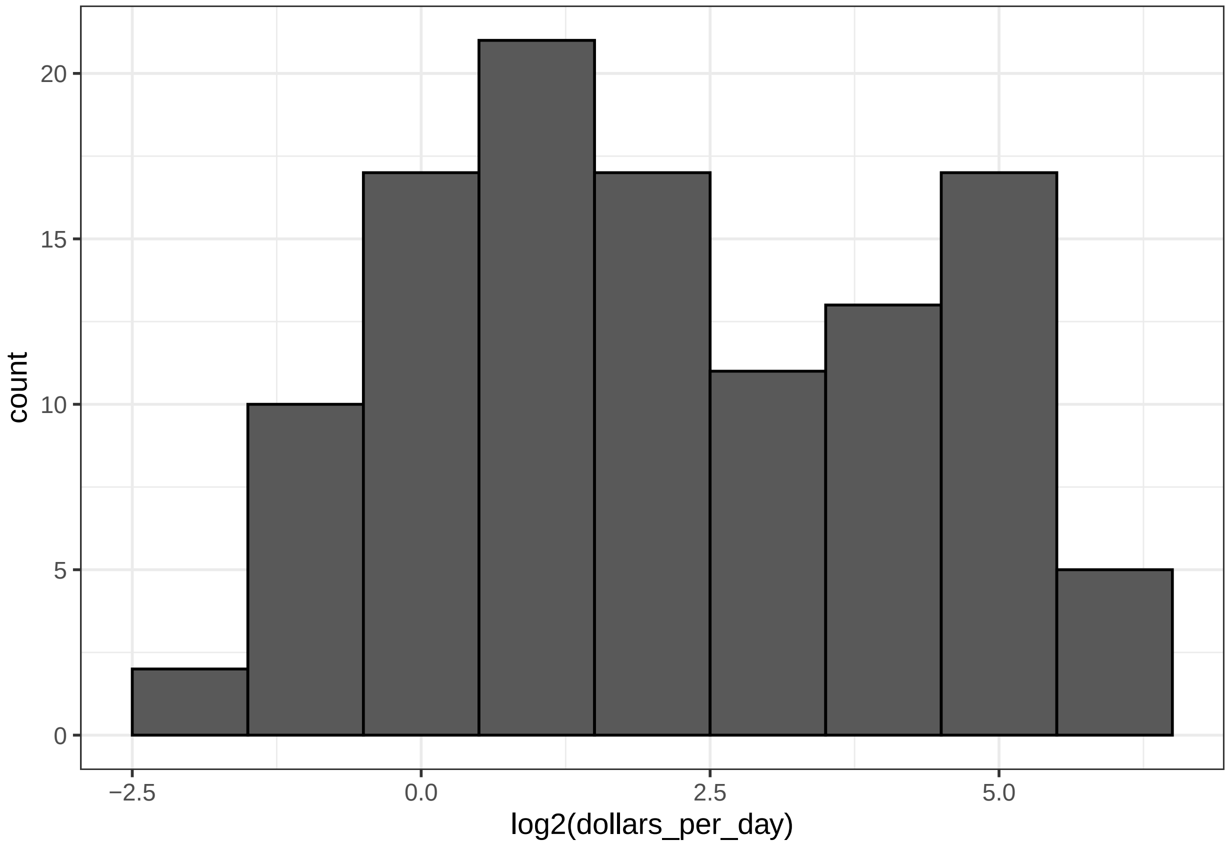
Log transformations convert multiplicative changes into additive changes.

Common transformations are the log base 2 transformation and the log base 10 transformation. The choice of base depends on the range of the data. The natural log is not recommended for visualization because it is difficult to interpret.

```
gapminder <- gapminder %>%
    mutate(dollars_per_day = gdp/population/365)

past_year <- 1970
gapminder %>%
    filter(year == past_year & !is.na(gdp)) %>%
    ggplot(aes(dollars_per_day)) +
    geom_histogram(binwidth = 1, color = "black")
```




```
gapminder %>%
    filter(year == past_year & !is.na(gdp)) %>%
    ggplot(aes(log2(dollars_per_day))) +
    geom_histogram(binwidth = 1, color = "black")
```


count
20
15
10
5
0
−2.5
0.0
2.5
5.0
log2(dollars_per_day)