Data Visualization - 4. Show the Right Numbers

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Code Horizons

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Show the Right Numbers

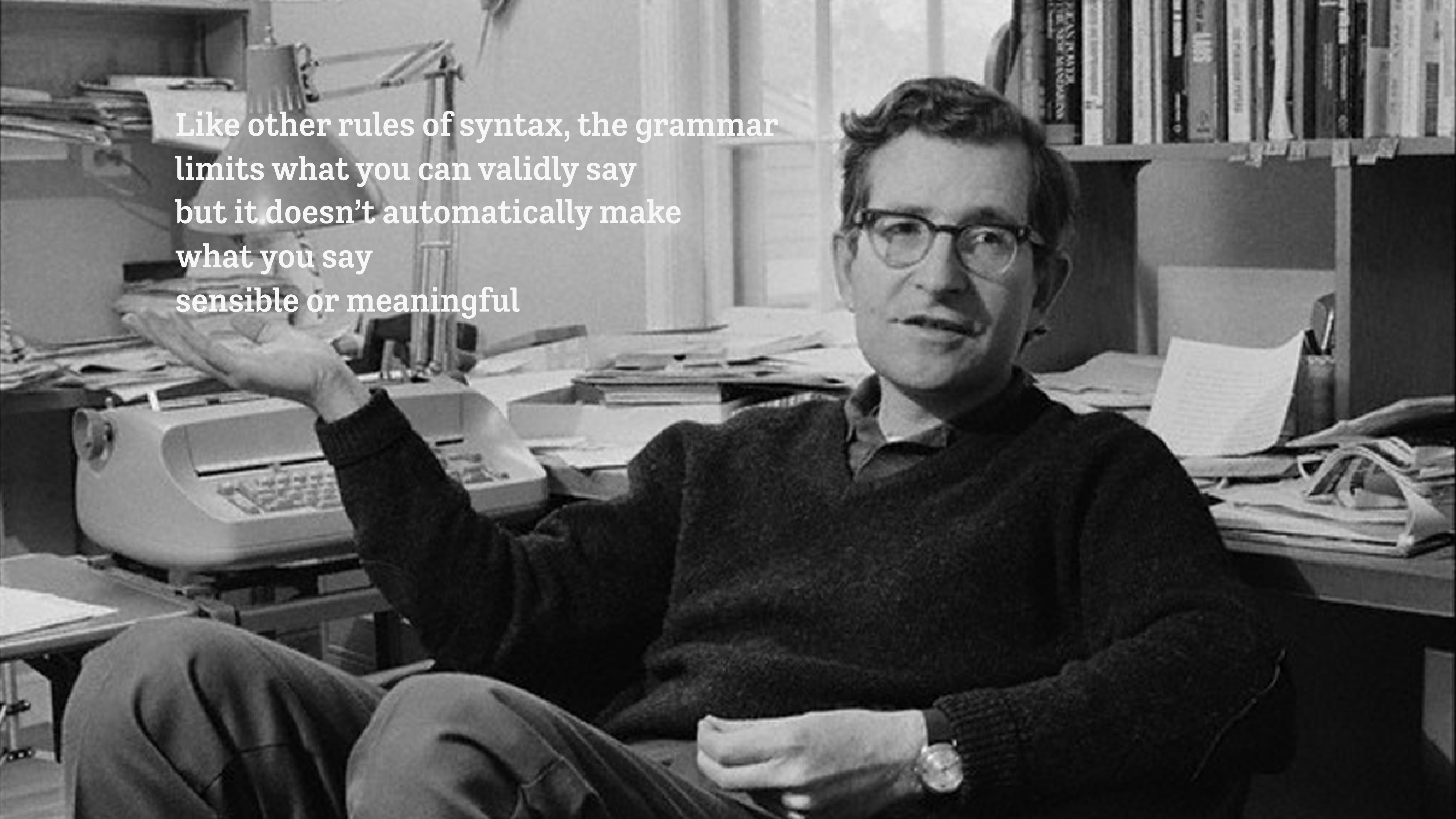
Load the packages we need

```r
library(tidyverse)      # Your friend and mine
library(gapminder)      # Gapminder data
library(here)           # Portable file paths
library(socviz)         # Handy socviz functions
```

`ggplot` implements a **grammar** of graphics

A grammar of graphics

The grammar is a set of rules for how to produce graphics from data, by *mapping* data to or *representing* it by geometric objects (like points and lines) that have aesthetic attributes (like position, color, size, and shape), together with further rules for transforming data if needed, for adjusting scales and their guides, and for projecting results onto some coordinate system.


Like other rules of syntax, the grammar
limits what you can validly say
but it doesn’t automatically make
what you say
sensible or meaningful

Grouped data and the `group` aesthetic

Try to make a lineplot

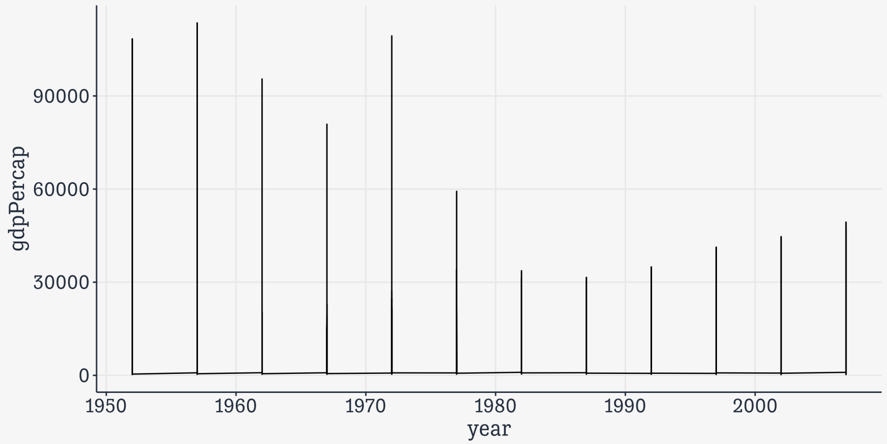
```r
p <- ggplot(data = gapminder,
            mapping = aes(x = year,
                          y = gdpPercap))
```

Try to make a lineplot

```
p <- ggplot(data = gapminder,
            mapping = aes(x = year,
                          y = gdpPercap)) +
  geom_line()
```

Try to make a lineplot

```r
p <- ggplot(data = gapminder,
            mapping = aes(x = year,
                          y = gdpPercap)) +
  geom_line()

p
```



Try to make a lineplot

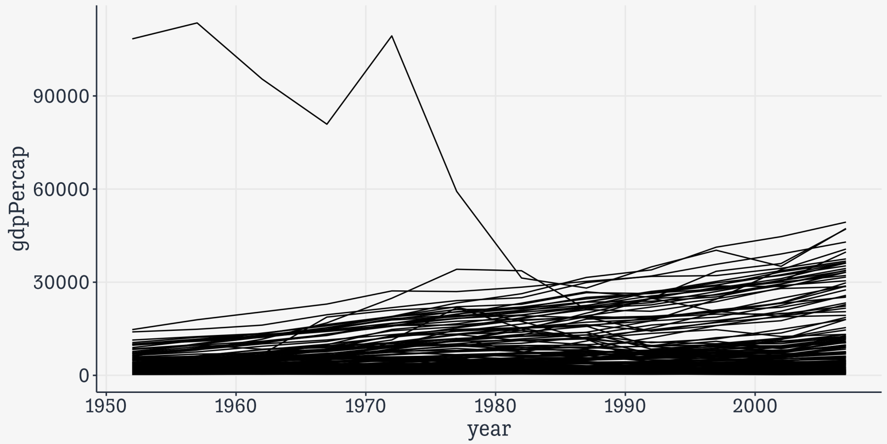
```r
p <- ggplot(data = gapminder,
            mapping = aes(x = year,
                          y = gdpPercap))
```

Try to make a lineplot

```r
p <- ggplot(data = gapminder,
            mapping = aes(x = year,
                          y = gdpPercap)) +
  geom_line(mapping = aes(group = country))
```

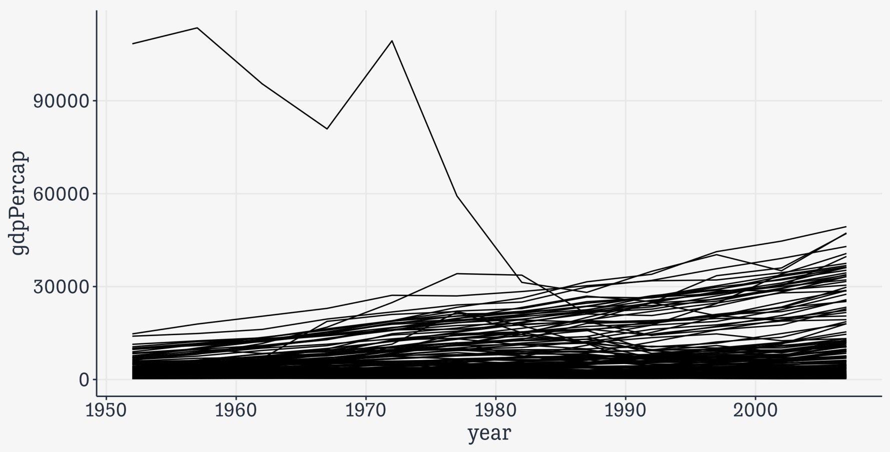
Try to make a lineplot

```r
p <- ggplot(data = gapminder,
            mapping = aes(x = year,
                          y = gdpPercap)) +
  geom_line(mapping = aes(group = country))

p
```



Try to make a lineplot

```
p <- ggplot(data = gapminder,
            mapping = aes(x = year,
                          y = gdpPercap)) +
  geom_line(mapping = aes(group = country))

p
```



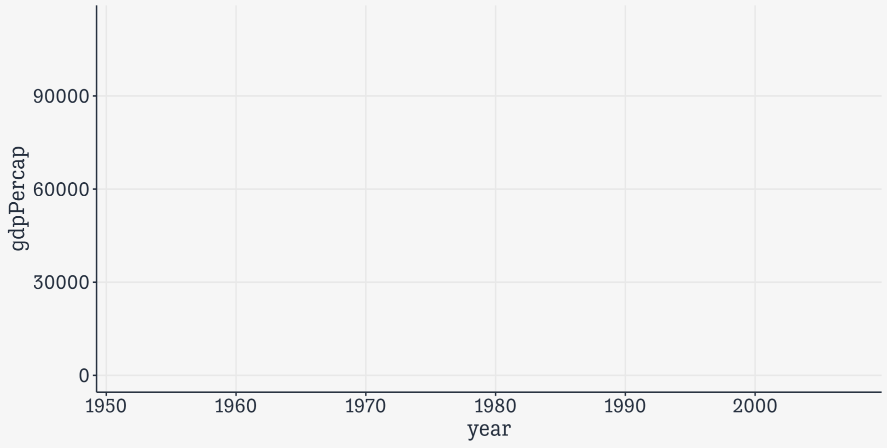
Facet the plot

```
1  gapminder
```

```
# A tibble: 1,704 × 6
   country     continent  year lifeExp      pop
gdpPercap
   <fct>       <fct>     <int>   <dbl>    <int>
<dbl>
 1 Afghanistan Asia       1952    28.8  8425333
779.
 2 Afghanistan Asia       1957    30.3  9240934
821.
 3 Afghanistan Asia       1962    32.0 10267083
853.
 4 Afghanistan Asia       1967    34.0 11537966
836.
 5 Afghanistan Asia       1972    36.1 13079460
740.
 6 Afghanistan Asia       1977    38.4 14880372
786.
 7 Afghanistan Asia       1982    39.9 12881816
978.
```

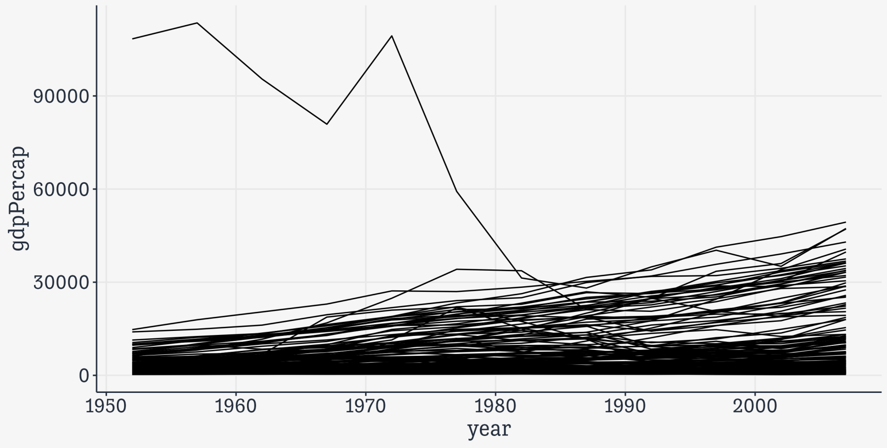
Facet the plot

```
gapminder |>
  ggplot(mapping =
           aes(x = year,
           y = gdpPercap))
```



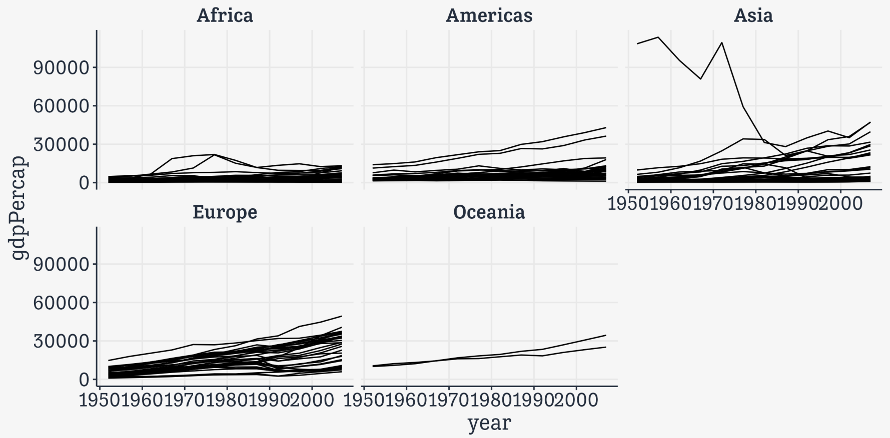
Facet the plot

```r
gapminder |>
  ggplot(mapping =
           aes(x = year,
           y = gdpPercap)) +
  geom_line(mapping = aes(group = country))
```



Facet the plot

```r
gapminder |>
  ggplot(mapping =
           aes(x = year,
           y = gdpPercap)) +
  geom_line(mapping = aes(group = country))
  facet_wrap(~ continent)
```



Faceting is very powerful

Faceting

A facet is not a geom; it's a way of arranging repeated geoms by some additional variable

Facets use R's "formula" syntax: `facet_wrap(~ continent)`

Read the `~` as "on" or "by"

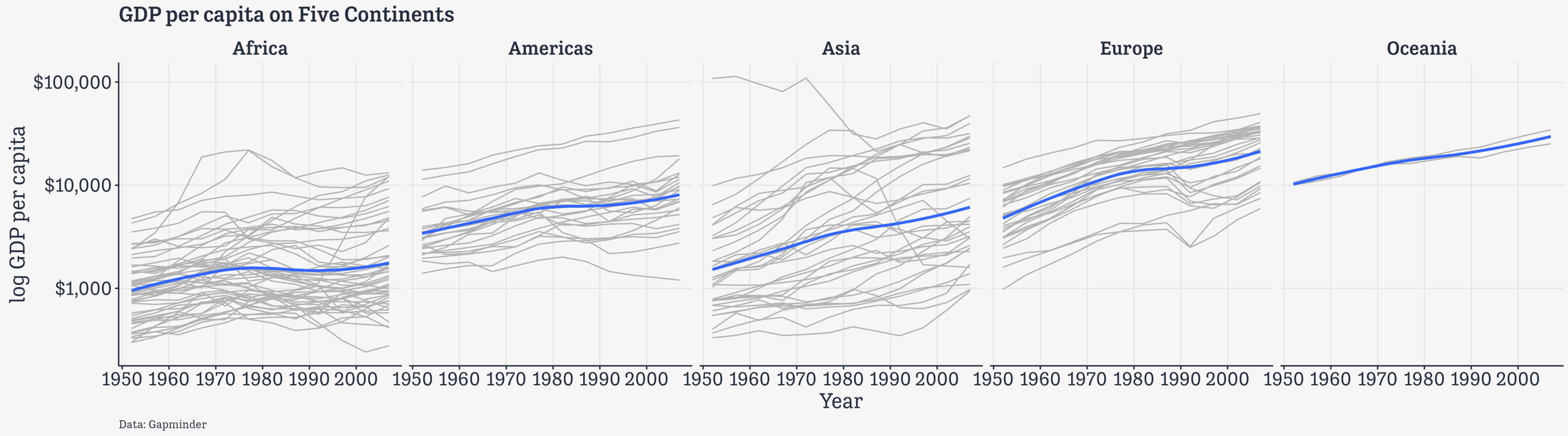
Faceting

You can also use this syntax: `facet_wrap(vars(continent))`

This is newer, and consistent with other ways of referring to variables within tidyverse functions.

Facets in action

```r
p <- ggplot(data = gapminder,
            mapping = aes(x = year,
                          y = gdpPercap))

p_out <- p + geom_line(color="gray70",
              mapping=aes(group = country)) +
    geom_smooth(size = 1.1,
                method = "loess",
                se = FALSE) +
    scale_y_log10(labels=scales::label_dollar()) +
    facet_wrap(~ continent, ncol = 5) +#<<
    labs(x = "Year",
         y = "log GDP per capita",
         title = "GDP per capita on Five Continents",
         caption = "Data: Gapminder")
```



A more polished faceted plot.

One-variable summaries

The `midwest` dataset

County-level census data for Midwestern U.S. Counties

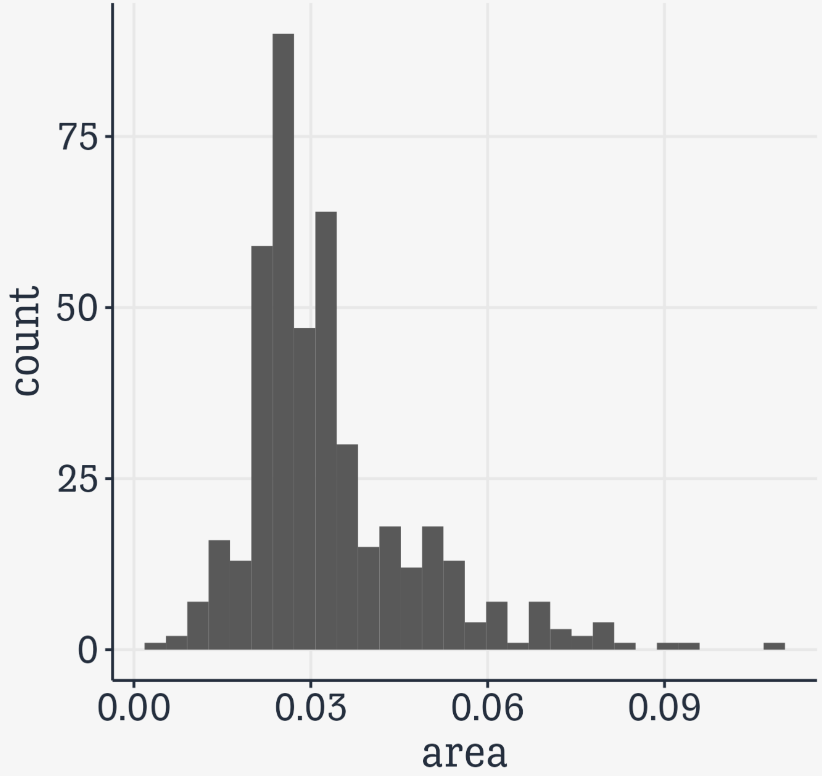
```
midwest
```

```
# A tibble: 437 × 28
     PID county  state  area poptotal popdensity popwhite popblack popamerindian
   <int> <chr>   <chr> <dbl>    <int>      <dbl>    <int>    <int>         <int>
 1   561 ADAMS   IL    0.052    66090      1271.    63917     1702            98
 2   562 ALEXAN… IL    0.014    10626       759      7054     3496            19
 3   563 BOND    IL    0.022    14991       681.    14477      429            35
 4   564 BOONE   IL    0.017    30806      1812.    29344      127            46
 5   565 BROWN   IL    0.018     5836       324.     5264      547            14
 6   566 BUREAU  IL    0.05     35688       714.    35157       50            65
 7   567 CALHOUN IL    0.017     5322       313.     5298        1             8
 8   568 CARROLL IL    0.027    16805       622.    16519      111            30
 9   569 CASS    IL    0.024    13437       560.    13384       16             8
10   570 CHAMPA… IL    0.058   173025      2983.   146506    16559           331
# ℹ 427 more rows
# ℹ 19 more variables: popasian <int>, popother <int>, percwhite <dbl>,
#   percblack <dbl>, percamerindan <dbl>, percasian <dbl>, percother <dbl>,
#   popadults <int>, perchsd <dbl>, percollege <dbl>, percprof <dbl>,
#   poppovertyknown <int>, percpovertyknown <dbl>, percbelowpoverty <dbl>,
#   percchildbelowpovert <dbl>, percadultpoverty <dbl>,
```

`stat_` functions behind the scenes

```r
p <- ggplot(data = midwest,
            mapping = aes(x = area))

p + geom_histogram()
```

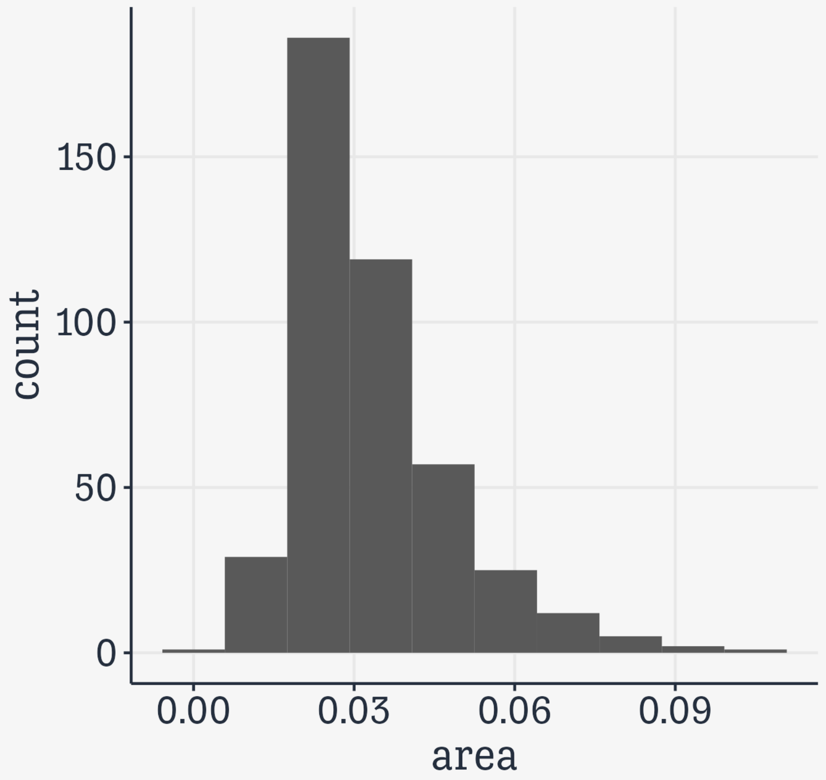
```
`stat_bin()` using `bins = 30`. Pick better
value with `binwidth`.
```



Here the default `stat_` function for this geom has to make a choice. It is

`stat_` functions behind the scenes

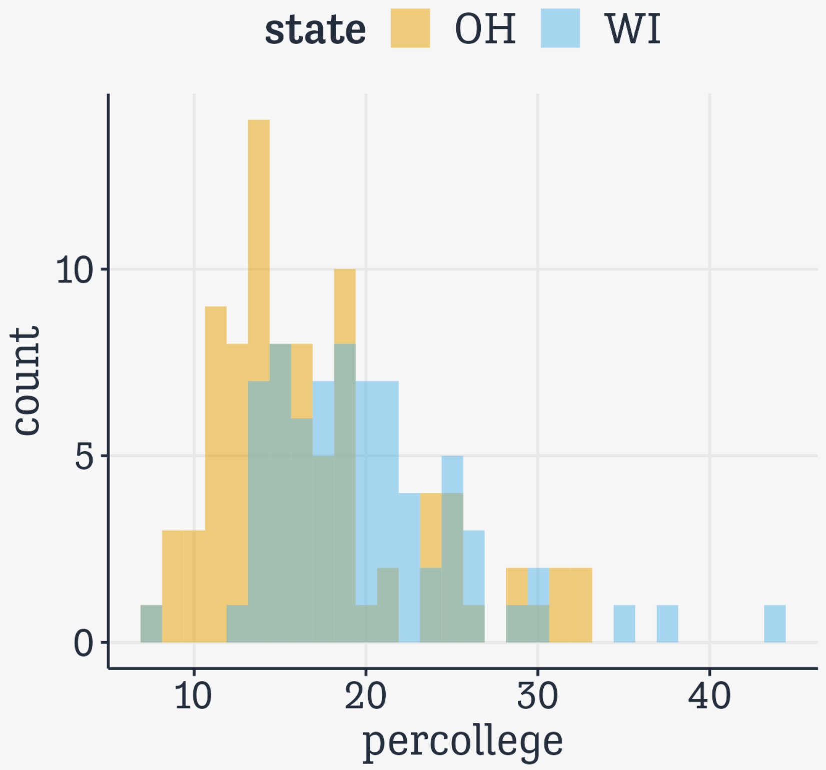
```r
p <- ggplot(data = midwest,
            mapping = aes(x = area))

p + geom_histogram(bins = 10)
```



We can choose *either* the number of bins *or* the `binwidth`

Compare two distributions

```r
## Two state codes
oh_wi <- c("OH", "WI")

midwest |>
  filter(state %in% oh_wi) |>
  ggplot(mapping = aes(x = percollege,
                       fill = state)) +
  geom_histogram(alpha = 0.5,
                 position = "identity")
```

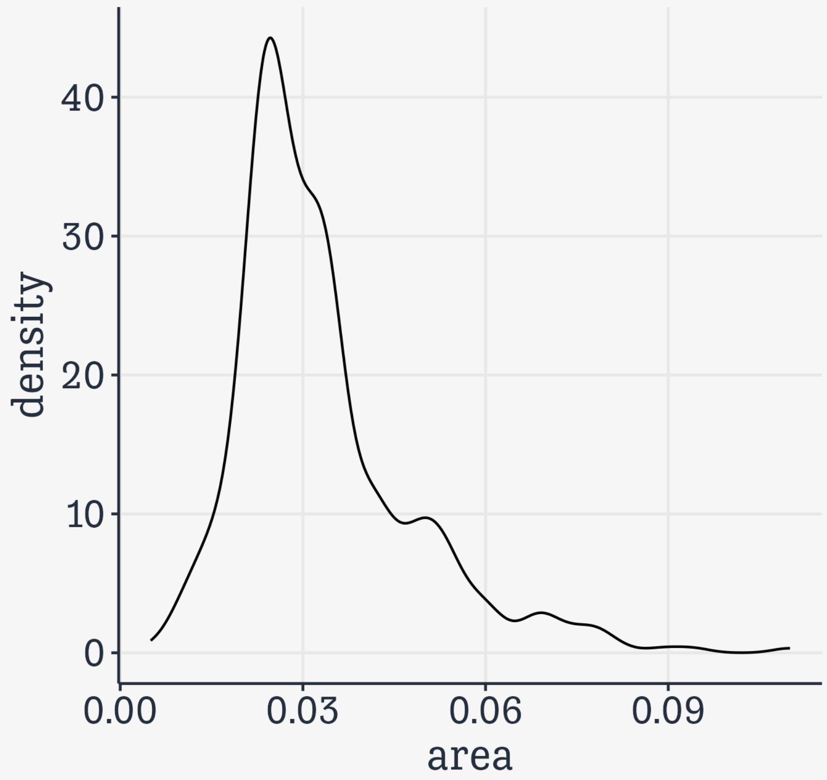


Here we do the whole thing in a pipeline using the pipe and the `dplyr` verb `filter()` to subset rows of the data by some condition.

Experiment with leaving the `position` argument out, or changing it to `"dodge"`.

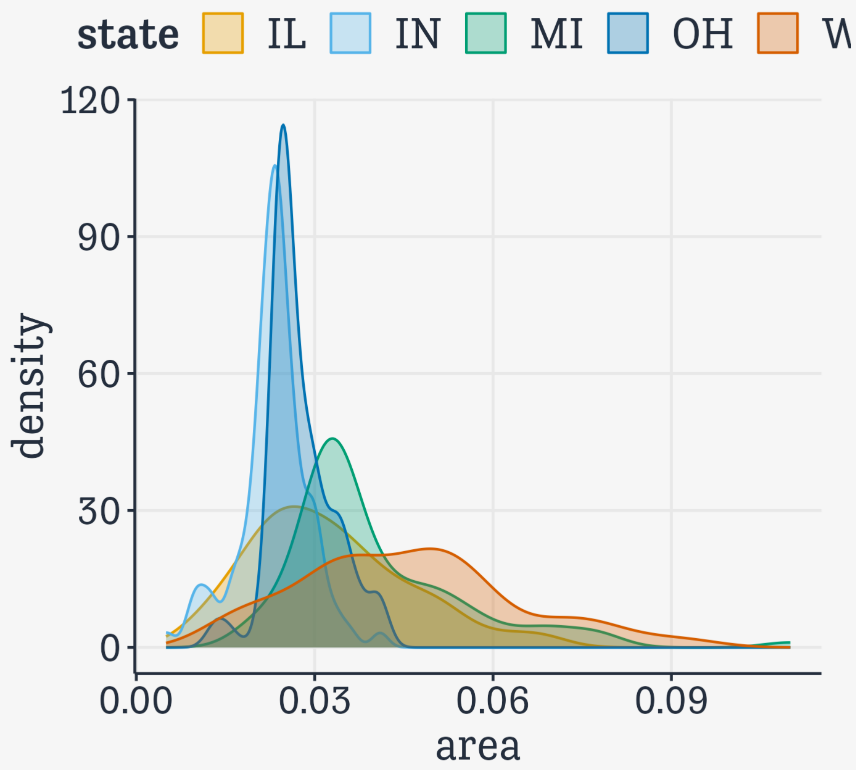
geom_density()

```
p <- ggplot(data = midwest,
            mapping = aes(x = area))

p + geom_density()
```



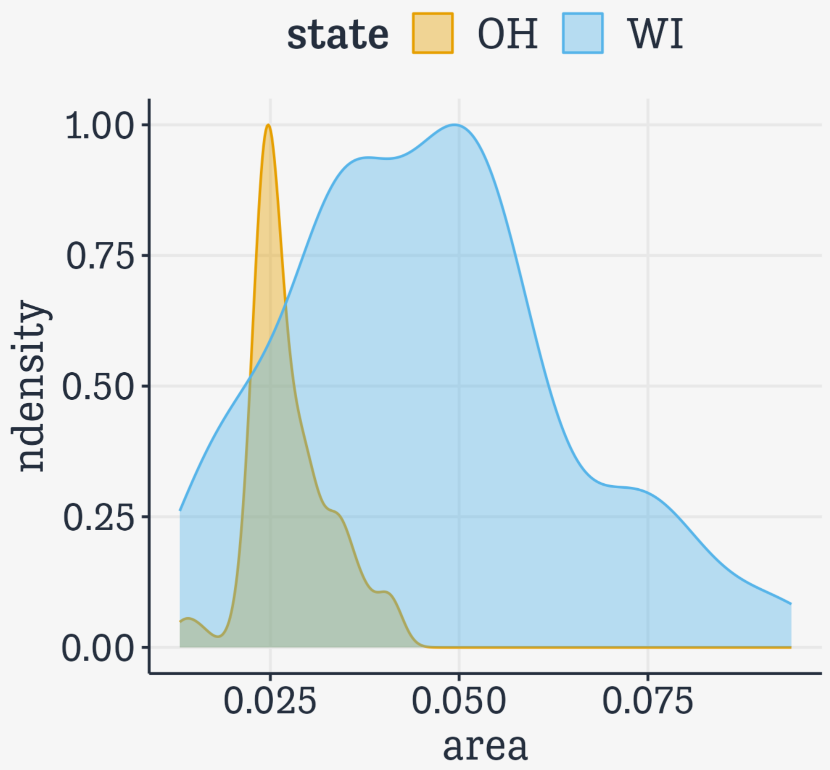
geom_density()

```
p <- ggplot(data = midwest,
            mapping = aes(x = area,
                          fill = state,
                          color = state))
p + geom_density(alpha = 0.3)
```



geom_density()

```
midwest |>
  filter(state %in% oh_wi) |>
  ggplot(mapping = aes(x = area,
                       fill = state,
                       color = state)) +
  geom_density(mapping = aes(y = after_stat(nde
               alpha = 0.4)
```



`ndensity` here is not in our data! It's *computed*. Histogram and density geoms have default statistics, but you can ask them to do more. The `after_stat` functions can do this work for us.

Compare subgroups to a reference distribution

Some made-up data

Consider 3,000 observations of some unit (e.g., a county) with summary measures for each group, and the population average.

```
df
```

```
# A tibble: 3,000 × 5
    unit   pop_a pop_b   pop_c pop_total
   <int>   <dbl> <dbl>   <dbl>     <dbl>
 1     1  1.29   1.93  -0.0869     1.09 
 2     2  0.522  0.536 -0.762      0.190
 3     3  2.14   1.47  -0.616      1.15 
 4     4  1.13   0.673 -0.242      0.575
 5     5  1.04   1.30   1.18       1.12 
 6     6  1.80   0.140  2.05       1.33 
 7     7  0.186  1.30  -0.709      0.476
 8     8 -0.953  0.520 -2.44      -0.767
 9     9  0.700  1.66  -1.09       0.749
10    10  0.0416 0.484 -0.180      0.177
# ℹ 2,990 more rows
```

Get the data into long format!

```r
df
```

```
# A tibble: 3,000 × 5
    unit   pop_a pop_b   pop_c pop_total
   <int>   <dbl> <dbl>   <dbl>     <dbl>
 1     1  1.29   1.93  -0.0869     1.09 
 2     2  0.522  0.536 -0.762      0.190
 3     3  2.14   1.47  -0.616      1.15 
 4     4  1.13   0.673 -0.242      0.575
 5     5  1.04   1.30   1.18       1.12 
 6     6  1.80   0.140  2.05       1.33 
 7     7  0.186  1.30  -0.709      0.476
 8     8 -0.953  0.520 -2.44      -0.767
 9     9  0.700  1.66  -1.09       0.749
10    10  0.0416 0.484 -0.180      0.177
# ℹ 2,990 more rows
```

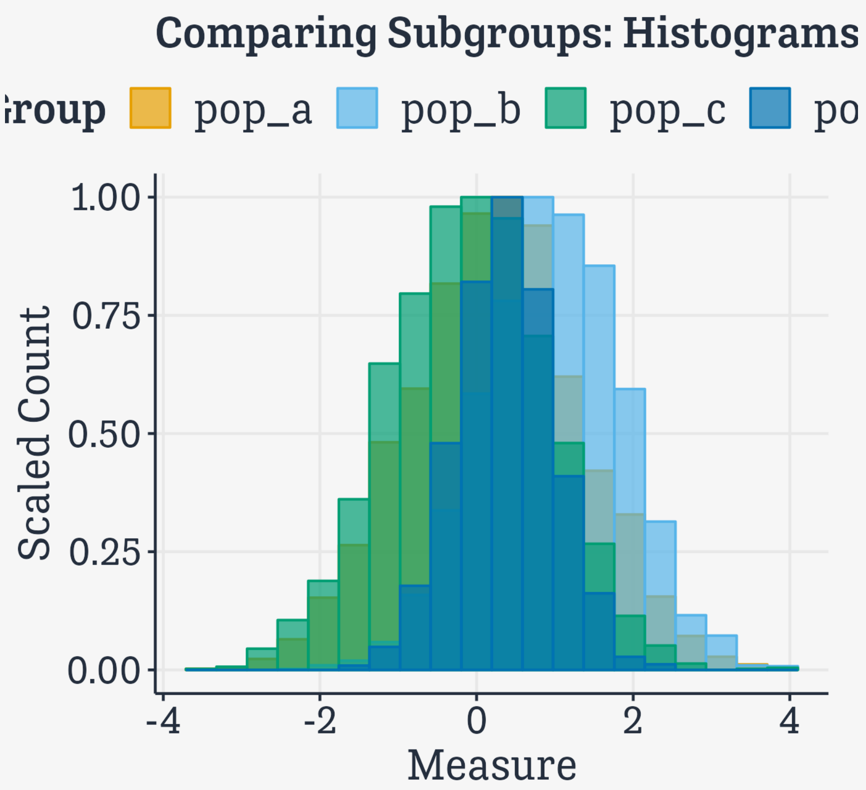
Get the data into long format!

```
df |>
  pivot_longer(cols = pop_a:p
```

```
# A tibble: 12,000 × 3
    unit name        value
   <int> <chr>       <dbl>
 1     1 pop_a      1.29
 2     1 pop_b      1.93
 3     1 pop_c     -0.0869
 4     1 pop_total  1.09
 5     2 pop_a      0.522
 6     2 pop_b      0.536
 7     2 pop_c     -0.762
 8     2 pop_total  0.190
 9     3 pop_a      2.14
10     3 pop_b      1.47
# ℹ 11,990 more rows
```

First effort: Hard to read

```r
df |>
  pivot_longer(cols = pop_a:pop_total)  |>
  ggplot() +
  geom_histogram(mapping = aes(x = value,
                               y = after_stat(n
                           color = name, fill = 
             stat = "bin", bins = 20,
             linewidth = 0.5, alpha = 0.7,
             position = "identity") +
  labs(x = "Measure", y = "Scaled Count", color
       fill = "Group",
       title = "Comparing Subgroups: Histograms
```



Again, `after_stat(ncount)` is computed.

A little pivot trick

```r
# Treat pop_a to pop_total as a single
df
```

```
# A tibble: 3,000 × 5
    unit   pop_a pop_b   pop_c pop_total
   <int>   <dbl> <dbl>   <dbl>     <dbl>
 1     1  1.29   1.93  -0.0869     1.09 
 2     2  0.522  0.536 -0.762      0.190
 3     3  2.14   1.47  -0.616      1.15 
 4     4  1.13   0.673 -0.242      0.575
 5     5  1.04   1.30   1.18       1.12 
 6     6  1.80   0.140  2.05       1.33 
 7     7  0.186  1.30  -0.709      0.476
 8     8 -0.953  0.520 -2.44      -0.767
 9     9  0.700  1.66  -1.09       0.749
10    10  0.0416 0.484 -0.180      0.177
# ℹ 2,990 more rows
```

A little pivot trick

```r
# Treat pop_a to pop_total as a single
df |>
  pivot_longer(cols = pop_a:pop_total)
```

```
# A tibble: 12,000 × 3
    unit name       value
   <int> <chr>      <dbl>
 1     1 pop_a     1.29
 2     1 pop_b     1.93
 3     1 pop_c    -0.0869
 4     1 pop_total 1.09
 5     2 pop_a     0.522
 6     2 pop_b     0.536
 7     2 pop_c    -0.762
 8     2 pop_total 0.190
 9     3 pop_a     2.14
10     3 pop_b     1.47
# ℹ 11,990 more rows
```

A little pivot trick

```
# Just treat pop_a to pop_c as the sing
# Notice that pop_total just gets repea
df
```

```
# A tibble: 3,000 × 5
    unit   pop_a pop_b   pop_c pop_total
   <int>   <dbl> <dbl>   <dbl>     <dbl>
 1     1  1.29   1.93  -0.0869     1.09
 2     2  0.522  0.536 -0.762      0.190
 3     3  2.14   1.47  -0.616      1.15
 4     4  1.13   0.673 -0.242      0.575
 5     5  1.04   1.30   1.18       1.12
 6     6  1.80   0.140  2.05       1.33
 7     7  0.186  1.30  -0.709      0.476
 8     8 -0.953  0.520 -2.44      -0.767
 9     9  0.700  1.66  -1.09       0.749
10    10  0.0416 0.484 -0.180      0.177
# ℹ 2,990 more rows
```

A little pivot trick

```r
# Just treat pop_a to pop_c as the sing
# Notice that pop_total just gets repea
df |>
  pivot_longer(cols = pop_a:pop_c)
```

```
# A tibble: 9,000 × 4
    unit pop_total name    value
   <int>     <dbl> <chr>   <dbl>
 1     1     1.09  pop_a  1.29
 2     1     1.09  pop_b  1.93
 3     1     1.09  pop_c -0.0869
 4     2     0.190 pop_a  0.522
 5     2     0.190 pop_b  0.536
 6     2     0.190 pop_c -0.762
 7     3     1.15  pop_a  2.14
 8     3     1.15  pop_b  1.47
 9     3     1.15  pop_c -0.616
10     4     0.575 pop_a  1.13
# ℹ 8,990 more rows
```

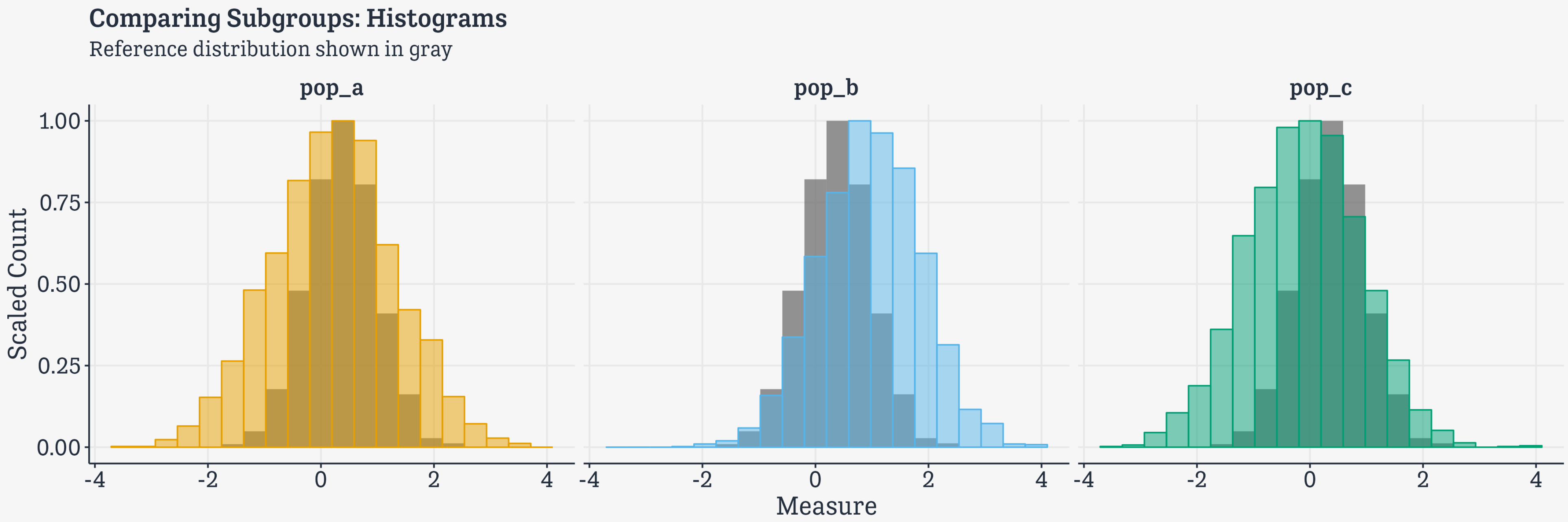
Now facet with that data

```r
p_out <- df |>
  pivot_longer(cols = pop_a:pop_c) |>
  ggplot() +
  geom_histogram(mapping = aes(x = pop_total, #<<
                               y = after_stat(ncount)),
                 bins = 20, alpha = 0.7,
                 fill = "gray40", linewidth = 0.5) +
  geom_histogram(mapping = aes(x = value, #<<
                               y = after_stat(ncount),
                           color = name, fill = name),
              stat = "bin", bins = 20, linewidth = 0.5,
              alpha = 0.5) +
  guides(color = "none", fill = "none") + #<<
  labs(x = "Measure", y = "Scaled Count",
       title = "Comparing Subgroups: Histograms",
       subtitle = "Reference distribution shown in gray")
  facet_wrap(~ name, nrow = 1)
```

Remember, we can layer geoms one on top of the other. Here we call `geom_histogram()` twice. What happens if you comment one or other of them out?

The call to `guides()` turns off the legend for the color and fill, because we don't need them.

Now facet with that data



Avoid counting up,
when necessary

Sometimes no counting is needed

```
titanic
```

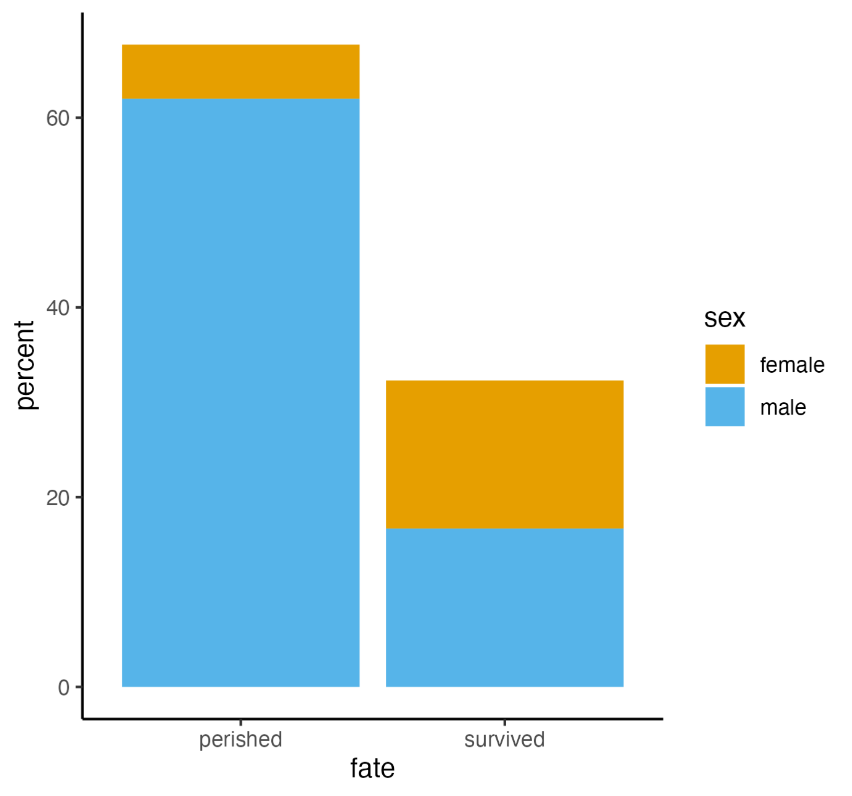
```
      fate    sex    n percent
1 perished   male 1364    62.0
2 perished female  126     5.7
3 survived   male  367    16.7
4 survived female  344    15.6
```

Here we just have a summary table and want to plot a few numbers directly in a bar chart.

geom_bar() wants to count up

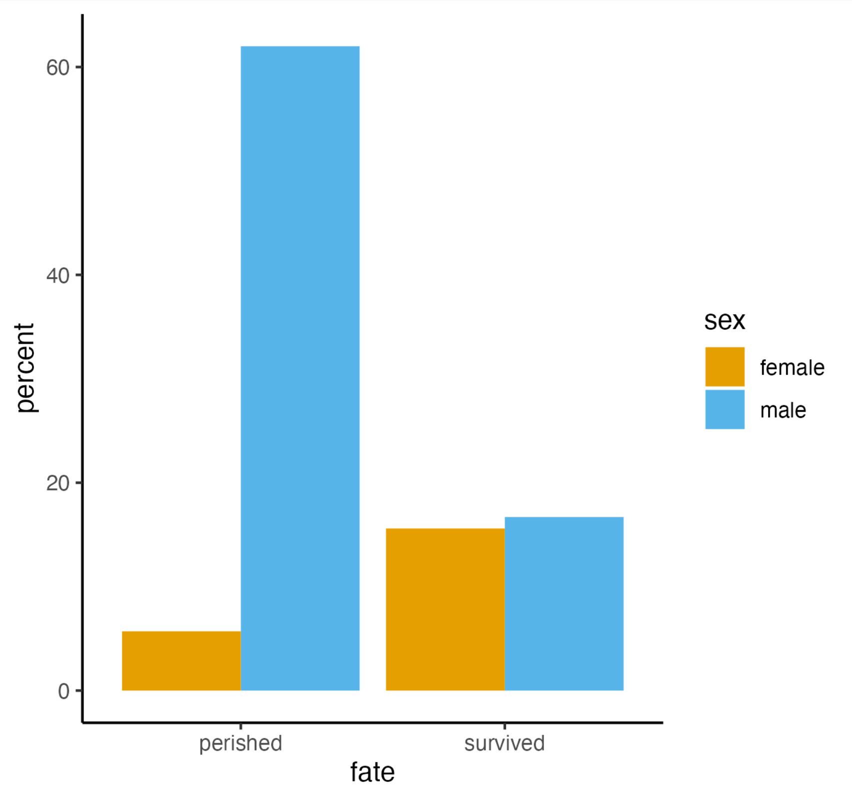
By default `geom_bar()` tries to count up data by category. (Really it's the `stat_count()` function that does this behind the scenes.) By saying `stat="identity"` we explicitly tell it not to do that. This also allows us to use a `y` mapping. Normally this would be the result of the counting up.

```
p <- ggplot(data = titanic,
            mapping = aes(x = fate,
                          y = percent,
                          fill = sex))
p + geom_bar(stat = "identity") #<<
```



`geom_bar()` stacks by default

```
p ← ggplot(data = titanic,
           mapping = aes(x = fate,
                         y = percent,
                         fill = sex))
p + geom_bar(stat = "identity",
             position = "dodge") #<<
```

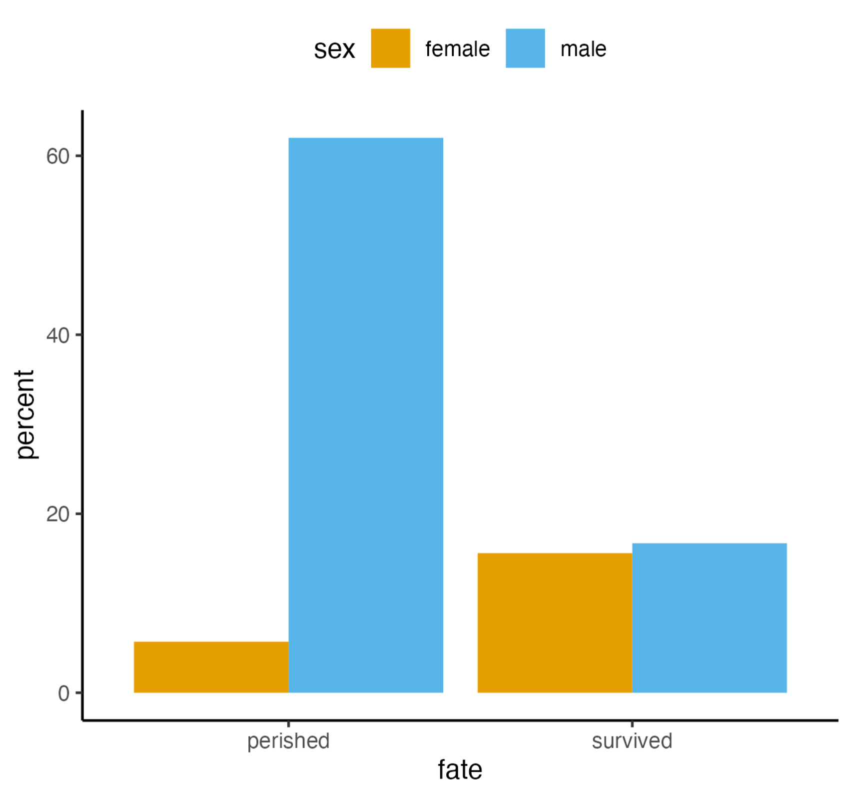


Position arguments adjust whether the things drawn are placed on top of one another (`"stack"`), side-by-side (`"dodge"`), or taken as-is (`"identity"`).

A quick theme() adjustment

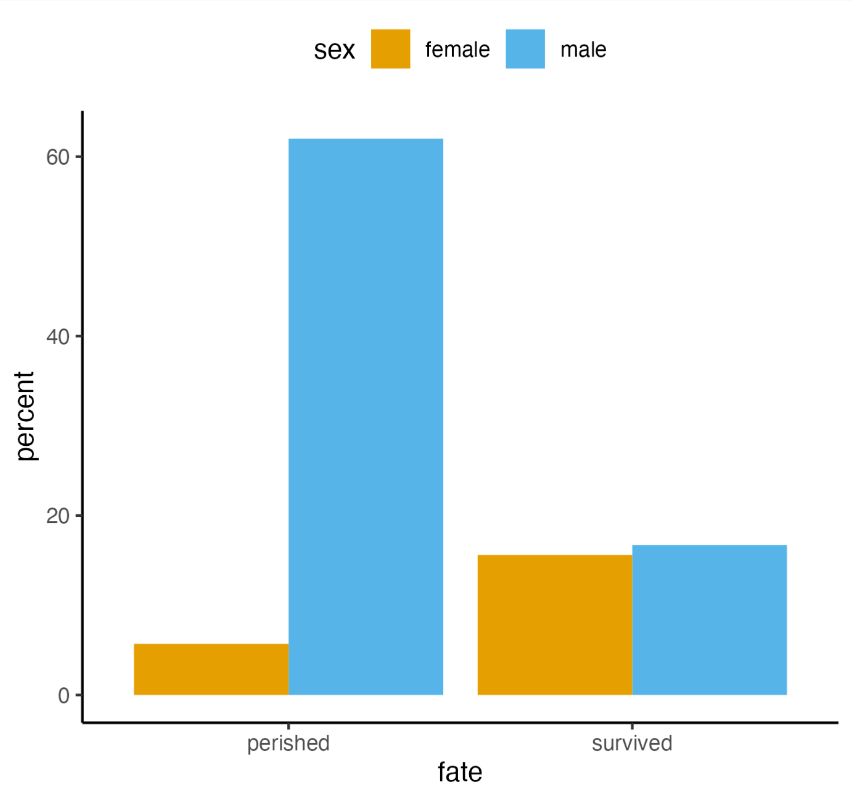
The theme() function controls the styling of parts of the plot that don't belong to its "grammatical" structure. That is, that are not contributing to directly representing data.

```
p <- ggplot(data = titanic,
            mapping = aes(x = fate,
                          y = percent,
                          fill = sex))
p + geom_bar(stat = "identity",
             position = "dodge") +
  theme(legend.position = "top") #<<
```



For convenience, use `geom_col()`

```
p <- ggplot(data = titanic,
            mapping = aes(x = fate,
                          y = percent,
                          fill = sex))
p + geom_col(position = "dodge") + #<<
  theme(legend.position = "top")
```



`geom_col()` assumes `stat = "identity"` by default. It's for when you want to directly plot a table of values, rather than create a bar chart by summing over one varible categorized by another.

Using `geom_col()` for thresholds

```
oecd_sum
```

```
# A tibble: 57 × 5
# Groups:   year [57]
    year other   usa  diff hi_lo
   <int> <dbl> <dbl> <dbl> <chr>
 1  1960  68.6  69.9 1.30  Below
 2  1961  69.2  70.4 1.20  Below
 3  1962  68.9  70.2 1.30  Below
 4  1963  69.1  70   0.900 Below
 5  1964  69.5  70.3 0.800 Below
 6  1965  69.6  70.3 0.700 Below
 7  1966  69.9  70.3 0.400 Below
 8  1967  70.1  70.7 0.600 Below
 9  1968  70.1  70.4 0.300 Below
10  1969  70.1  70.6 0.5   Below
# ℹ 47 more rows
```

Data comparing U.S. average life expectancy to the rest of the OECD average.

`diff` is difference in years with respect to the U.S.

`hi_lo` is a flag saying whether the OECD is above or below the U.S.

Using geom_col() for thresholds

```
p <- ggplot(data = oecd_sum,
            mapping = aes(x = year,
                          y = diff,
                          fill = hi_lo))

p_out <- p + geom_col() +
  geom_hline(yintercept = 0, linewidth = 1
  guides(fill = "none") +
  labs(x = NULL, #<<
       y = "Difference in Years",
       title = "The U.S. Life Expectancy Ga
       subtitle = "Difference between U.S.
       OECD average life expectancies, 196
       caption = "Data: OECD.")
```

`geom_hline()` doesn't take any data argument. It just draws a horizontal line with a given y-intercept.

`x = NULL` means "Don't label the x-axis (not even with the default value, the variable name)."

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