

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

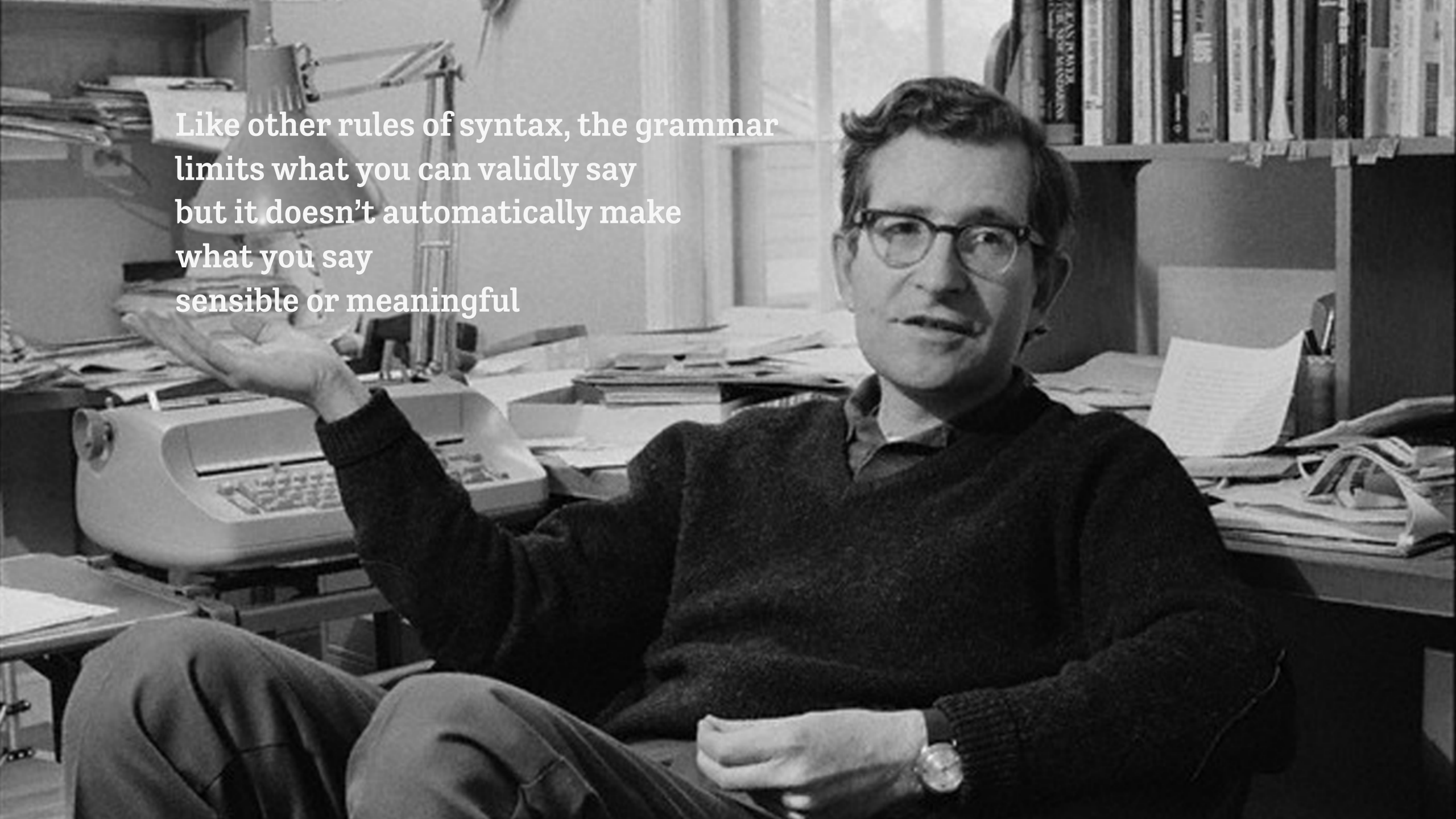
```
library(tidyverse)    # Your friend and mine  
library(gapminder)    # Gapminder data  
library(here)         # Portable file paths  
library(socviz)       # Handy socviz functions
```

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



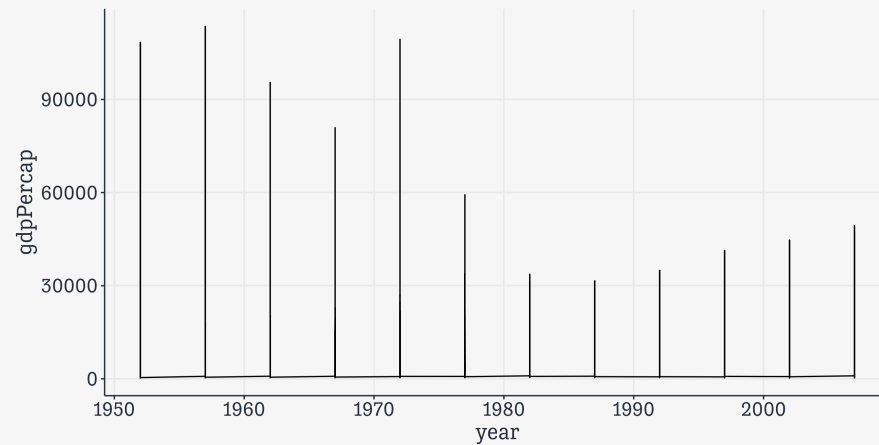
Grouped data and the group aesthetic

Try to make a lineplot

```
1 p ← ggplot(data = gapminder,  
2           mapping = aes(x = year,  
3                         y = gdpPercap))
```


Try to make a lineplot

```
1 p <- ggplot(data = gapminder,  
2             mapping = aes(x = year,  
3                           y = gdpPercap)) +  
4   geom_line()  
5  
6 p
```



Try to make a lineplot

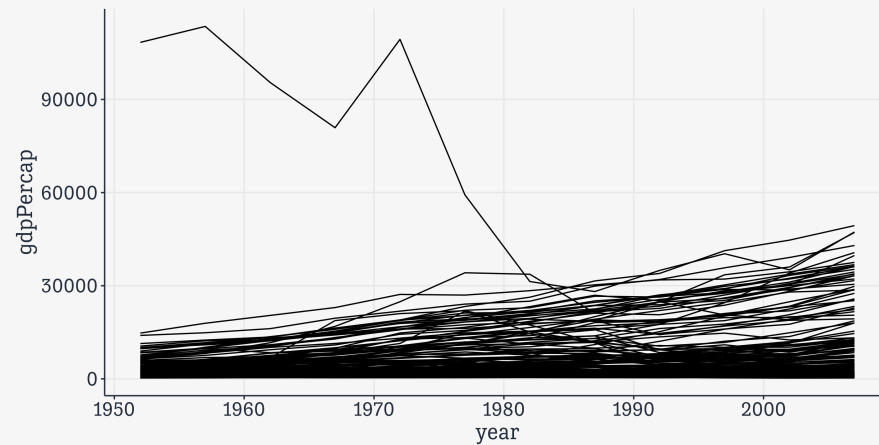
```
1 p ← ggplot(data = gapminder,  
2           mapping = aes(x = year,  
3                         y = gdpPercap))
```

Try to make a lineplot

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

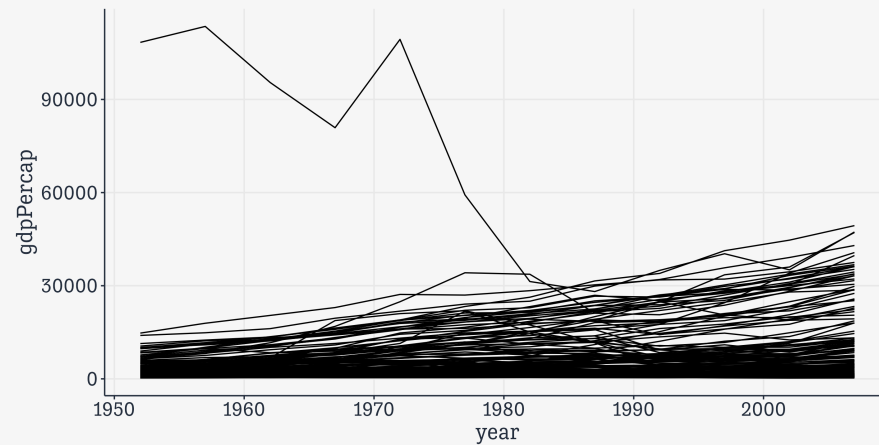
Try to make a lineplot

```
1 p <- ggplot(data = gapminder,  
2             mapping = aes(x = year,  
3                           y = gdpPercap)) +  
4   geom_line(mapping = aes(group = country))  
5  
6 p
```



Try to make a lineplot

```
1 p <- ggplot(data = gapminder,  
2             mapping = aes(x = year,  
3                           y = gdpPercap)) +  
4   geom_line(mapping = aes(group = country))  
5  
6 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.
```

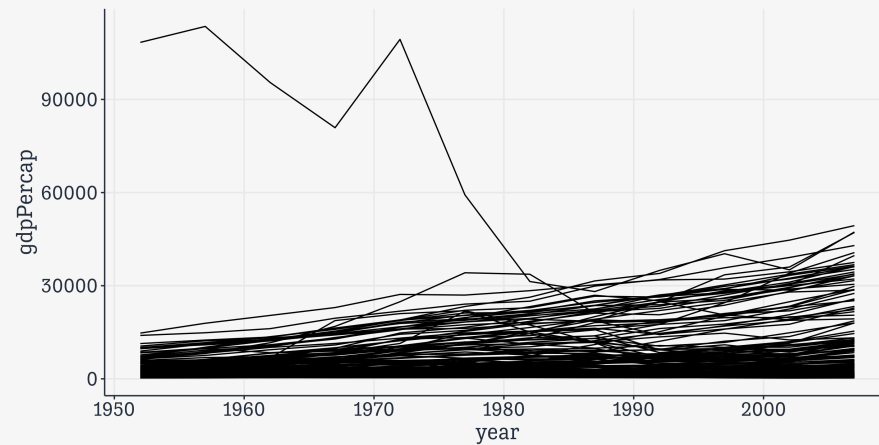
Facet the plot

```
1 gapminder ►  
2   ggplot(mapping =  
3     aes(x = year,  
4     y = gdpPercap))
```



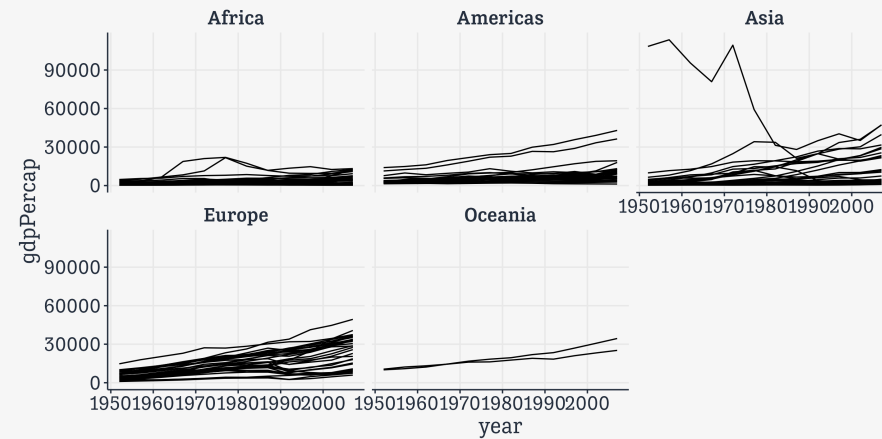
Facet the plot

```
1 gapminder ►  
2   ggplot(mapping =  
3     aes(x = year,  
4       y = gdpPercap)) +  
5   geom_line(mapping = aes(group = country))
```



Facet the plot

```
1 gapminder ►  
2   ggplot(mapping =  
3     aes(x = year,  
4       y = gdpPercap)) +  
5   geom_line(mapping = aes(group = country))  
6   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

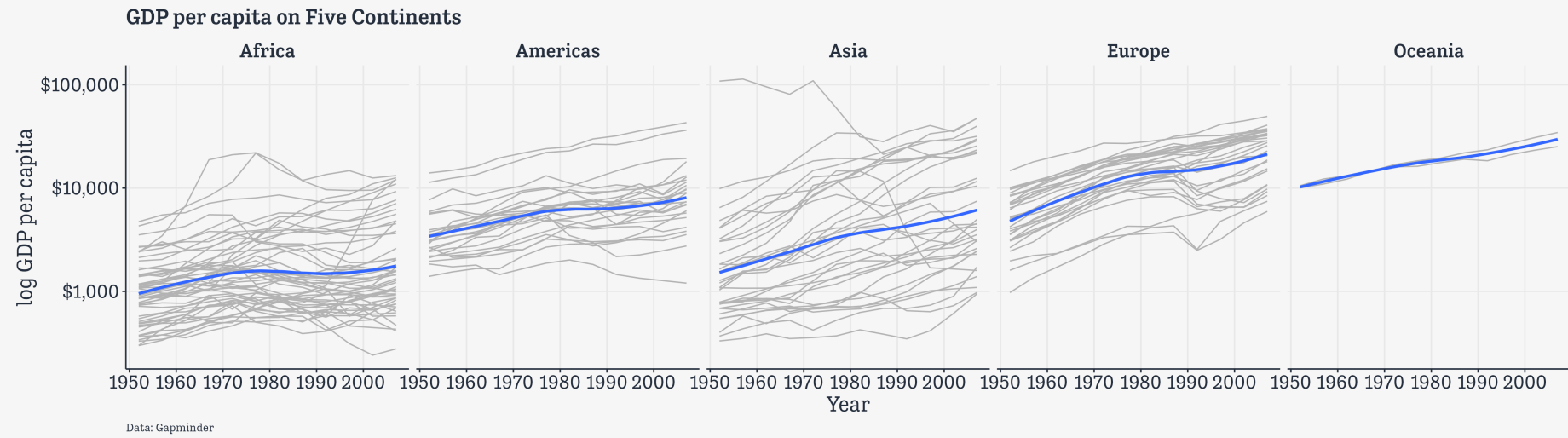
You can also use this syntax: `facet_wrap(vars(continent))`

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

Facets in action

```
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

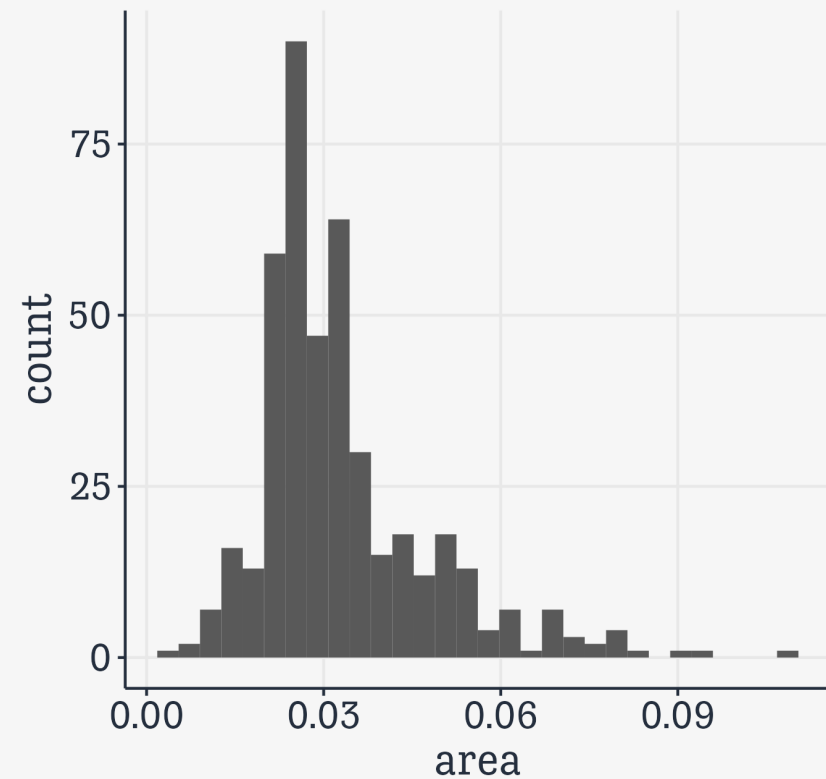
```
# i 427 more rows
```

```
# i 19 more variables: popasian <int>, popother <int>, percwhite <dbl>,  
# percblack <dbl>, percamerindian <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

```
p ← ggplot(data = midwest,  
            mapping = aes(x = area))  
  
p + geom_histogram()
```

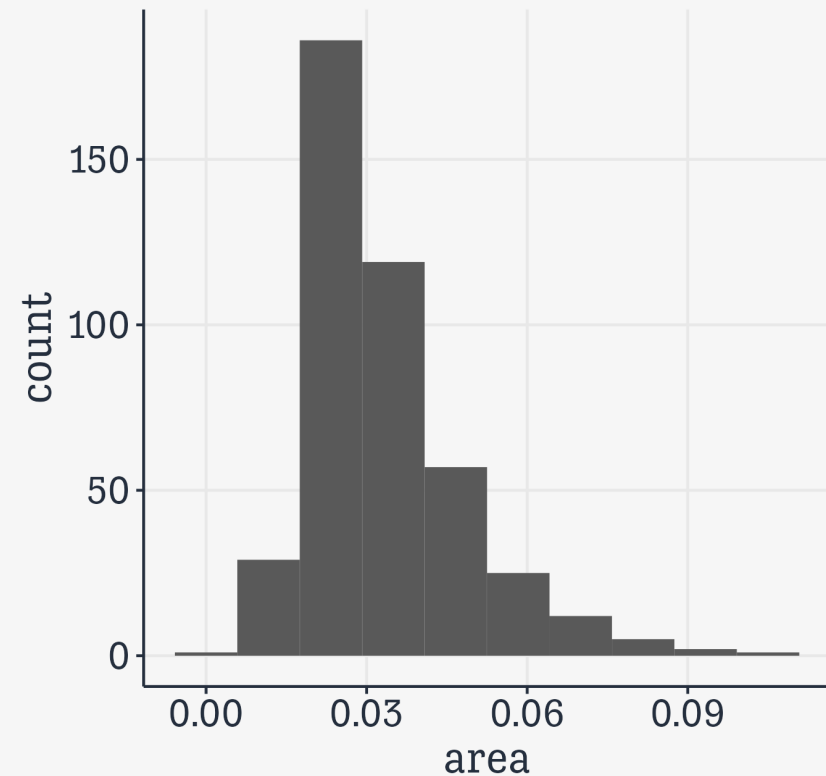
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



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

stat_ functions behind the scenes

```
p ← ggplot(data = midwest,  
            mapping = aes(x = area))  
  
p + geom_histogram(bins = 10)
```

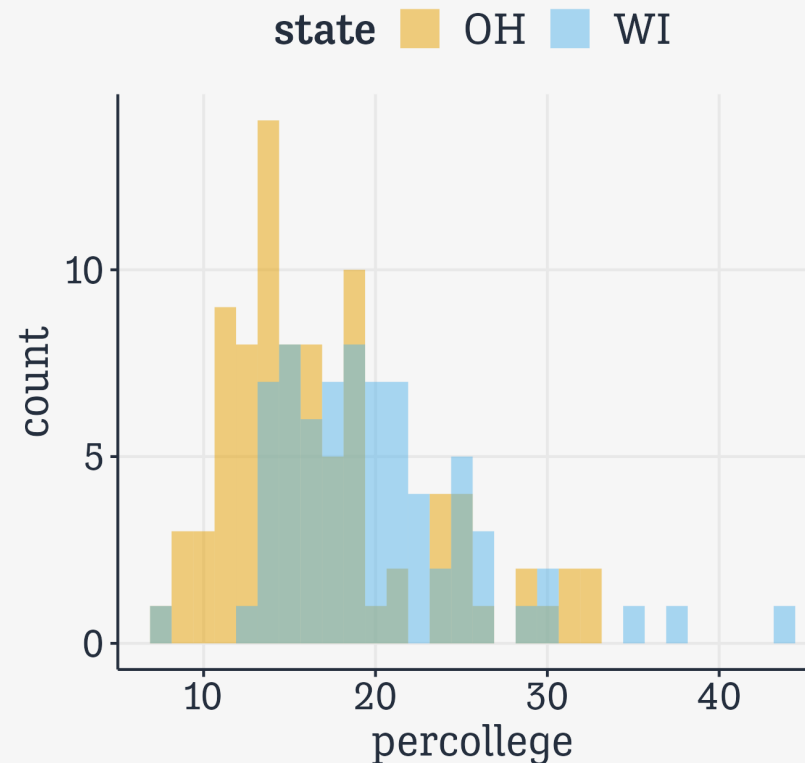


We can choose *either* the number of bins *or* the `binwidth`

Compare two distributions

```
## 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")
```

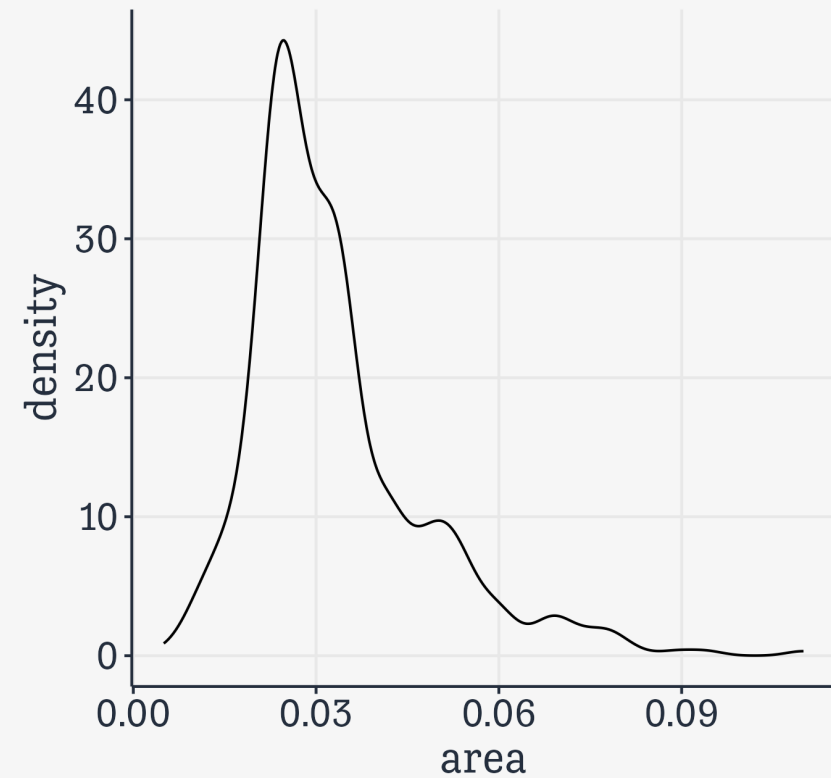


Here we do the whole thing in a **pipeline** using the pipe and the **dplyr** verb **filter()** to subset rows of the data by some condition.

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

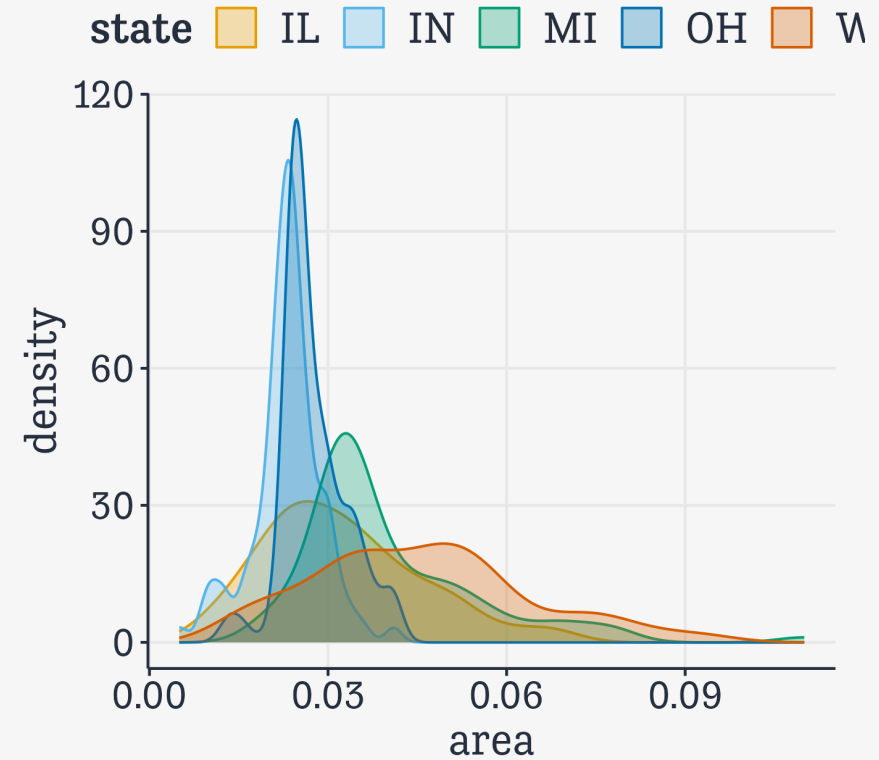
geom_density()

```
p ← ggplot(data = midwest,  
            mapping = aes(x = area))  
  
p + geom_density()
```



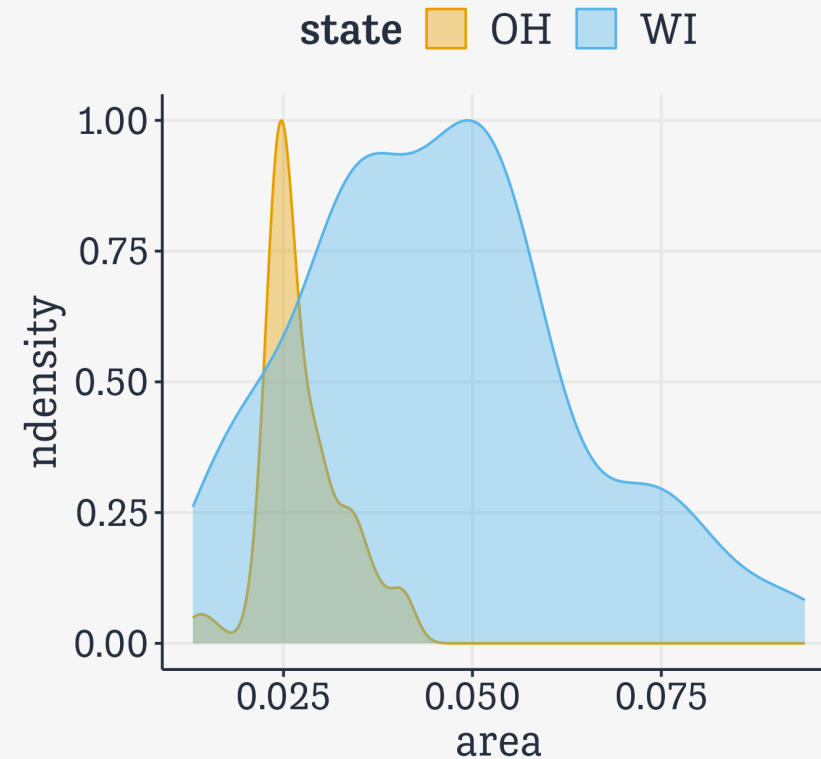
geom_density()

```
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!

```
1 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
```

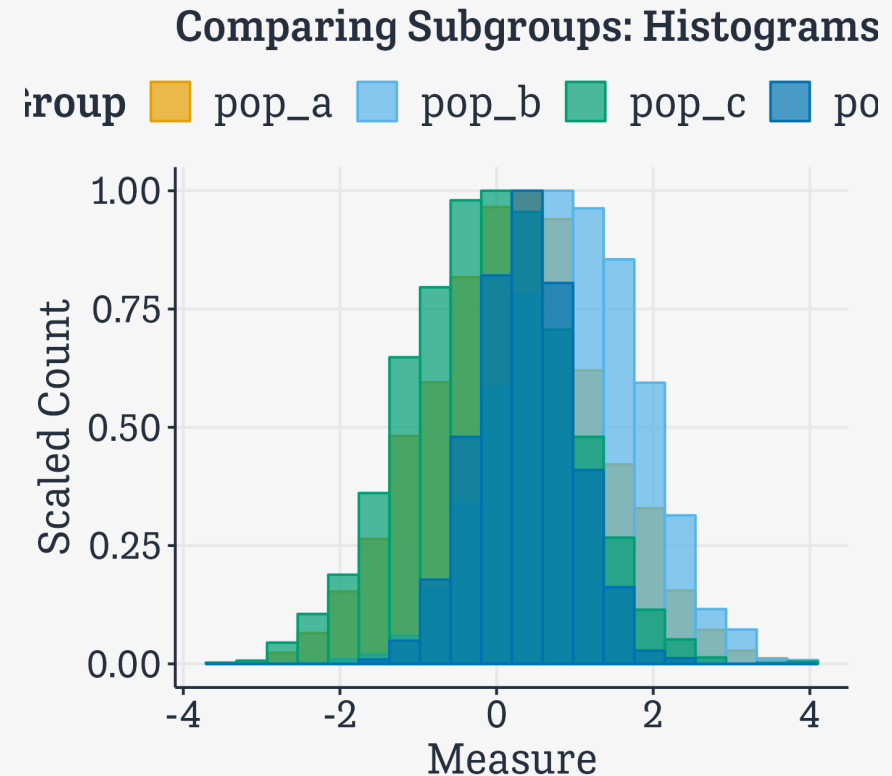
Get the data into long format!

```
1 df ▶  
2 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

```
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

```
1 # Treat pop_a to pop_total as a single  
2 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

```
1 # Treat pop_a to pop_total as a single  
2 df ▶  
3   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

```
1 # Just treat pop_a to pop_c as the sing
2 # Notice that pop_total just gets repe
3 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

```
1 # Just treat pop_a to pop_c as the sing
2 # Notice that pop_total just gets repe
3 df ►
4   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

```
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)
```

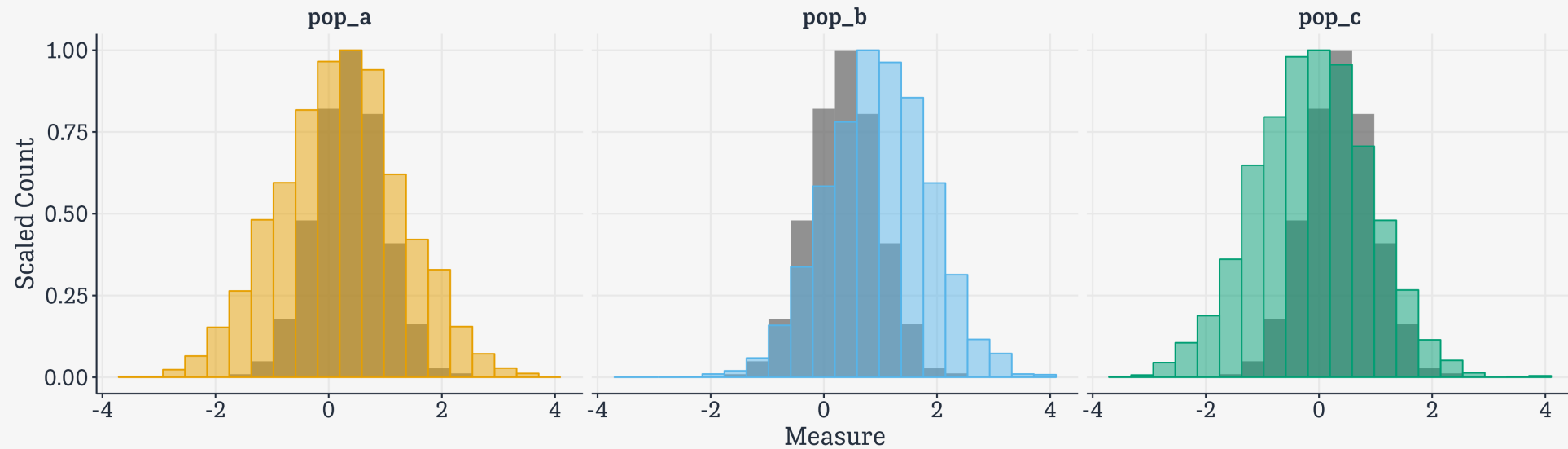
Remember, we can layer geoms one on top of the other. Here we call `geom_histogram()` twice. What happens if you comment one or other of them out?

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

Now facet with that data

Comparing Subgroups: Histograms

Reference distribution shown in gray



**Avoid counting up,
when necessary**

Sometimes no counting is needed

```
titanic
```

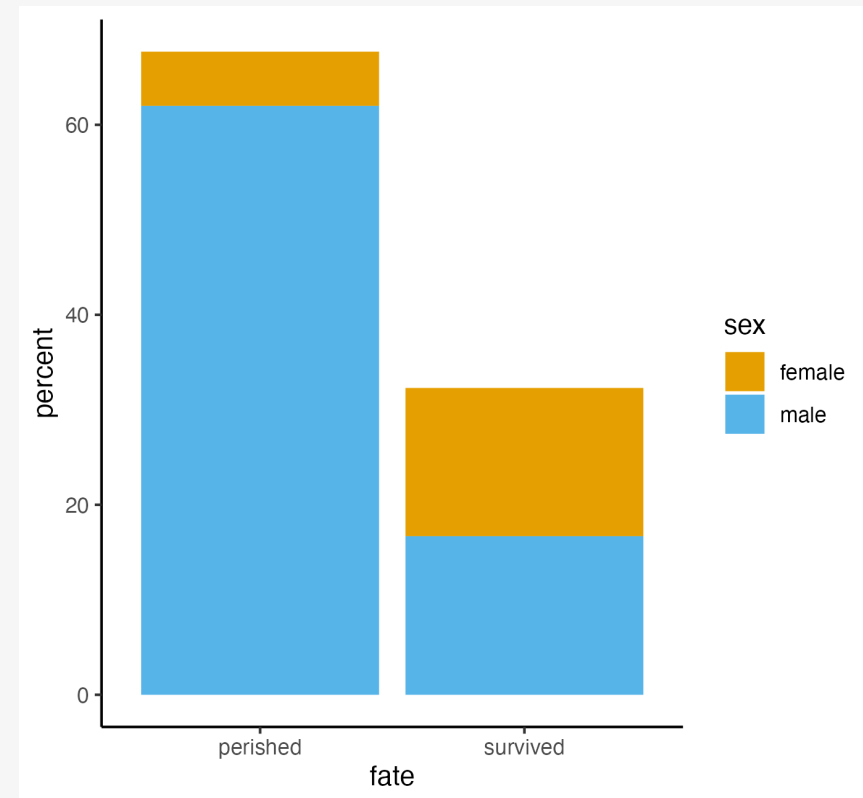
	fate	sex	n	percent
1	perished	male	1364	62.0
2	perished	female	126	5.7
3	survived	male	367	16.7
4	survived	female	344	15.6

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

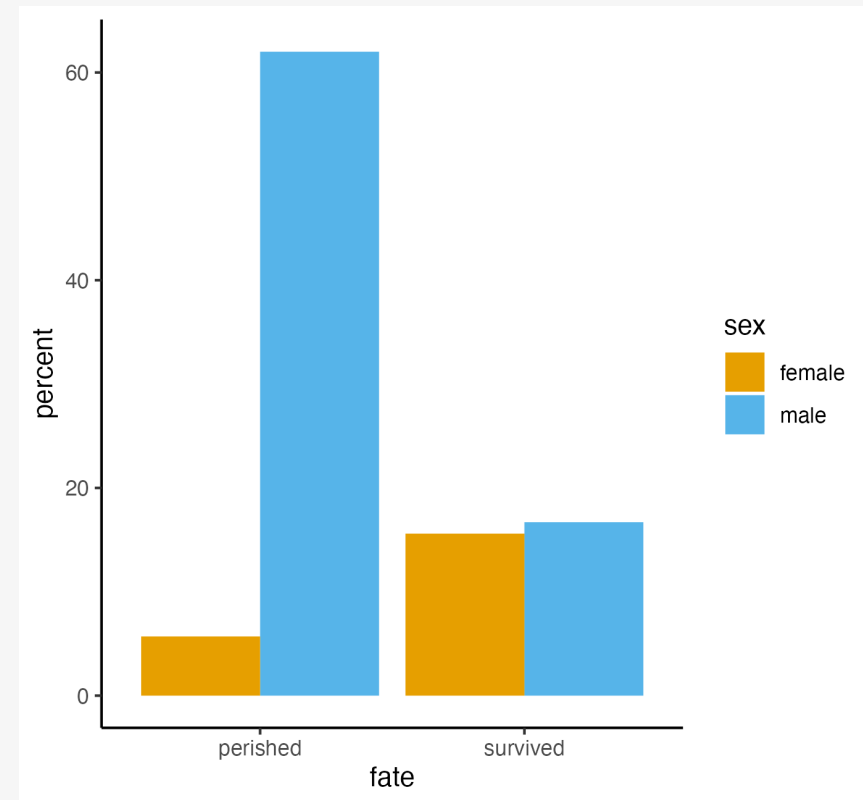
By default `geom_bar()` tries to count up data by category. (Really it's the `stat_count()` function that does this behind the scenes.) By saying `stat="identity"` we explicitly tell it not to do that. This also allows us to use a `y` mapping. Normally this would be the result of the counting up.

```
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") #<<
```

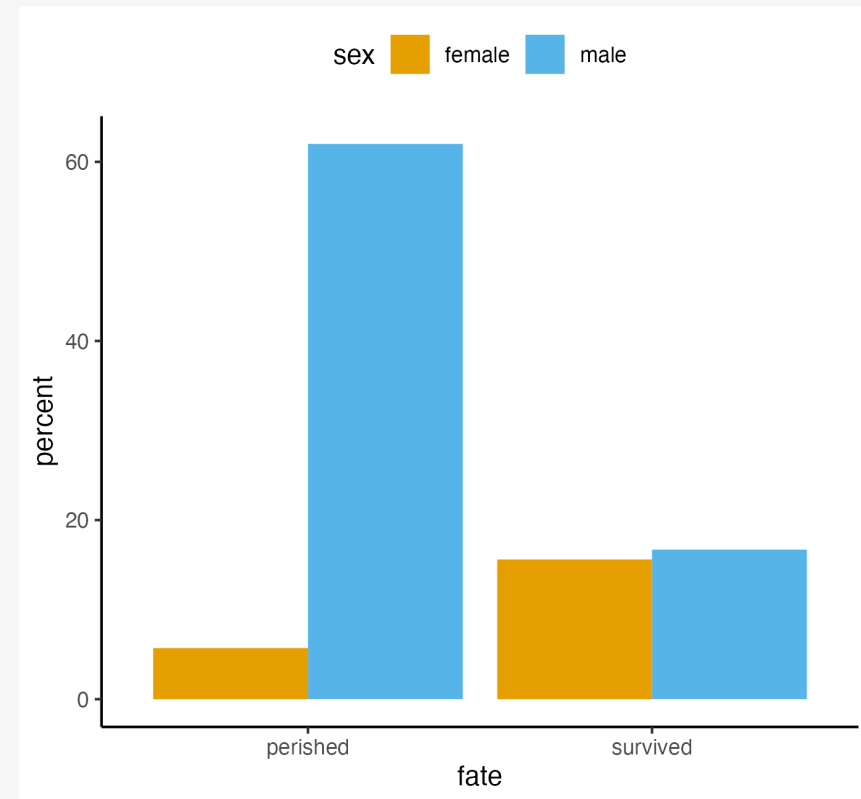


Position arguments adjust whether the things drawn are placed on top of one another ("**stack**"), side-by-side ("**dodge**"), or taken as-is ("**identity**").

A quick `theme()` adjustment

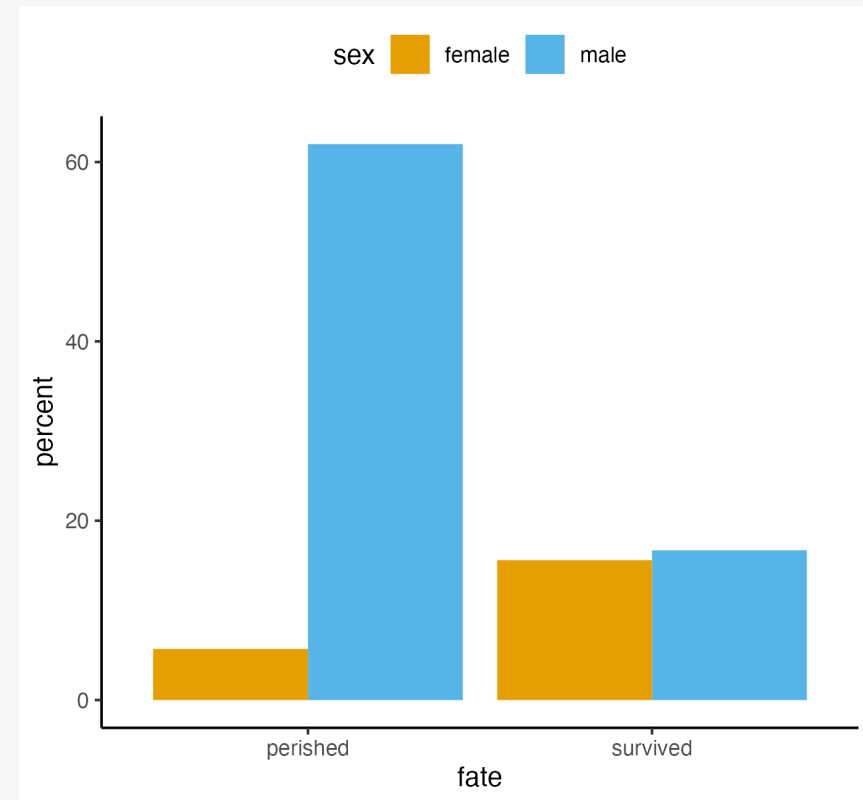
The `theme()` function controls the styling of parts of the plot that don't belong to its “grammatical” structure. That is, that are not contributing to directly representing data.

```
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 variable 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 Gap",
       subtitle = "Difference between U.S.
                  OECD average life expectancies, 1960-2014",
       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)."

Using `geom_col()` for thresholds

