

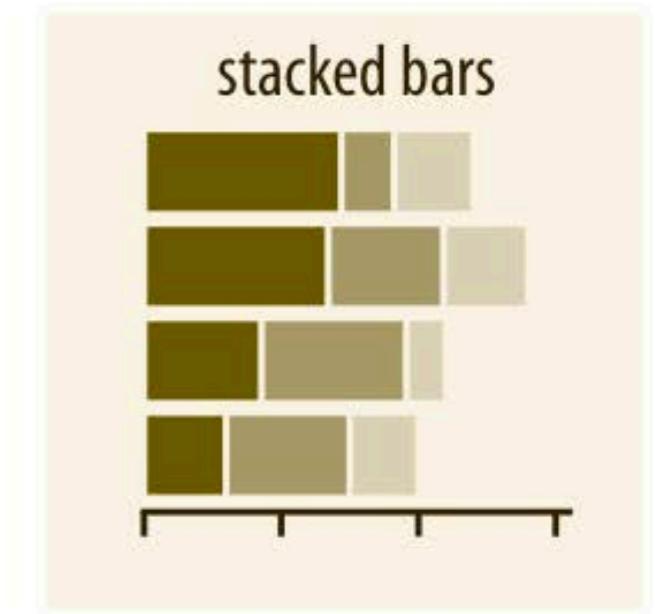
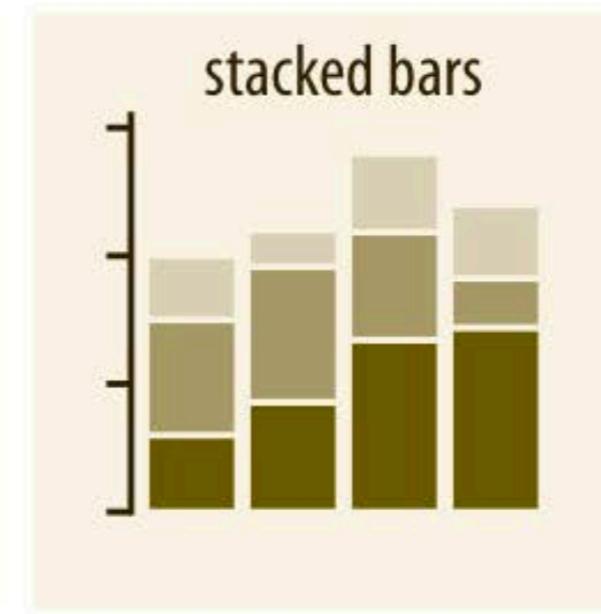
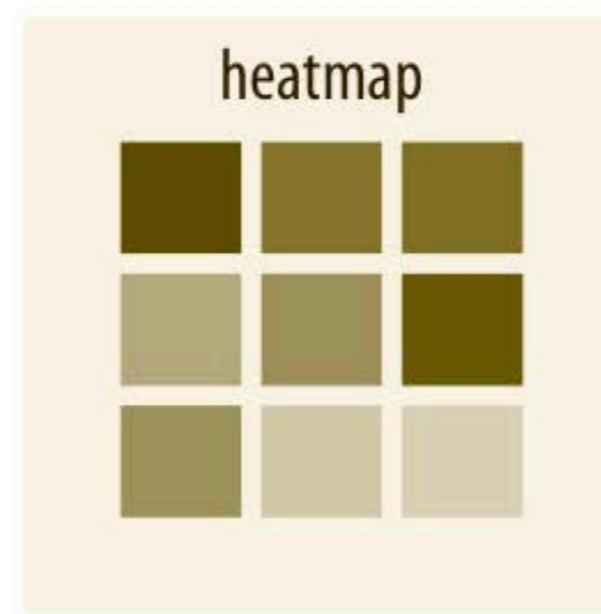
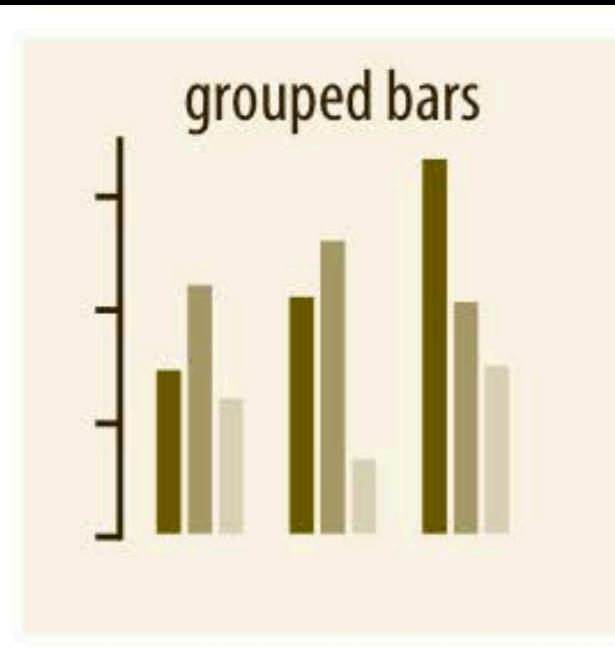
ANT 6973: DATA VISUALIZATION AND EXPLORATION

VISUALIZING DISTRIBUTIONS AND UNCERTAINTY

PREVIOUSLY...

PREVIOUSLY...

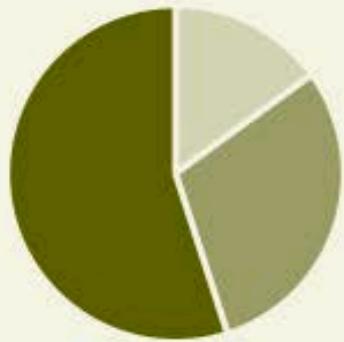
- Visualizing amounts with bar charts (and variants)



PREVIOUSLY...

- Visualizing proportions with pies, stacked bars, and stacked areas

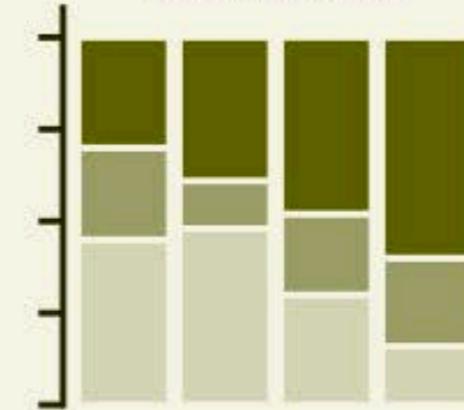
pie chart



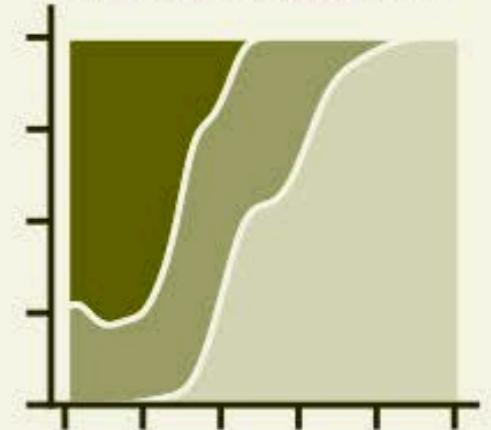
multiple pie charts



stacked bars



stacked densities



PREVIOUSLY...

- Import from a .csv file using `read_csv()` the `readr` package.

```
my_data <- read_csv("path/to/data.csv")
```

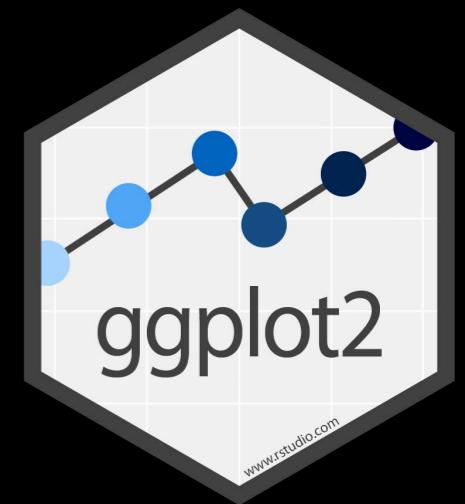
New R object where
data will be stored

readr
function

Path of data file relative
to project home

PREVIOUSLY...

- Stats
- Position adjustments
- Coordinates
- Facets
- Scales
- Themes



```
ggplot(data = <DATA>) +  
  <GEOM_FUNCTION>(  
    mapping = aes(<MAPPINGS>),  
    stat = <STAT>,  
    position = <POSITION>  
) +  
  <COORDINATE_FUNCTION> +  
  <FACET_FUNCTION> +  
  <SCALE_FUNCTION> +  
  <THEME_FUNCTION>
```

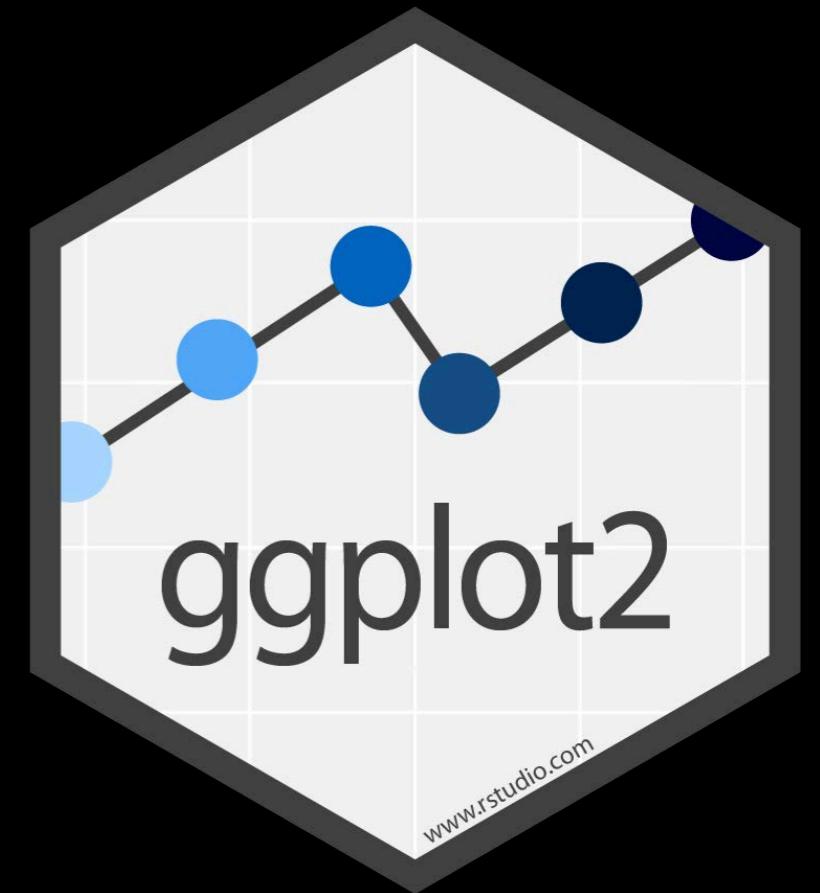
Required

Not required,
sensible
defaults
supplied

TODAY'S TOPICS

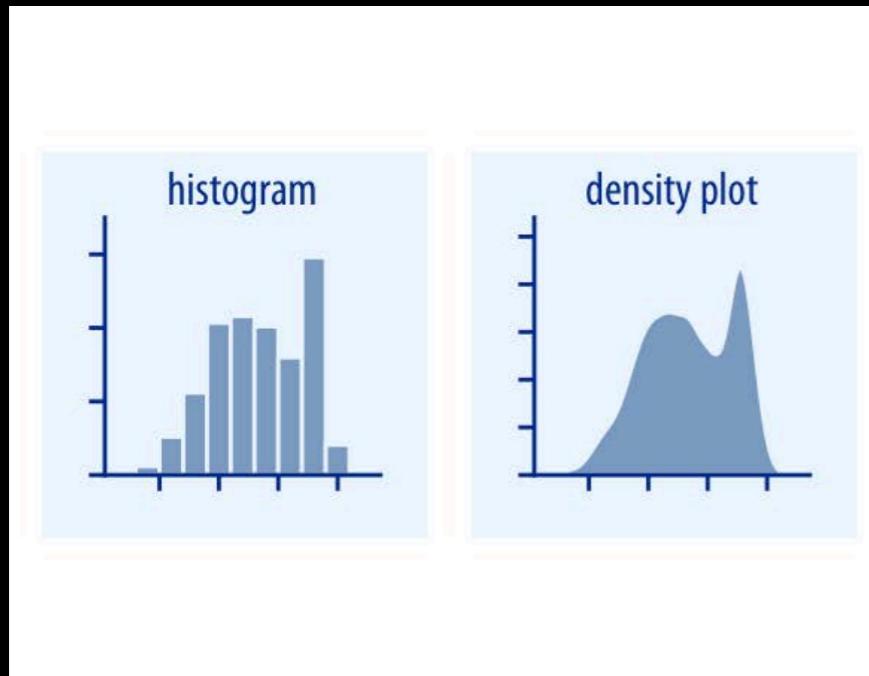
- Visualizing single distributions
- Visualizing multiple distributions
- Visualizing uncertainty
- Activities:
 - Body mass distributions of late Quaternary mammals

VISUALIZING DISTRIBUTIONS

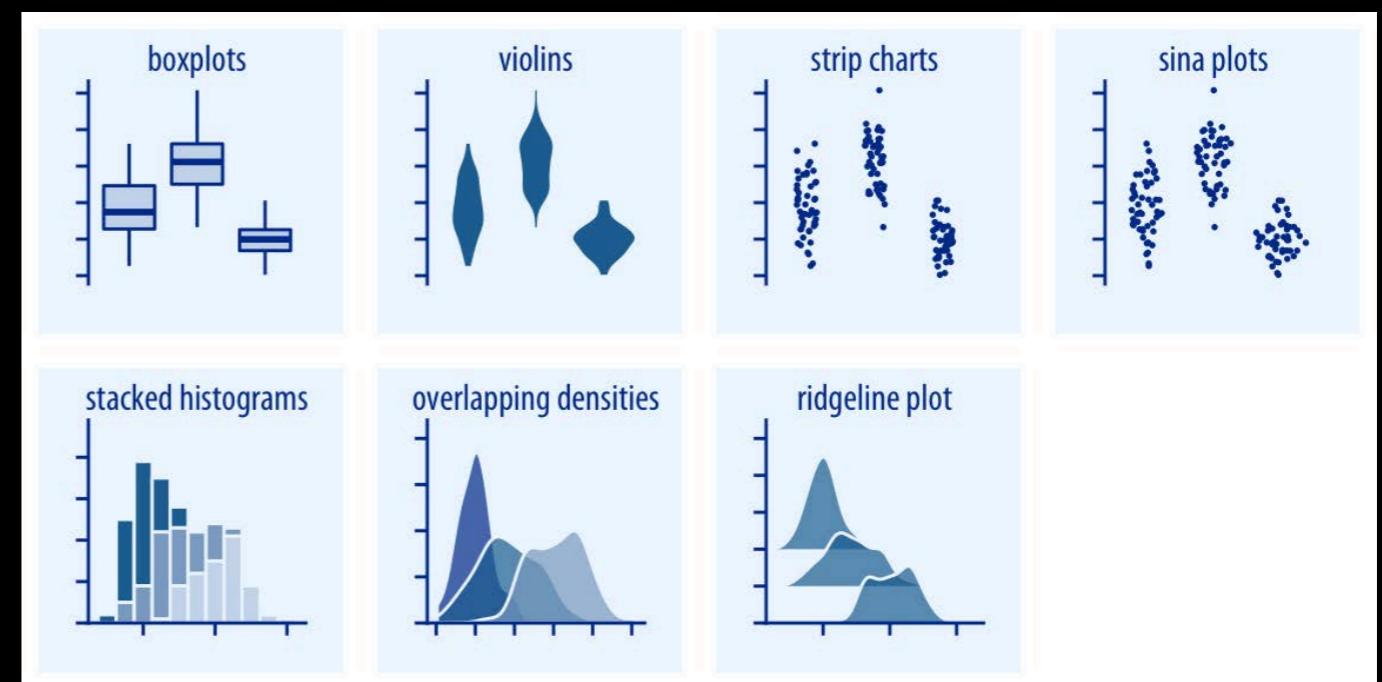


VISUALIZING DISTRIBUTIONS

Single distributions



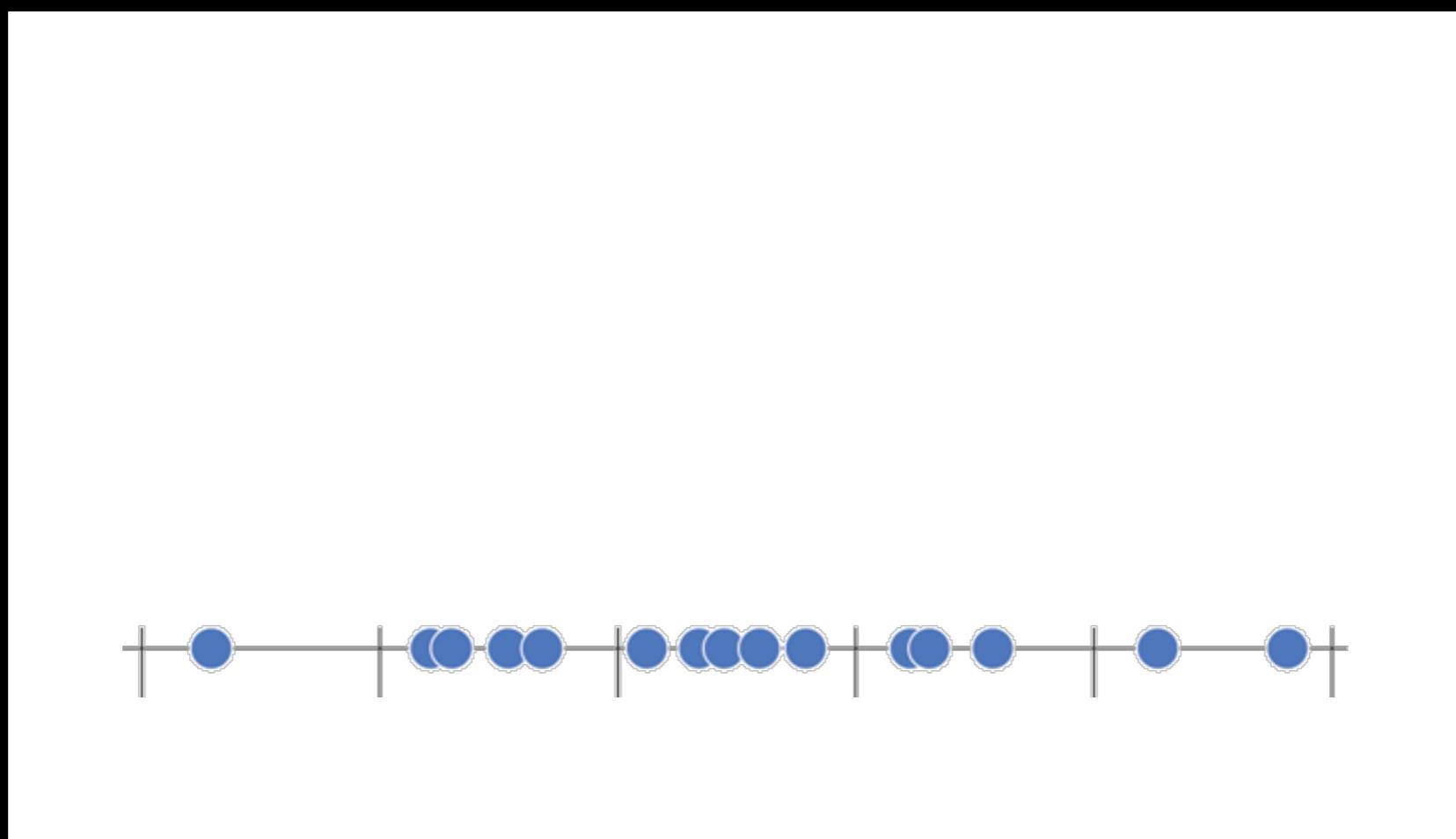
Multiple distributions



HISTOGRAMS

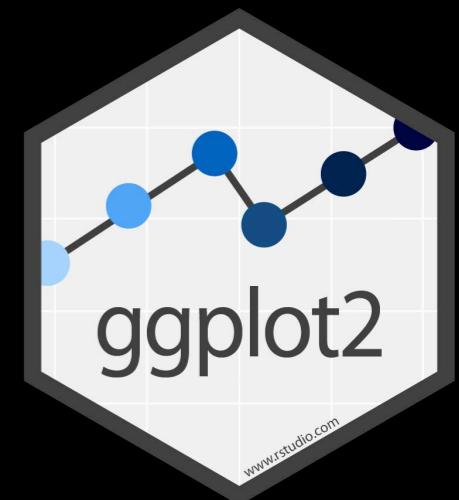
HISTOGRAMS

- Shows the distribution of a **single variable**
- Breaks the data apart into specific bins and shows *count* of cases in each bin

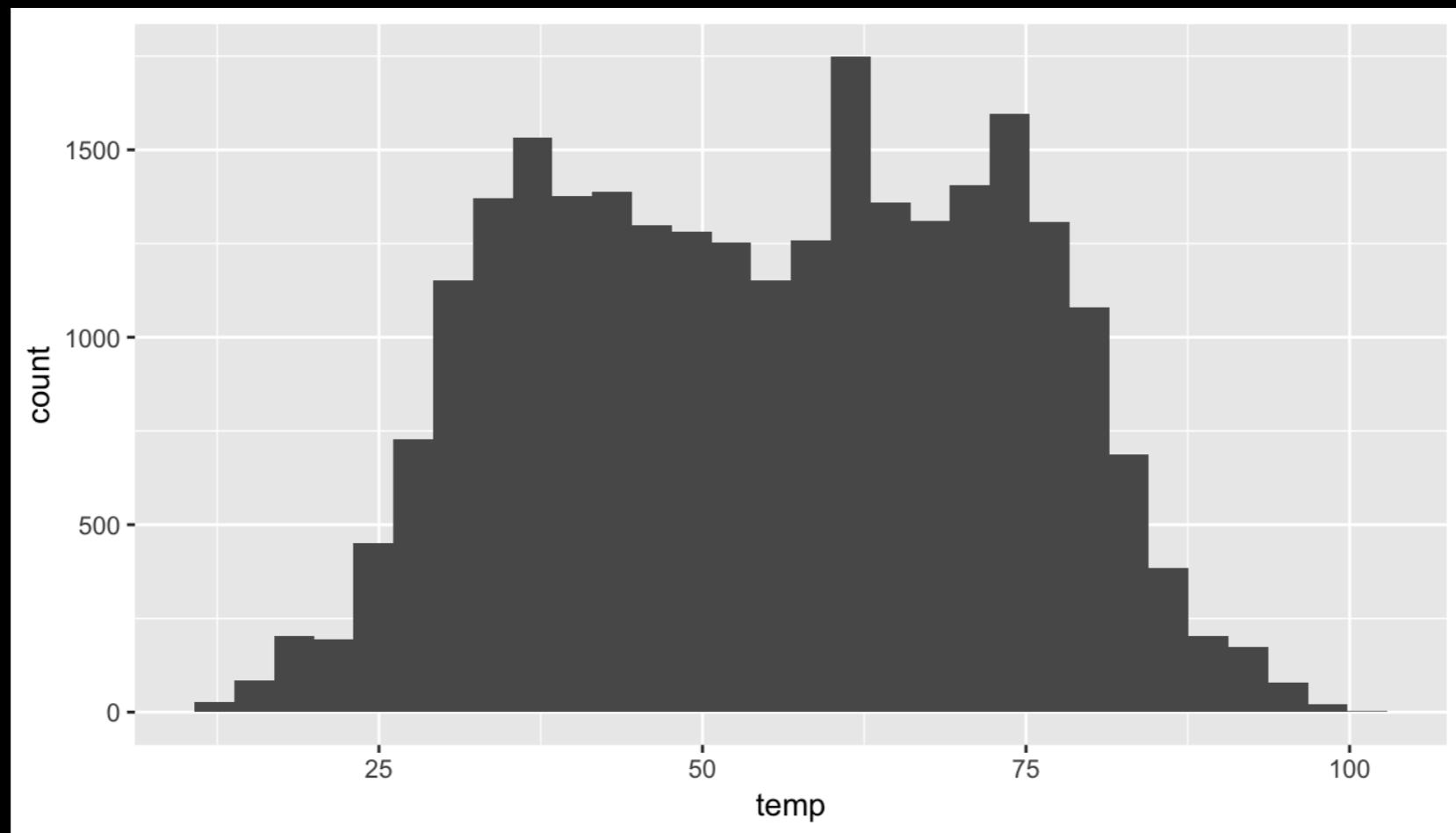


HISTOGRAMS

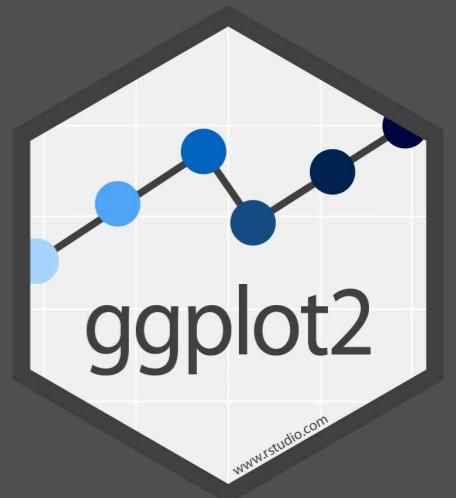
Major difference
with bar charts



- Geometric object is `geom_histogram()`
- One `numeric` variable mapped to `x` in `aes()`
- `y-aesthetic` computed automatically (don't map anything to `y`)



YOUR TURN



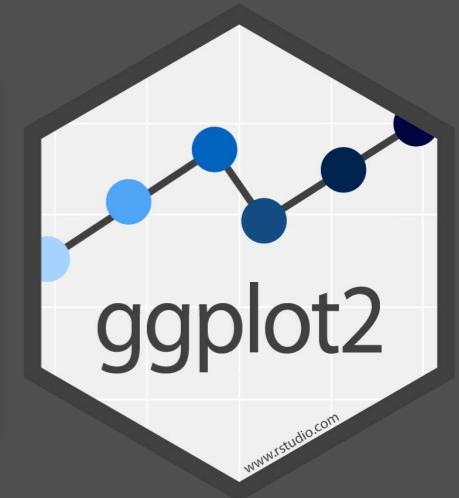
- Download the late Quaternary mammals data set from the course website (“`late_quaternary_mammals.RDS`”). This is a file format for single R objects.
- Read the file into R using:

```
lqm <- readRDS("your-path/late_quaternary_mammals.RDS")
```



YOUR TURN

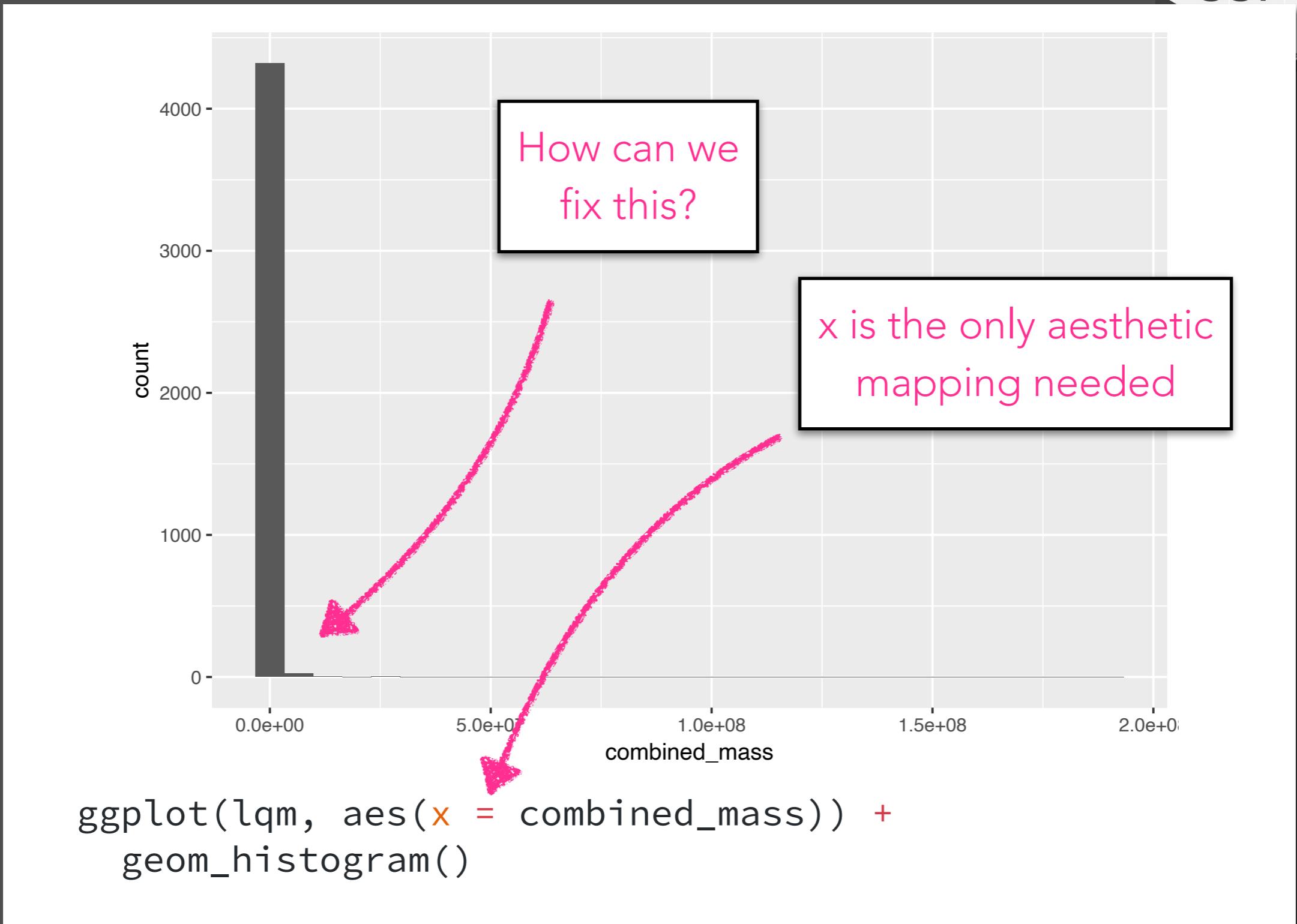
Average of
M/F body
masses (g)



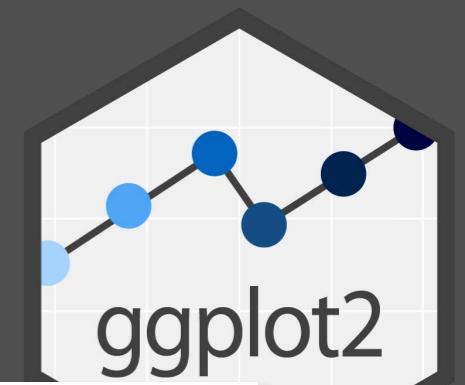
$\log_{10}(\text{combined_mass})$

continent	status	order	family	genus	species	log_mass	combined_mass	reference
Africa	extant	Artiodactyla	Bovidae	Addax	nasomaculatus	4.85	70000.3	60
Africa	extant	Artiodactyla	Bovidae	Aepyceros	melampus	4.72	52500.1	63, 70
Africa	extant	Artiodactyla	Bovidae	Alcelaphus	buselaphus	5.23	171001.5	63, 70
Africa	extant	Artiodactyla	Bovidae	Ammodorcas	clarkei	4.45	28049.8	60
Africa	extant	Artiodactyla	Bovidae	Ammotragus	lervia	4.68	48000.0	75
Africa	extant	Artiodactyla	Bovidae	Antidorcas	marsupialis	4.59	39049.9	60
Africa	extinct	Artiodactyla	Bovidae	Antidorcas	bondi	4.53	34000.0	1
Africa	extinct	Artiodactyla	Bovidae	Antidorcas	australis	4.60	40000.0	2
Africa	extant	Artiodactyla	Bovidae	Bos	taurus	5.95	900000.0	-999
Africa	extant	Artiodactyla	Bovidae	Capra	walie	5.00	100000.0	-999

YOUR TURN



YOUR TURN



count

400
300
200
100
0

0

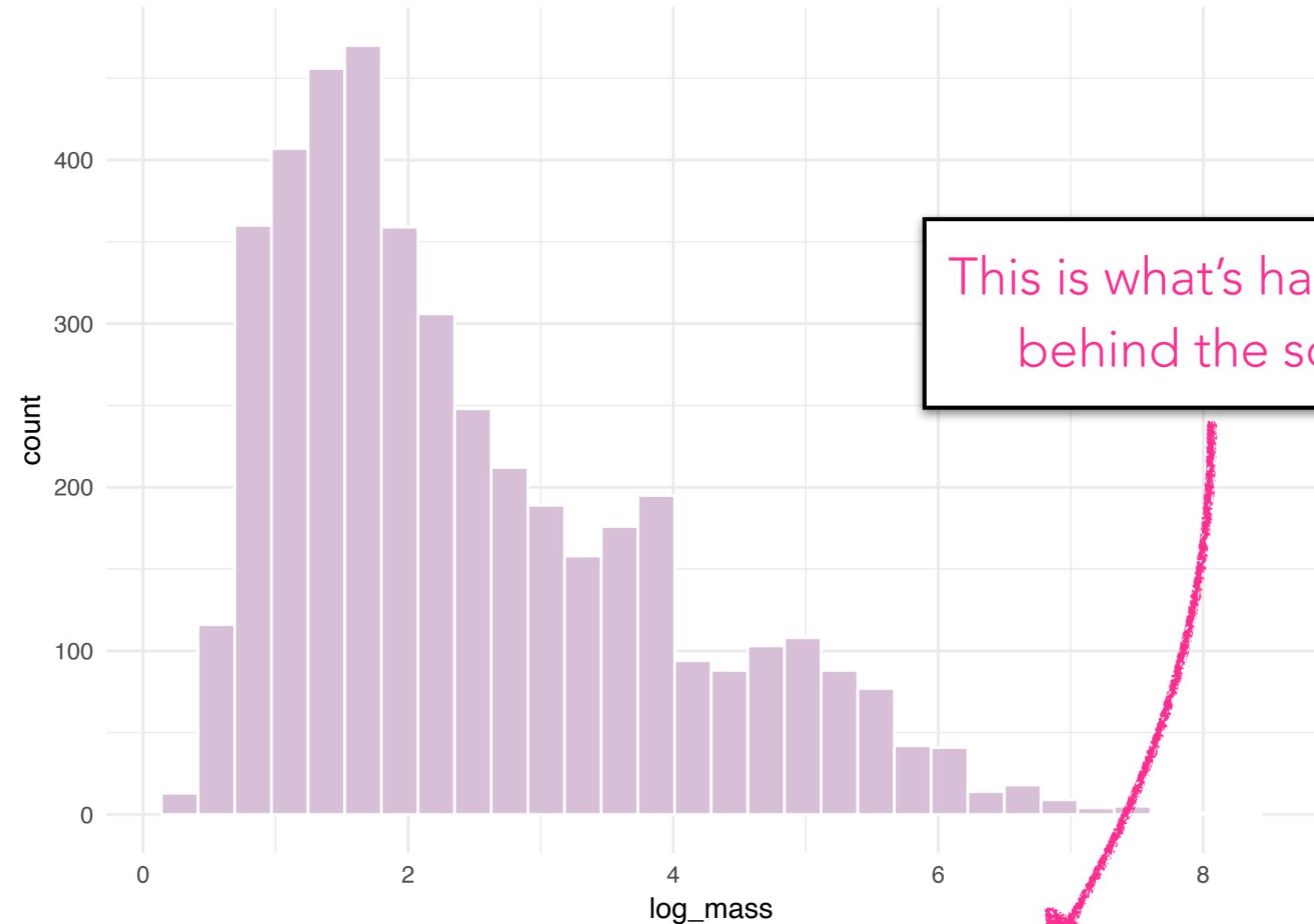
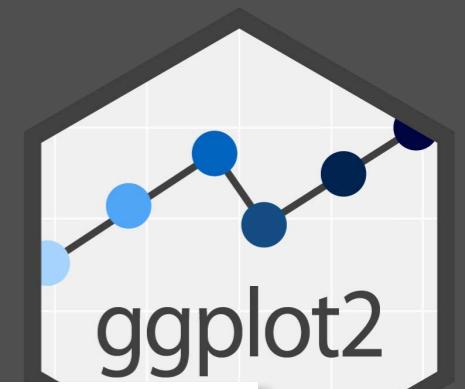
2

log_mass

8

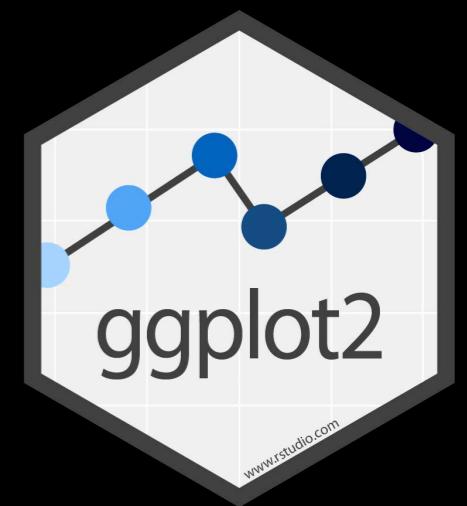
```
ggplot(lqm, aes(x = log_mass)) +  
  geom_histogram(fill = "thistle", color = "white")
```

YOUR TURN



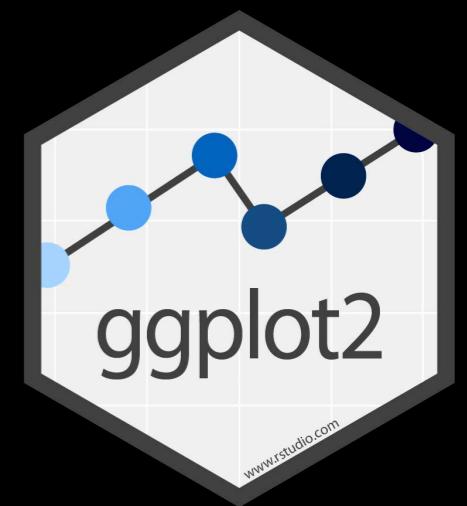
```
ggplot(lqm, aes(x = log_mass, y = stat(count))) +  
  geom_histogram(fill = "thistle", color = "white")
```

HISTOGRAMS



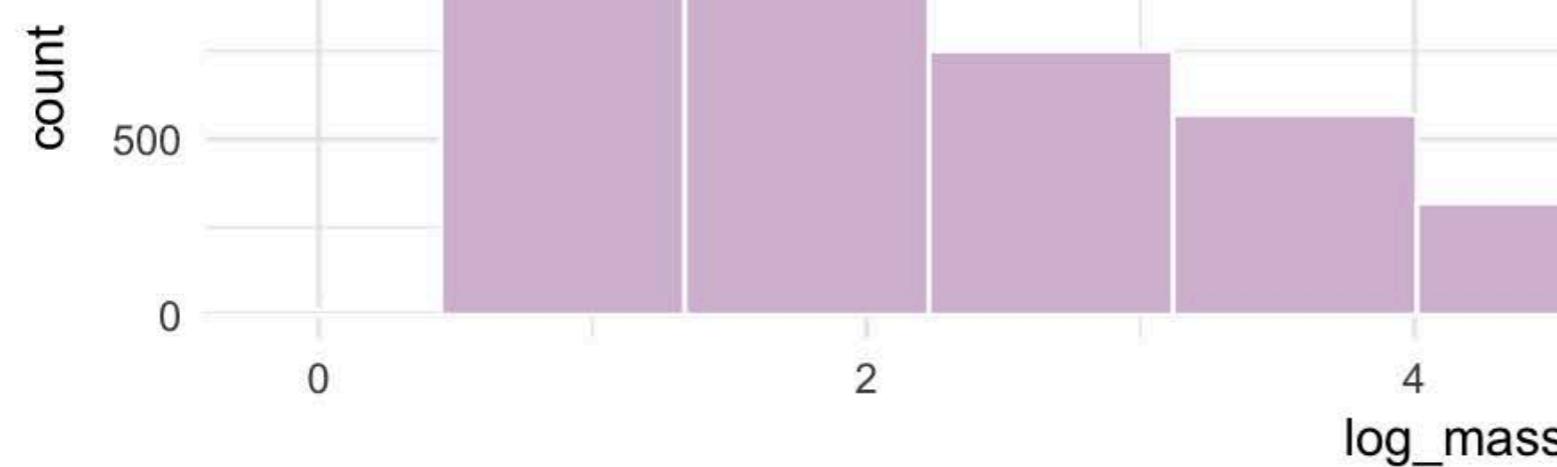
- When making a histogram, always explore multiple bin widths.
 - Binning behavior can be modified using:
 - bins: `geom_histogram(bins = 30)`
 - binwidth: `geom_histogram(binwidth = 1)`
 - breaks: `geom_histogram(breaks = 0:10)`
- # of bins
- width of one bin in units of x
- sequence of bin boundaries

HISTOGRAMS

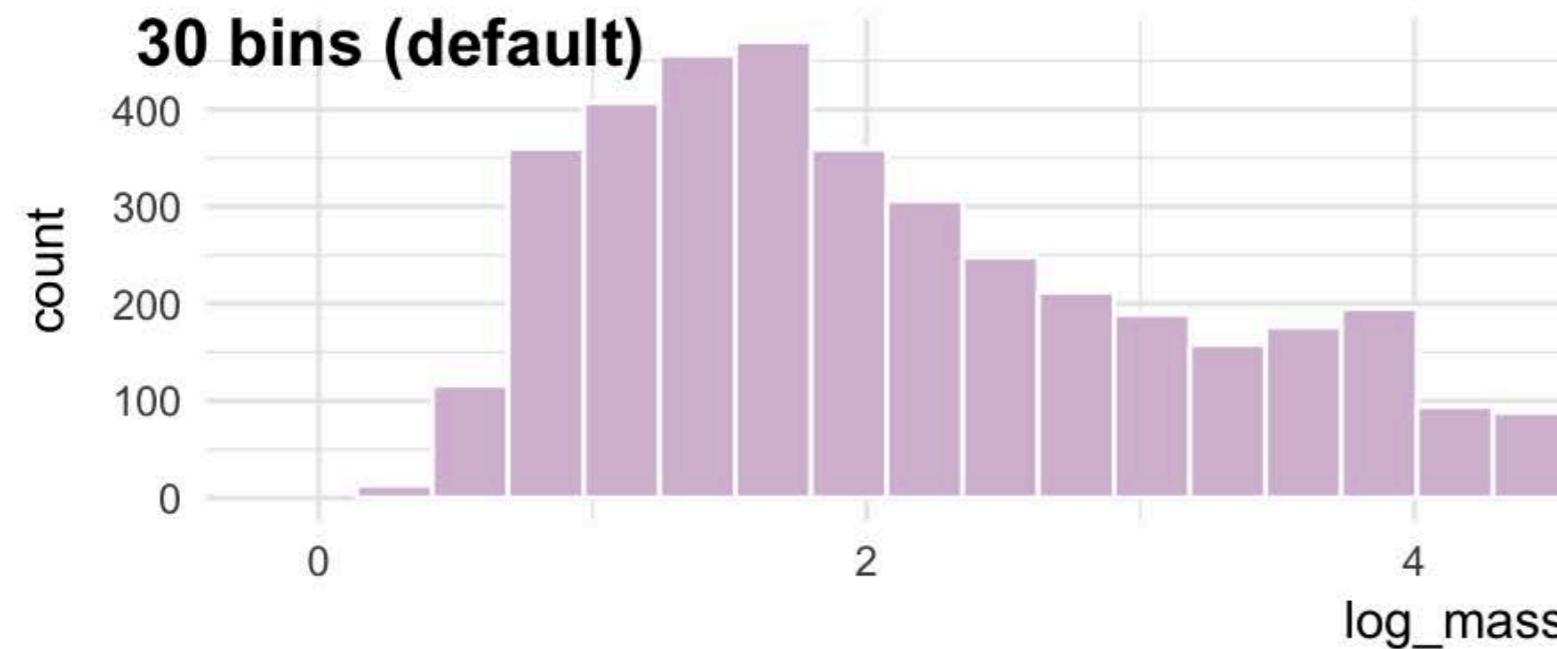


- When making a histogram, always explore multiple bin widths.
- Binning behavior can be modified using:
 - bins: `geom_histogram(bins = 30)`
 - binwidth: `geom_histogram(binwidth = 1)`
 - breaks: `geom_histogram(breaks = 0:10)`

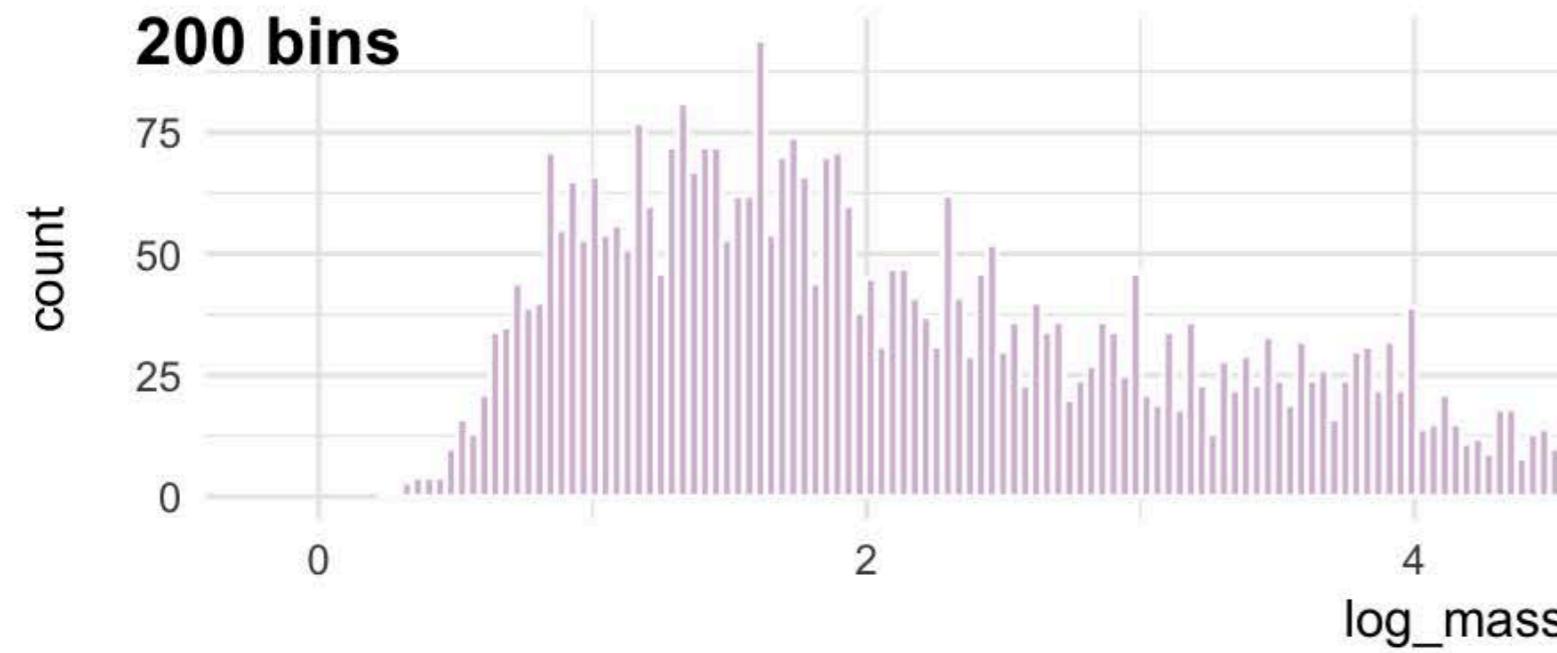
10 bins



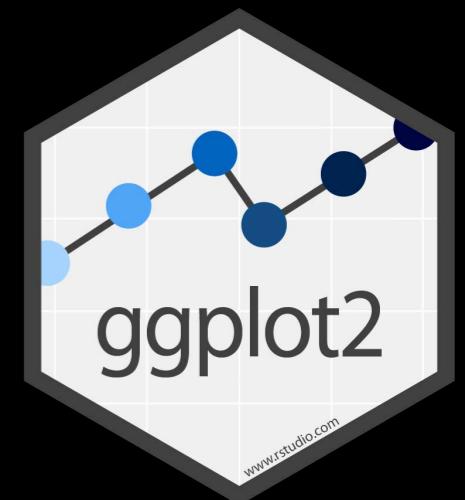
30 bins (default)



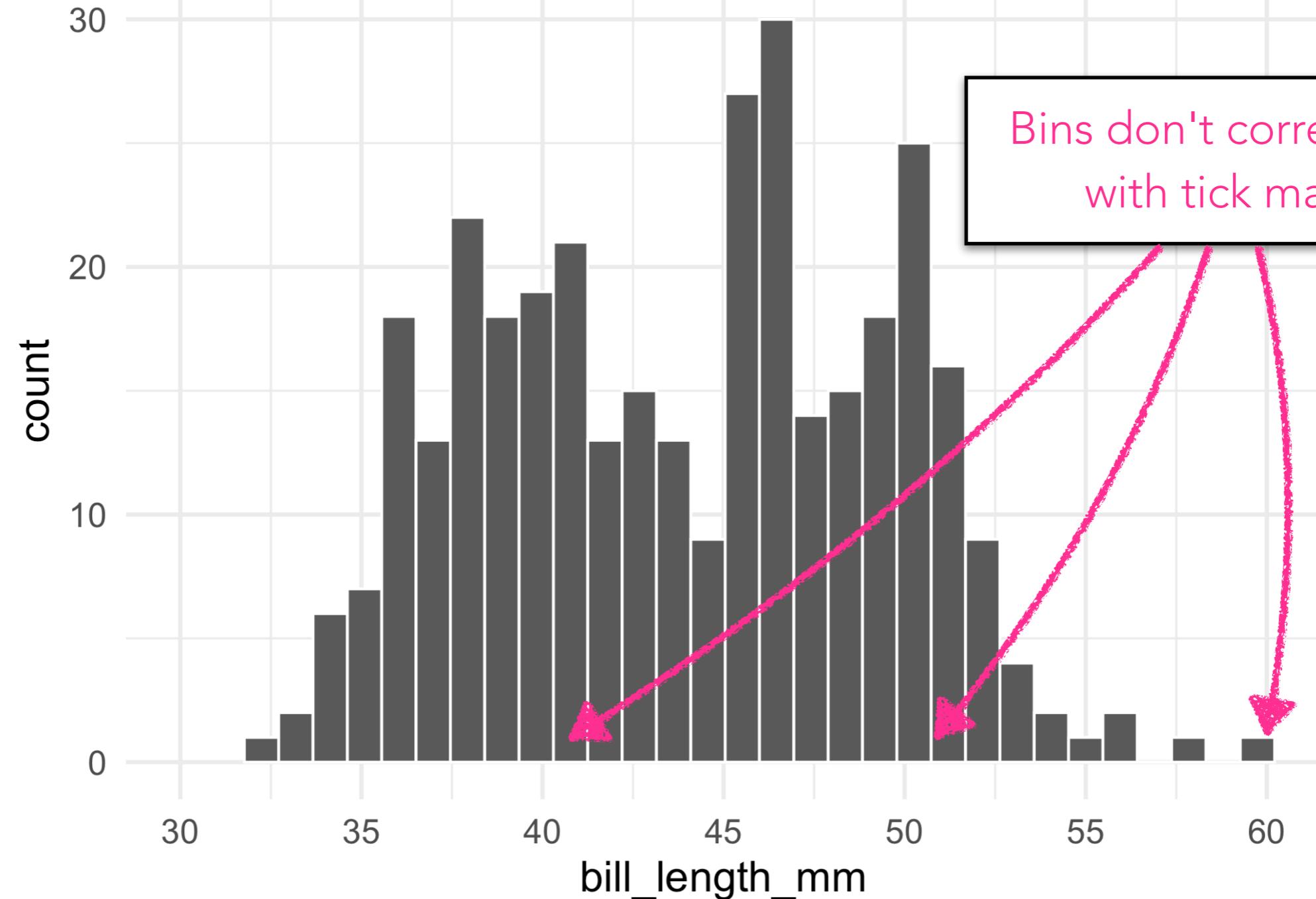
200 bins



HISTOGRAMS



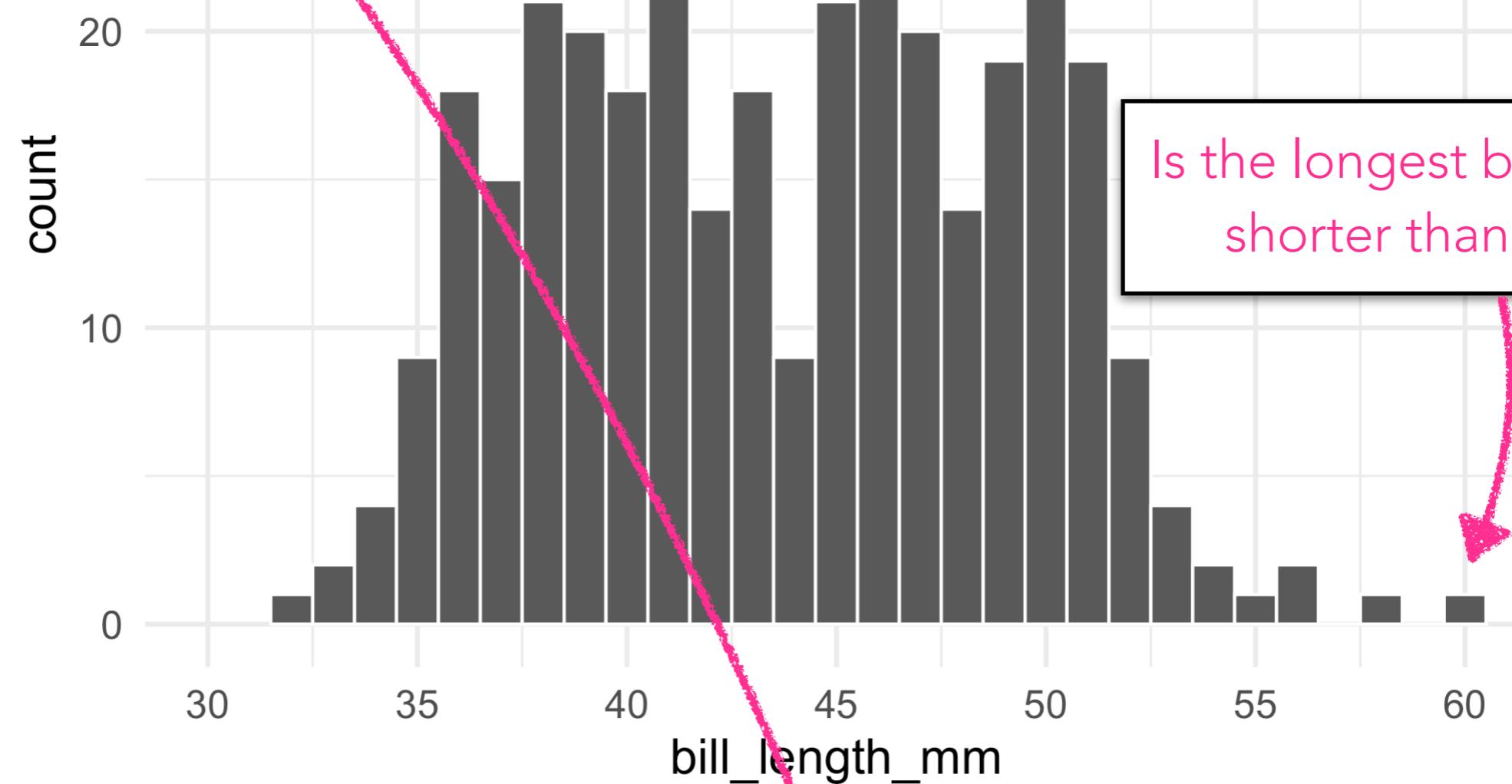
- *Also pay attention to the bin positions!*
The defaults don't always make sense.
- Binning positions can be modified with **ONE** (not both) of the following:
 - center: an x value for the center of one of the bins (the rest will be calculated)
 - boundary: an x value for the boundary between any two bins (the rest will be calculated)



```
ggplot(penguins, aes(x = bill_length_mm)) +  
  geom_histogram(color = "white", bins = 30)
```



Looks better when
binwidth set to integer unit

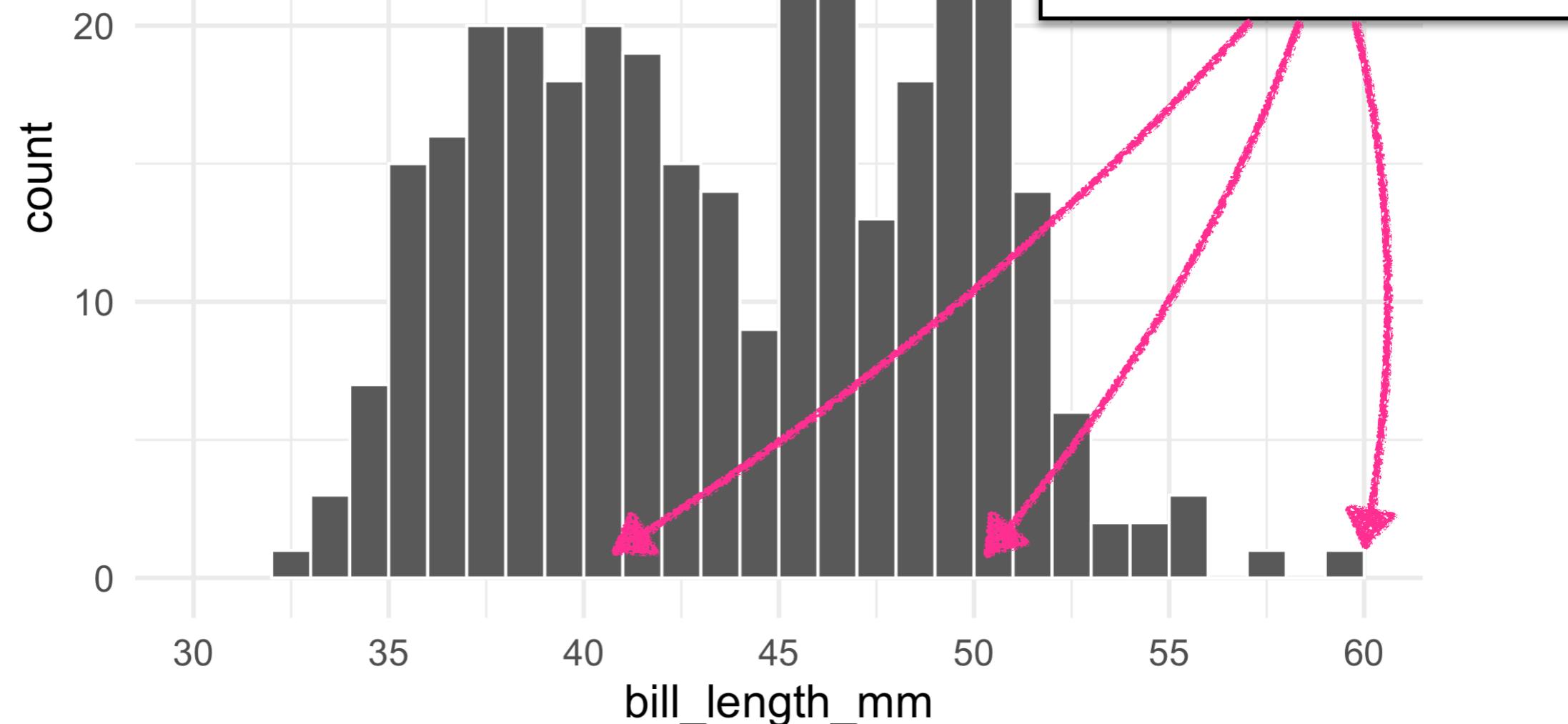


Is the longest bill longer or
shorter than 60 mm?

```
ggplot(penguins, aes(x = bill_length_mm)) +  
  geom_histogram(color = "white", binwidth = 1)
```

How else could we achieve
this using center?

We can shift the bars by
setting the boundary

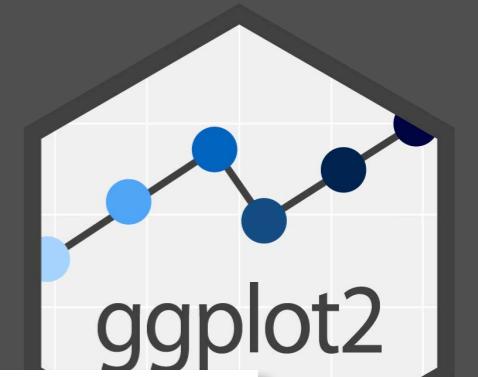


```
ggplot(penguins, aes(x = bill_length_mm)) +  
  geom_histogram(color = "white", binwidth = 1, boundary = 40)
```

HISTOGRAMS

- Histograms are generally bad at showing multiple distributions together
- For example...

YOUR TURN



Try to predict what this will do...

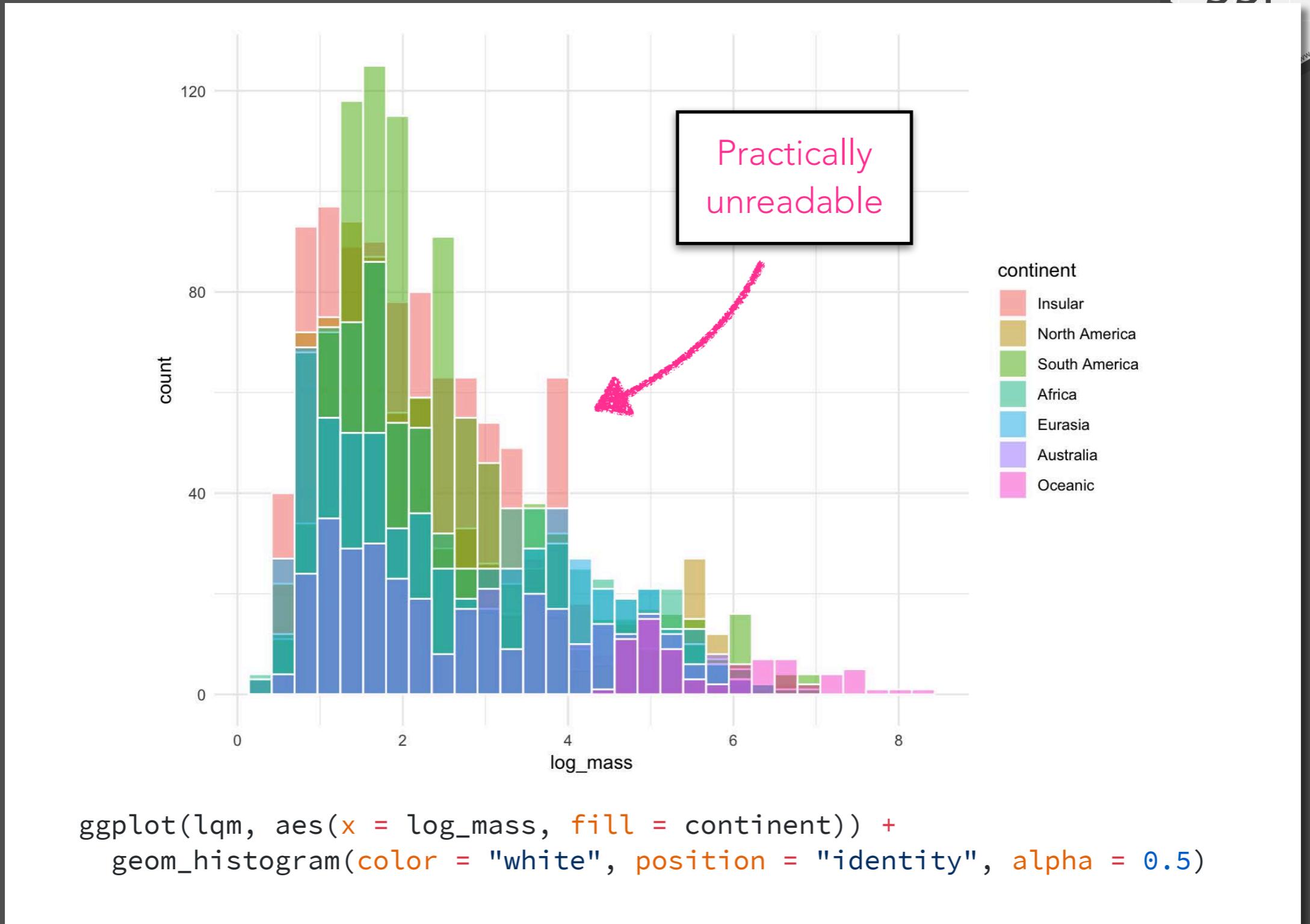
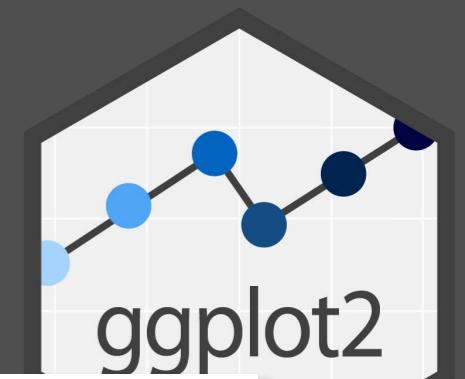
Different
fill color
for each
continent

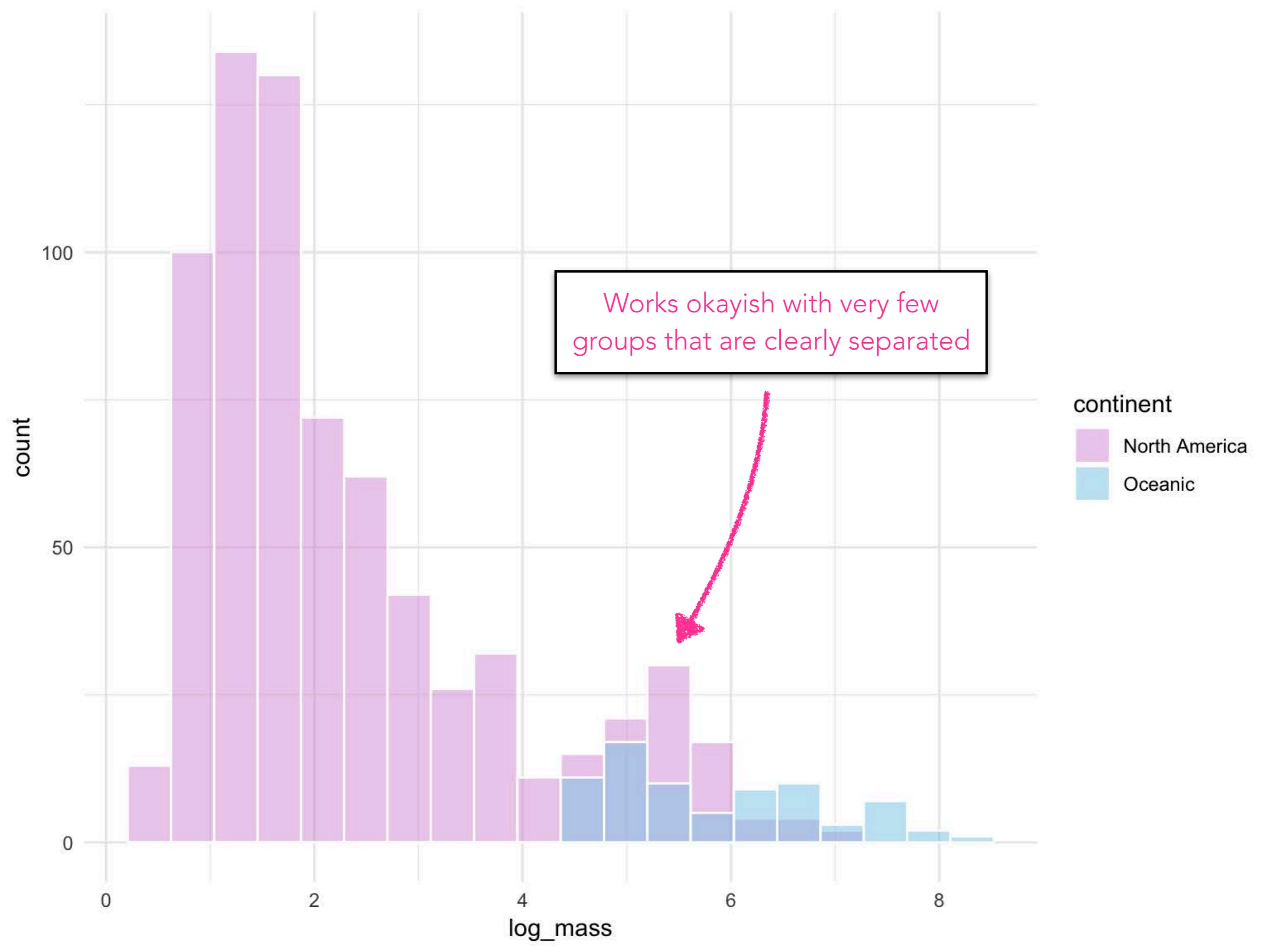
Makes
histograms
overlap

Makes them
partially
transparent

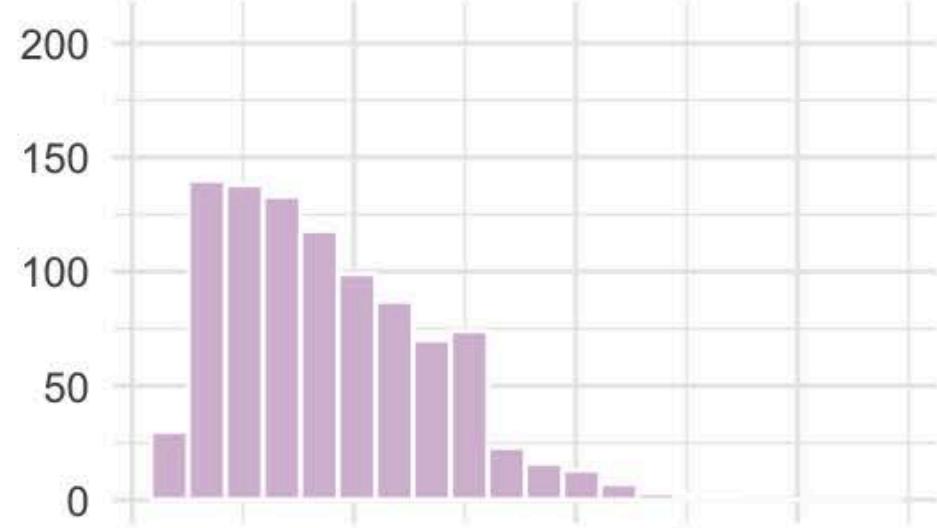
```
ggplot(lqm, aes(x = log_mass, fill = continent)) +  
  geom_histogram(color = "white", position = "identity", alpha = 0.5)
```

YOUR TURN

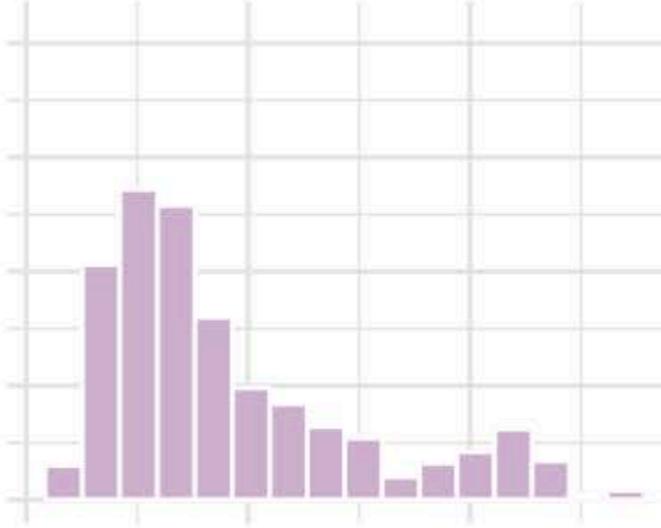




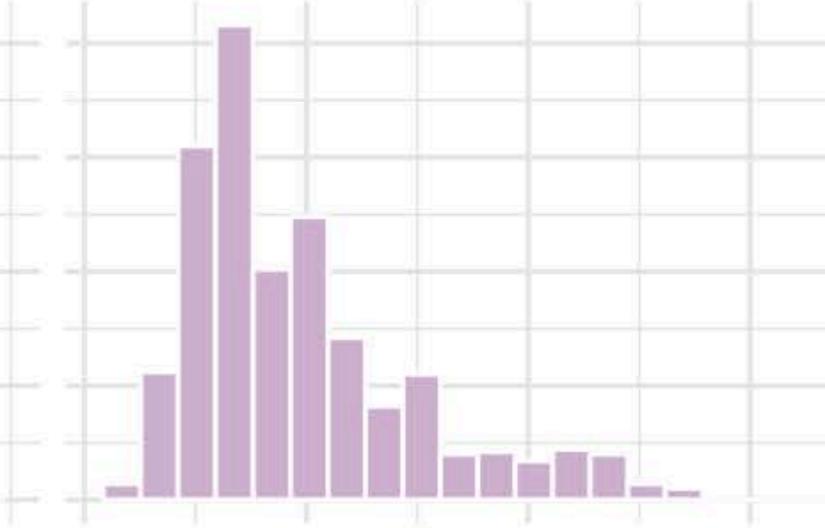
Insular



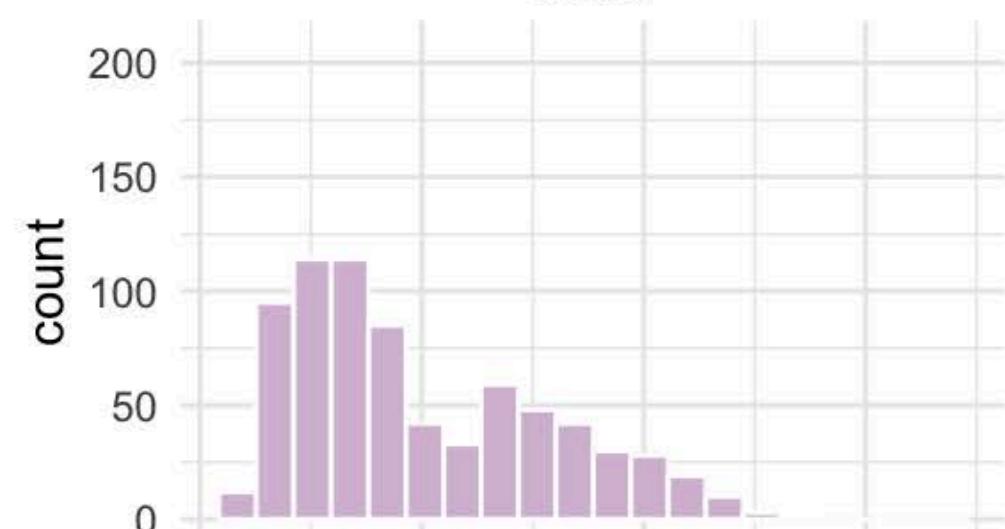
North America



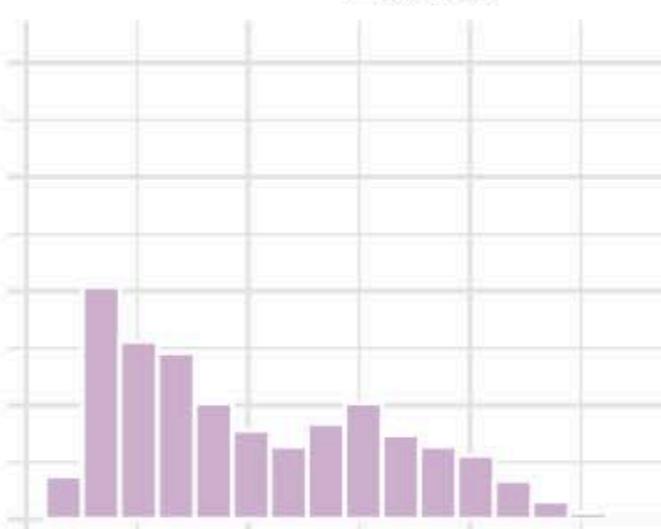
South America



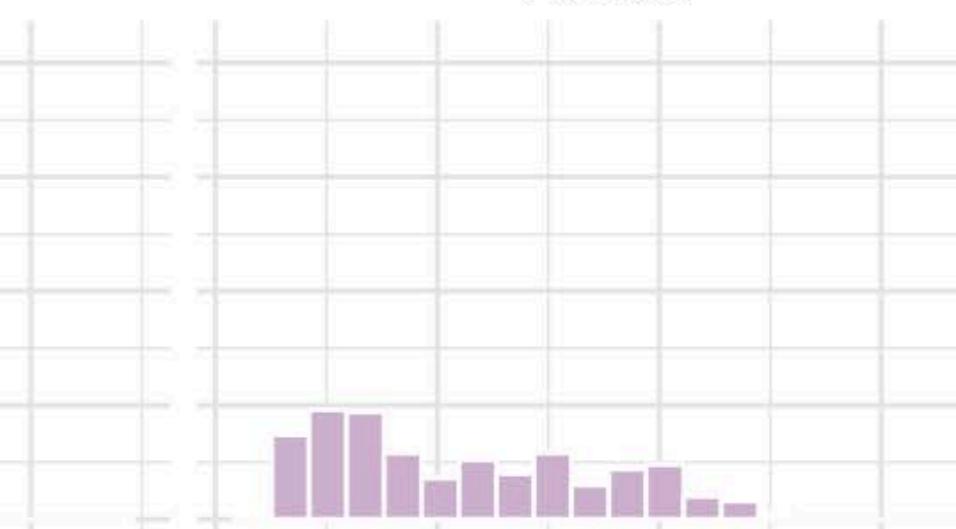
Africa



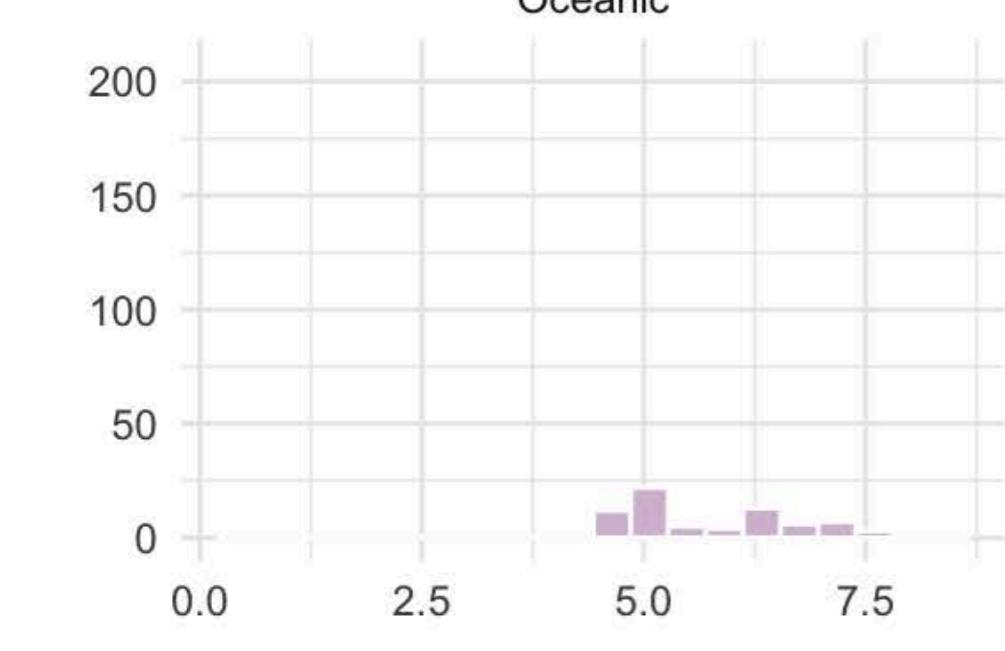
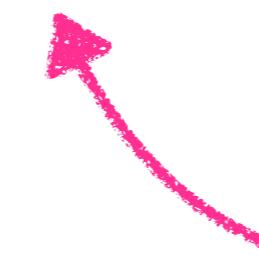
Eurasia



Australia

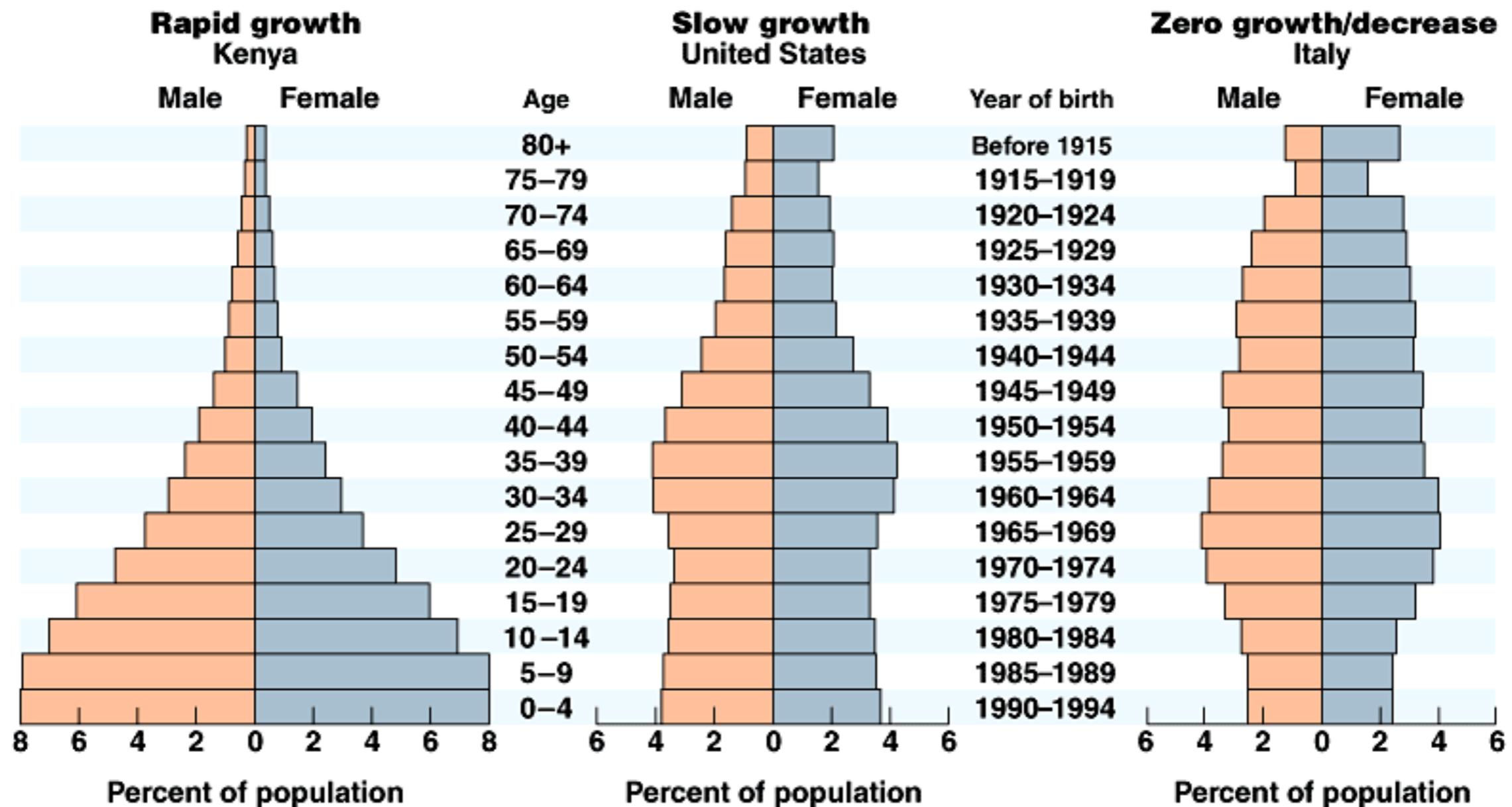


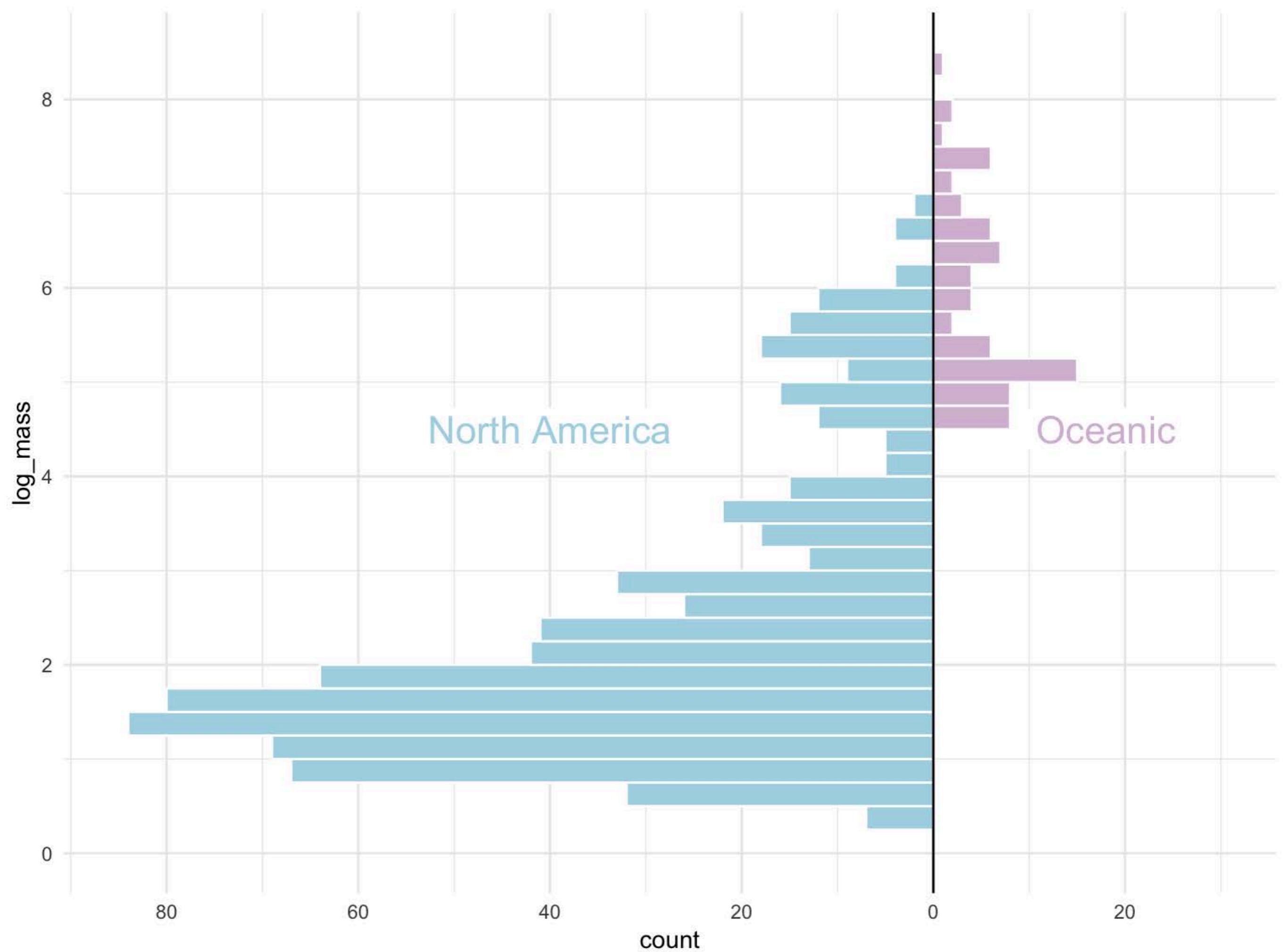
Oceanic

log₁₀ mass

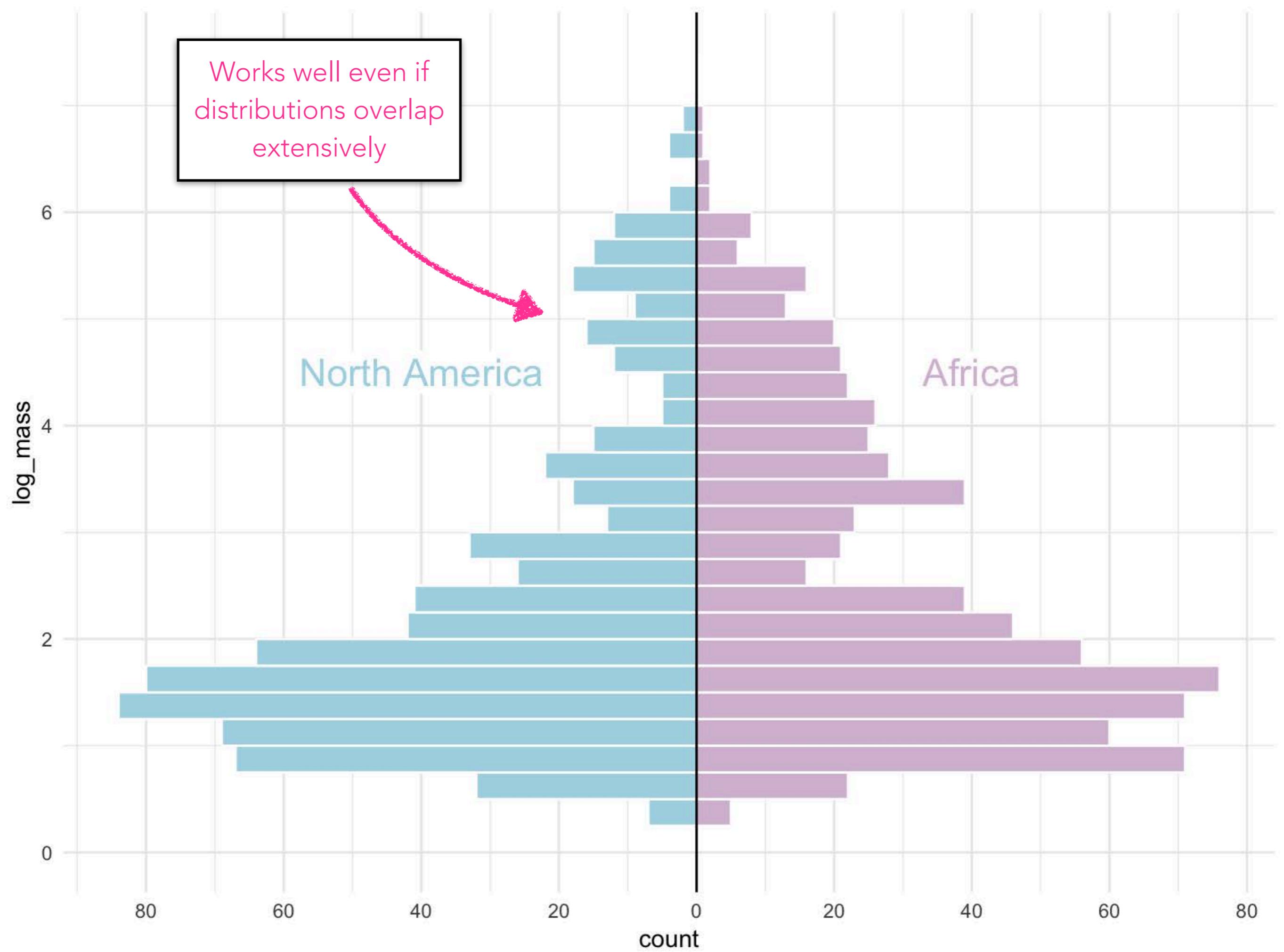
Better as small multiples,
but direct comparisons
more difficult

"Age pyramid" style plot is ideal for comparing two (and only two) distributions

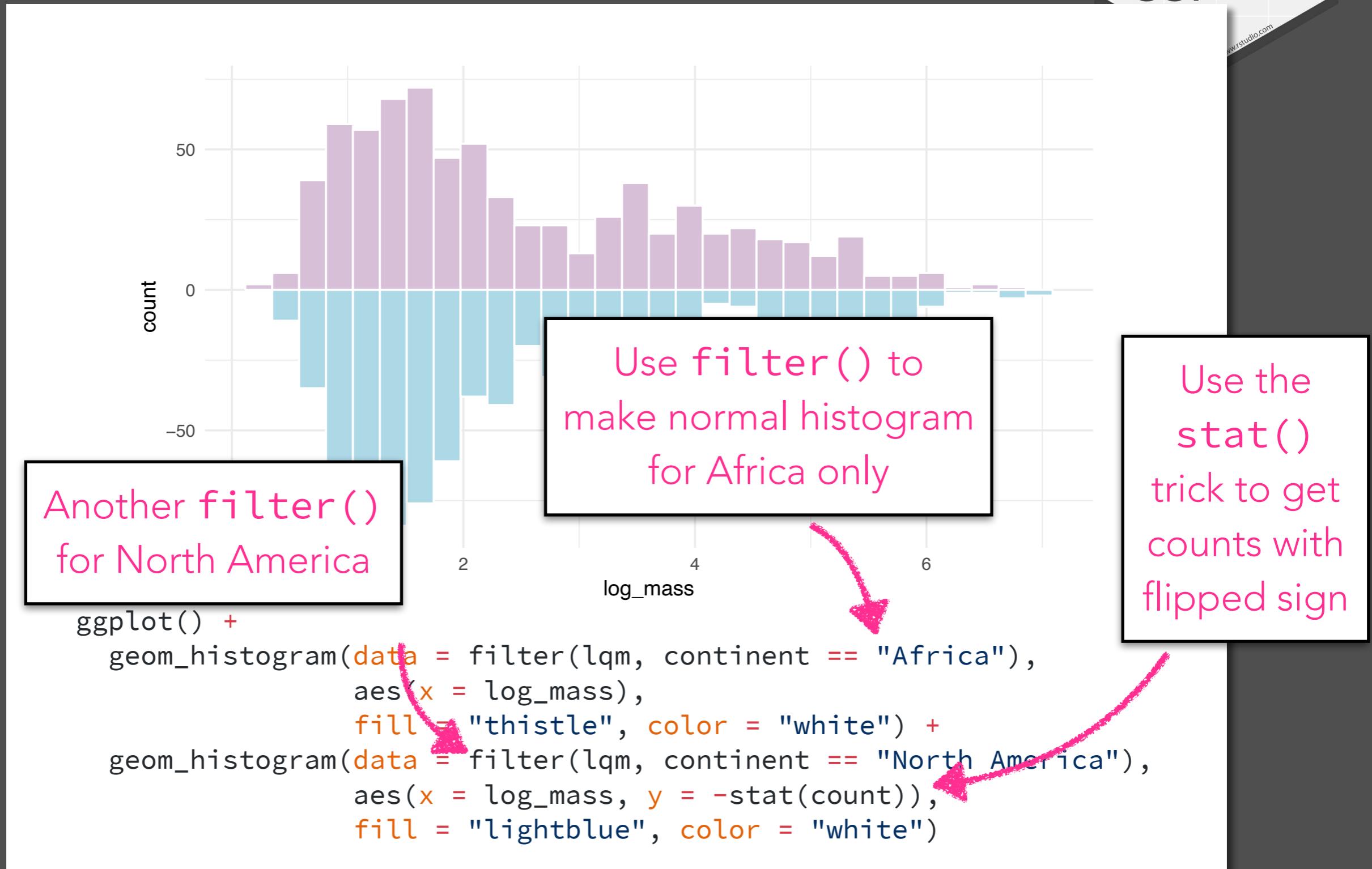
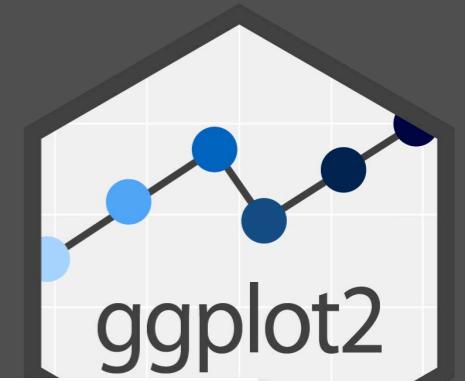




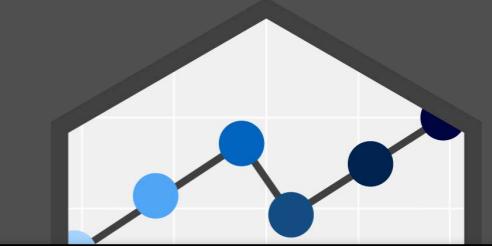
Works well even if
distributions overlap
extensively



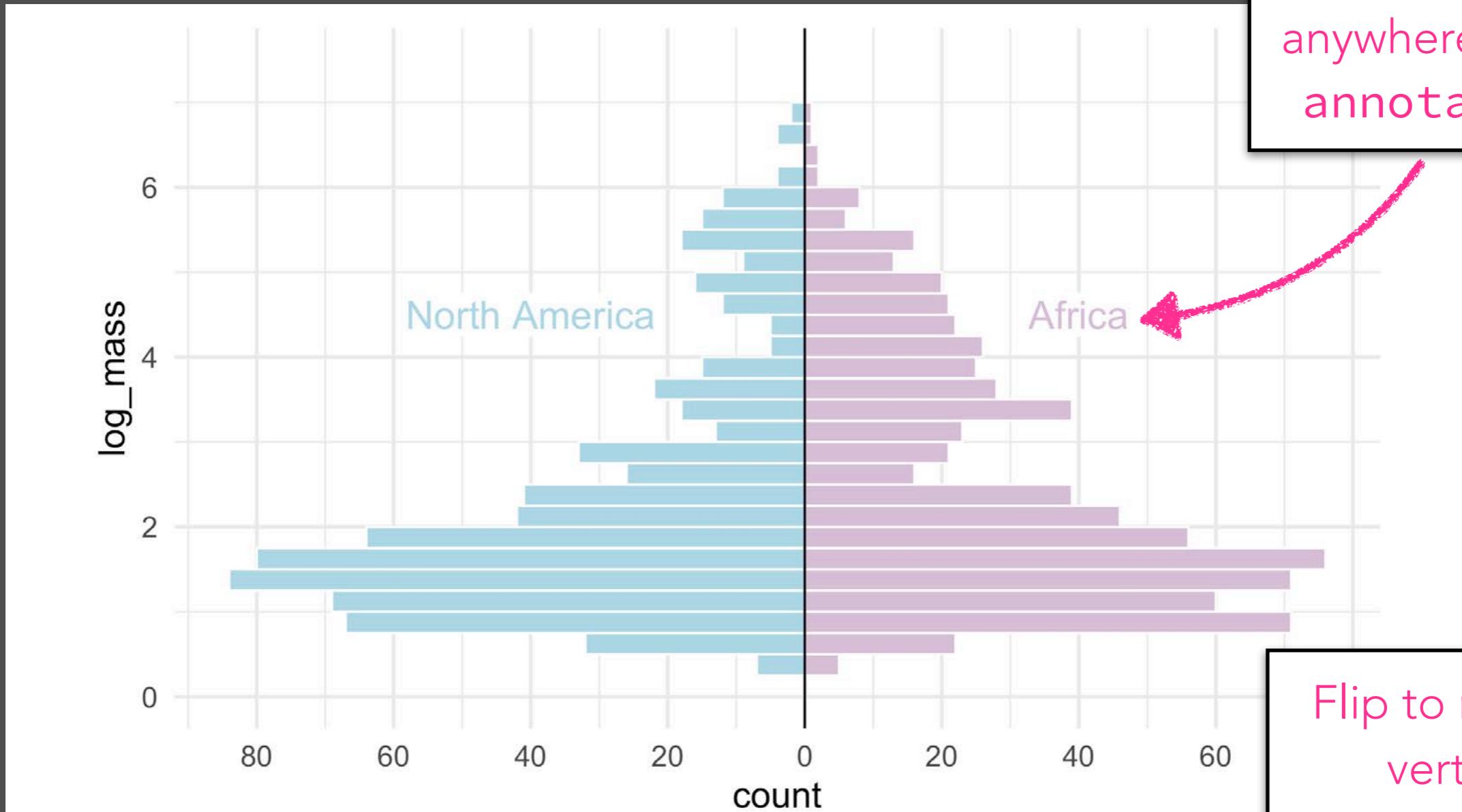
A STARTER...



A STARTER...



Add text
anywhere using
annotate()

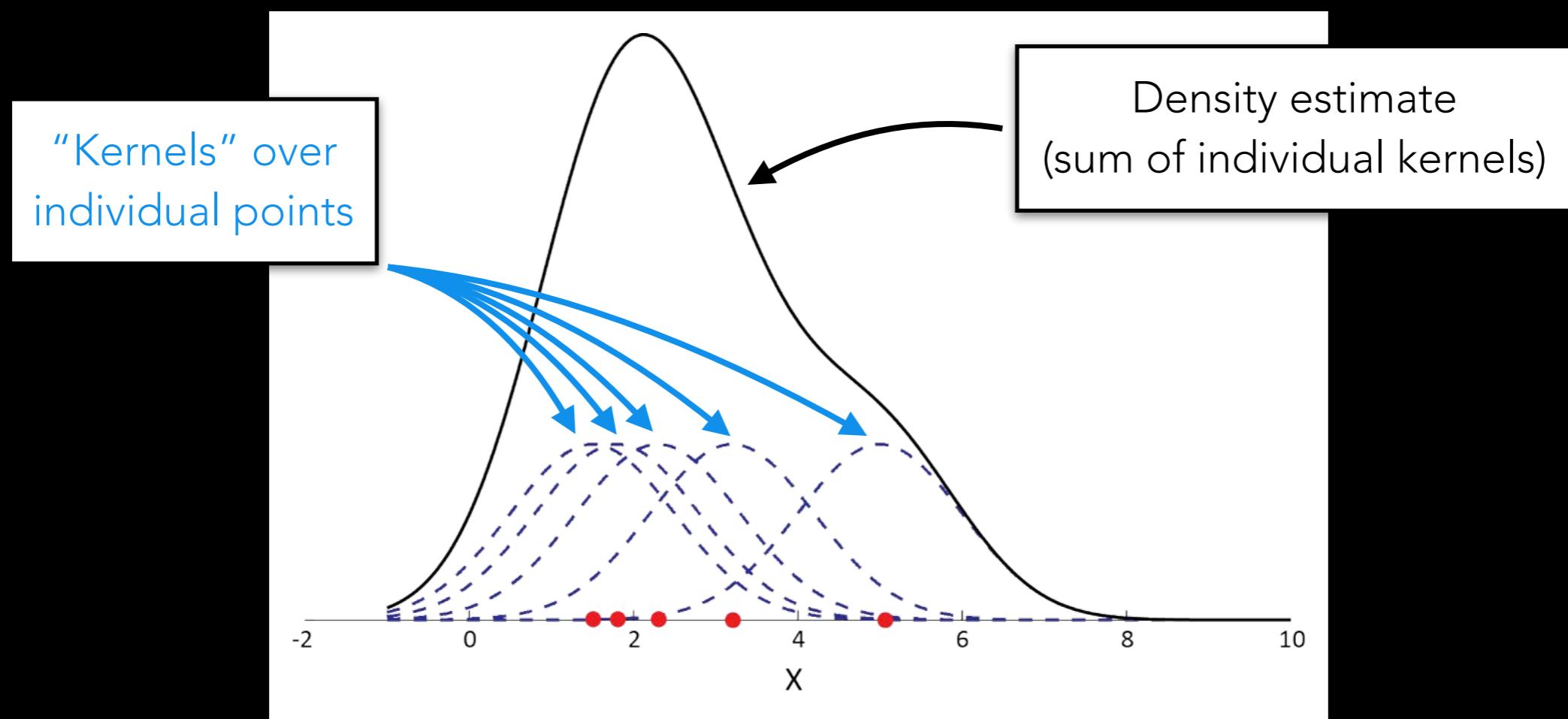


Flip to make it
vertical

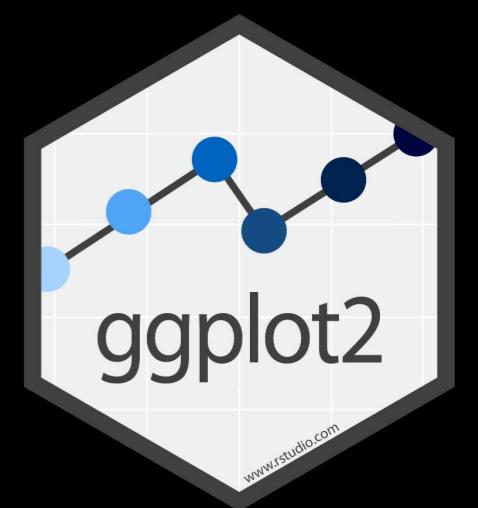
```
... +
  annotate(geom = "text", y = 40, x = 4.5, label = "Africa",
           color = "thistle", size = 6) +
  annotate(geom = "text", y = -40, x = 4.5, label = "North America",
           color = "lightblue", size = 6) +
  coord_flip()
```

DENSITY PLOTS

- Like histograms, density plots show the distribution of a single variable
- Uses smoothing to estimate the *density* of points over a continuous range of data values.

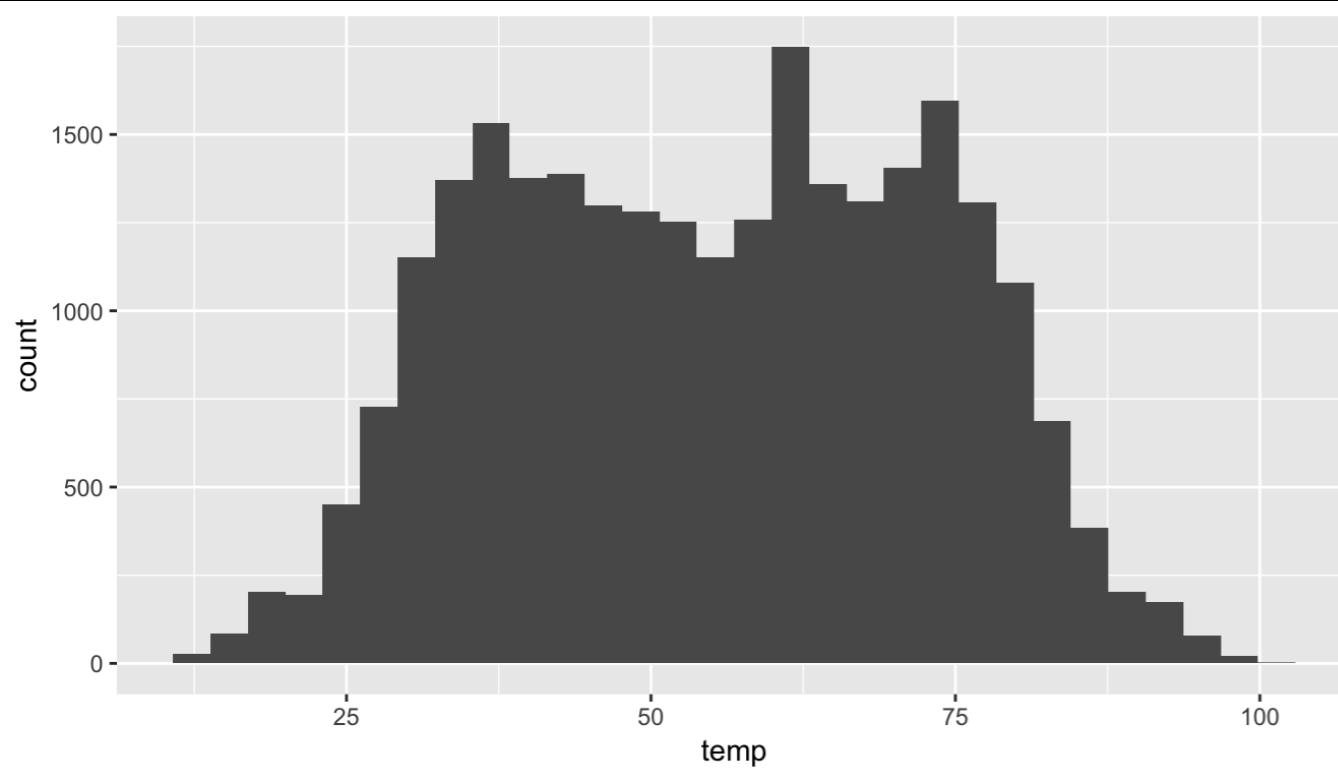


DENSITY PLOTS

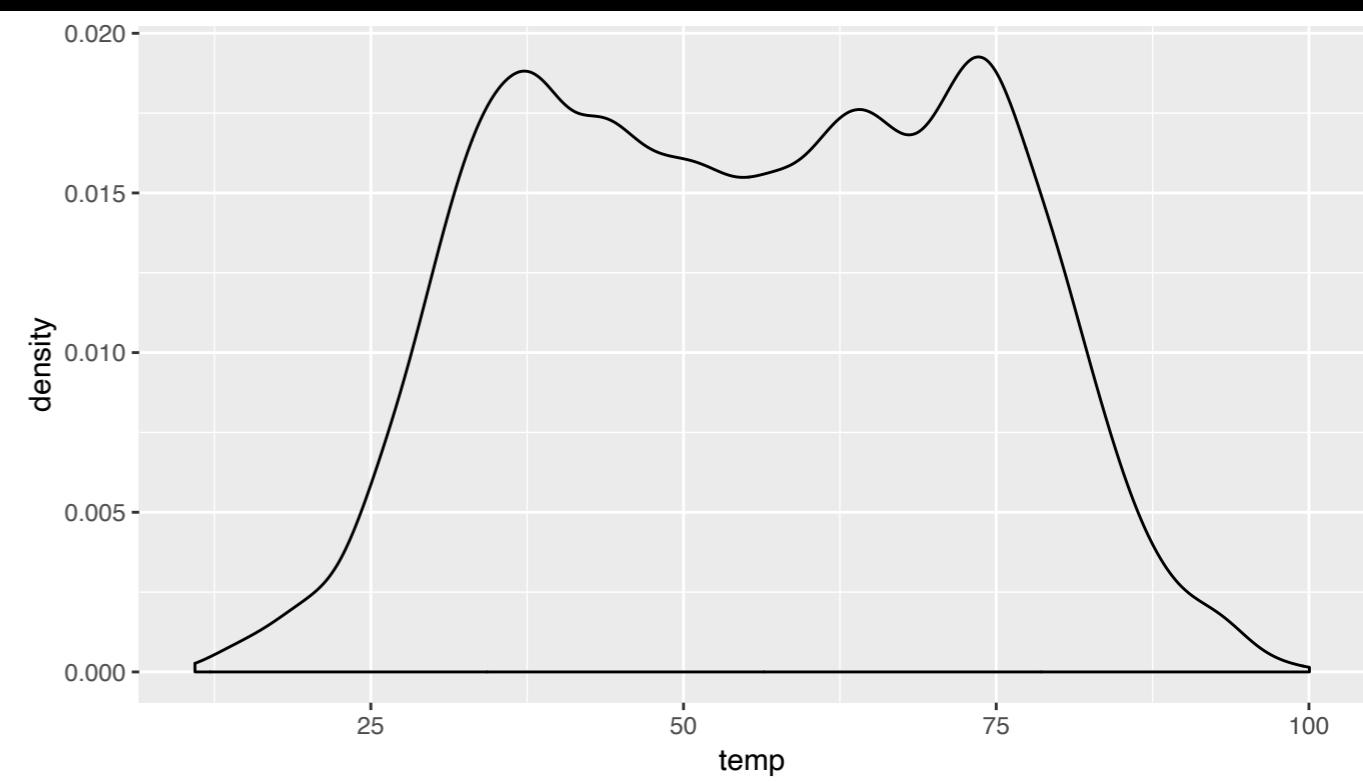


- Geometric object is `geom_density()`
- Aesthetic mappings are same as for histogram

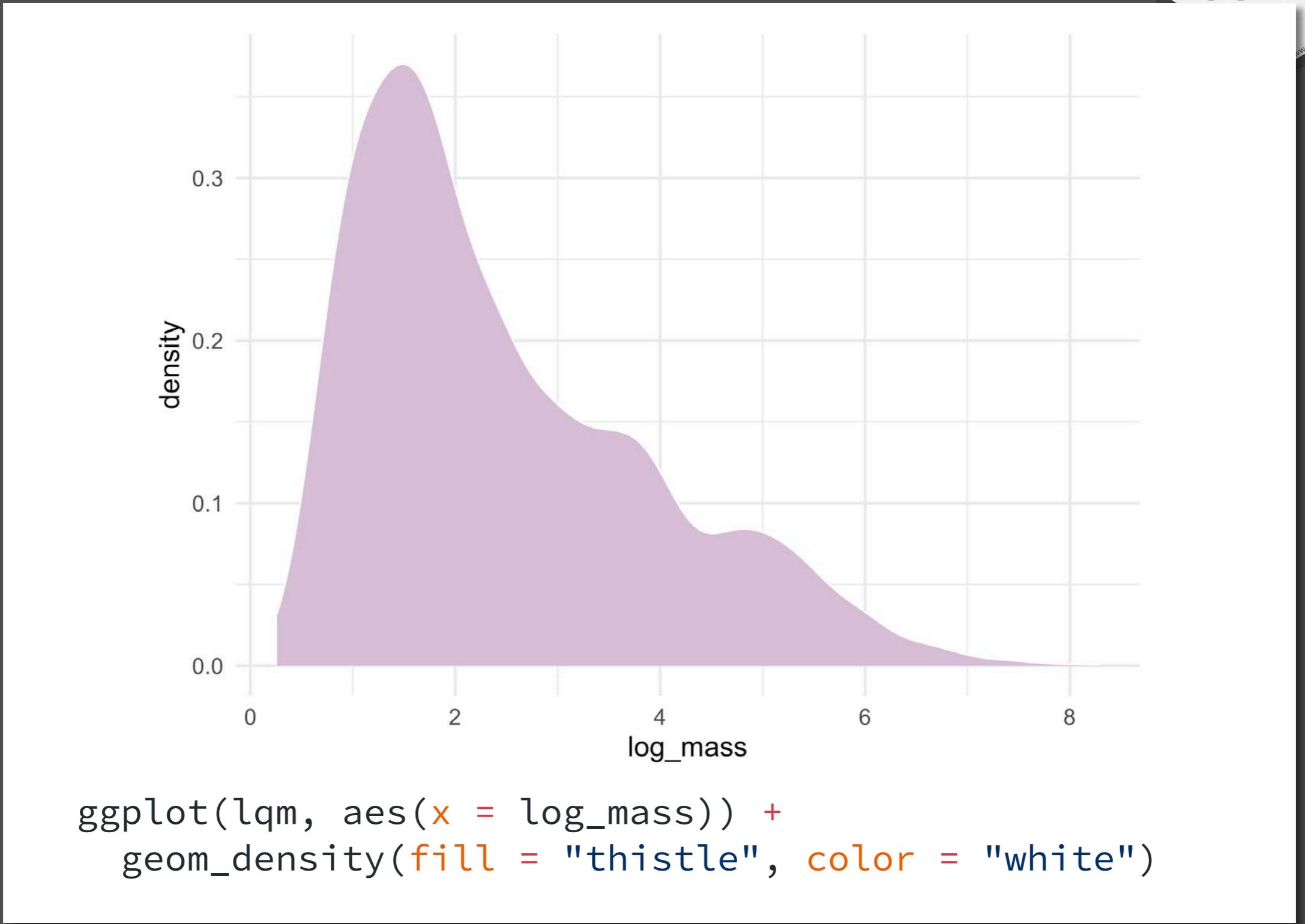
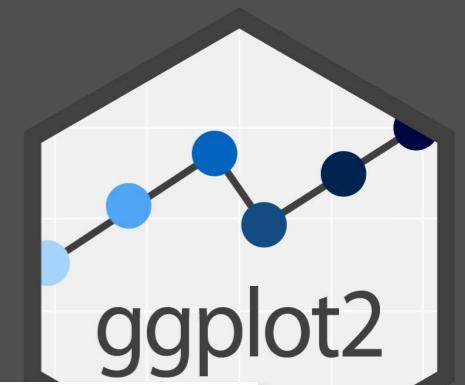
Histogram



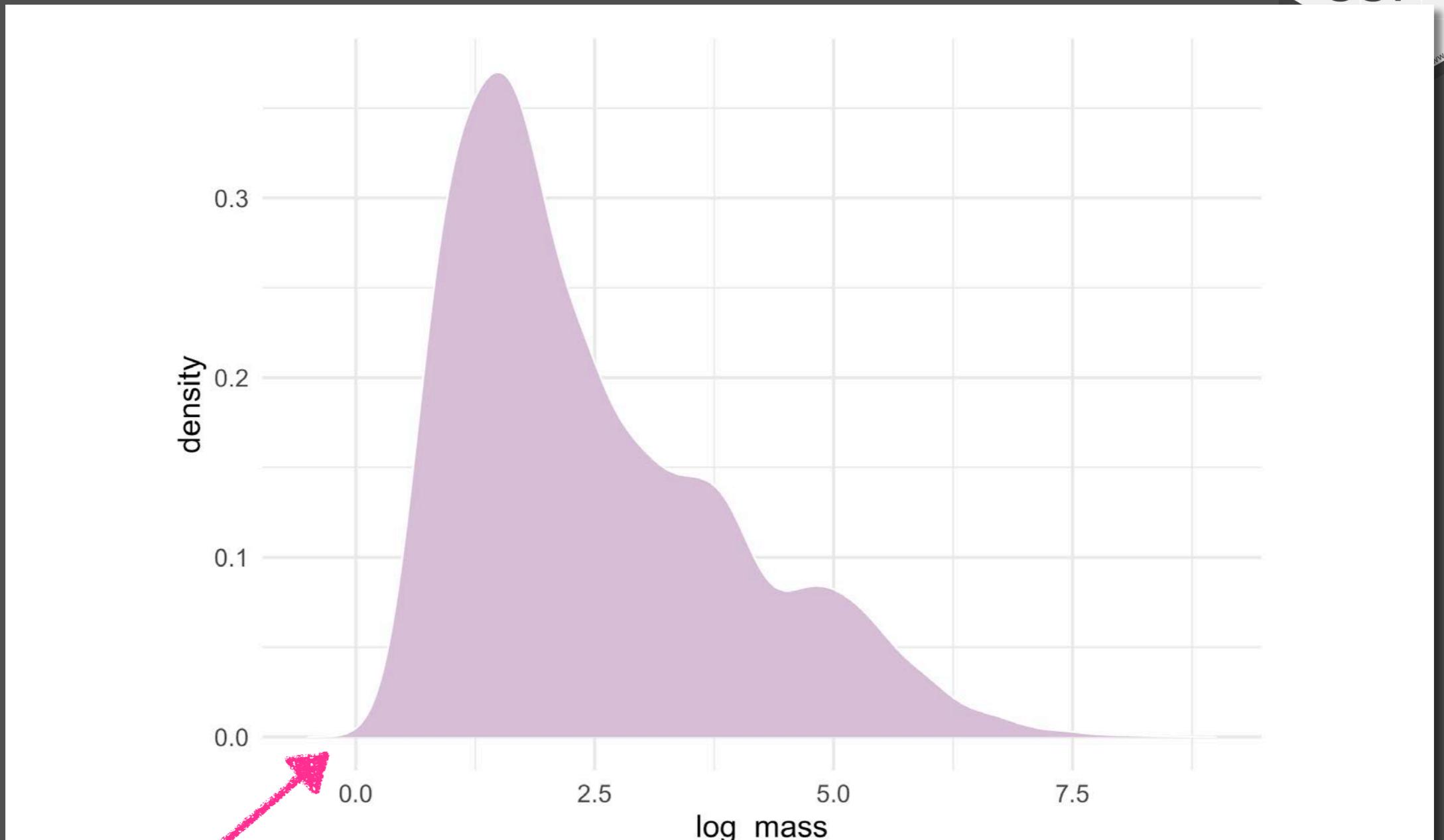
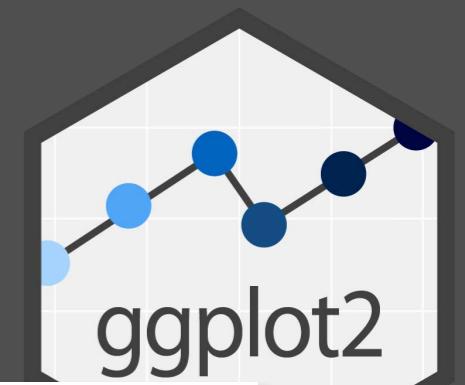
Density plot



YOUR TURN

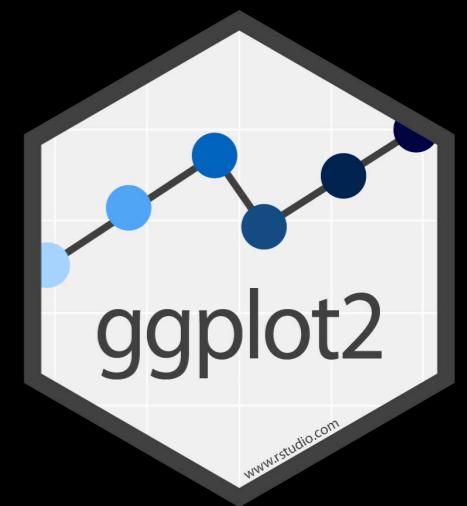


YOUR TURN



Be careful with density plots—they can show nonsensical data.

DENSITY PLOTS

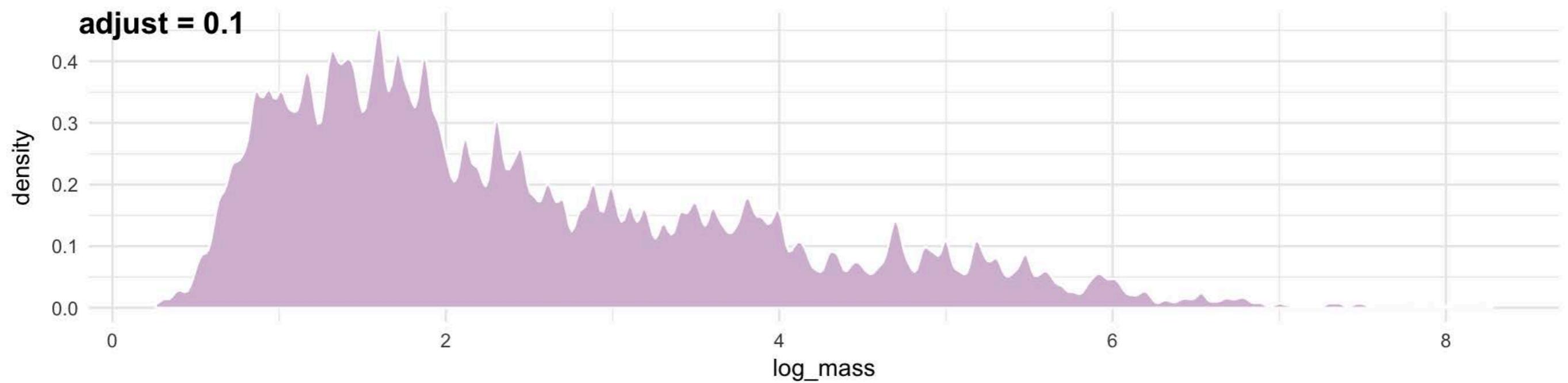


- Like histograms, the visual appearance of density plots depends on the amount of smoothing.
- Smoothing behavior can be adjusted in various complex ways, but the only one you're likely to use is:
 - `adjust: geom_density(adjust = 1)`

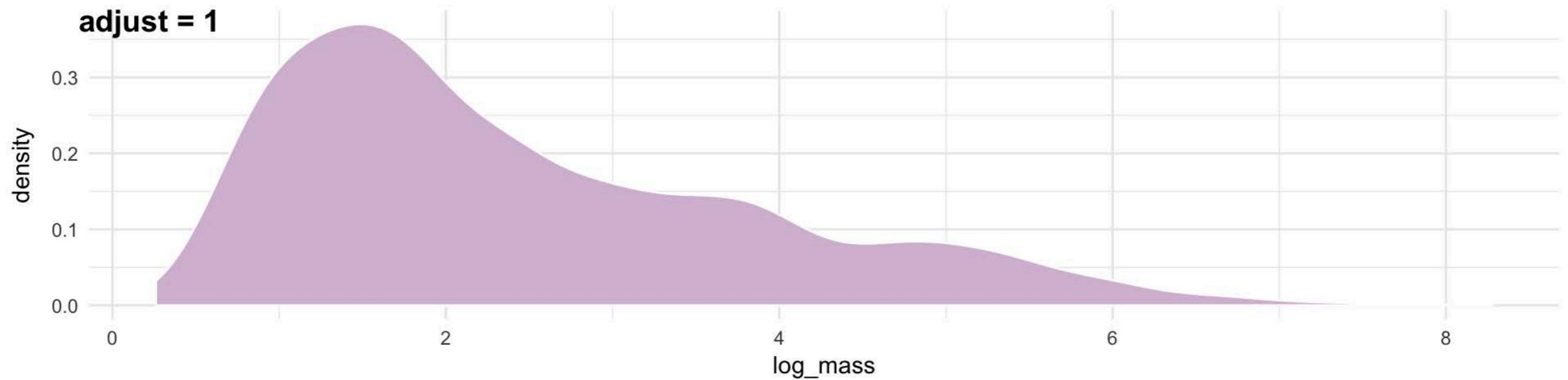


Multiplier for
the amount of
smoothing
(1 = default)

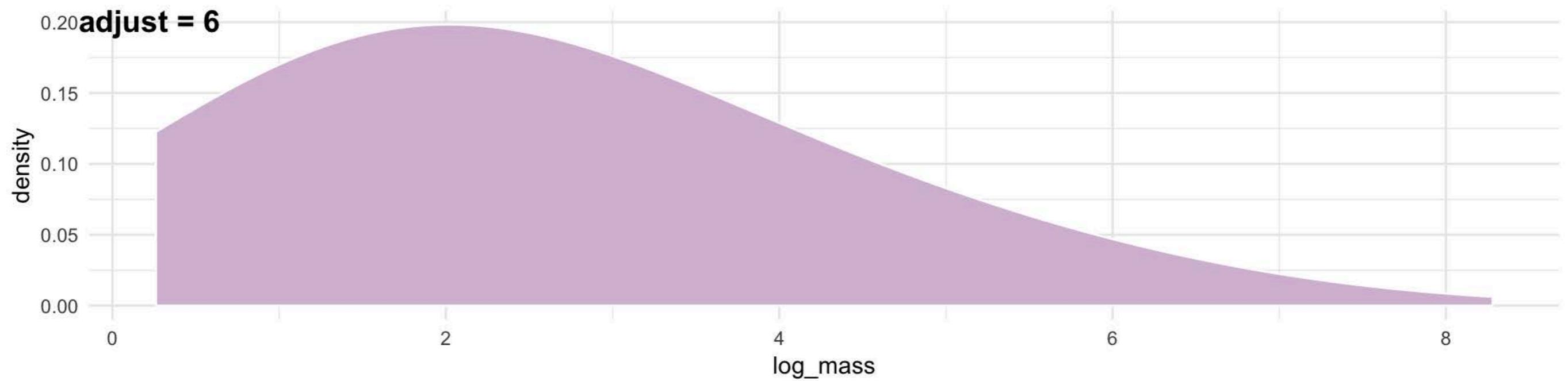
adjust = 0.1



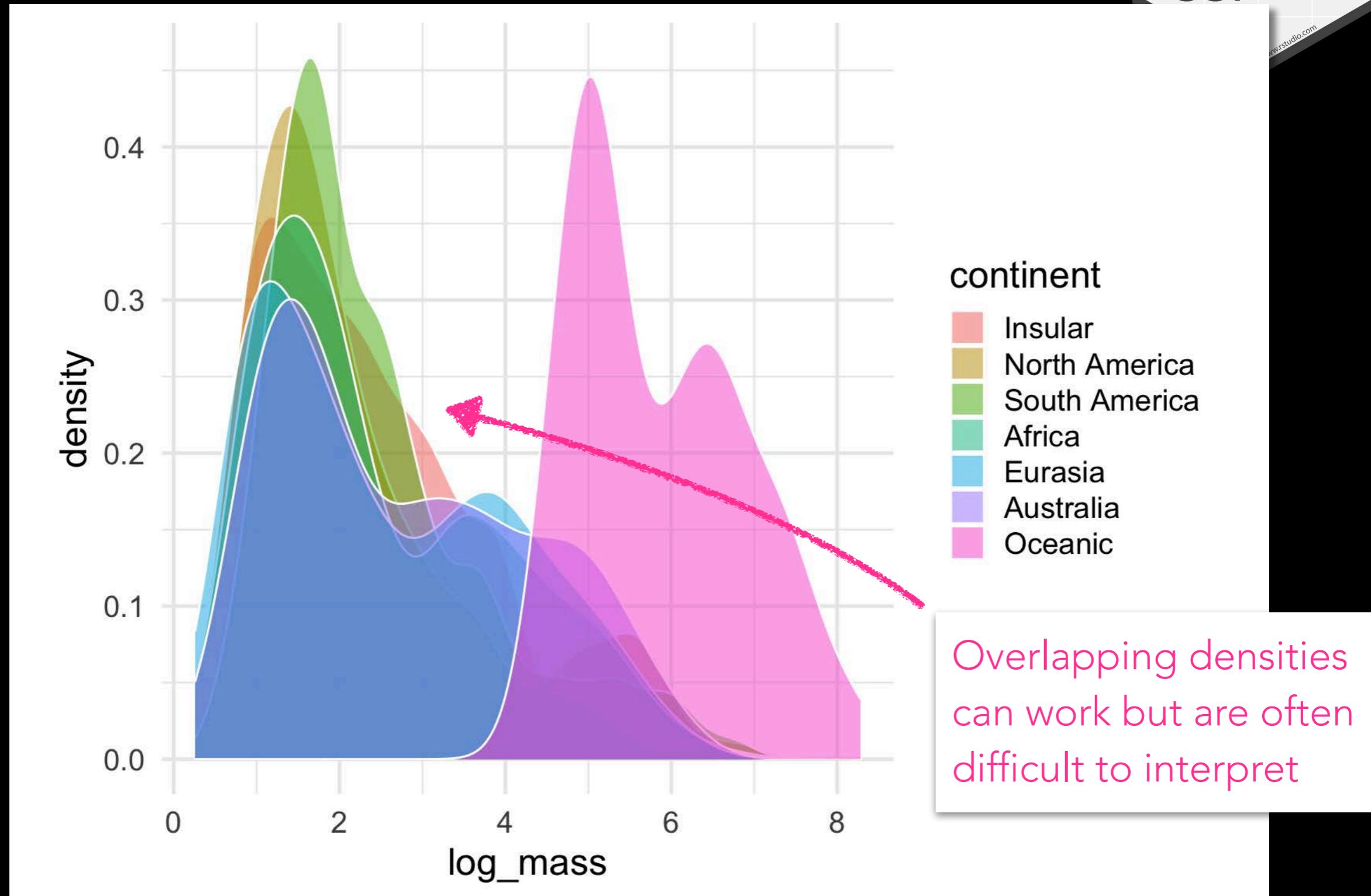
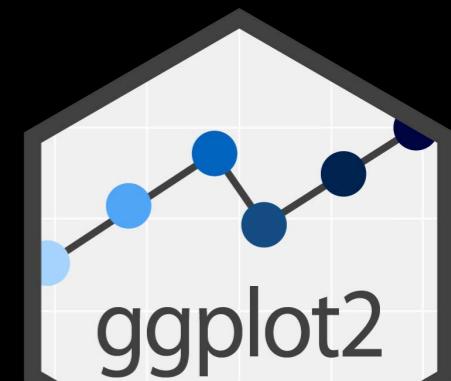
adjust = 1



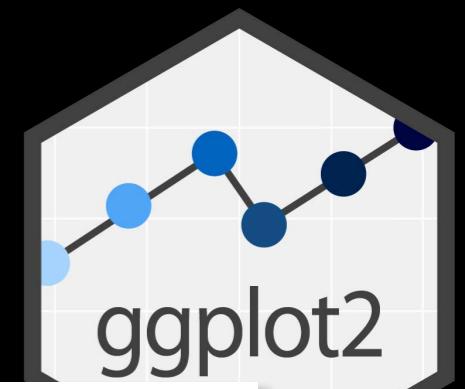
adjust = 6



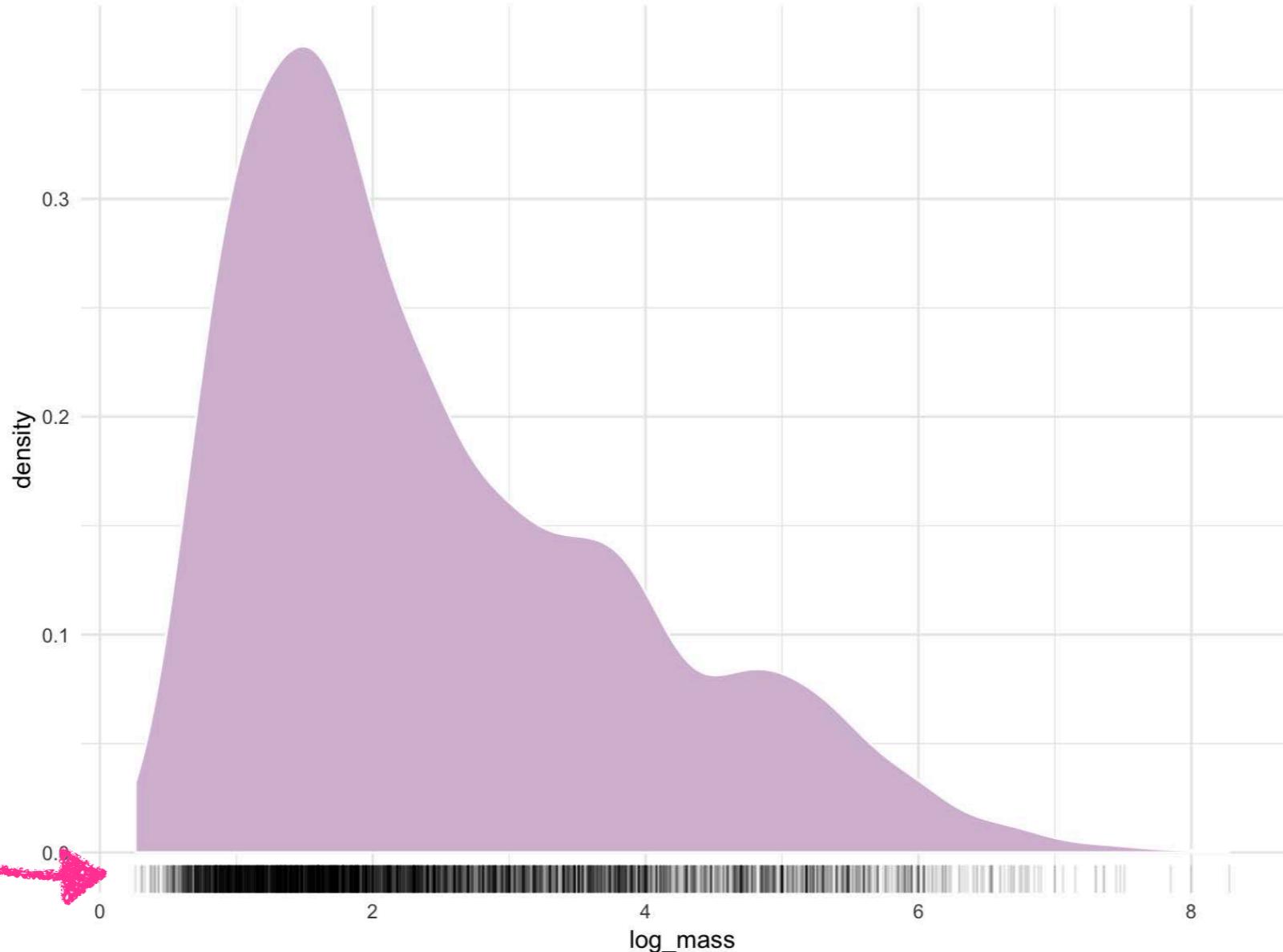
DENSITY PLOTS



DENSITY PLOTS

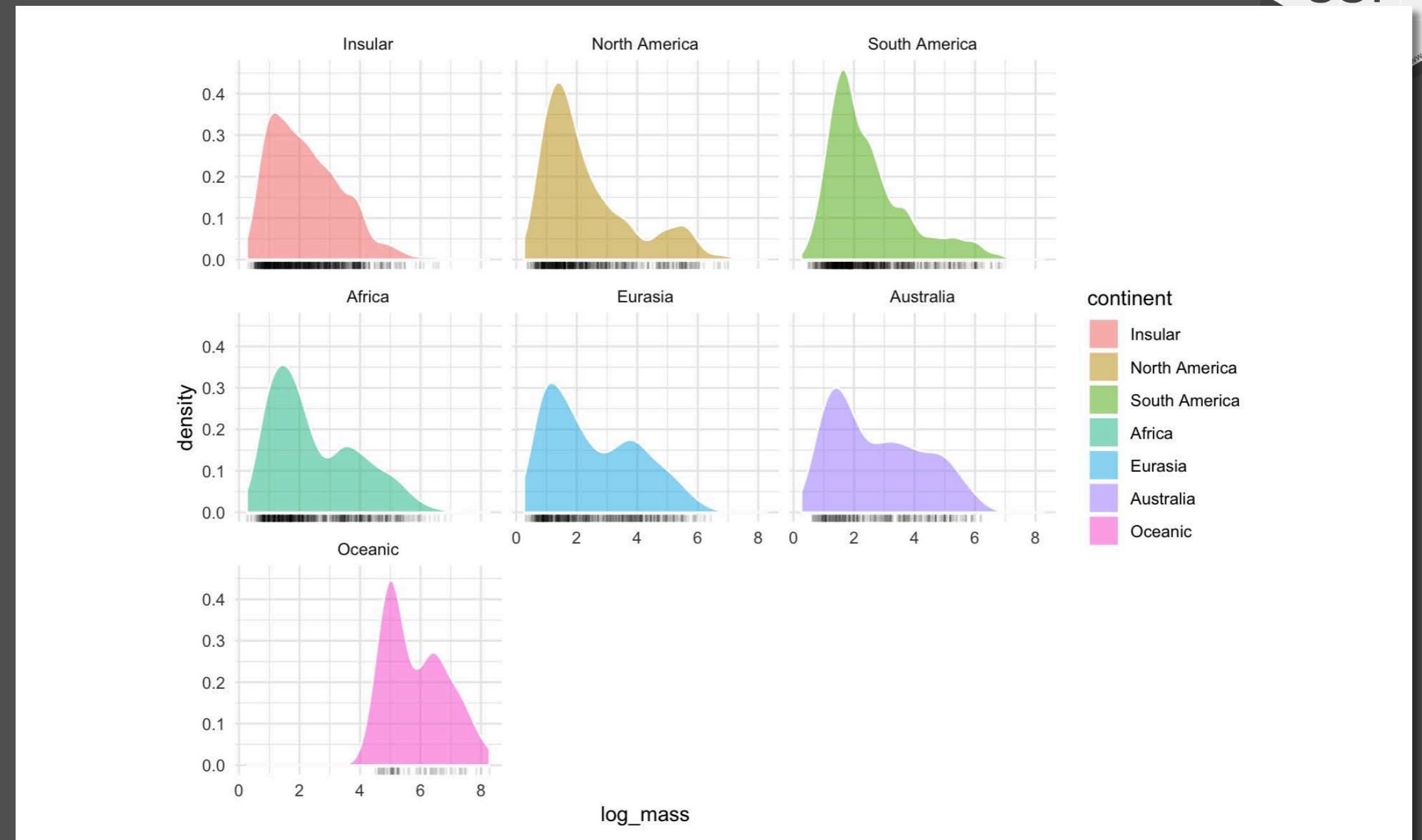
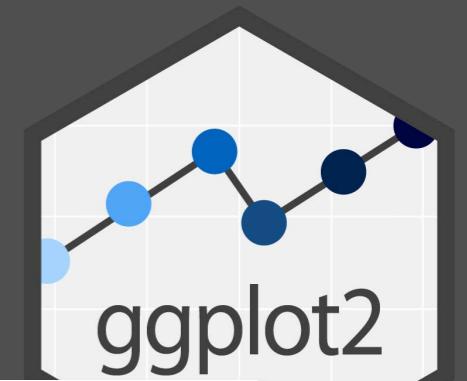


Rug plot shows data points as small marks along axis



```
ggplot(lqm, aes(x = log_mass)) +  
  geom_density(fill = "thistle", color = "white") +  
  geom_rug(alpha = 0.1)
```

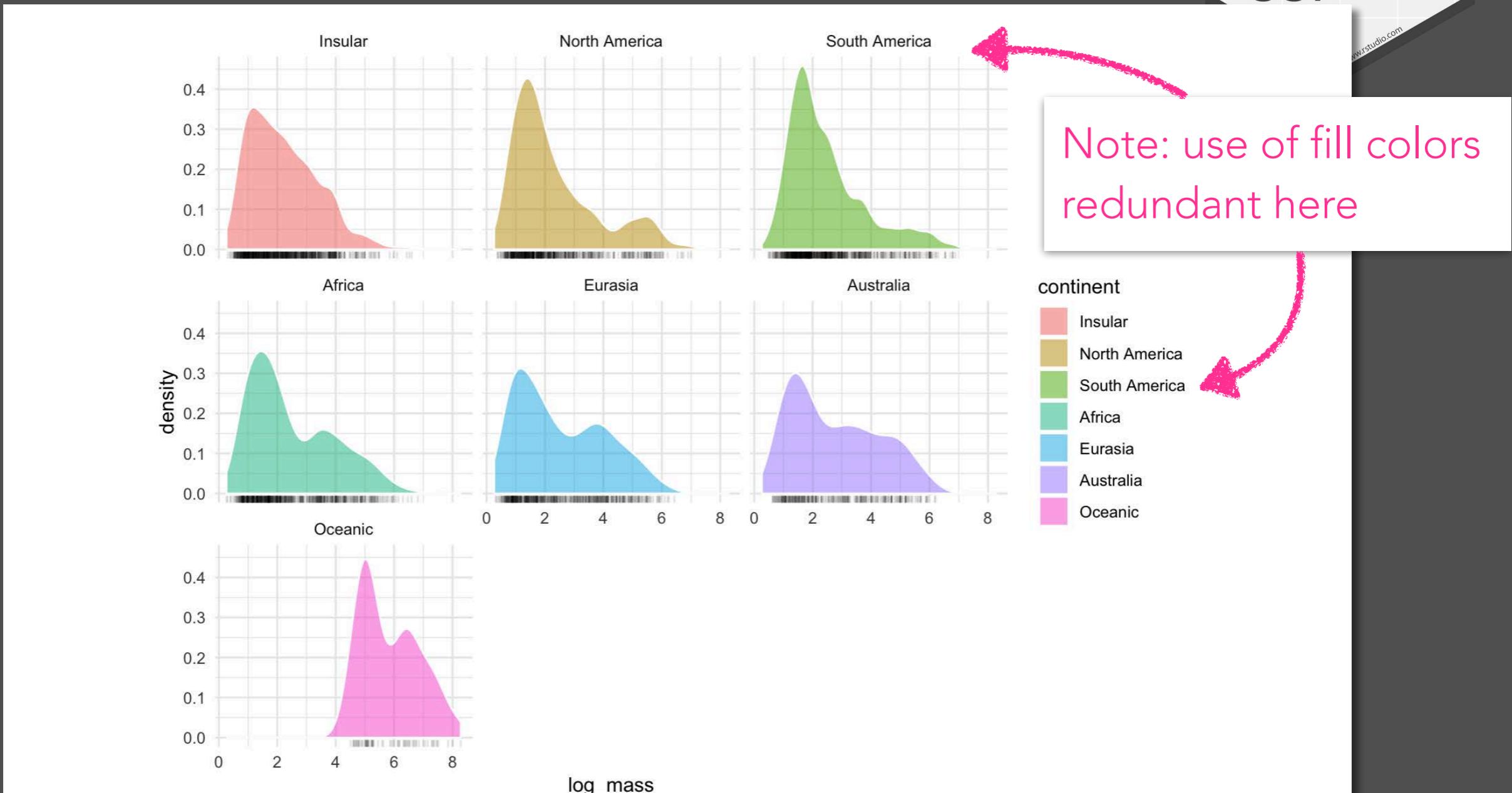
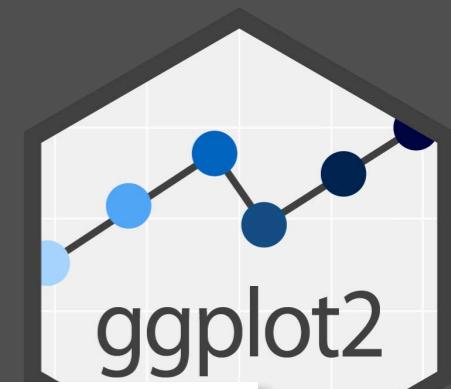
YOUR TURN



Try to reverse-engineer this plot.

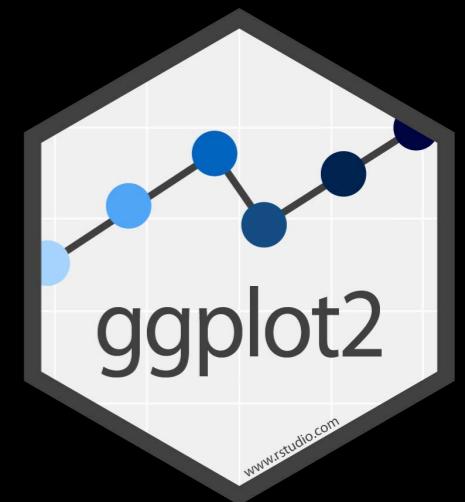


YOUR TURN



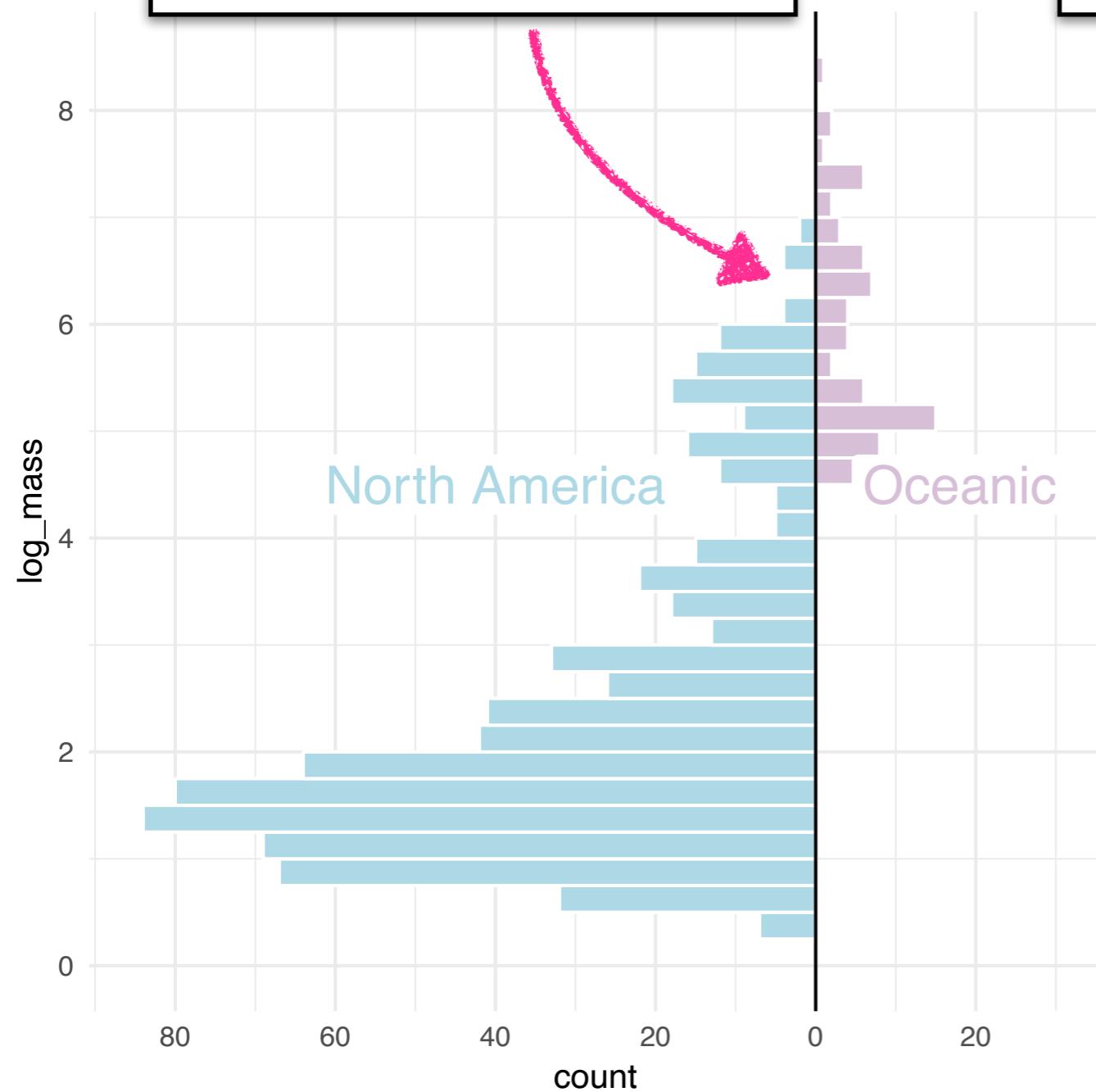
```
ggplot(lqm, aes(x = log_mass, fill = continent)) +  
  geom_density(color = NA, alpha = 0.5) +  
  geom_rug(alpha = 0.1) +  
  facet_wrap(vars(continent))
```

HISTOGRAMS VS. DENSITY PLOTS

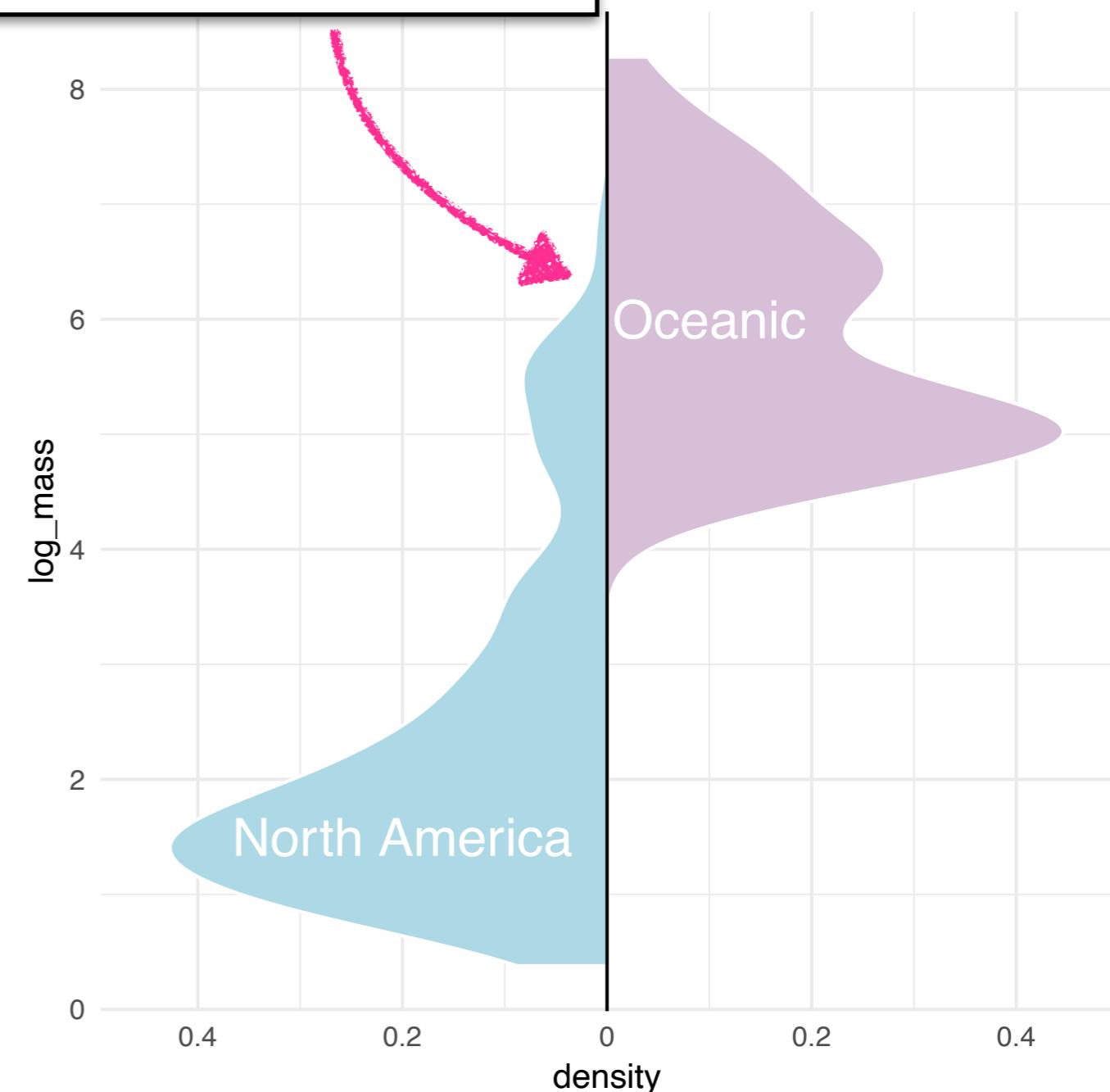


- Histograms are much more common, and are therefore more familiar to a wide audience
- Histograms use a more intuitive stat (count vs. density)
- Whereas the appearance of a histograms depends on sample size, densities are *scaled*

Smaller sample size for
“Oceanic” means bars
are small

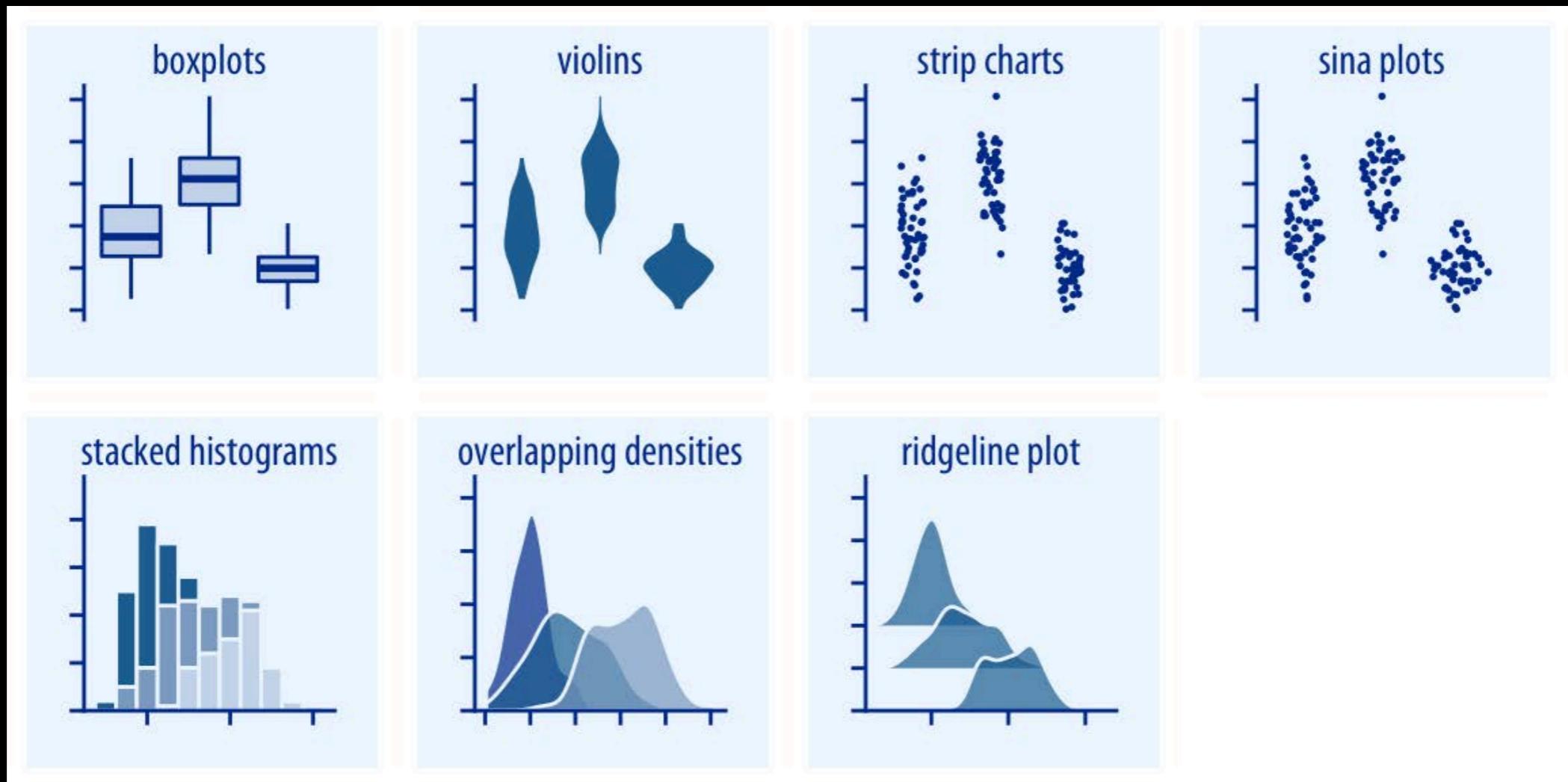


Densities have equal
areas (area under the
curve sums to 1)

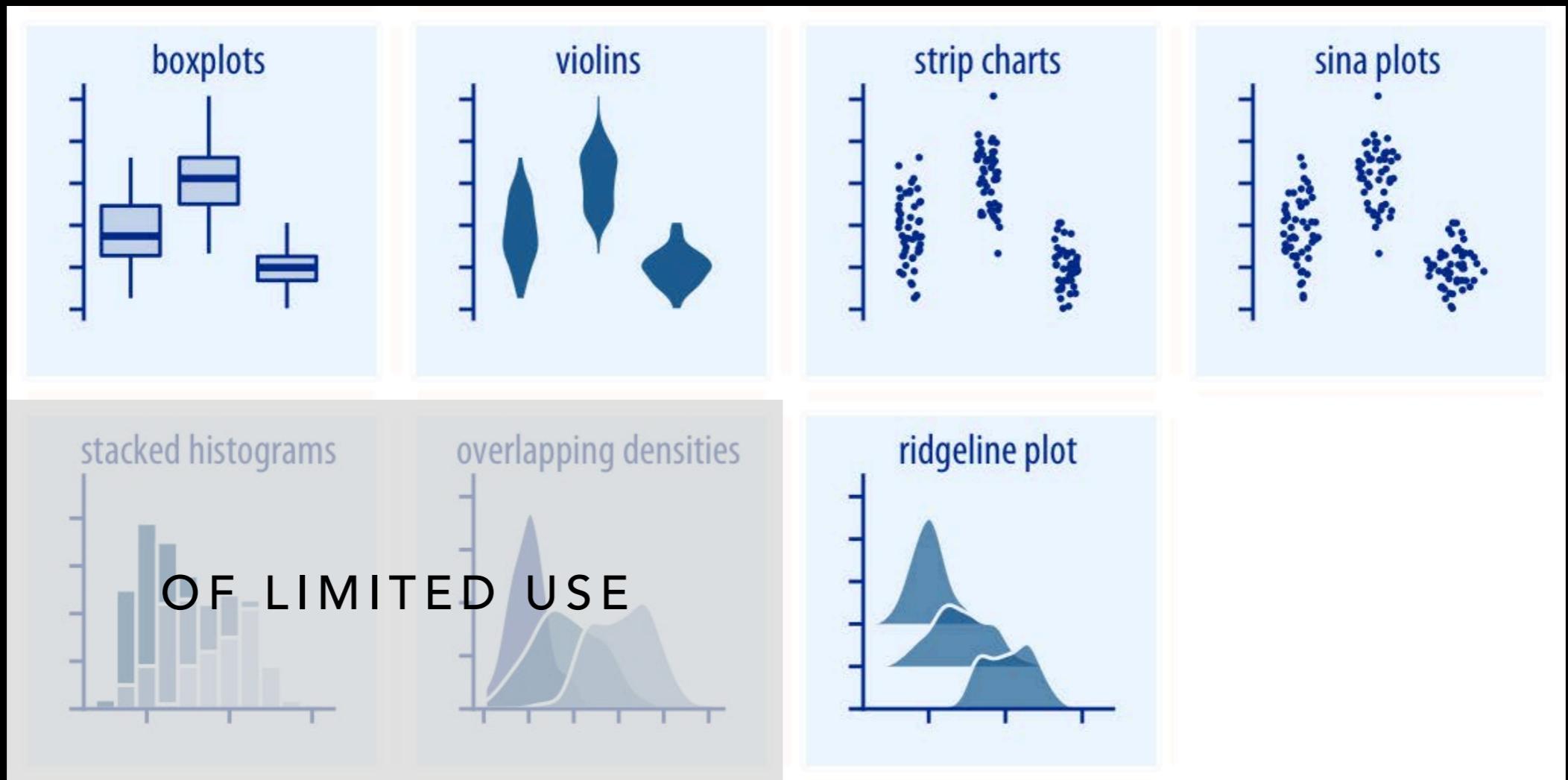


WHAT IF YOU NEED TO SHOW
MULTIPLE DISTRIBUTIONS TOGETHER?

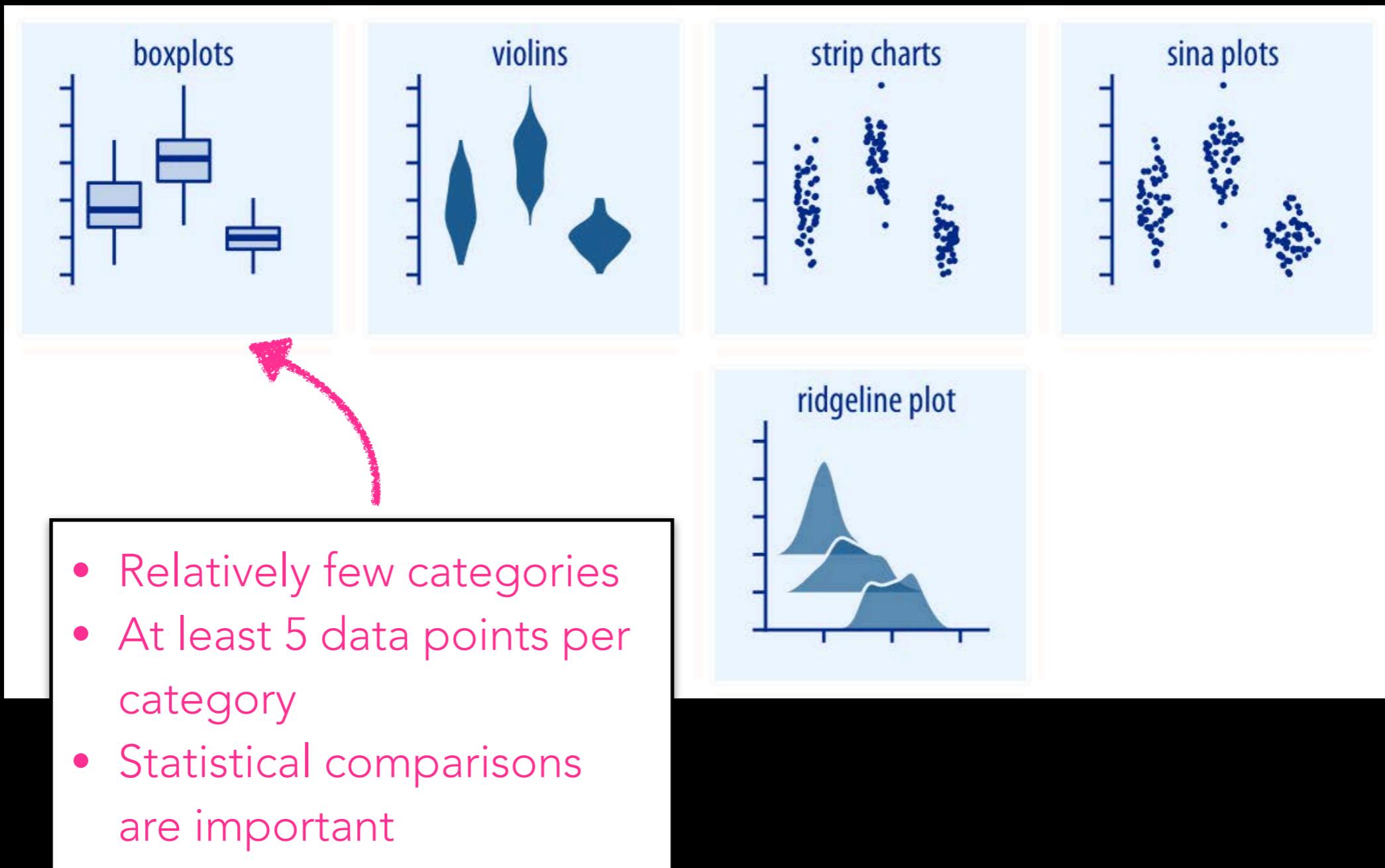
WHAT IF YOU NEED TO SHOW MULTIPLE DISTRIBUTIONS TOGETHER?



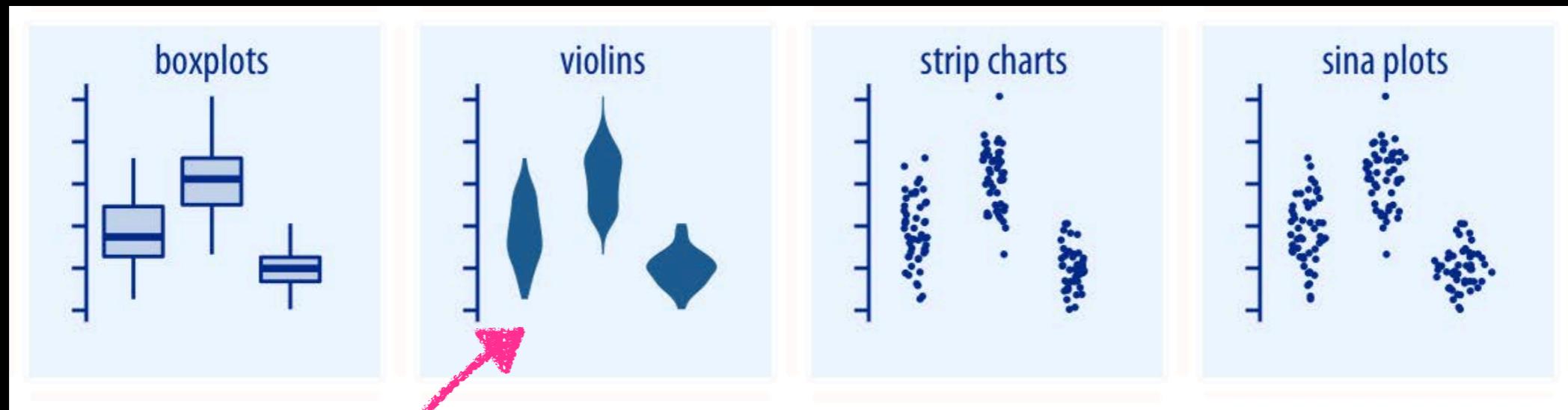
WHAT IF YOU NEED TO SHOW MULTIPLE DISTRIBUTIONS TOGETHER?



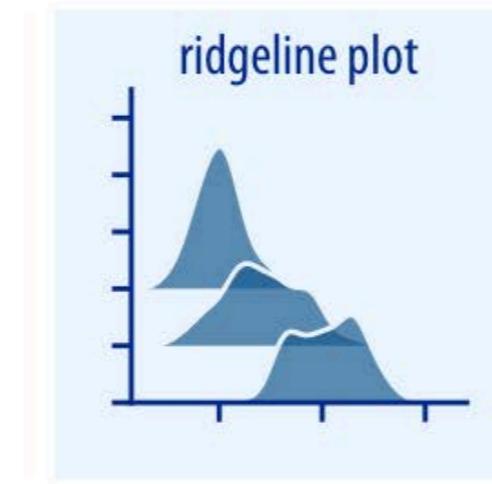
USAGE GUIDELINES



USAGE GUIDELINES



- Relatively few categories
- At least 5 data points per category
- You want a more nuanced comparison of the *shapes* of the distributions rather than statistical values



USAGE GUIDELINES

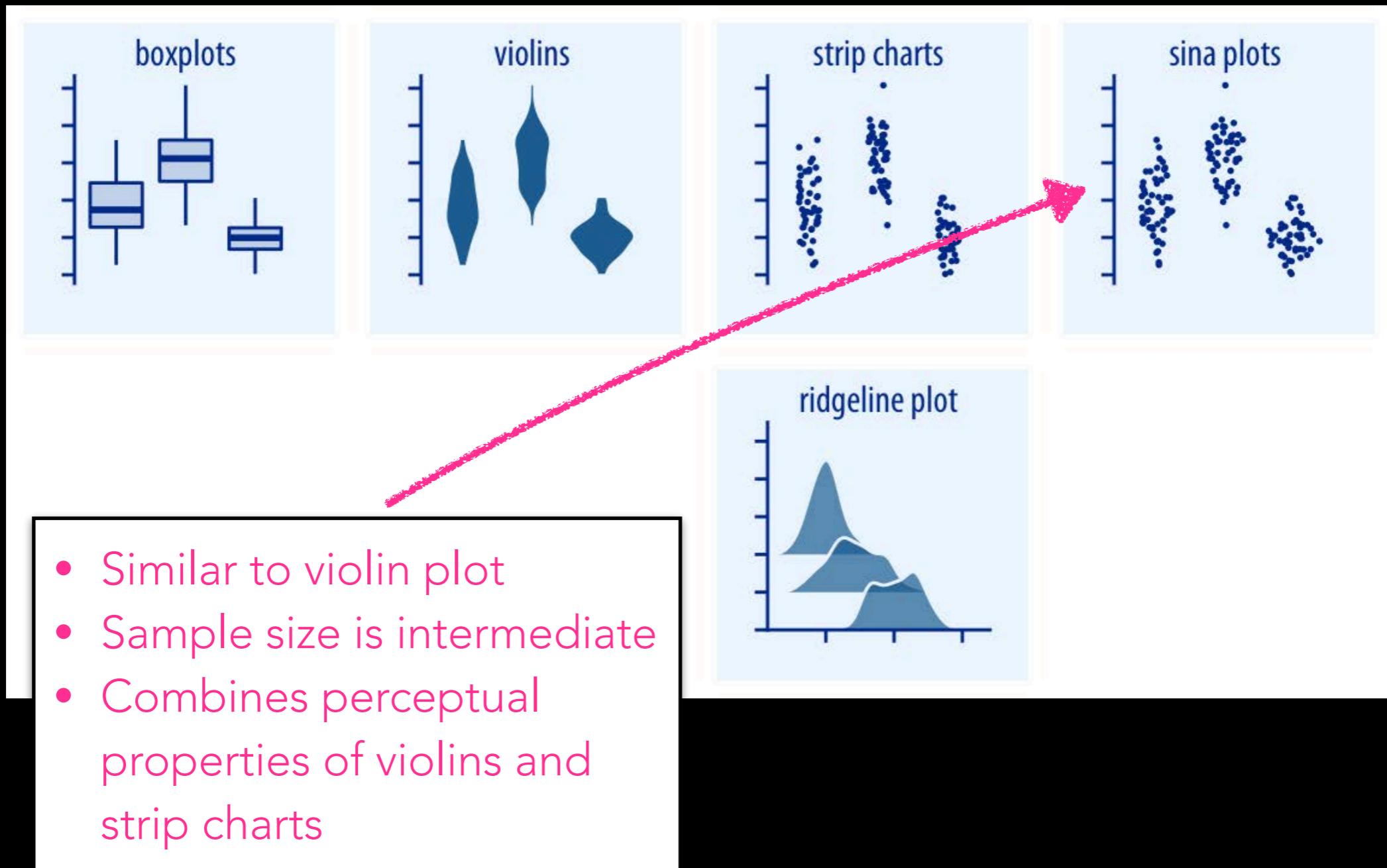
The figure displays five types of data visualizations:

- boxplots**: Shows four boxplots with varying median positions and whisker lengths.
- violins**: Shows three violins representing density distributions.
- strip charts**: Shows three vertical clusters of individual data points.
- sina plots**: Shows three vertical clusters of individual data points.
- ridgeline plot**: Shows multiple overlapping density ridges across a horizontal axis.

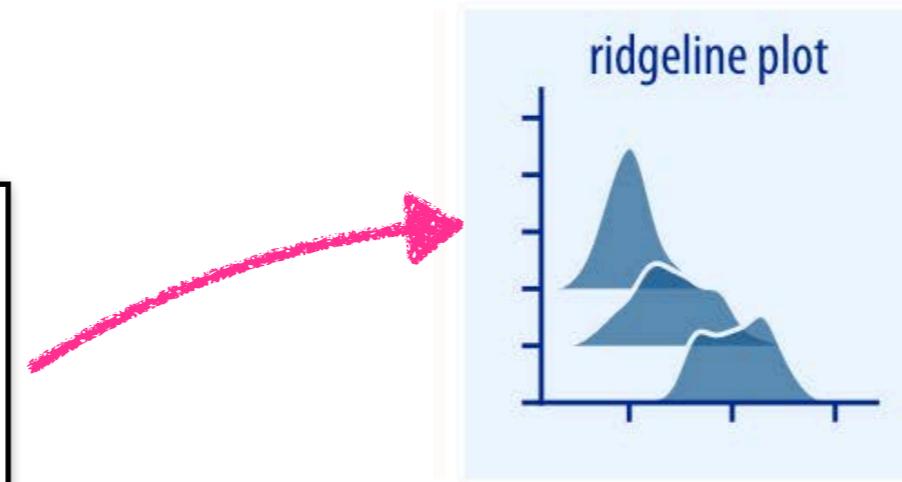
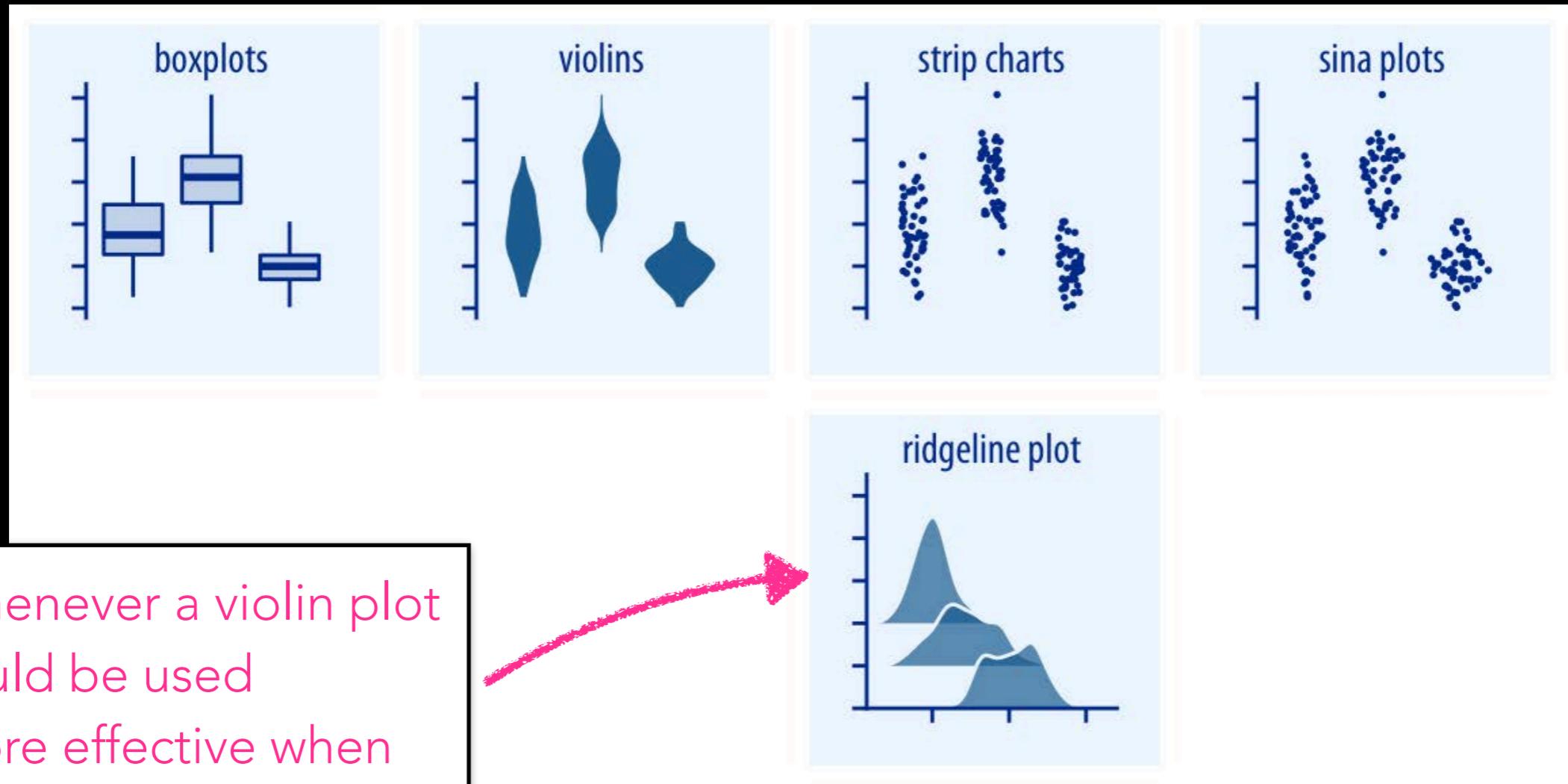
A red arrow points from the "strip charts" panel to a callout box containing the following guidelines:

- You need to show raw data for any reason
- You have fewer than 5 data points in some categories

USAGE GUIDELINES



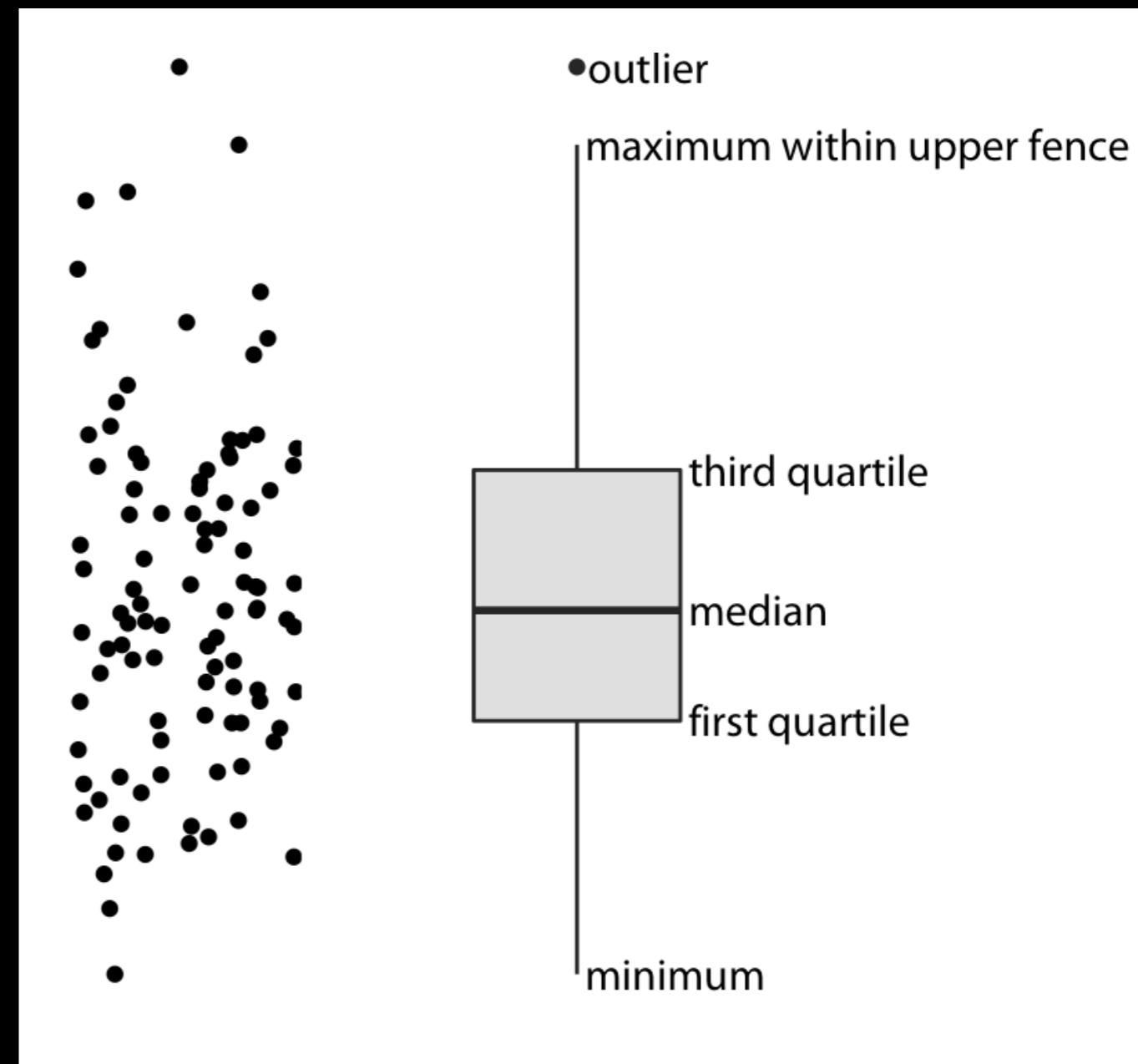
USAGE GUIDELINES



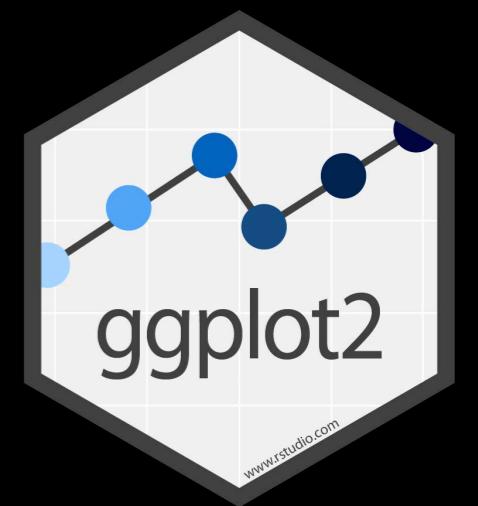
BOXPLOTS

BOXPLOTS

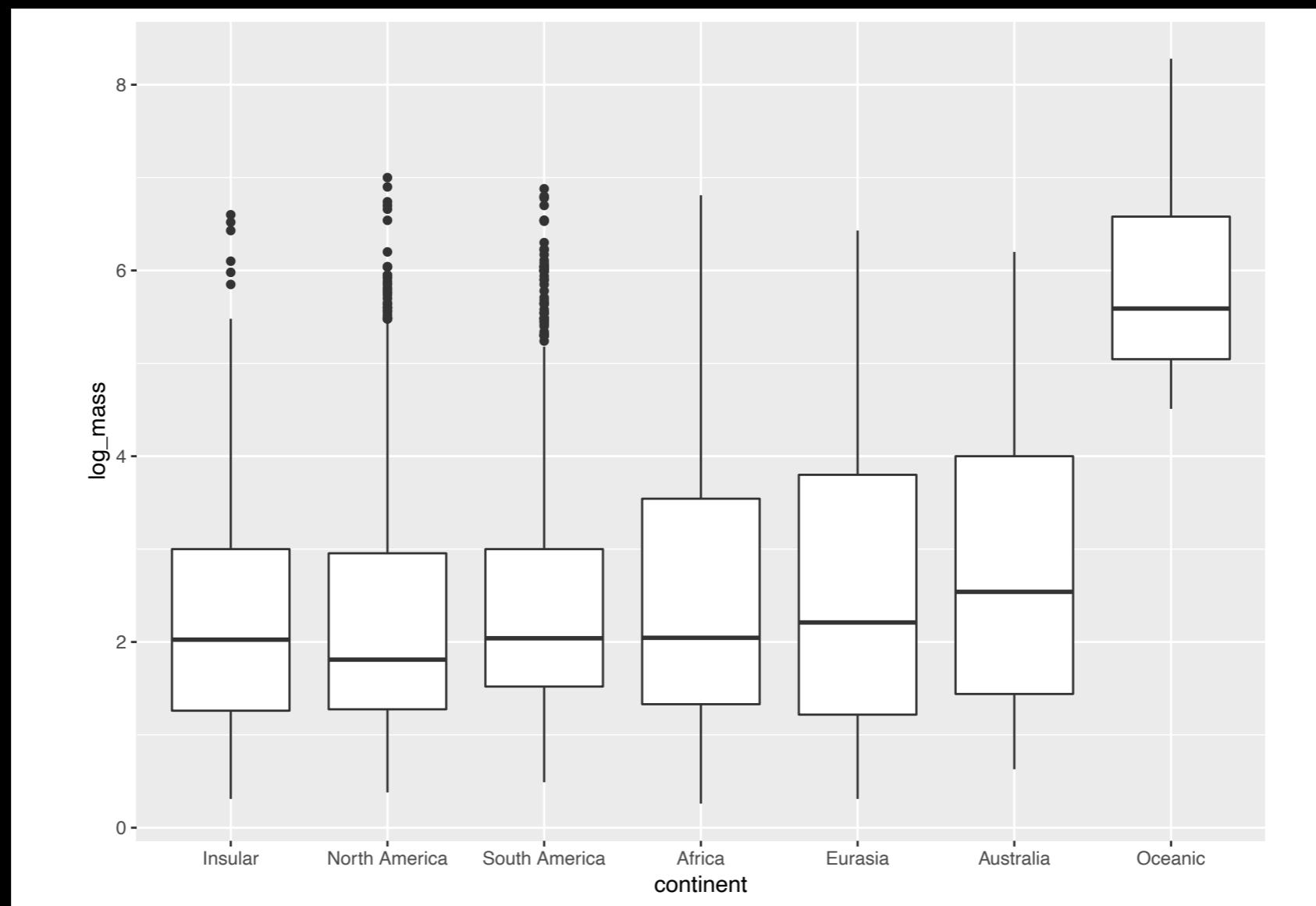
- Each box plot shows a **standardized set** of 5 statistical summaries of the distribution, as well as individual outliers
- Very common in scientific lit
- But beware of using with lay audience (e.g., “what does the line sticking out of the top show exactly?”)



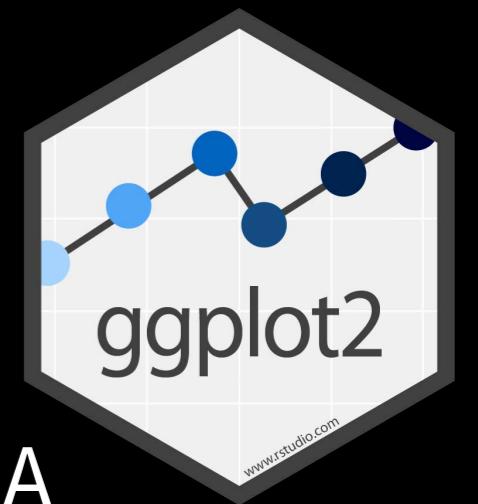
BOXPLOTS



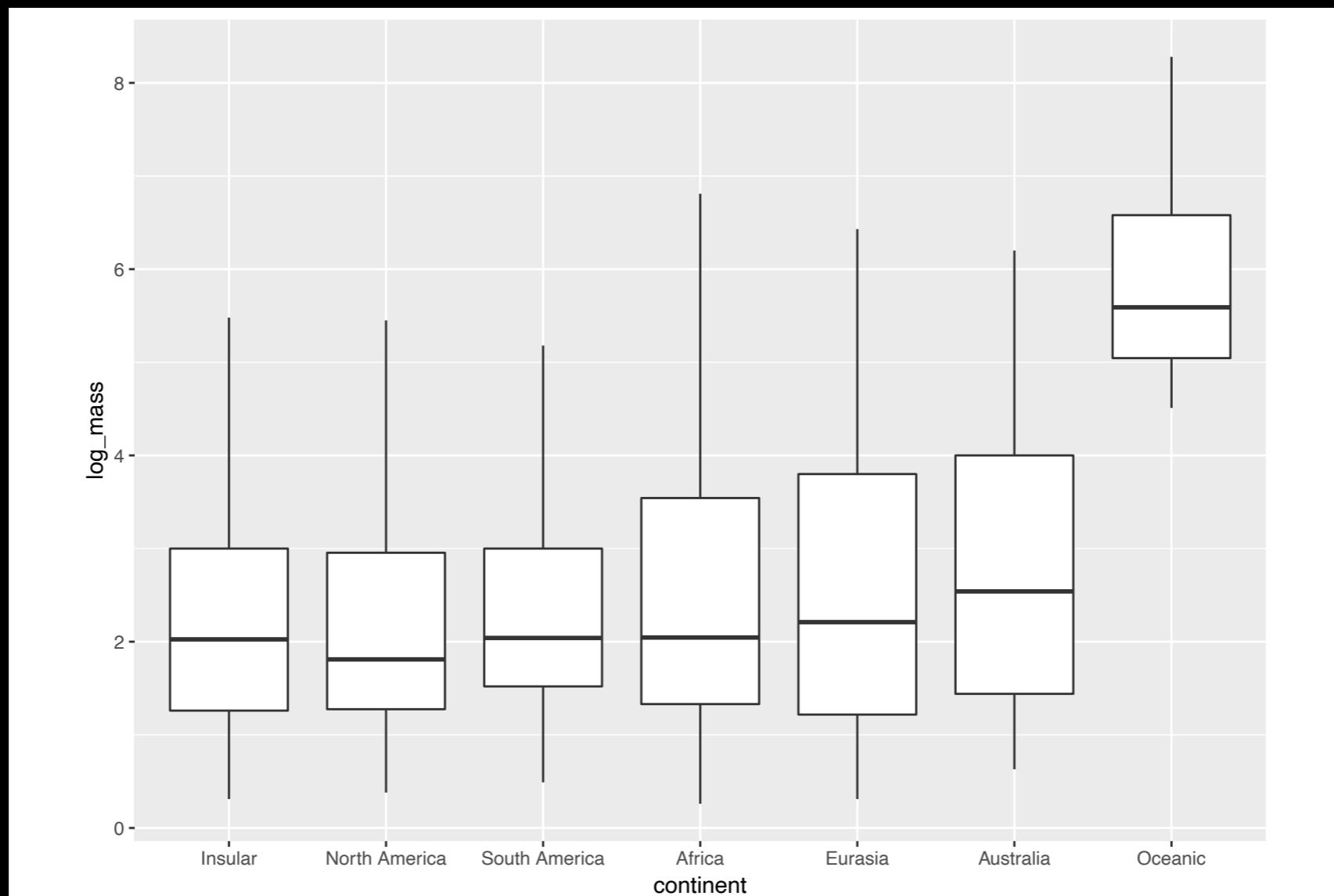
- Geometric object is `geom_boxplot()`
- Categorical variable to mapped to x, and numeric variable mapped to y



BOXPLOTS



- Suppress outliers with `outlier.shape = NA`

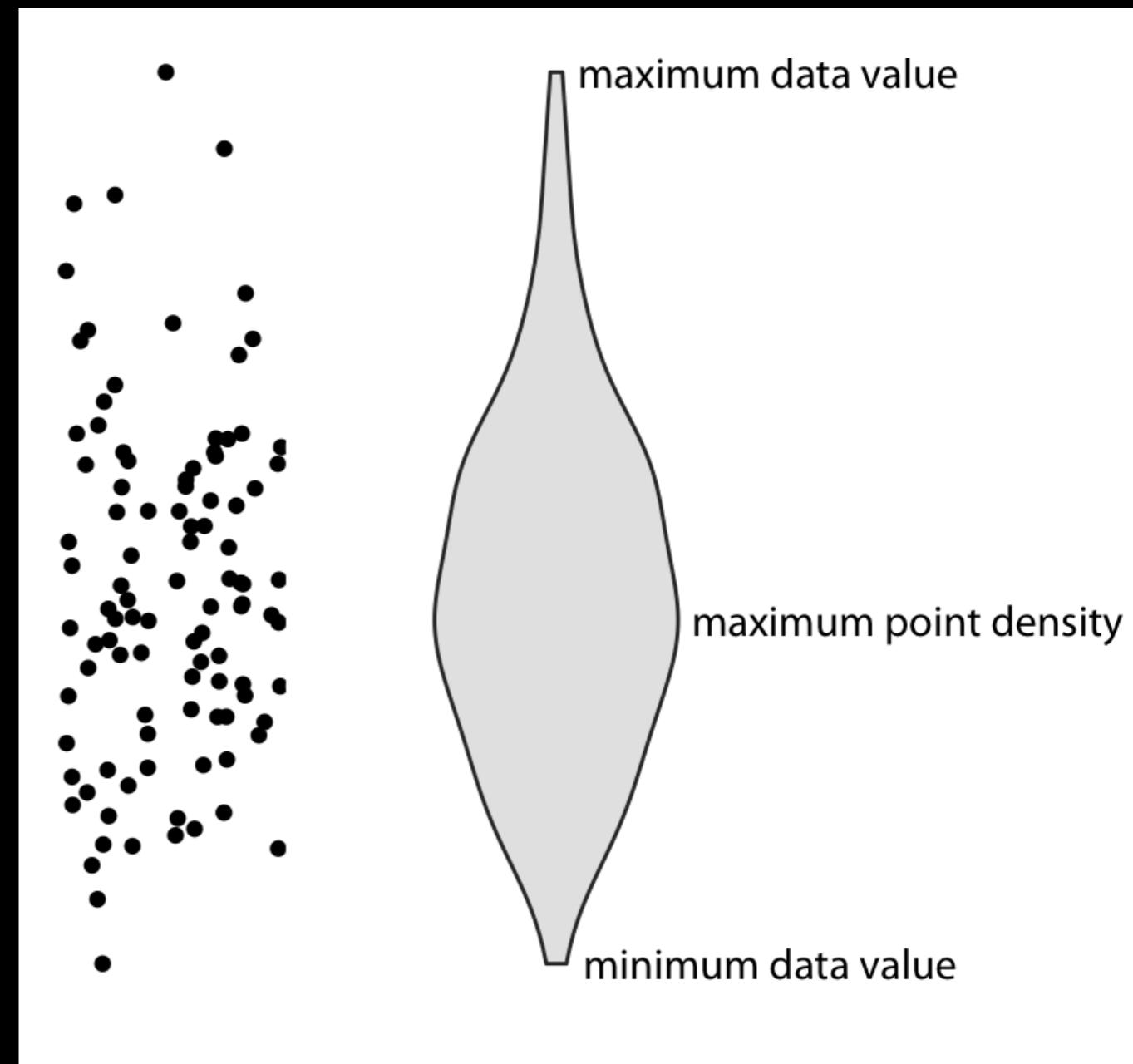


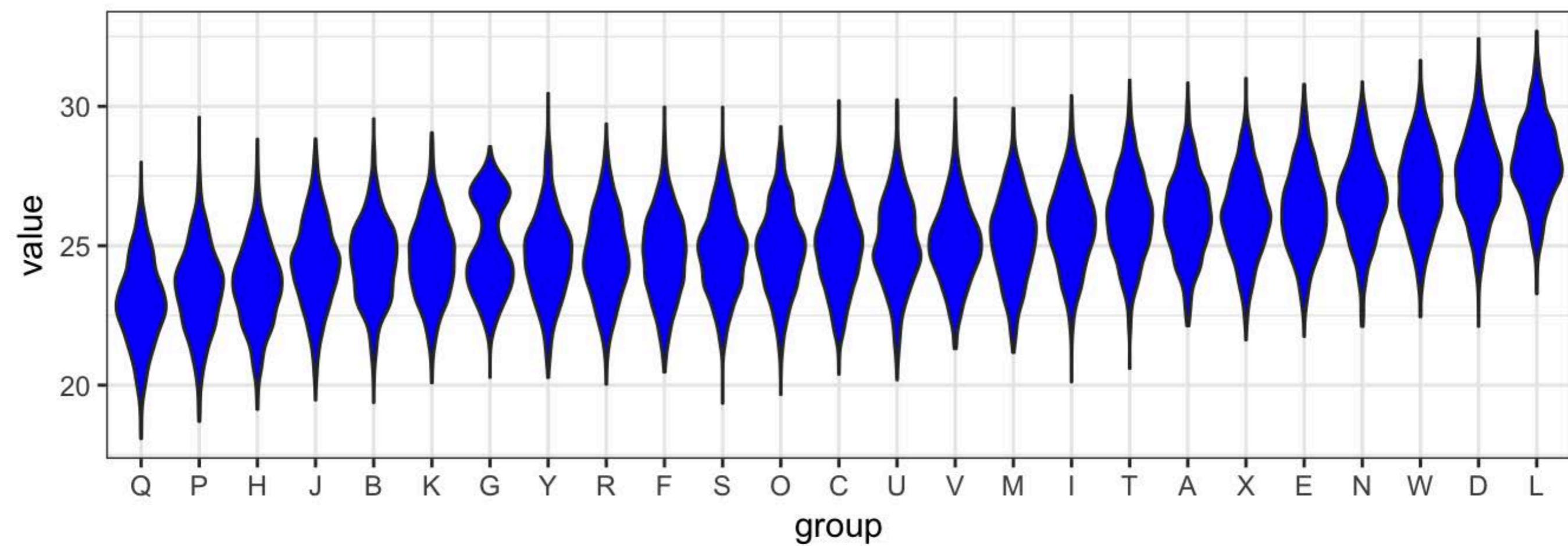
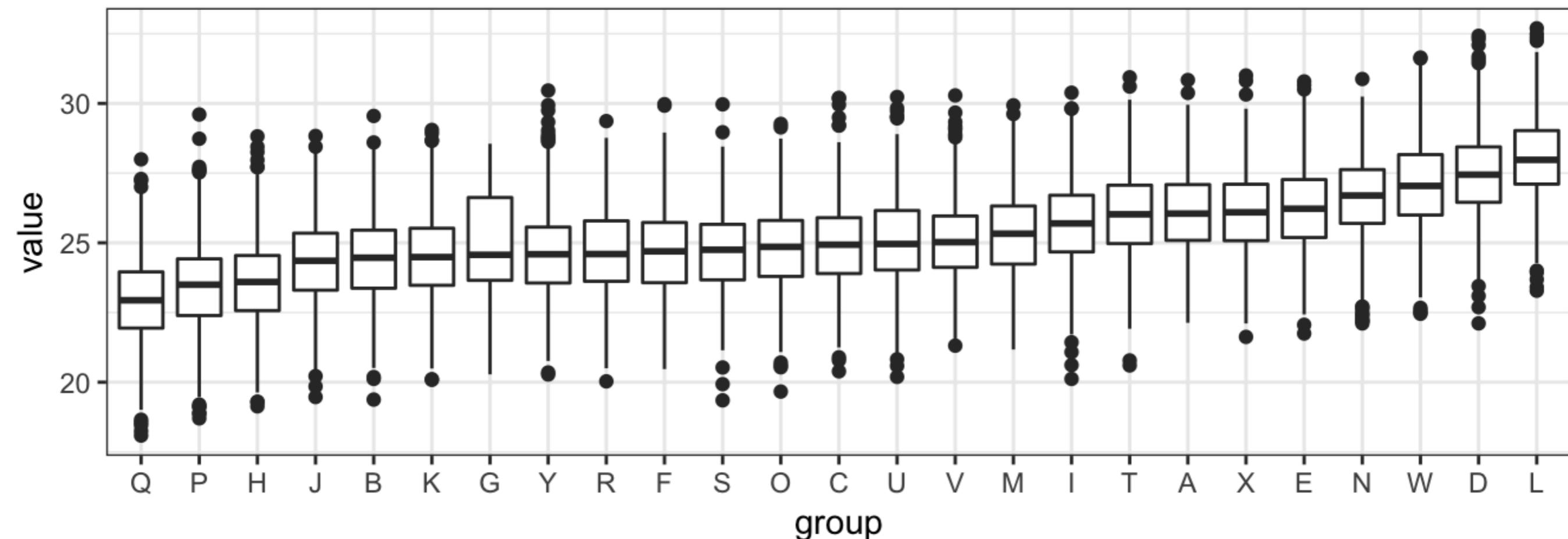
```
ggplot(lqm, aes(x = continent, y = log_mass)) +  
  geom_boxplot(outlier.shape = NA)
```

VIOLIN PLOTS

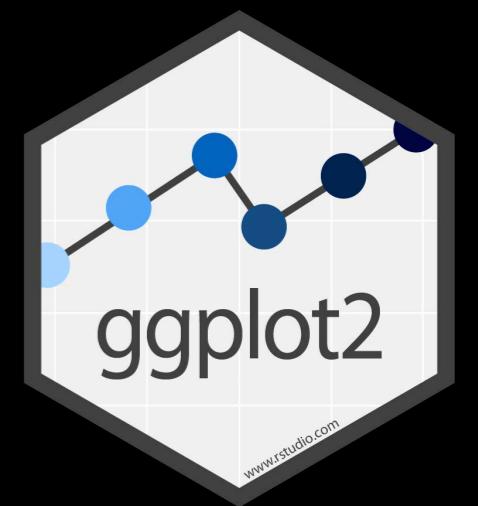
VIOLIN PLOTS

- Each violin is essentially a density plot rotated vertically and mirrored across the vertical
- Less standardized and precise, but also easier to intuit
- Better at showing multi-modal distributions

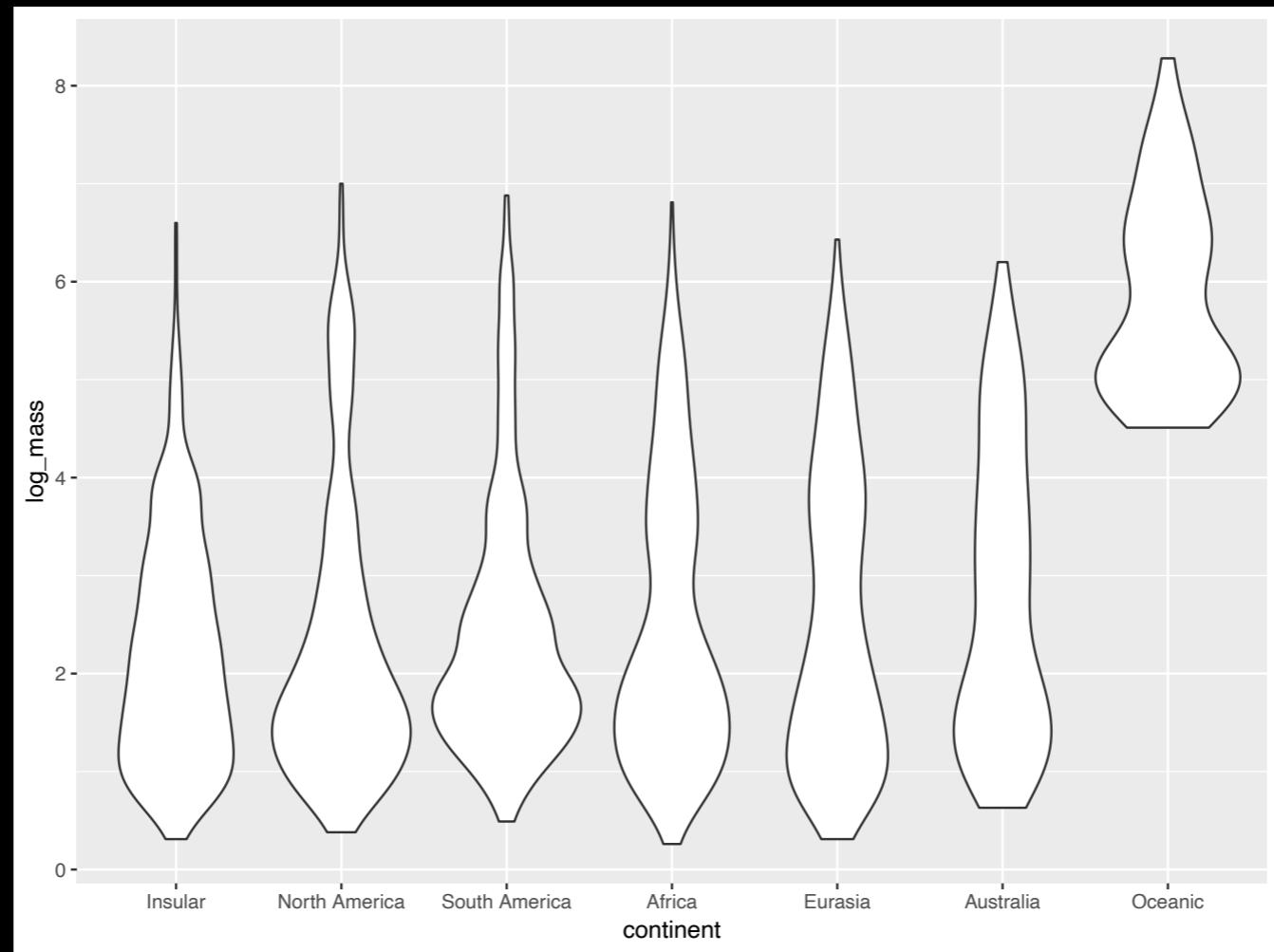




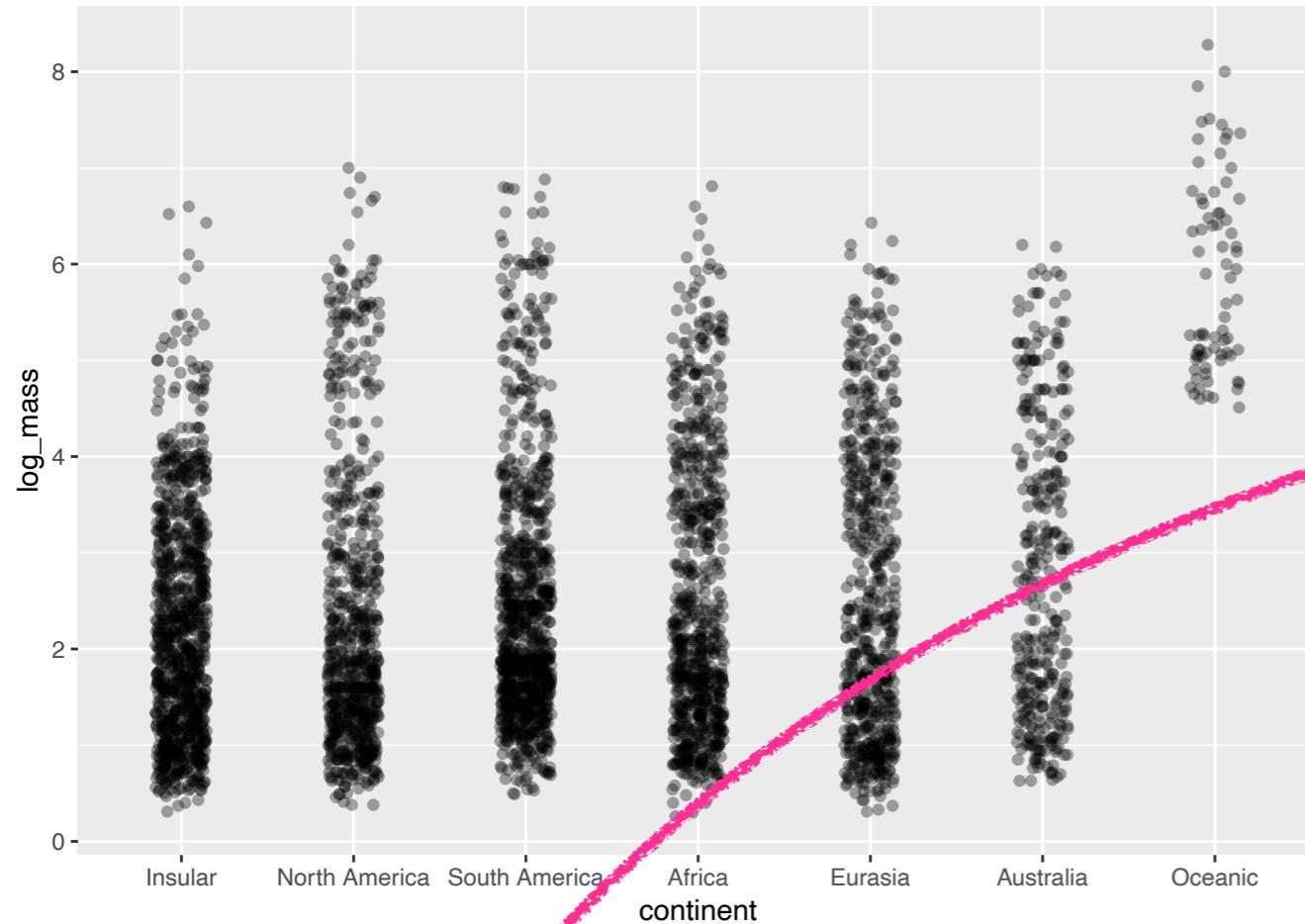
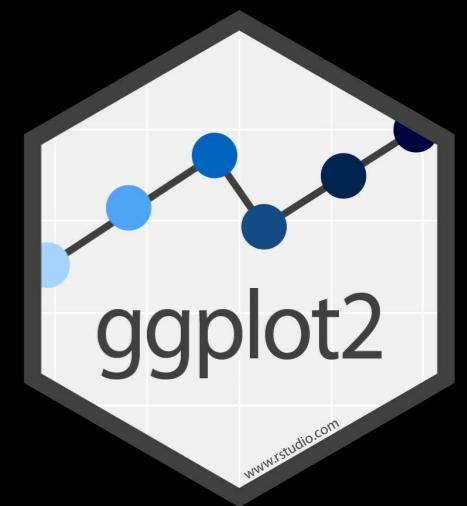
VIOLIN PLOTS



- Geometric object is `geom_violin()`
- Mappings same as boxplot



STRIP PLOTS

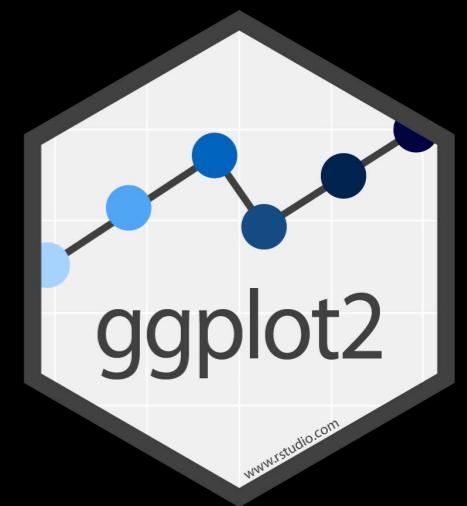


geom_jitter()
makes randomly
displaced points

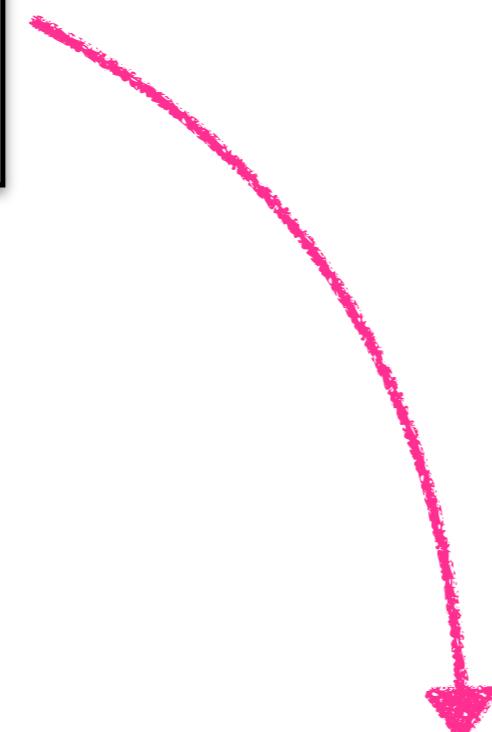
height and width
parameters control
amount of jitter

```
ggplot(lqm, aes(x = continent, y = log_mass)) +  
  geom_jitter(width = 0.15, height = 0, alpha = 0.35)
```

SINA PLOTS

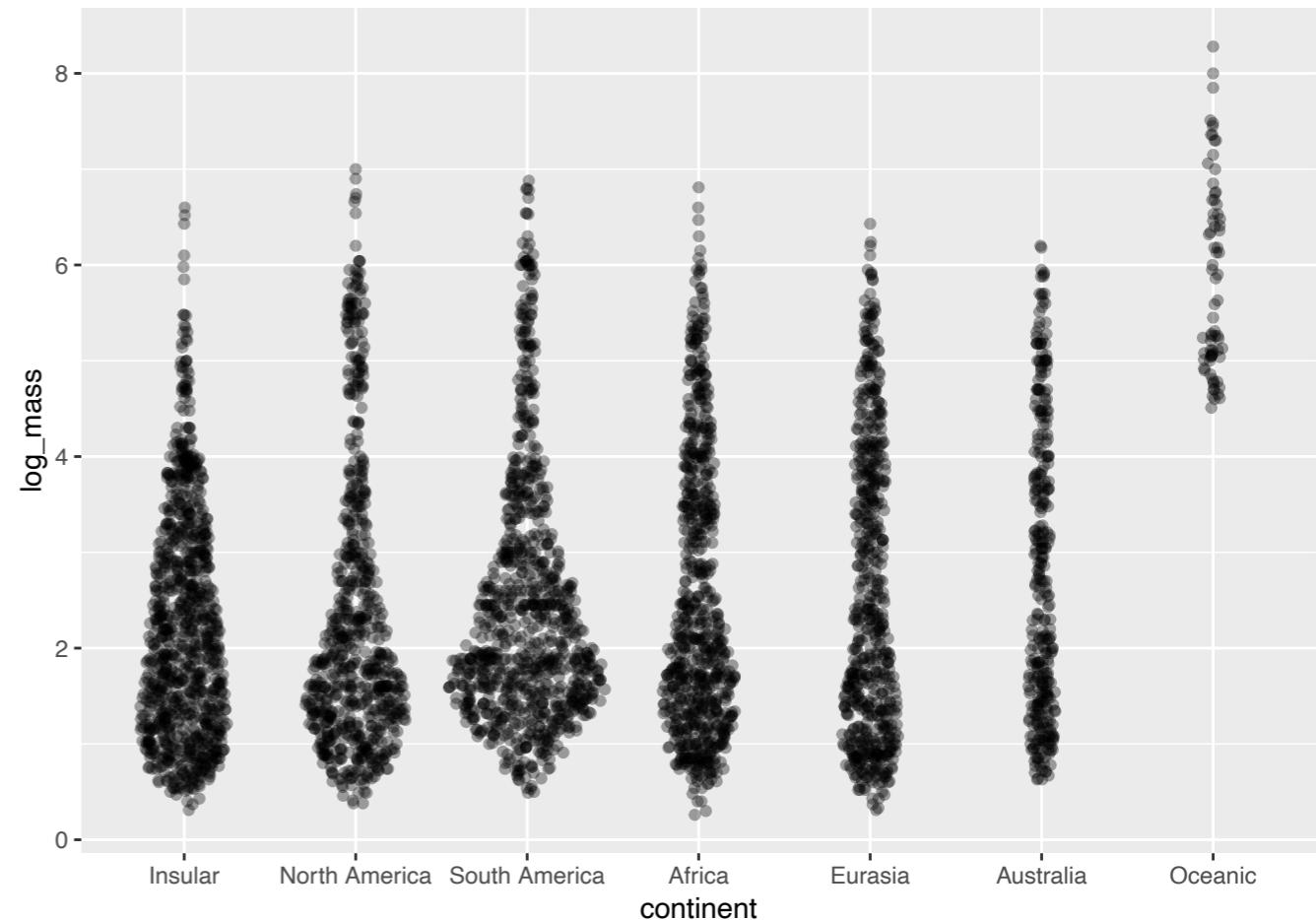


Not a default geom!
Provided by the
“ggforce” package.



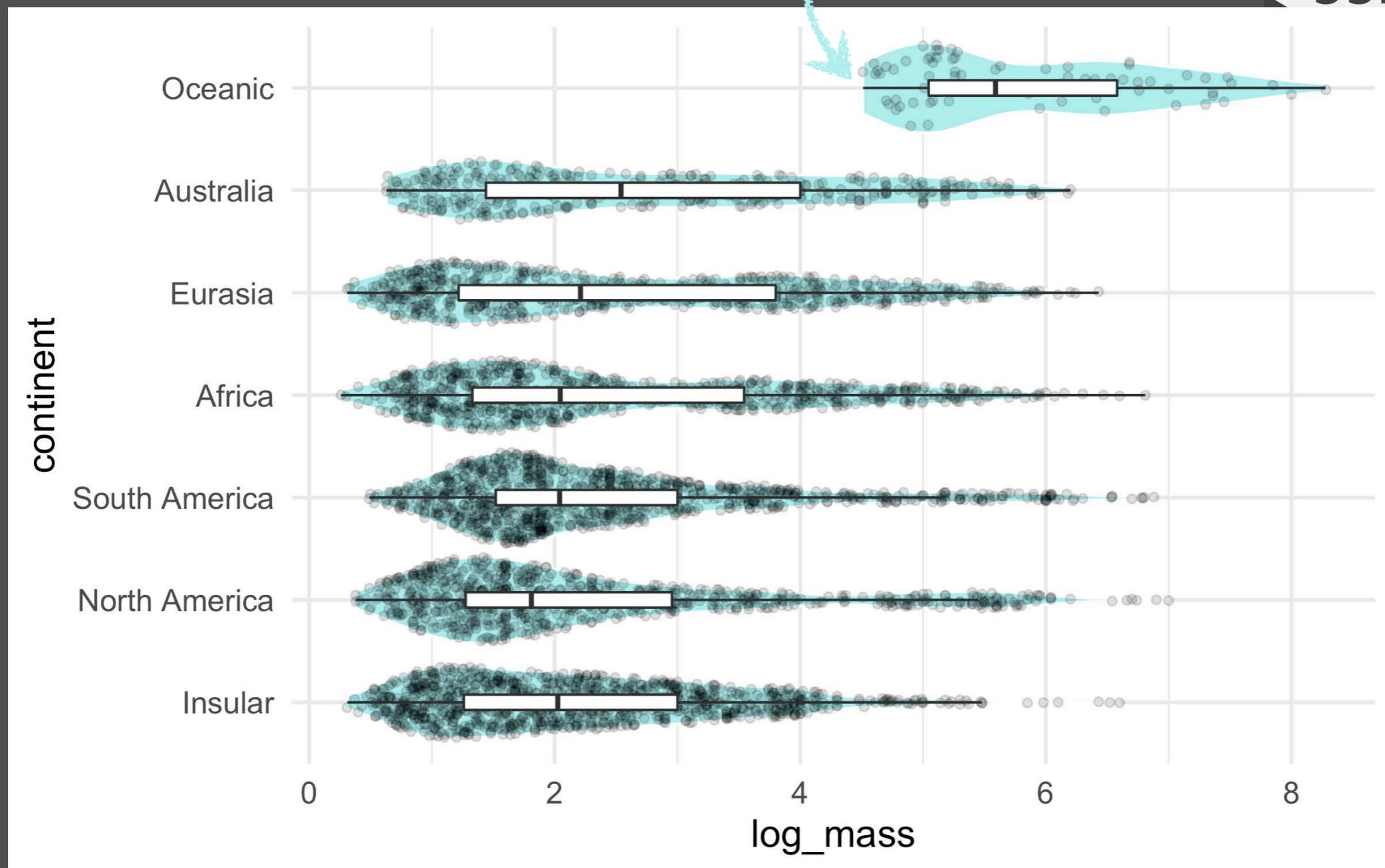
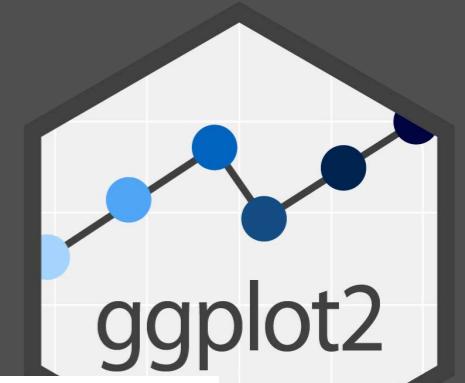
library("ggforce")

```
ggplot(lqm, aes(x = continent, y = log_mass)) +  
  geom_sina(alpha = 0.15)
```



YOUR TURN

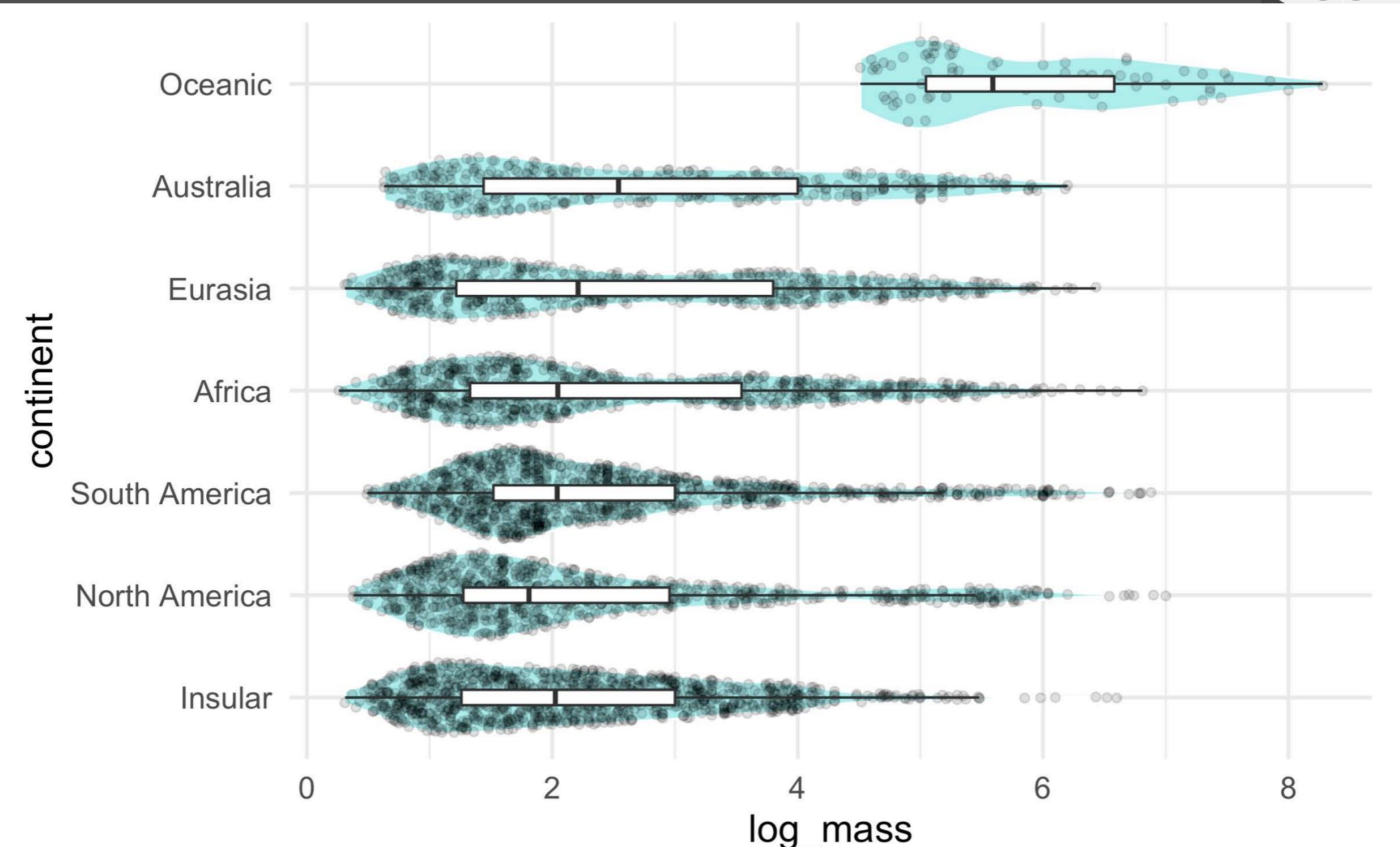
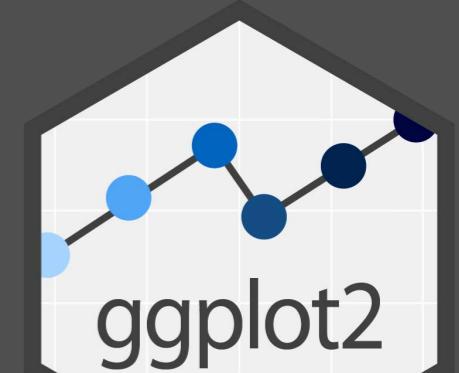
fill is "paleturquoise"



Try to reverse-engineer this (rather busy) plot.



YOUR TURN

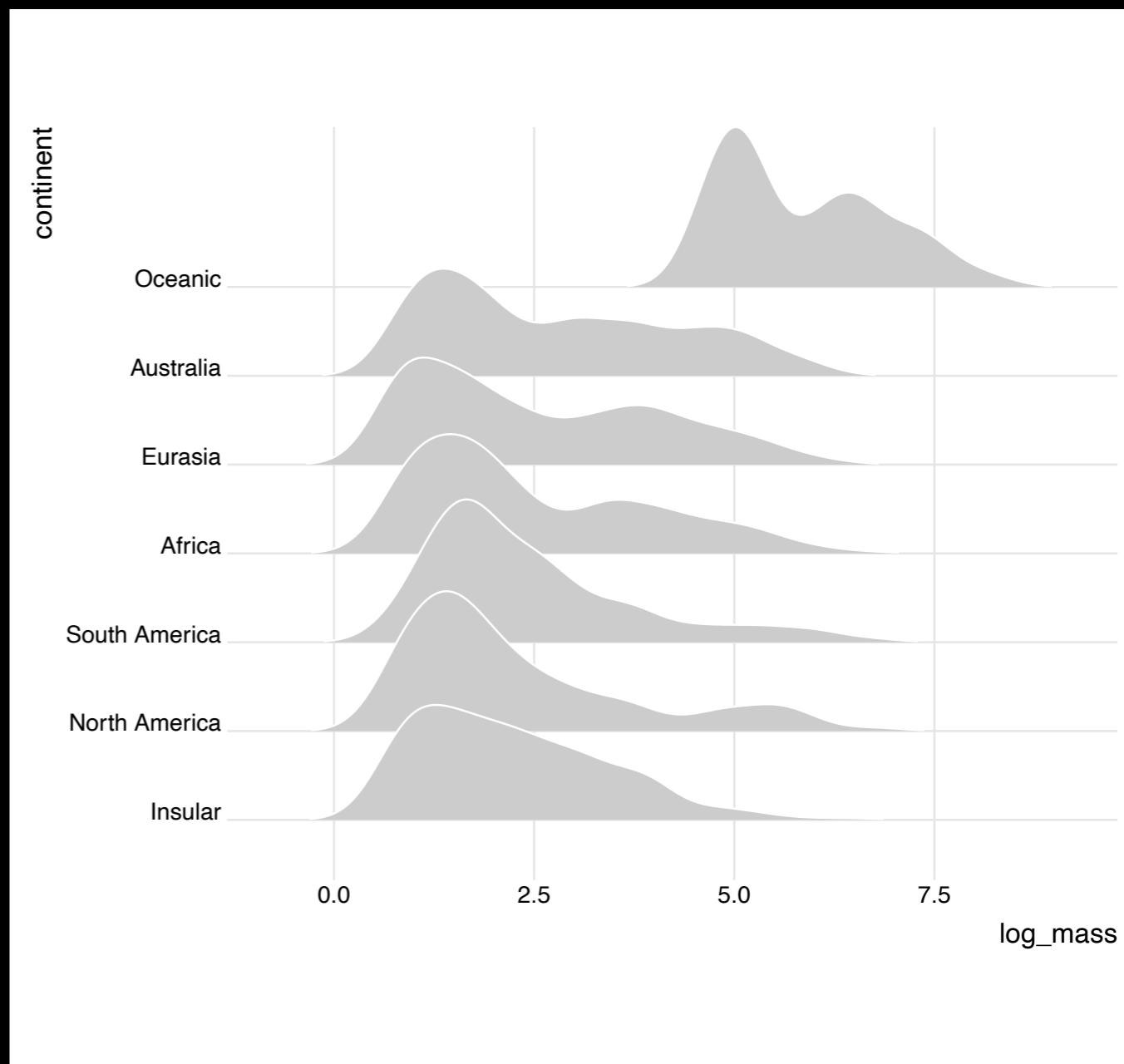


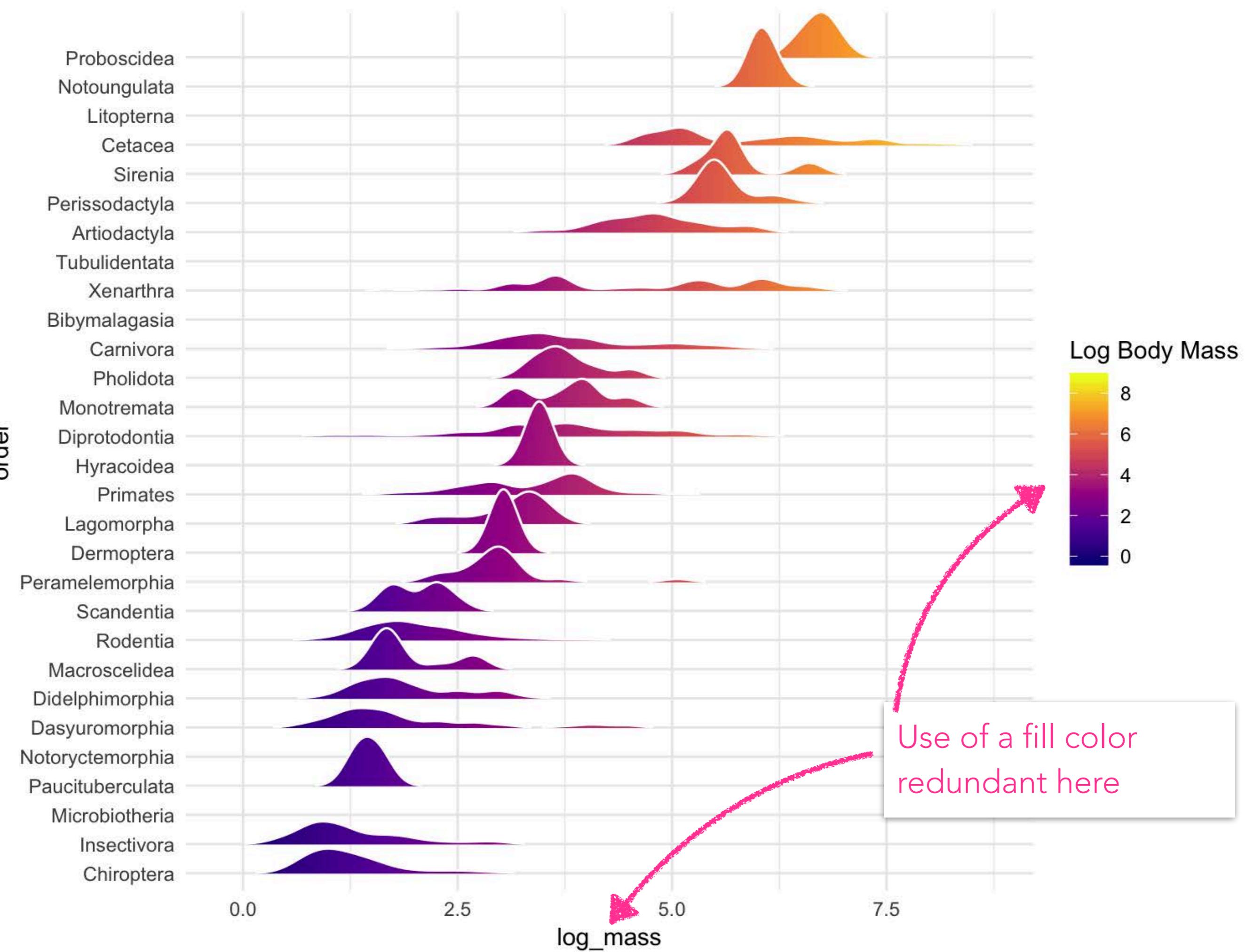
```
ggplot(lqm, aes(x = continent, y = log_mass)) +  
  geom_violin(fill = "paleturquoise", color = NA) +  
  geom_sina(alpha = 0.15) +  
  geom_boxplot(fill = "white", width = 0.15, outlier.shape = NA) +  
  coord_flip()
```

RIDGELINE PLOTS

RIDGELINE PLOTS

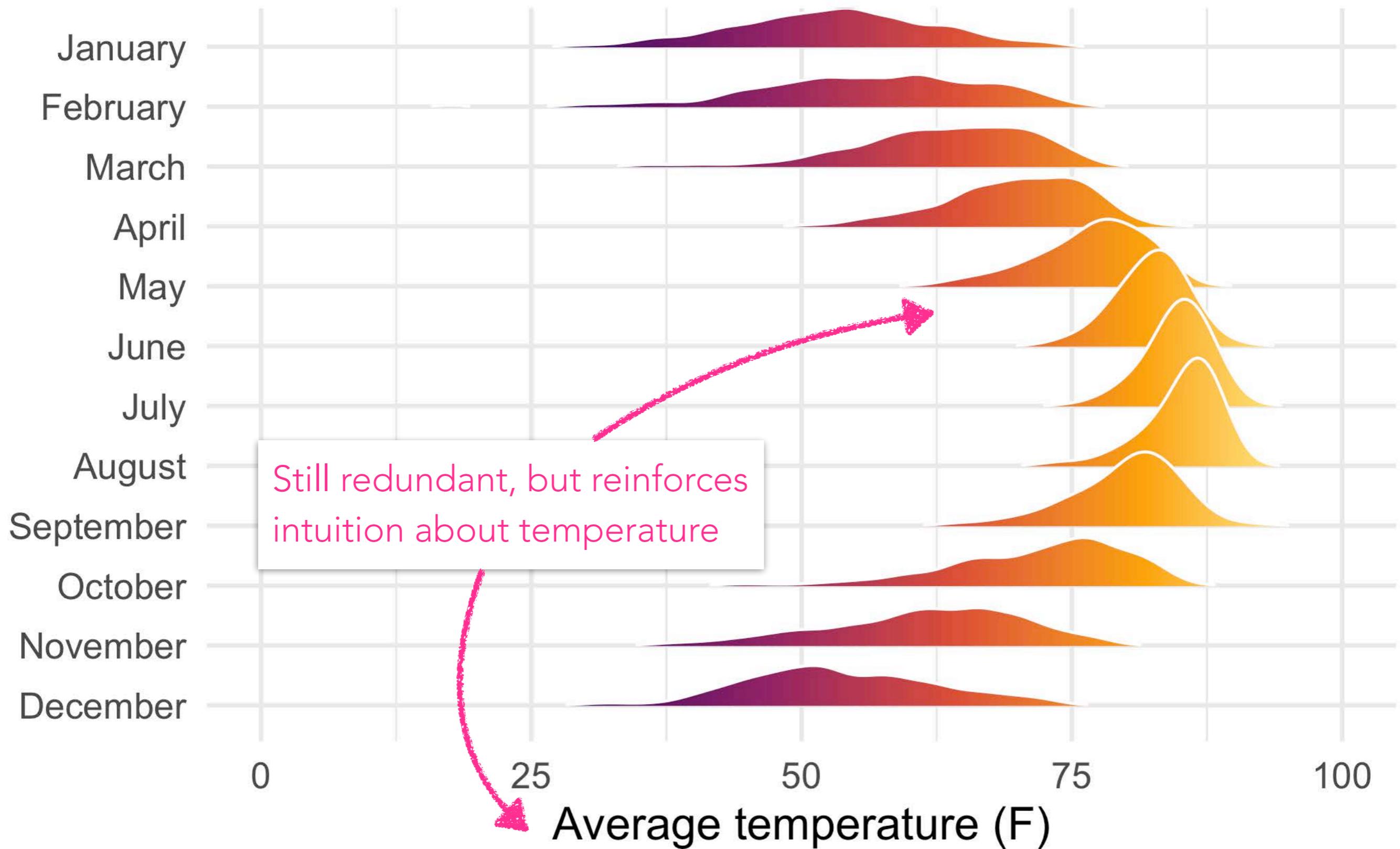
- Each ridge is a vertically offset density plot
- Rarely used, but easy to compare shapes and relative heights
- Not good if specific statistical values are of interest.





SATX Climate

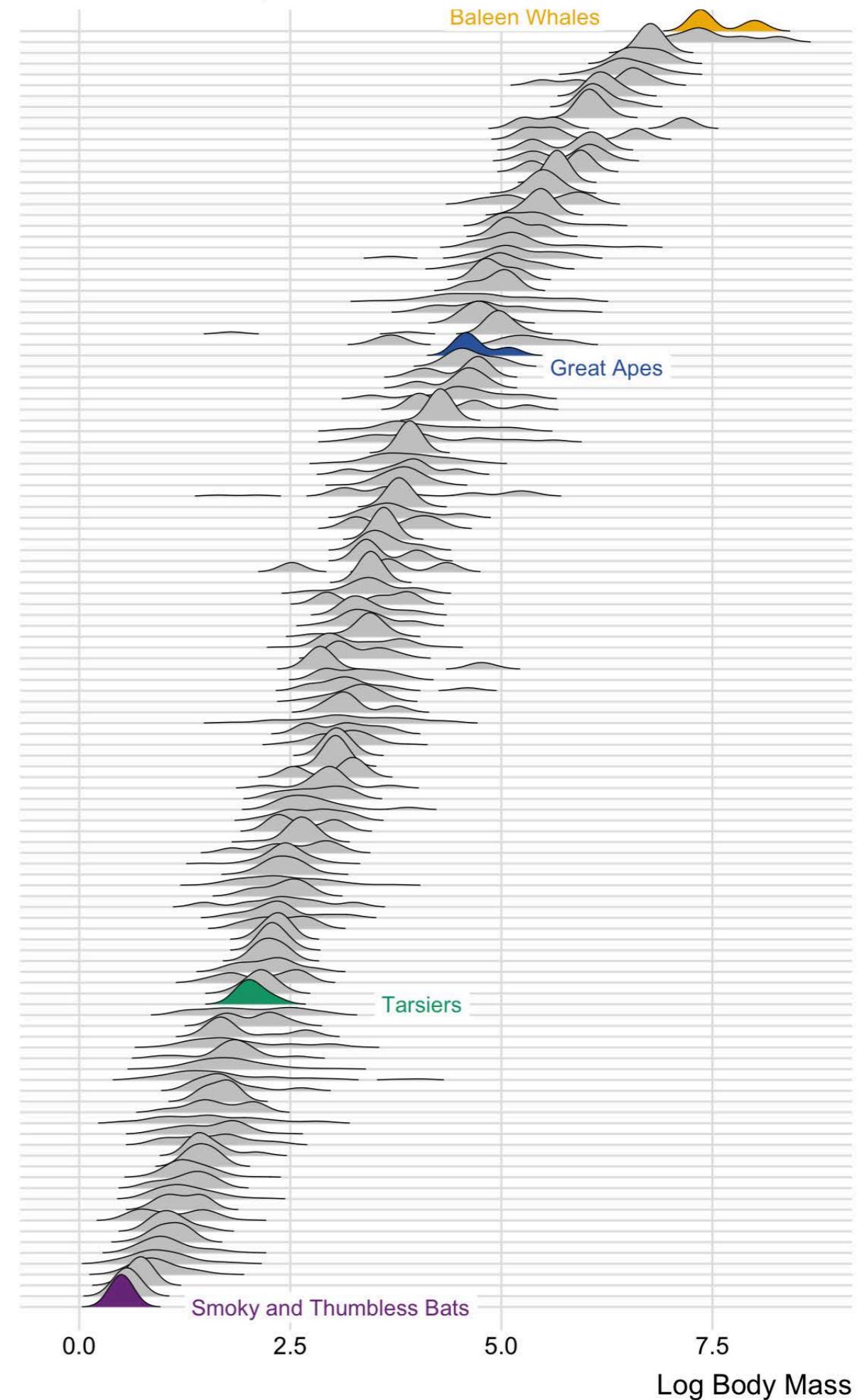
1946 - 2021



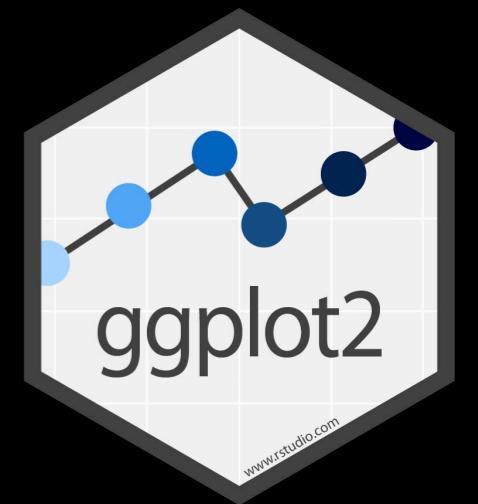
RIDGELINE PLOT

- Only method we have discussed that remains readable with large number of distributions

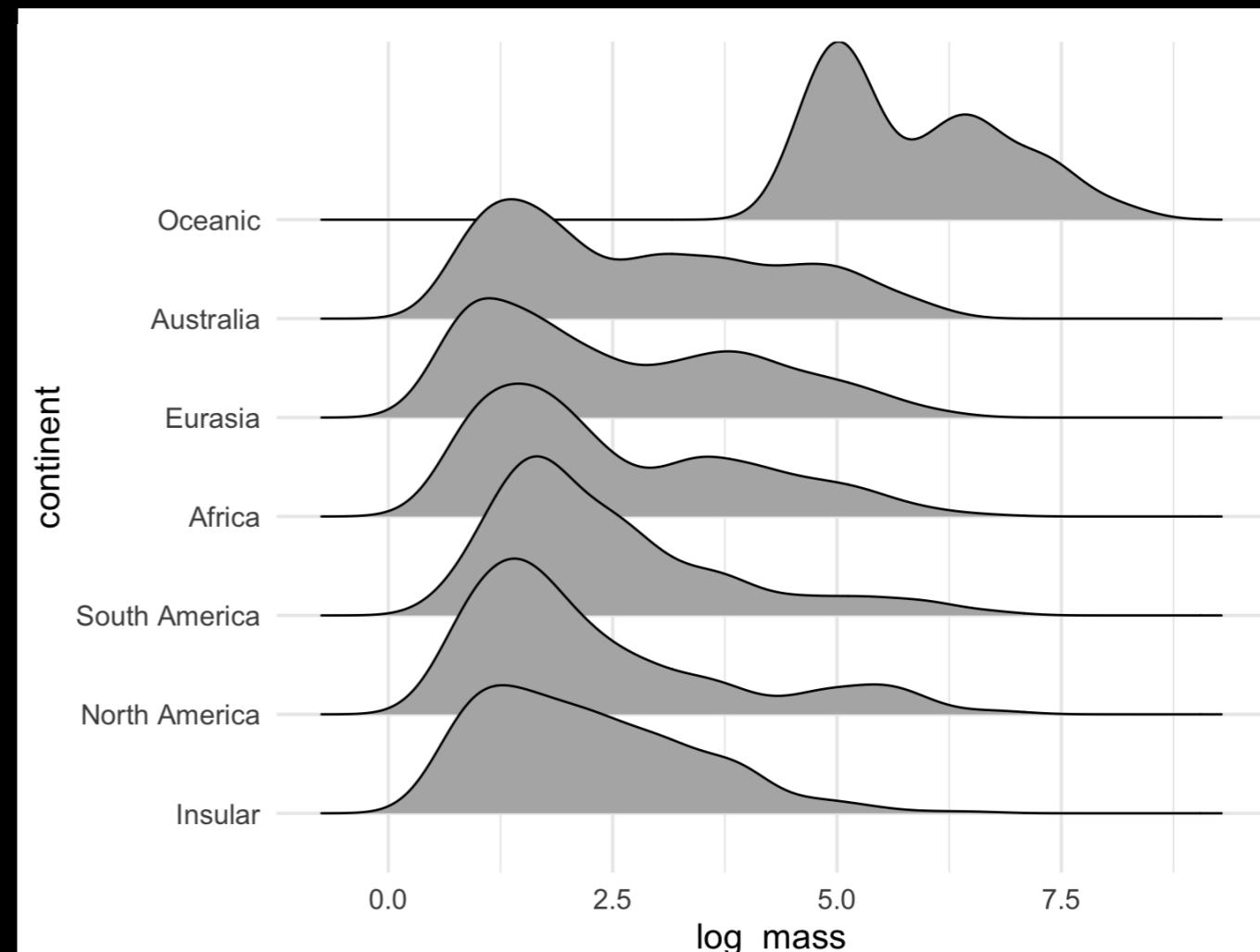
Families of Quaternary Mammals



RIDGE LINE PLOTS



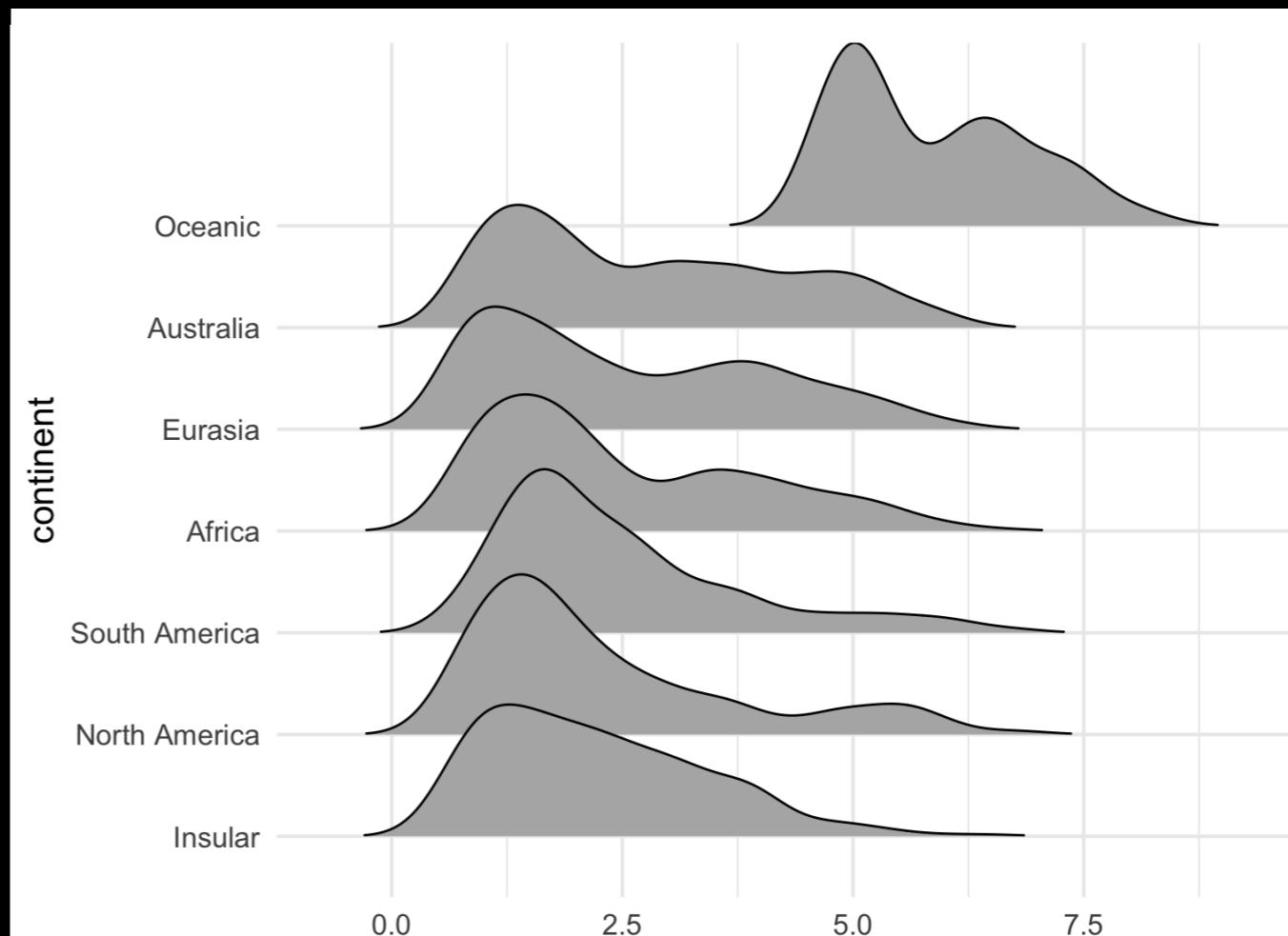
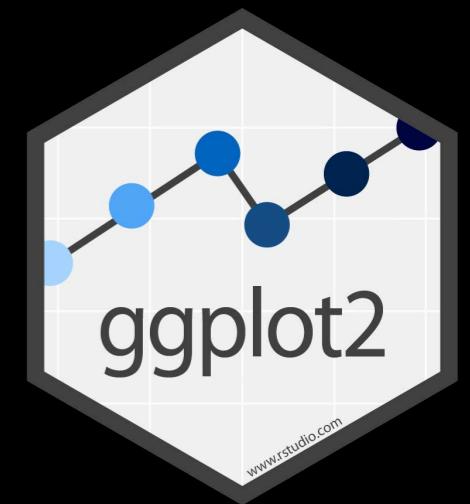
- Not a default geom—provided by “ggridges” package
- Basic geometric object is `geom_density_ridges()`
- Like density plot, numeric variable mapped to x but categorical variable to mapped to y



```
library("ggridges")  
  
ggplot(lqm, aes(x = log_mass, y = continent)) +  
  geom_density_ridges()
```

RIDGE LINE PLOTS

- Not a default geom— provided by “ggridges” package
- Basic geometric object is `geom_density_ridges()`
- Like density plot, numeric variable mapped to x but categorical variable to mapped to y



```
library("ggridges")
```

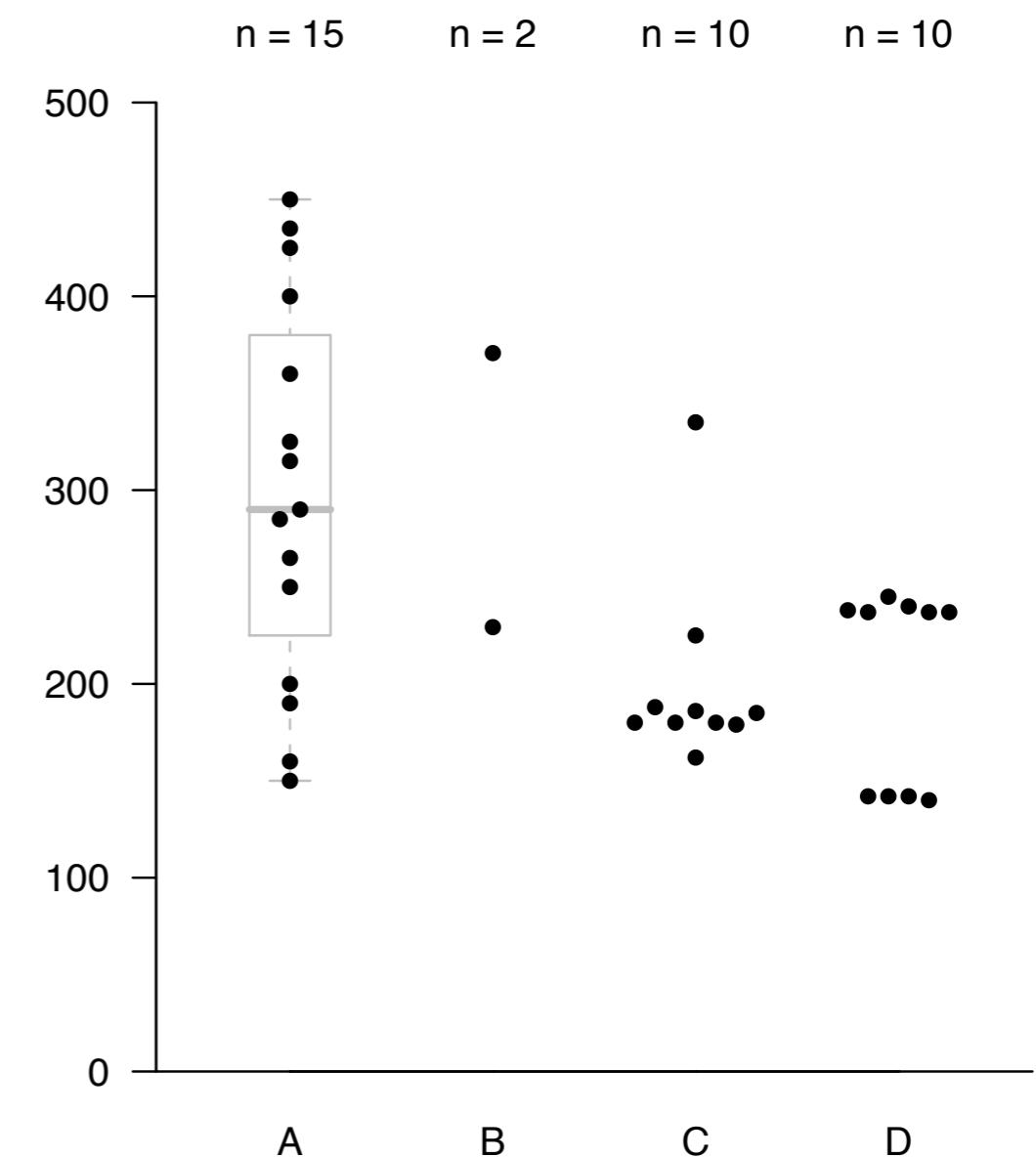
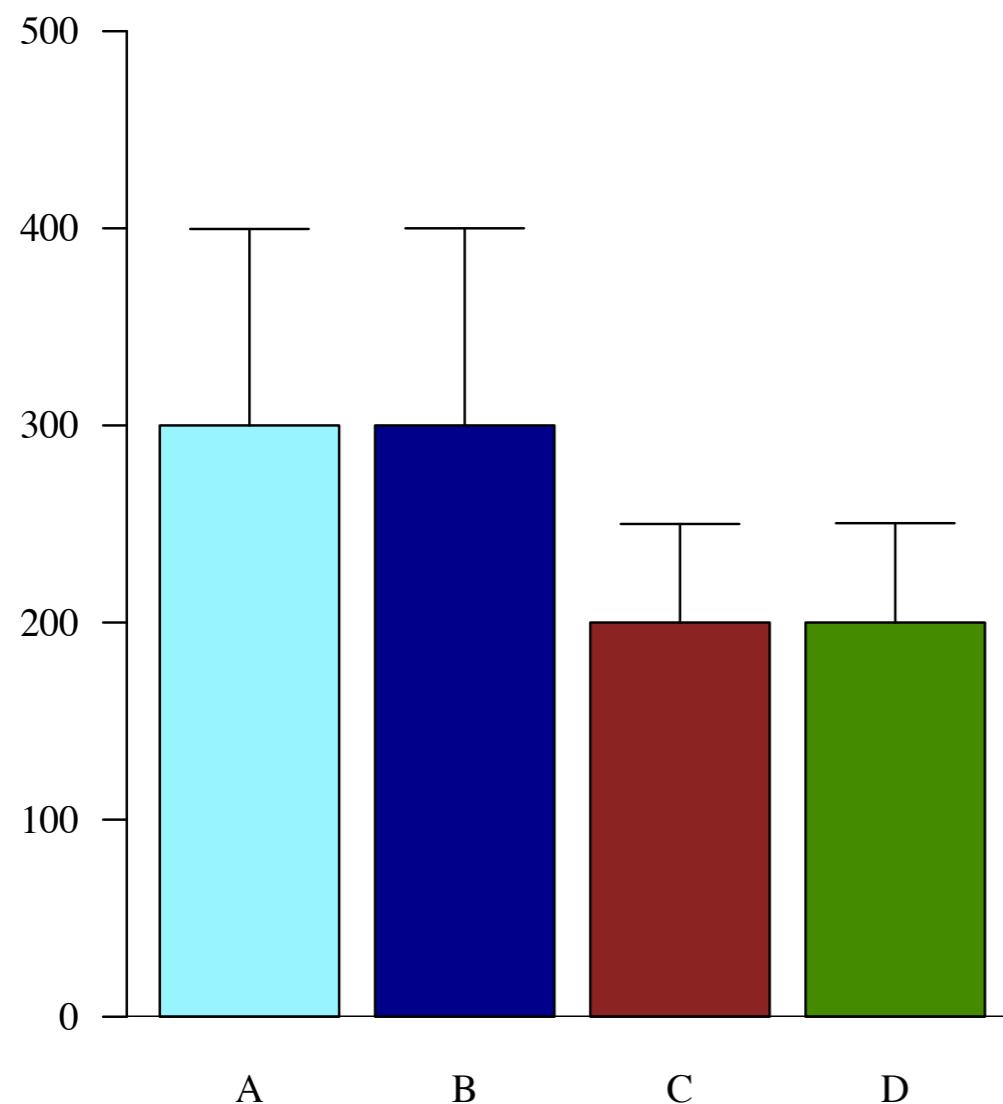
```
ggplot(lqm, aes(x = log_mass, y = continent)) +  
  geom_density_ridges(rel_min_height = 0.005)
```

Cleaner look: cuts off long tails.

WHAT ABOUT A “DYNAMITE PLOT”?



DON'T USE THEM FOR DISTRIBUTIONS



VISUALIZING UNCERTAINTY

VISUALIZING UNCERTAINTY

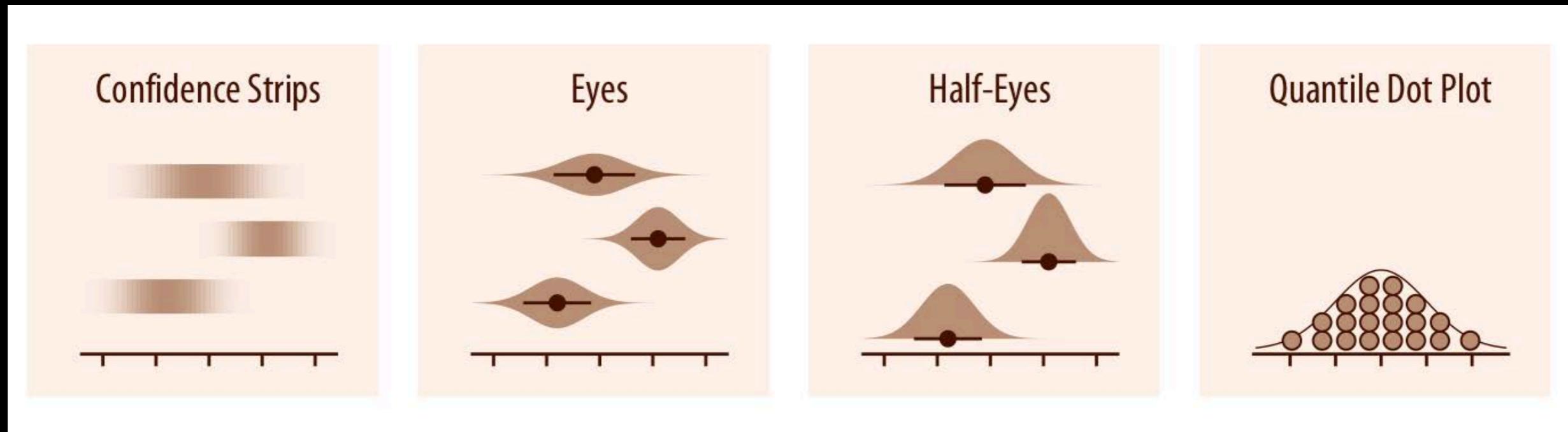
Showing uncertainty intervals around a measurement/estimate



Very common approaches

VISUALIZING UNCERTAINTY

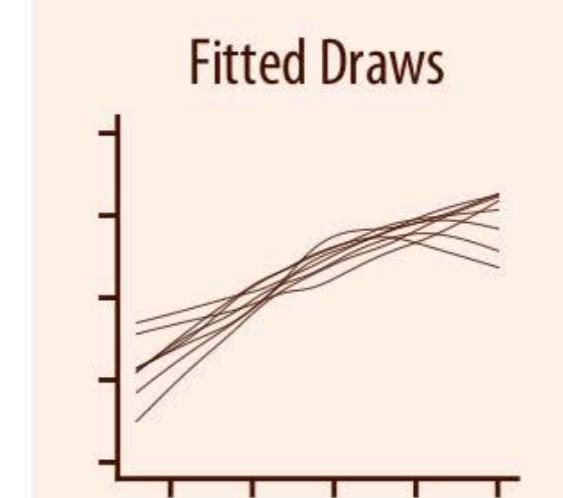
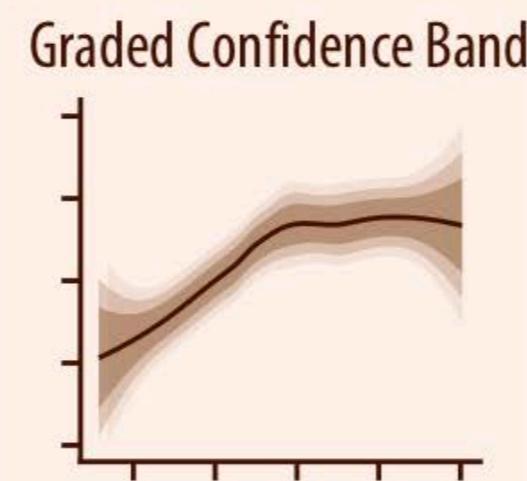
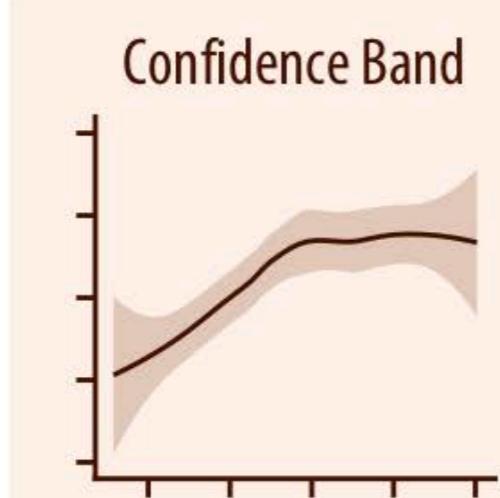
Showing continuous uncertainty around an estimate

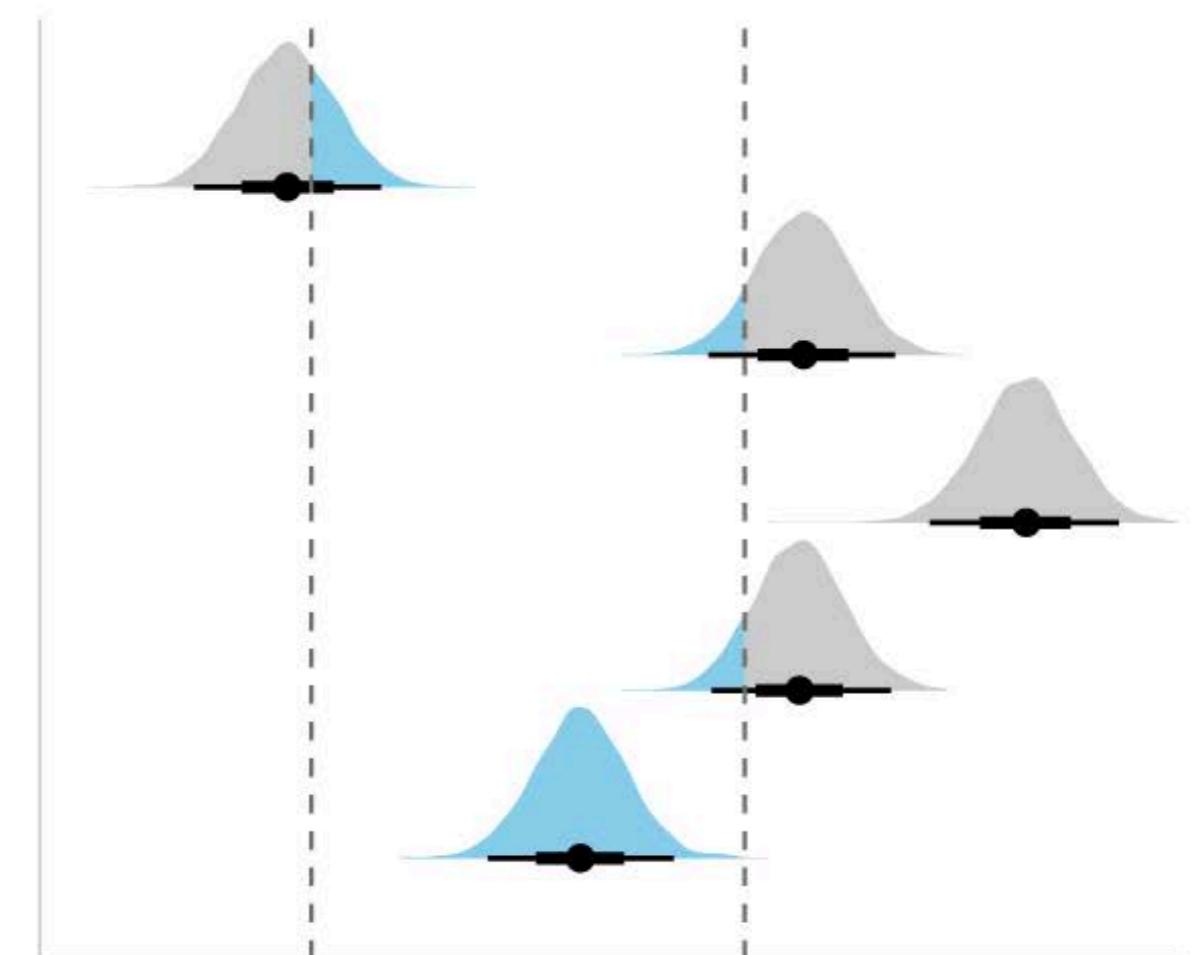
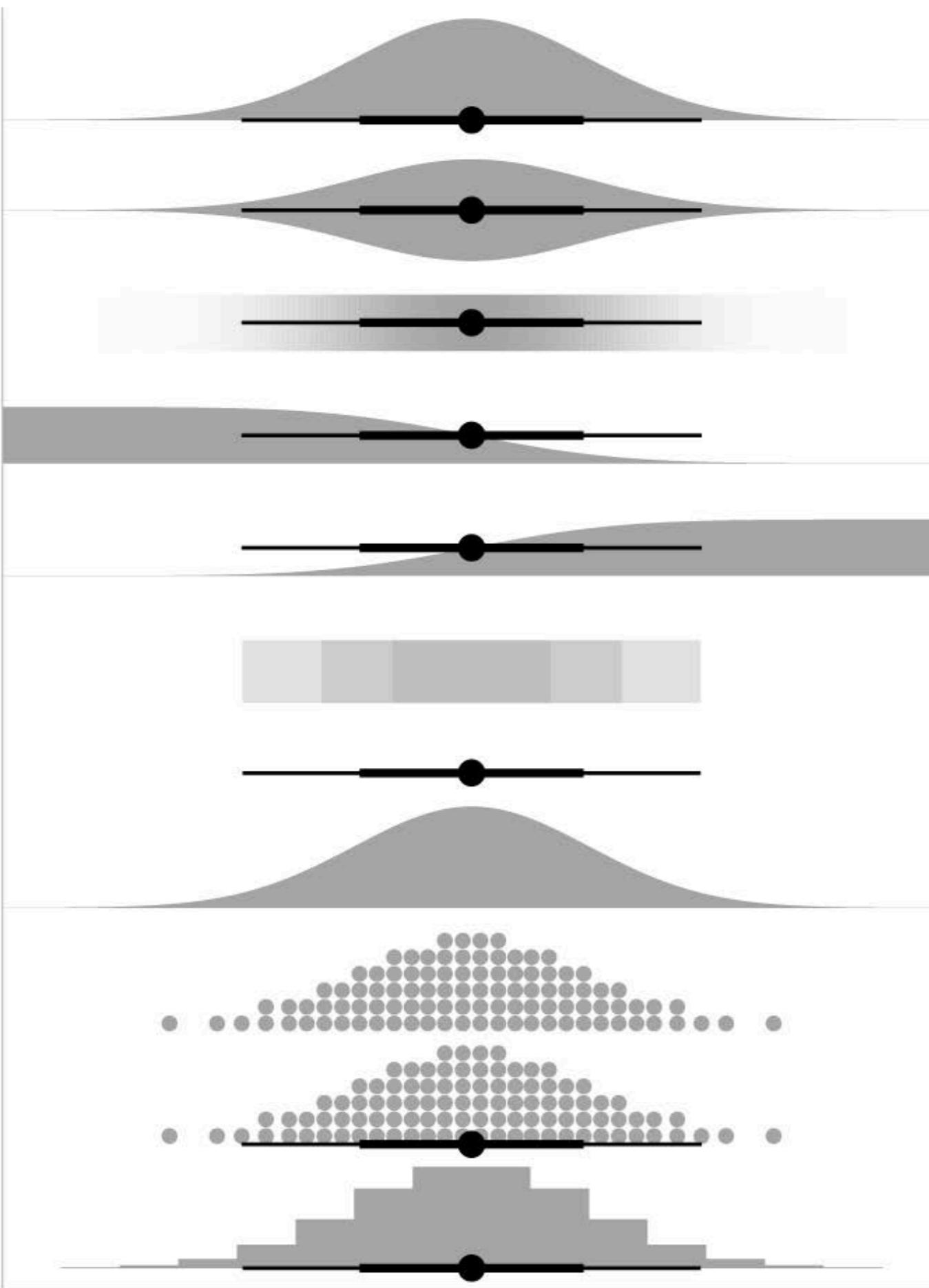


Less-common approaches

VISUALIZING UNCERTAINTY

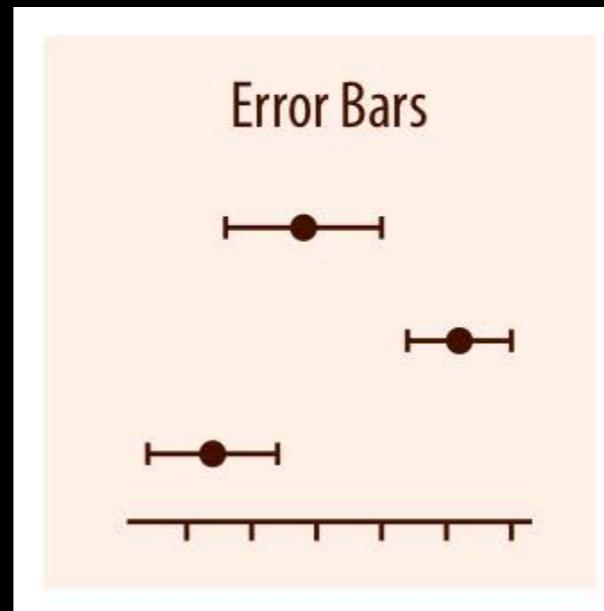
Showing uncertainty around smooth lines





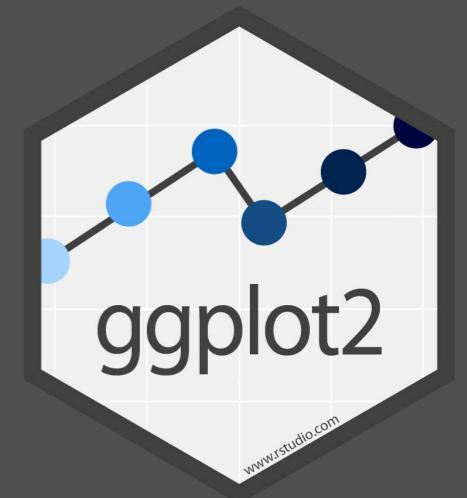
VISUALIZING UNCERTAINTY

Showing uncertainty intervals around a measurement/estimate



The workhorse: error bars

YOUR TURN

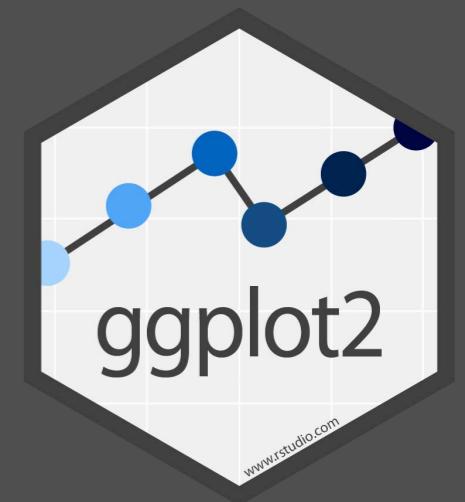


- Download the model summary data set from the course website ("model_summary.csv"). This is a file format for single R objects.
- Read the file into R using:

```
model_summary <- read_csv("your-path/model_summary.csv")
```

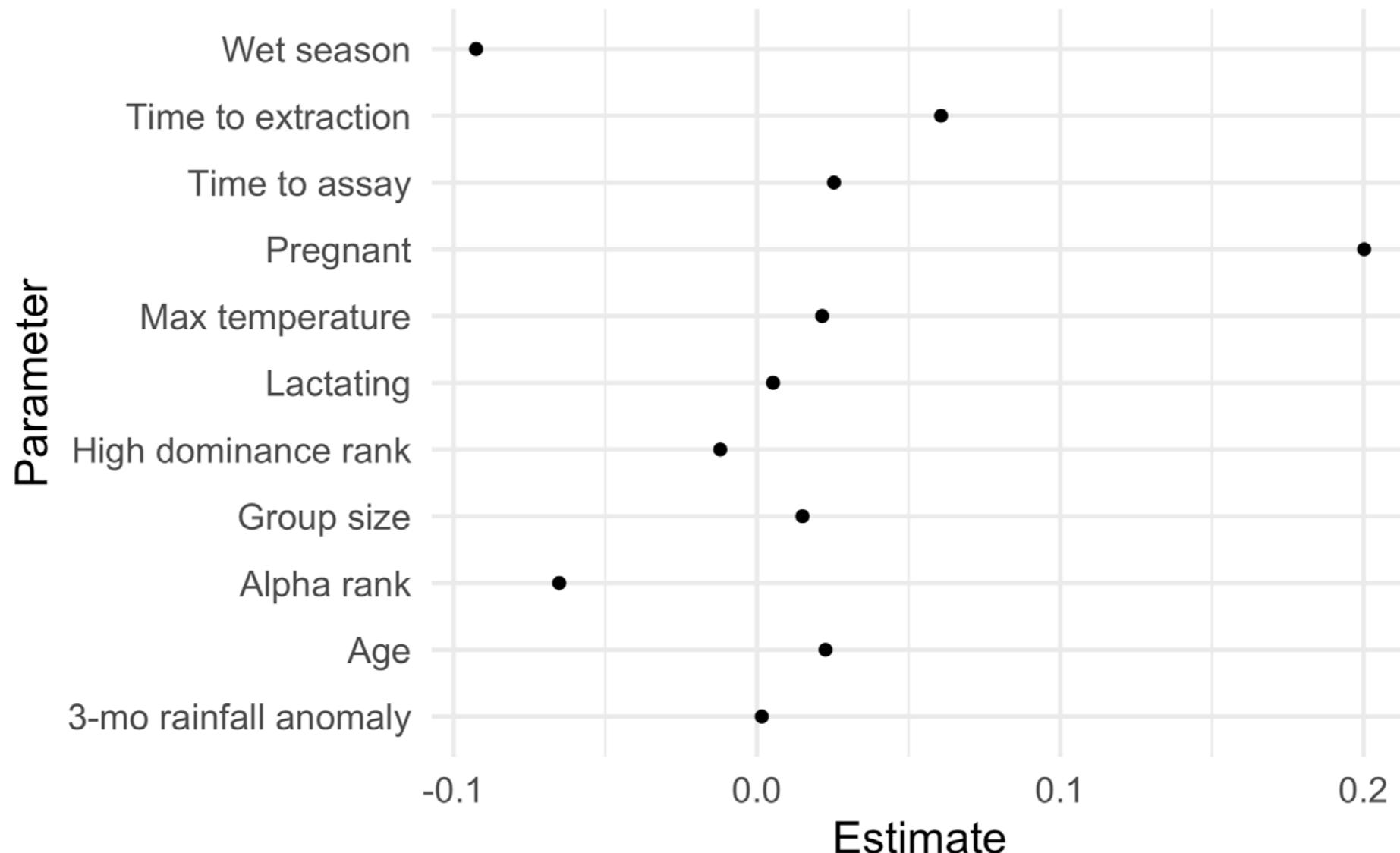
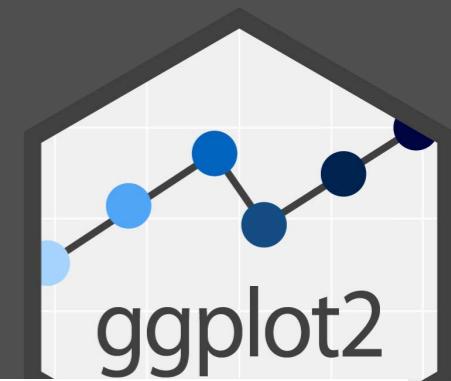


YOUR TURN



parameter	mean	std_error	lower	upper
Lactating	0.0053	0.0089	-0.0094	0.0198
Pregnant	0.2002	0.0097	0.1842	0.2163
Wet season	-0.0926	0.0084	-0.1063	-0.0786
Group size	0.0150	0.0071	0.0033	0.0267
Alpha rank	-0.0652	0.0316	-0.1171	-0.0133
High dominance rank	-0.0121	0.0104	-0.0293	0.0050
Max temperature	0.0215	0.0043	0.0144	0.0286
3-mo rainfall anomaly	0.0016	0.0037	-0.0044	0.0077
Time to extraction	0.0607	0.0044	0.0534	0.0680
Time to assay	0.0254	0.0040	0.0189	0.0321

YOUR TURN

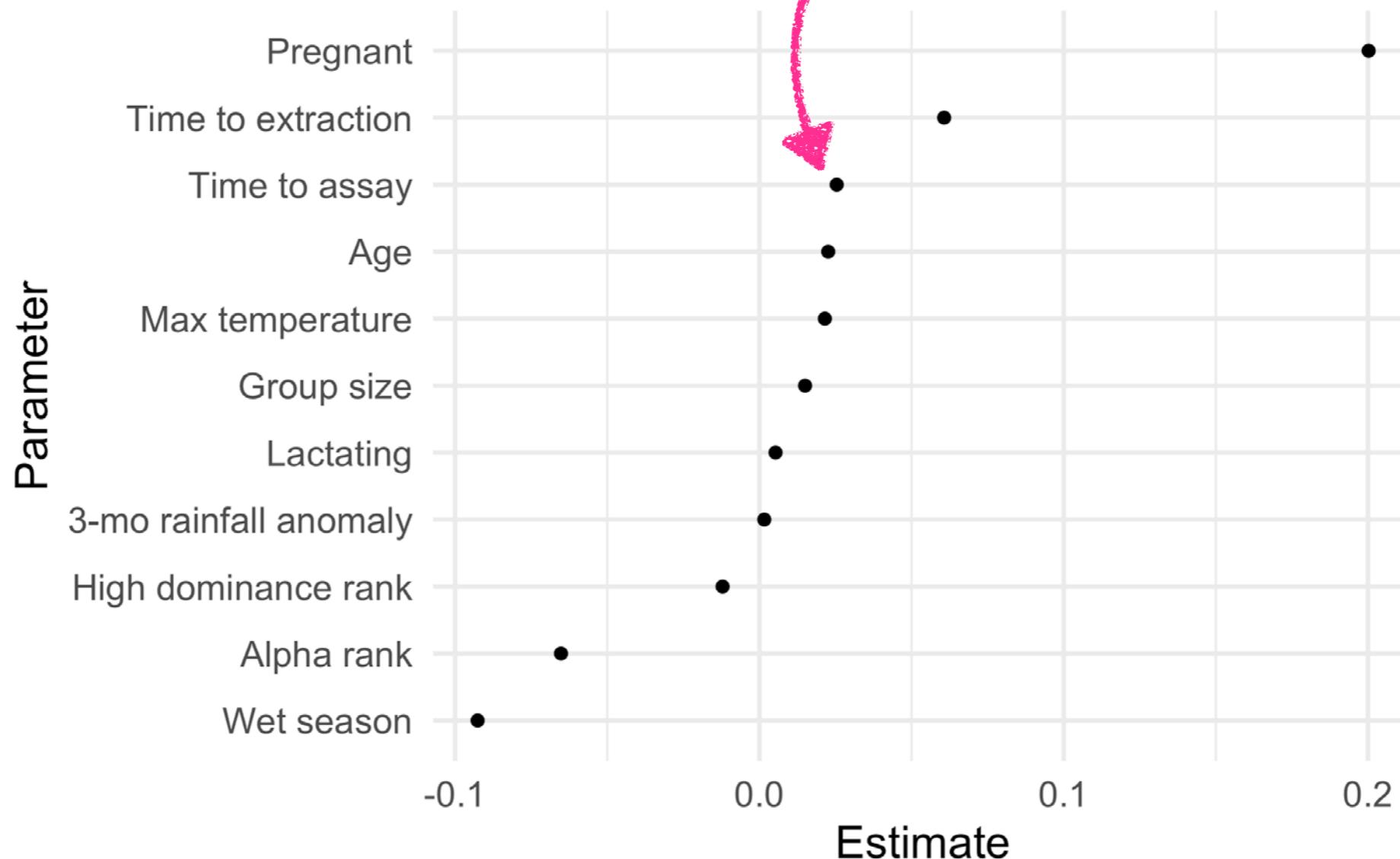


```
ggplot(model_summary, aes(x = mean, y = parameter)) +  
  geom_point(size = 2) +  
  labs(x = "Estimate", y = "Parameter")
```

YOUR TURN

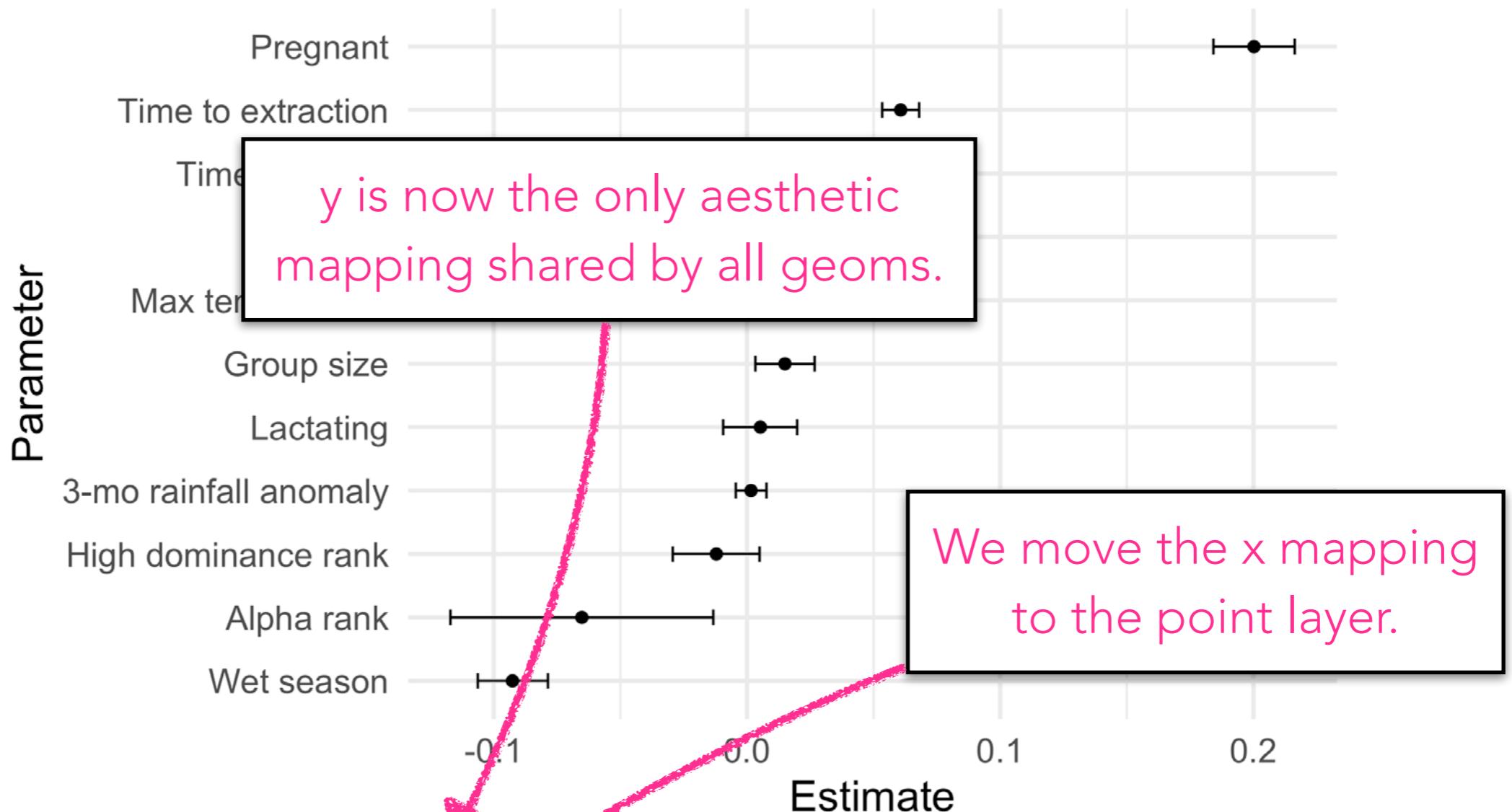
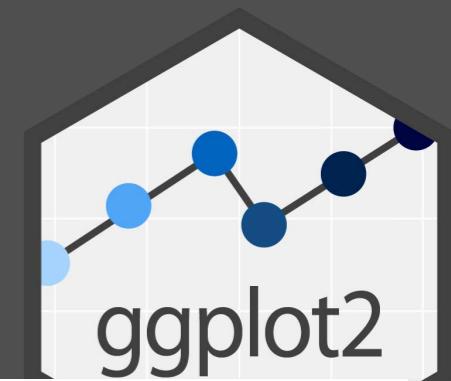
Reordering by mean looks cleaner
and improves interpretation.

ggplot2



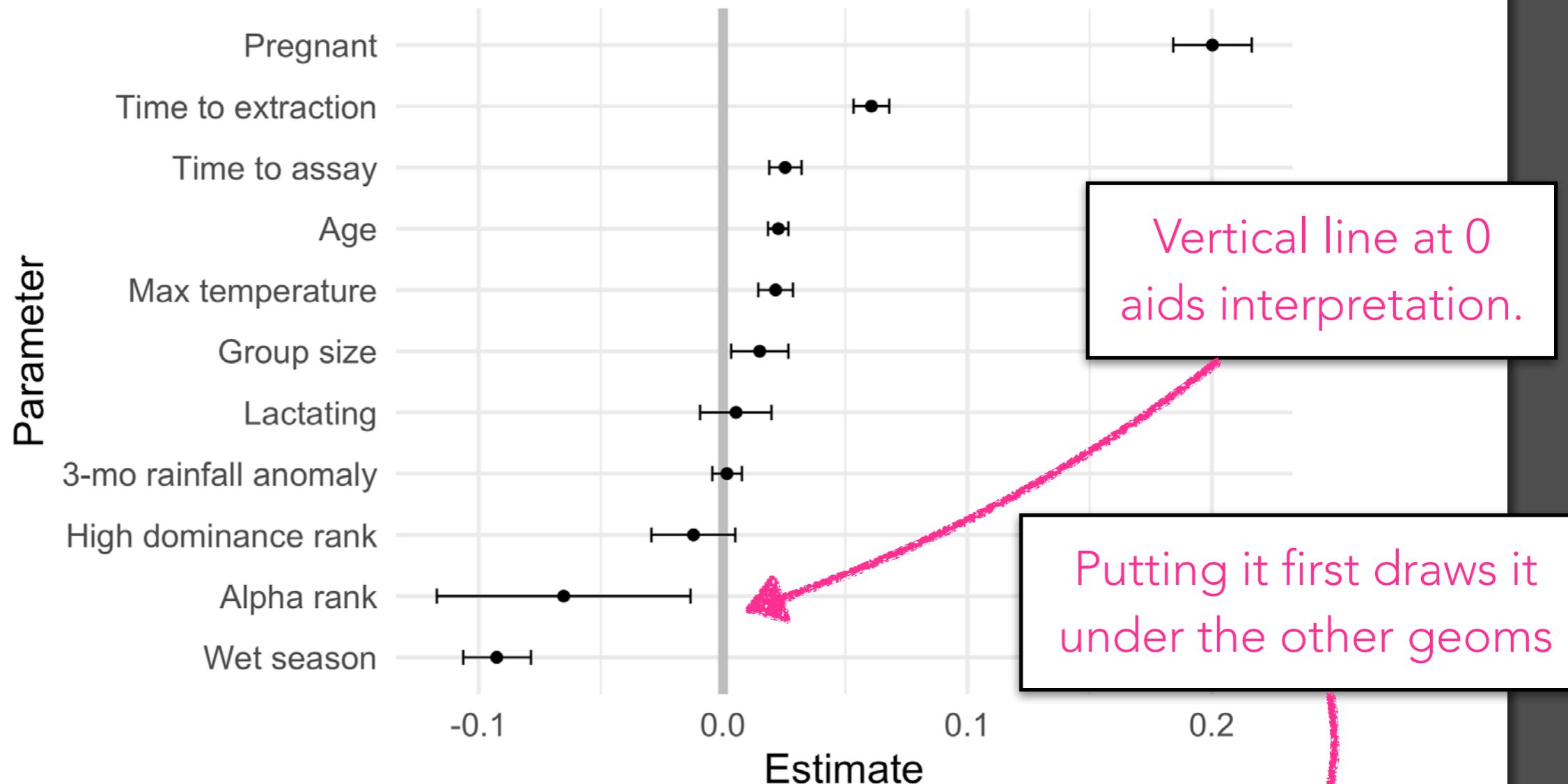
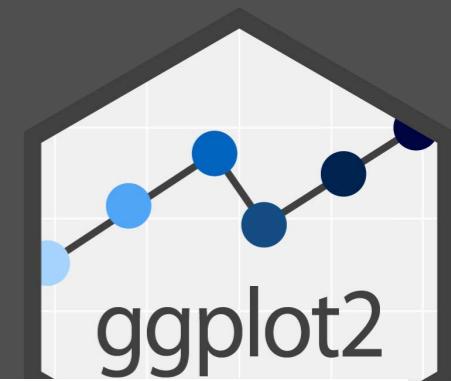
```
ggplot(model_summary, aes(x = mean, y = fct_reorder(parameter, mean))) +  
  geom_point(size = 2) +  
  labs(x = "Estimate", y = "Parameter")
```

YOUR TURN



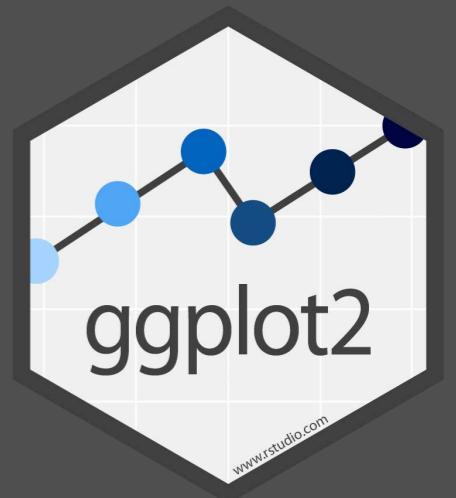
```
ggplot(model_summary, aes(y = fct_reorder(parameter, mean))) +  
  geom_errorbarh(aes(xmin = lower, xmax = upper), height = 0.25) +  
  geom_point(aes(x = mean), size = 2) +  
  labs(x = "Estimate", y = "Parameter")
```

YOUR TURN



```
ggplot(model_summary, aes(y = fct_reorder(parameter, mean))) +  
  geom_vline(xintercept = 0, color = "gray", size = 2) +  
  geom_errorbarh(aes(xmin = lower, xmax = upper), height = 0.25) +  
  geom_point(aes(x = mean), size = 2) +  
  labs(x = "Estimate", y = "Parameter")
```

YOUR TURN



- Go to this week's assignments on the course website.
- Download the **quaternary-mammals.Rmd** R Markdown file.
- Follow the instructions to visualize distributions

