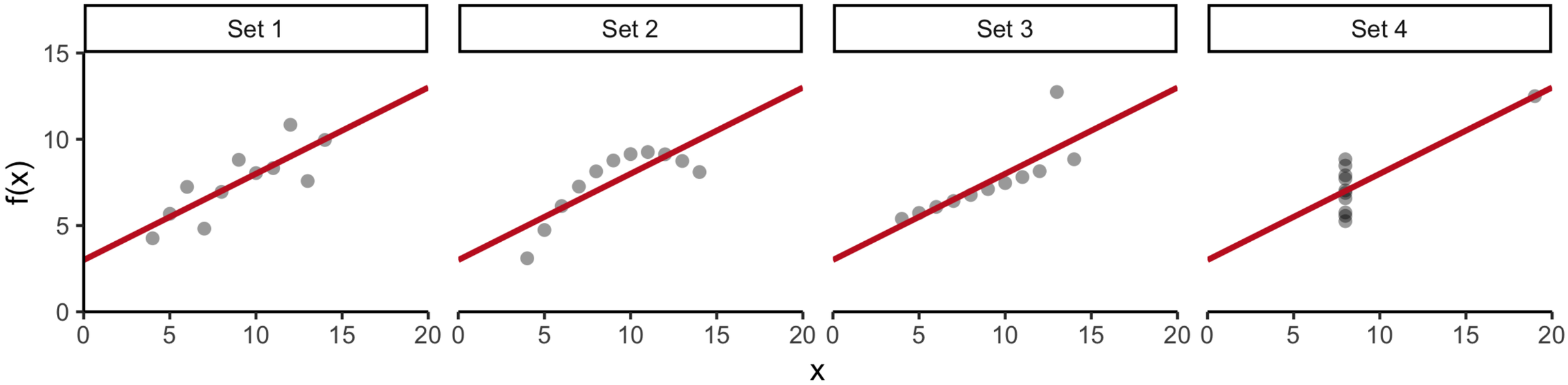
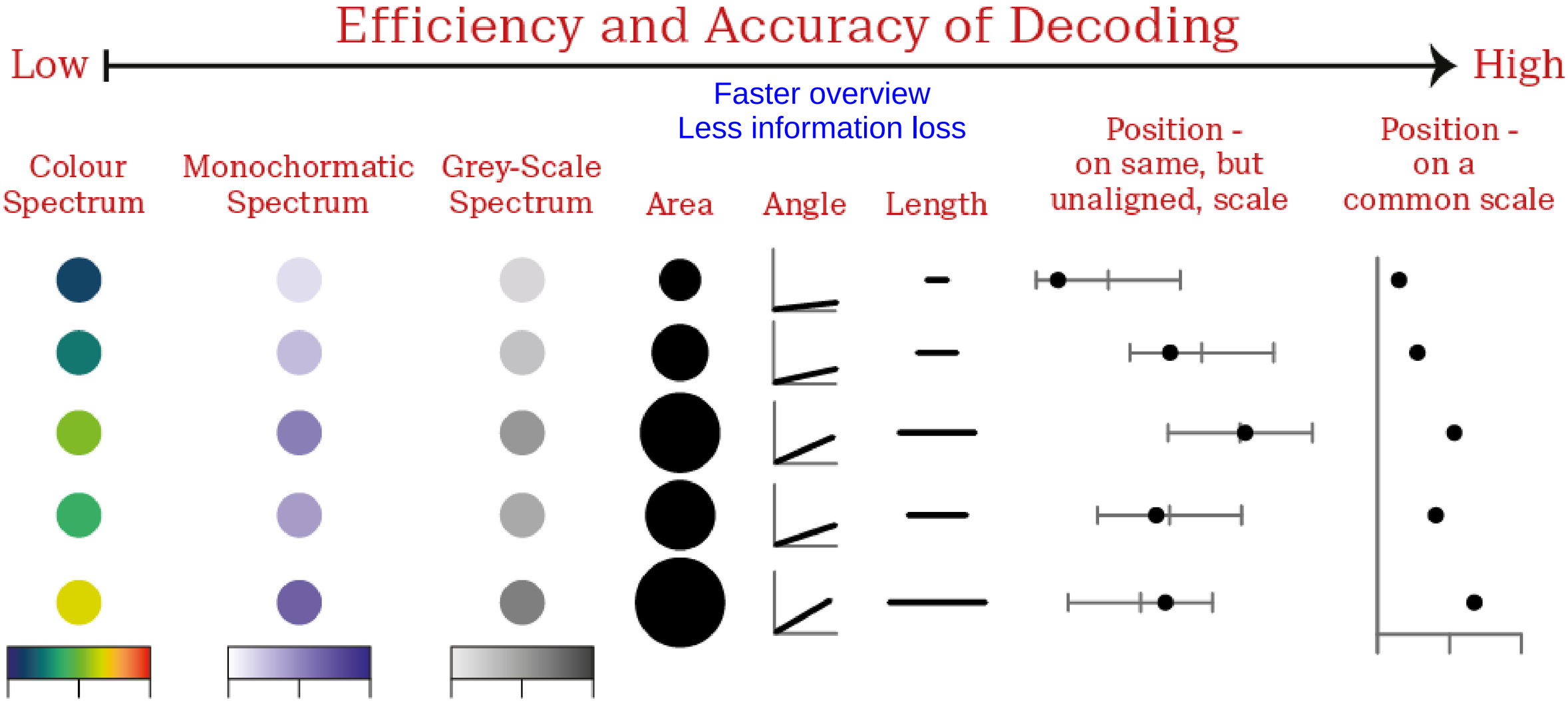
Anscombe's plots

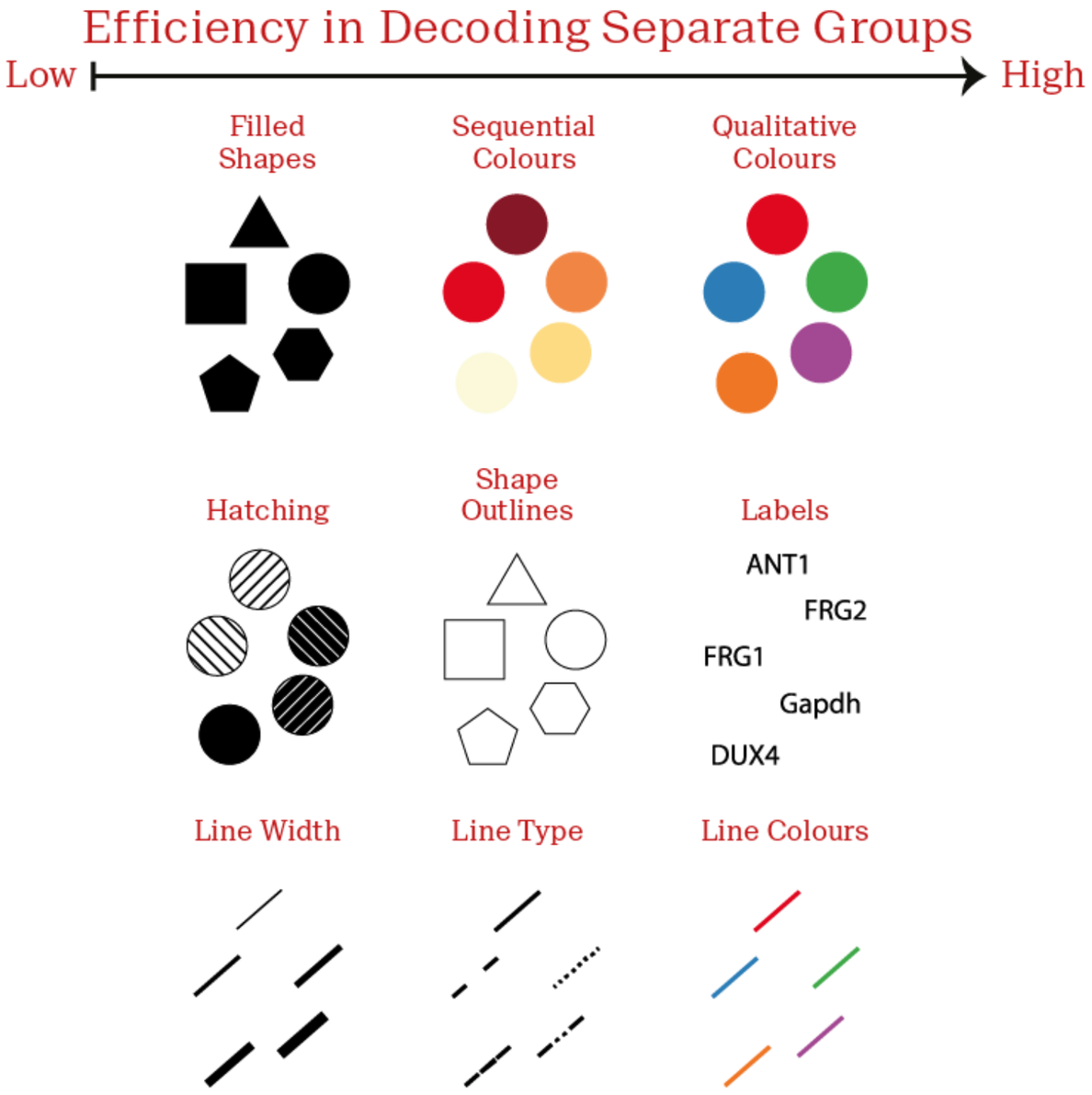


Typical visible aesthetics

Aesthetic	Description
x	X axis position
y	Y axis position
fill	Fill color
color	Color of points, outlines of other geoms
size	Area or radius of points, thickness of lines

Aesthetic	Description
alpha	Transparency
linetype	line dash pattern
labels	Text on a plot or axes
shape	Shape


Efficiency and Accuracy of Decoding
Low
High
Faster overview
Less information loss
Colour Spectrum
Monochormatic Spectrum
Grey-Scale Spectrum
Area
Angle
Length
Position - on same, but unaligned, scale
Position - on a common scale


Efficiency in Decoding Separate Groups
Low
High
Filled Shapes
Sequential Colours
Qualitative Colours
Hatching
Shape Outlines
Labels
ANT1
FRG2
FRG1
Gapdh
DUX4
Line Width
Line Type
Line Colours

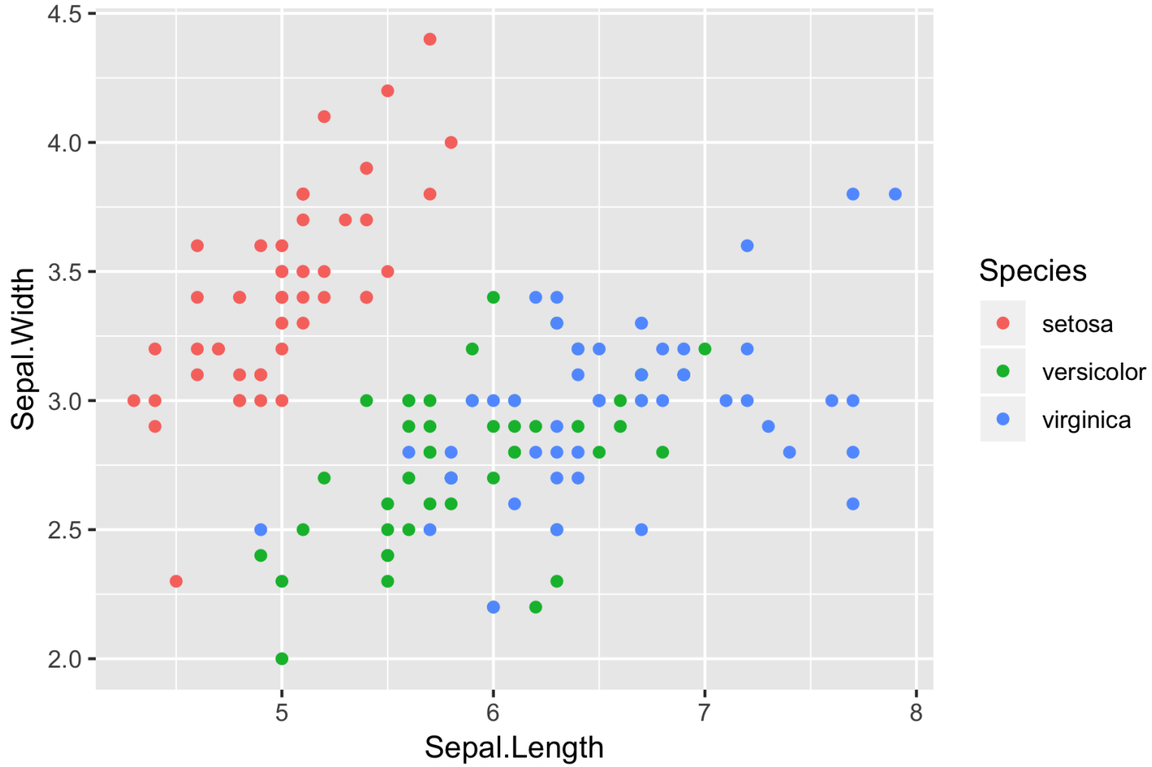
Positions

Adjustment for overlapping

- identity
- dodge
- stack
- fill
- jitter
- jitterdodge
- nudge

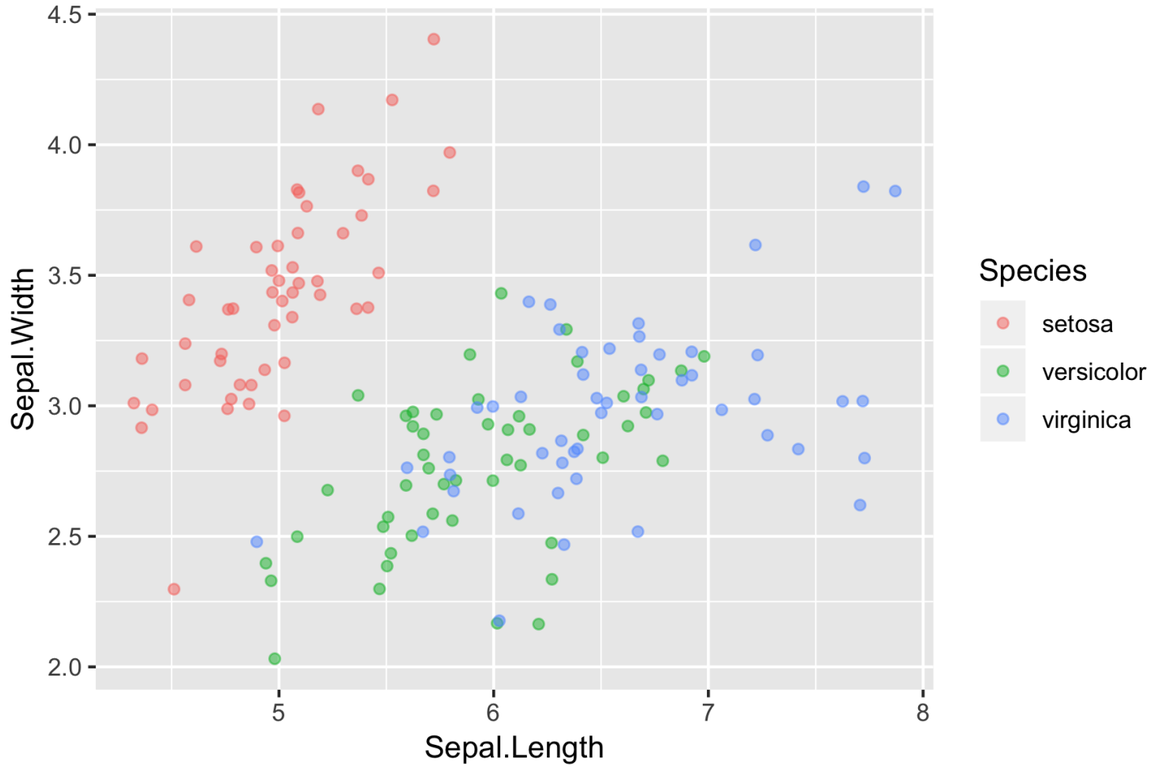
position = "identity" (default)

```
ggplot(iris, aes(x = Sepal.Length,
                 y = Sepal.Width,
                 color = Species)) +
  geom_point(position = "identity")
```



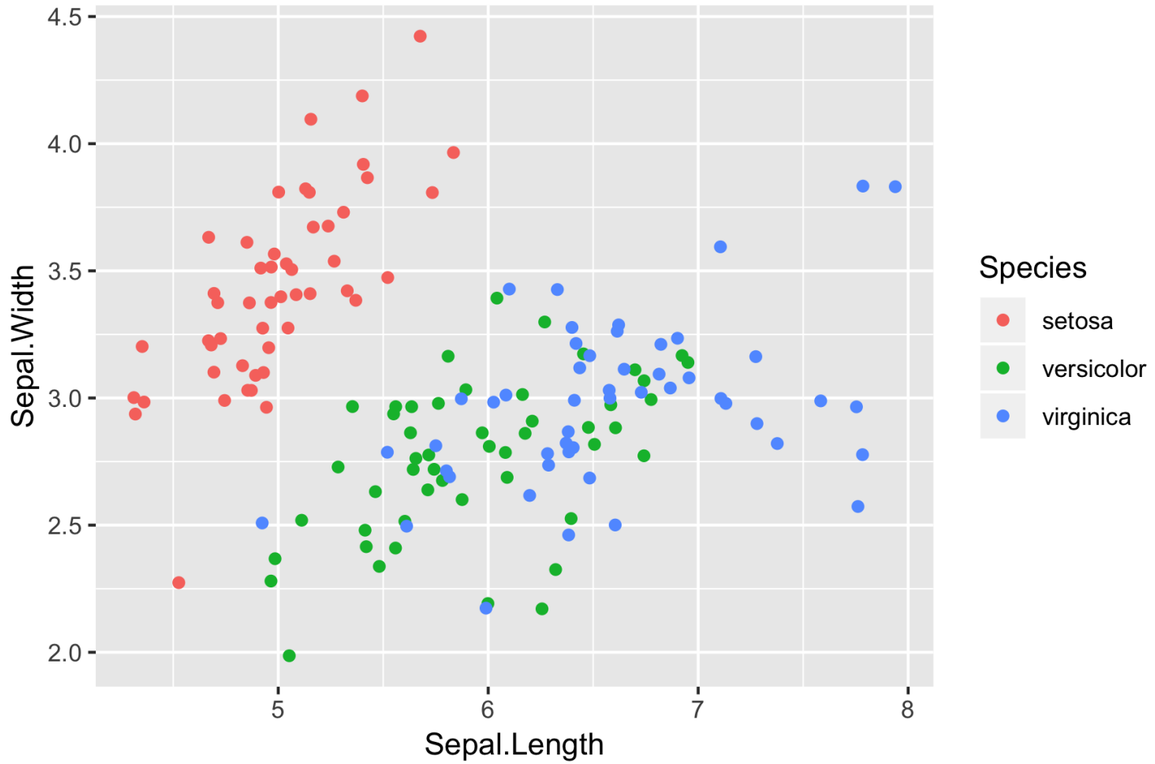
position = "jitter"

```
ggplot(iris, aes(x = Sepal.Length,
                 y = Sepal.Width,
                 color = Species)) +
  geom_point(position = "jitter")
```



position_jitter()

```
posn_j <- position_jitter(0.1,
                          seed = 136)

ggplot(iris, aes(x = Sepal.Length,
                 y = Sepal.Width,
                 color = Species)) +
  geom_point(position = posn_j)
```



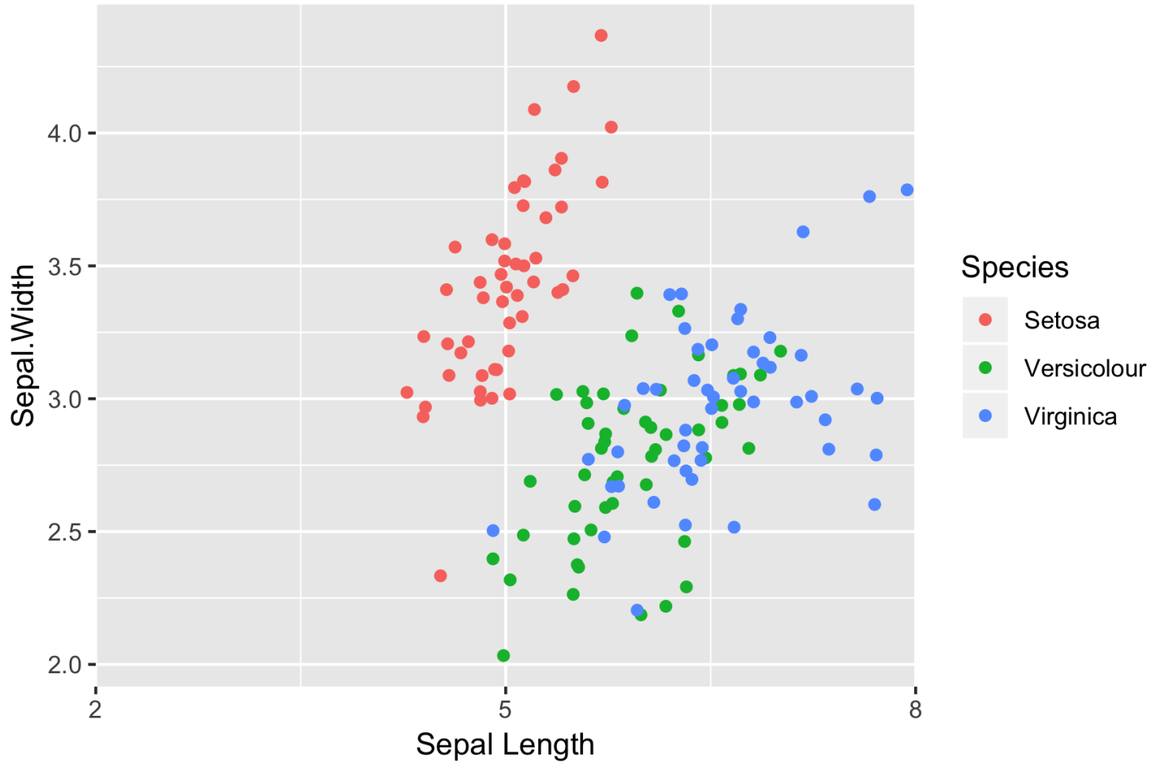
- Set arguments for the position
- Consistency across plots & layers

Scale functions

- **`scale_x_continuous()`**
- `scale_y_*()`
- **`scale_color_discrete()`**
  - Alternatively, `scale_colour_*()`
- `scale_fill_*()`
- `scale_shape_*()`
- `scale_linetype_*()`
- `scale_size_*()`

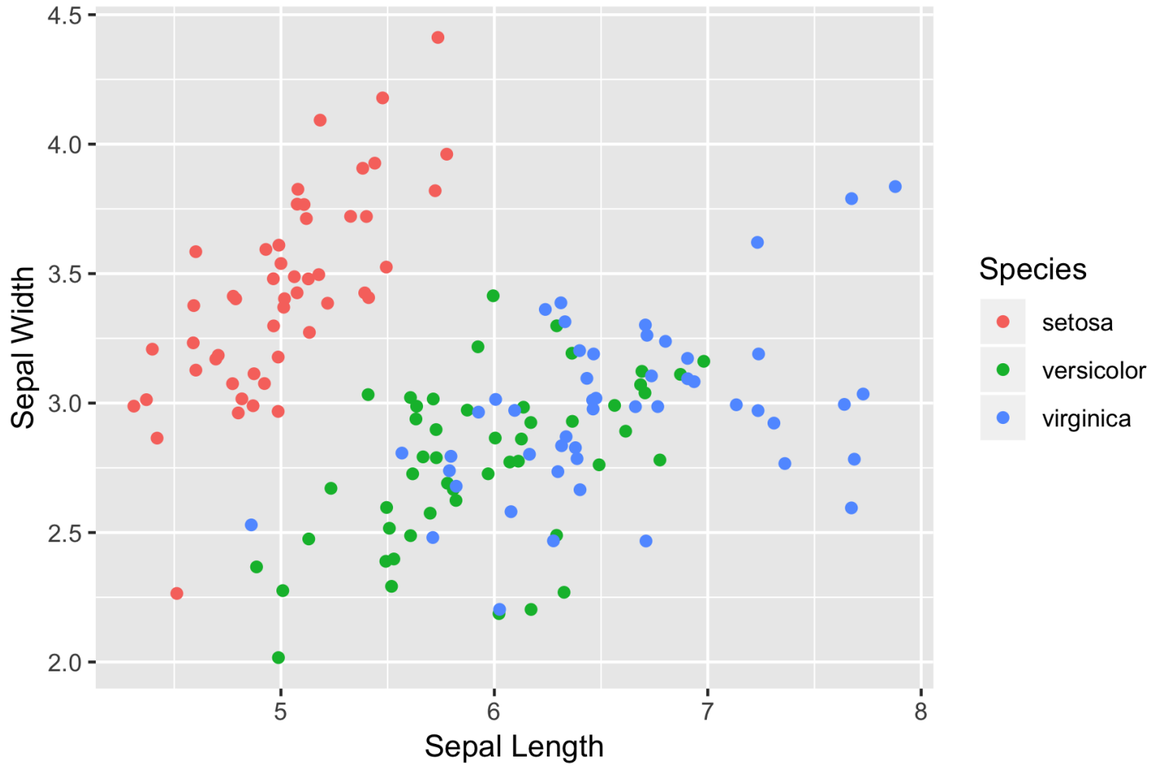
The labels argument

```
ggplot(iris, aes(x = Sepal.Length,
                 y = Sepal.Width,
                 color = Species)) +
  geom_point(position = "jitter") +
  scale_x_continuous("Sepal Length",
                     limits = c(2, 8),
                     breaks = seq(2, 8, 3),
                     expand = c(0, 0),
                     labels = c("Setosa",
                                "Versicolor",
                                "Virginica")) +
  scale_color_discrete("Species")
```

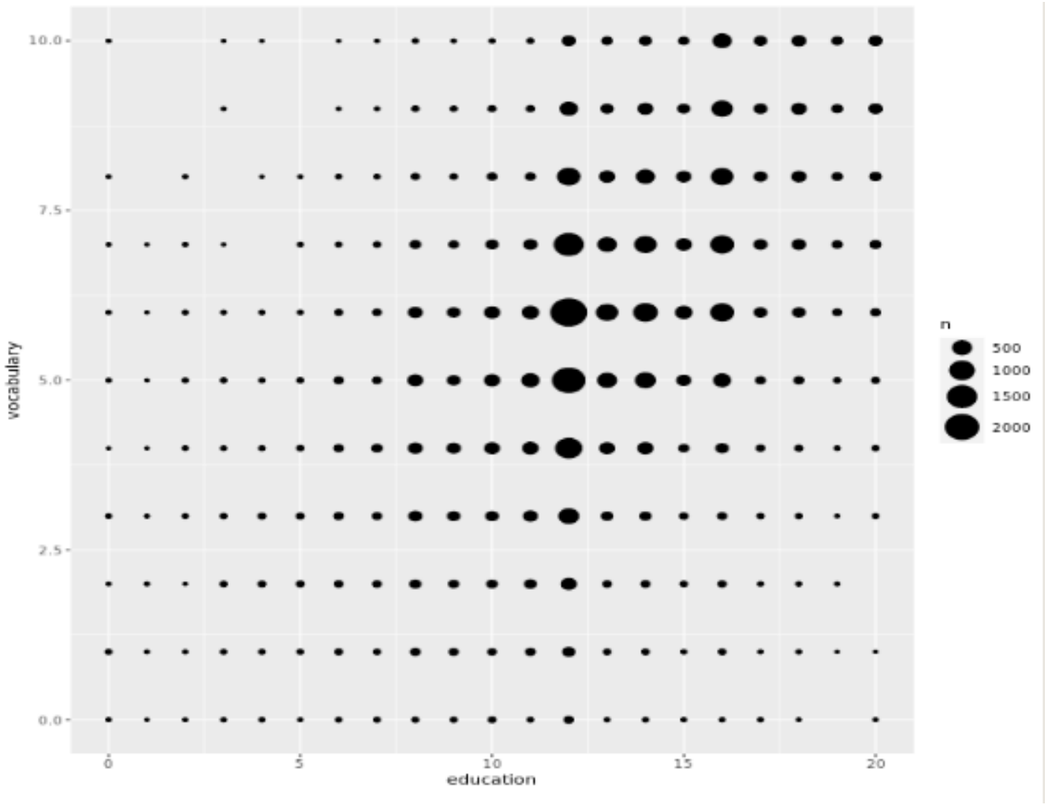


labs()

```
ggplot(iris, aes(x = Sepal.Length,
                 y = Sepal.Width,
                 color = Species)) +
  geom_point(position = "jitter") +
  labs(x = "Sepal Length",
       y = "Sepal Width",
       color = "Species")
```



```r
ggplot(Vocab, aes(x = education, y =
vocabulary)) +
  stat_sum() +
  # Add a size scale, from 1 to 10
  scale_size(range = c(1,10))
```



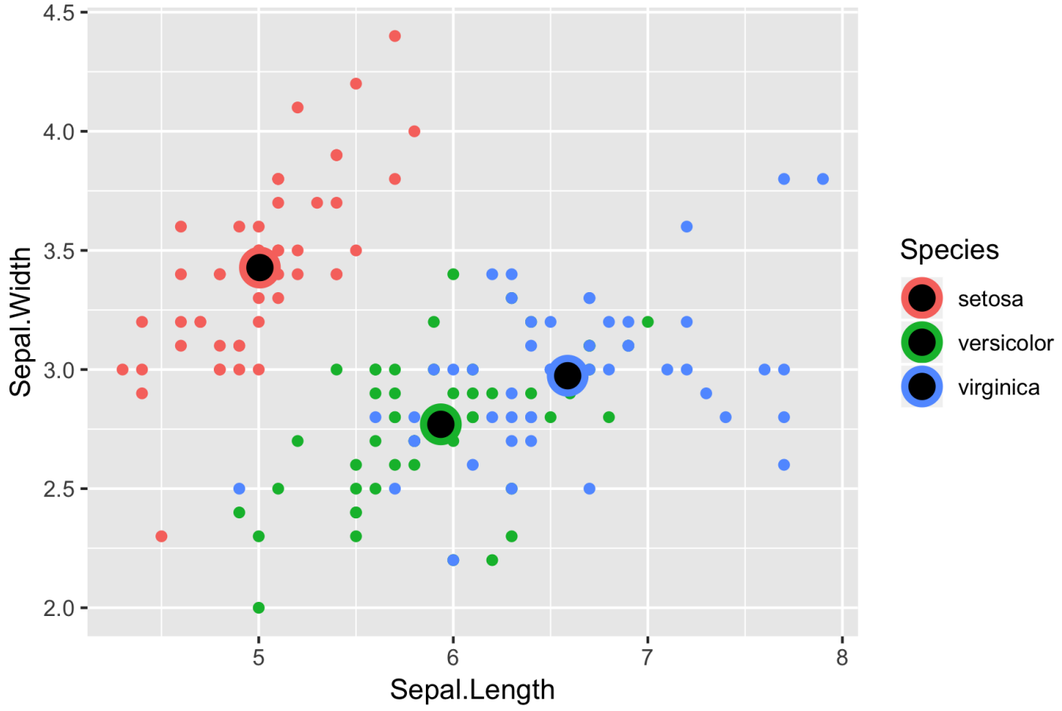
48 geometries

geom_*						
abline	contour	dotplot	jitter	pointrange	ribbon	spoke
area	count	errorbar	label	polygon	rug	step
bar	crossbar	errorbarh	line	qq	segment	text
bin2d	curve	freqpoly	linerange	qq_line	sf	tile
blank	density	hex	map	quantile	sf_label	violin
boxplot	density2d	histogram	path	raster	sf_text	vline
col	density_2d	hline	point	rect	smooth	

Shape attribute values

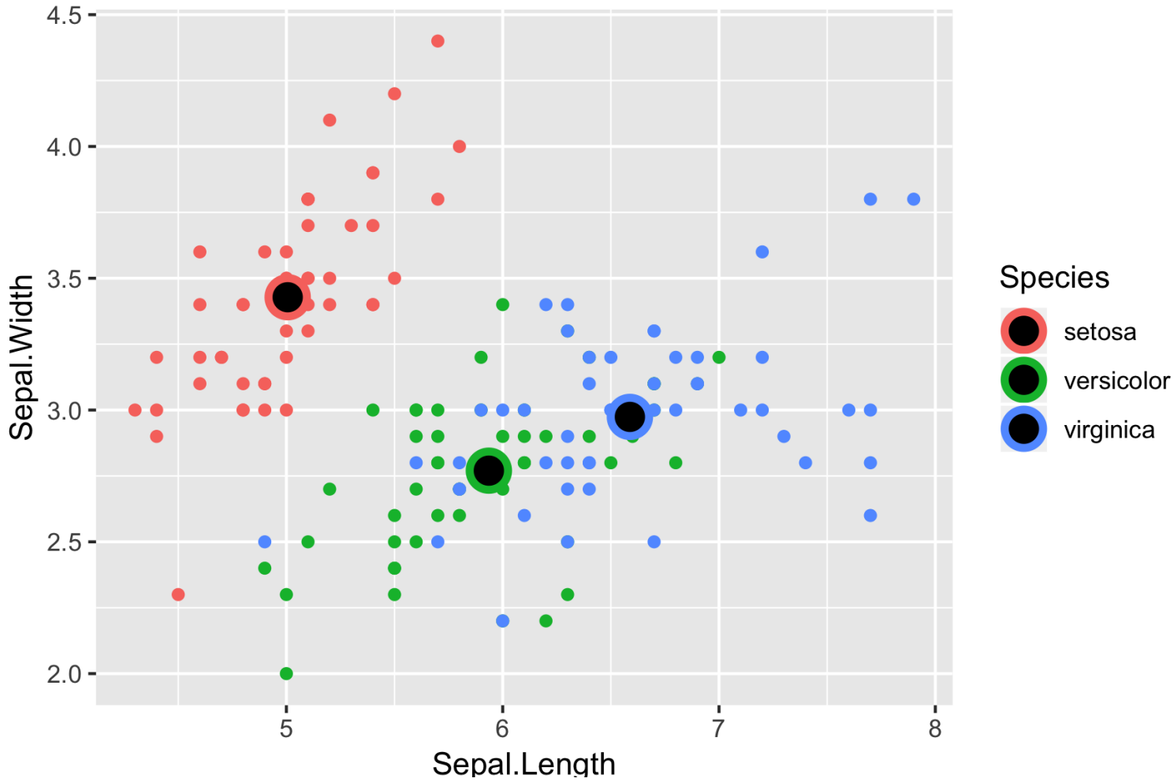
Example

```
ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width, col = Species)) +
  geom_point() +
  geom_point(data = iris.summary, shape = 21, size = 5,
             fill = "black", stroke = 2)
```



On-the-fly stats by ggplot2

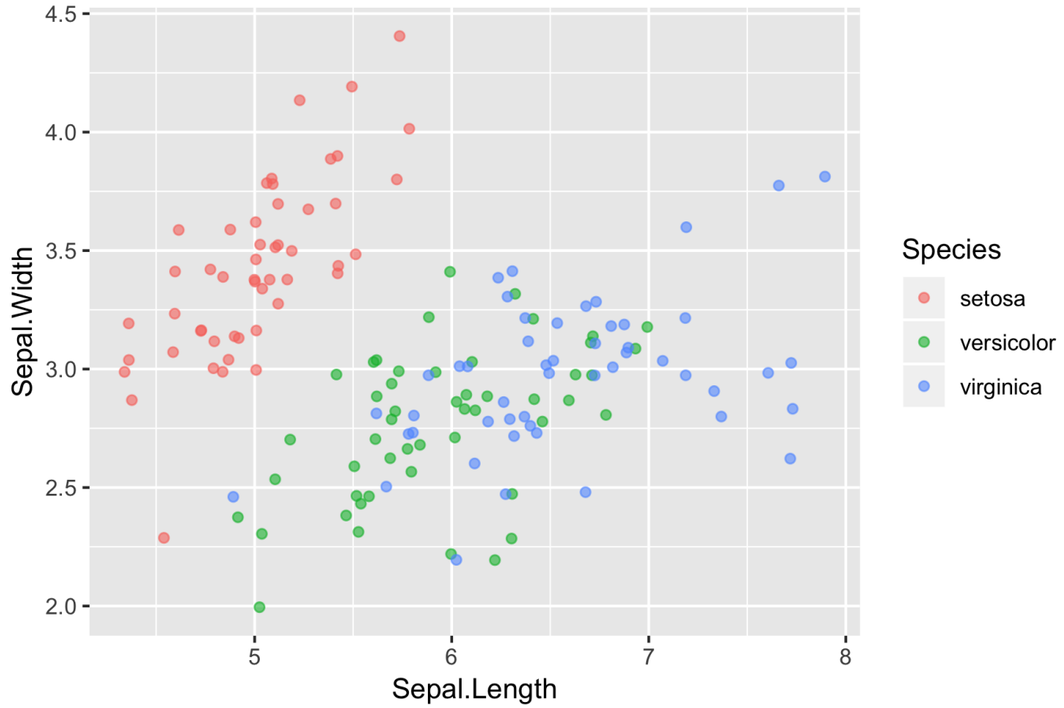
- See the second course for the stats layer.
- Note: Avoid plotting only the mean without a measure of spread, e.g. the standard deviation.



Don't forget to adjust alpha

- Combine jittering with alpha-blending if necessary

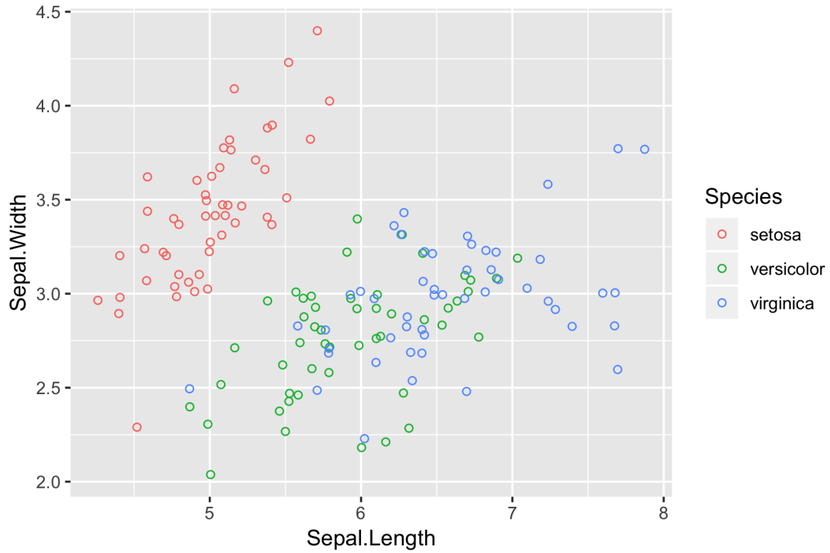
```
ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width, col = Species)) +
  geom_jitter(alpha = 0.6)
```



Hollow circles also help

- `shape = 1` is a. hollow circle.
- Not necessary to also use alpha-blending.

```
ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width, col = Species)) +
  geom_jitter(shape = 1)
```



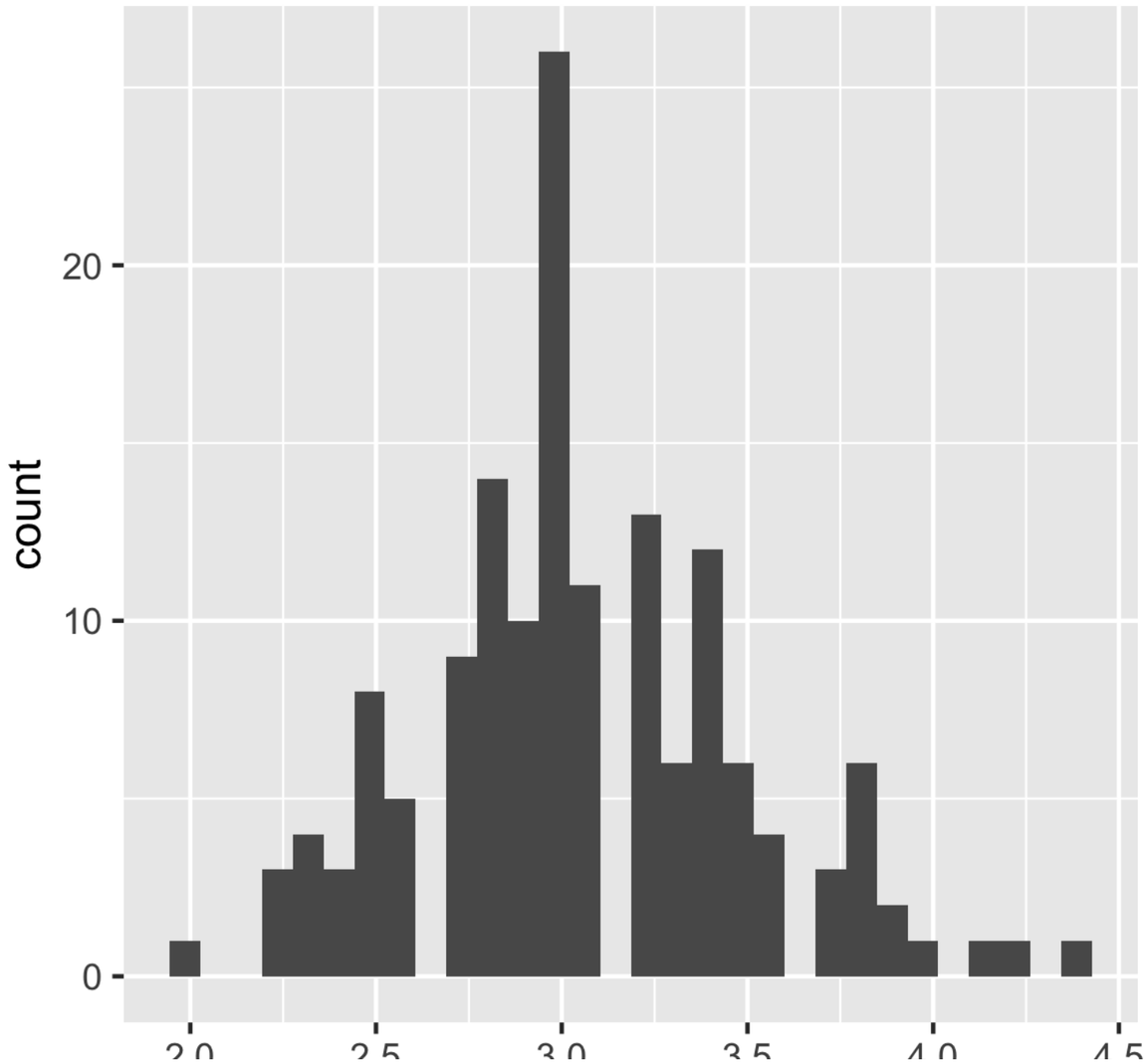
Default of 30 even bins

```
ggplot(iris, aes(x = Sepal.Width)) +
  geom_histogram()
```

- A plot of binned values
  - i.e. a statistical function

```
# Default bin width:
diff(range(iris$Sepal.Width))/30
```

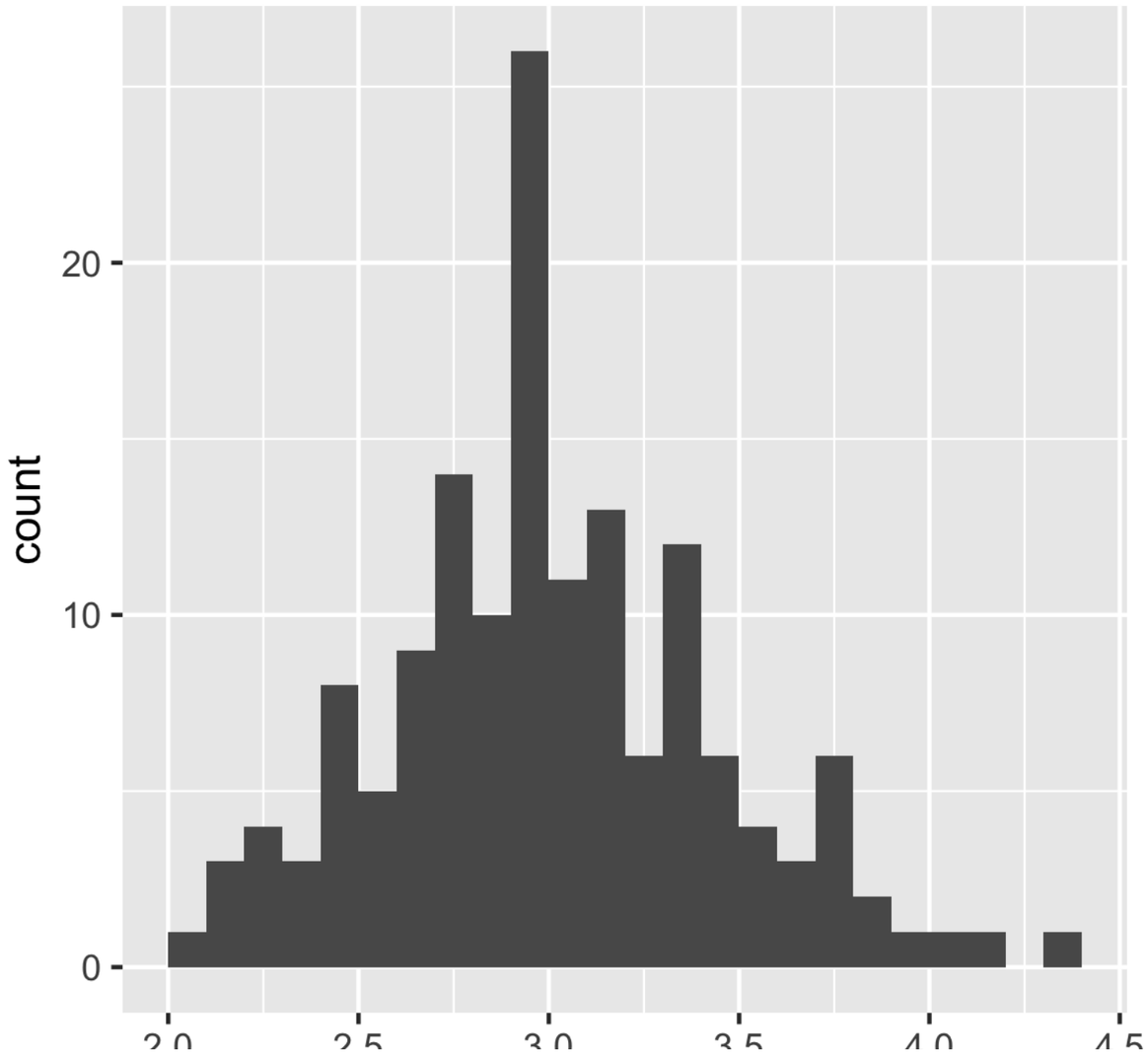
```
[1] 0.08
```



Re-position tick marks

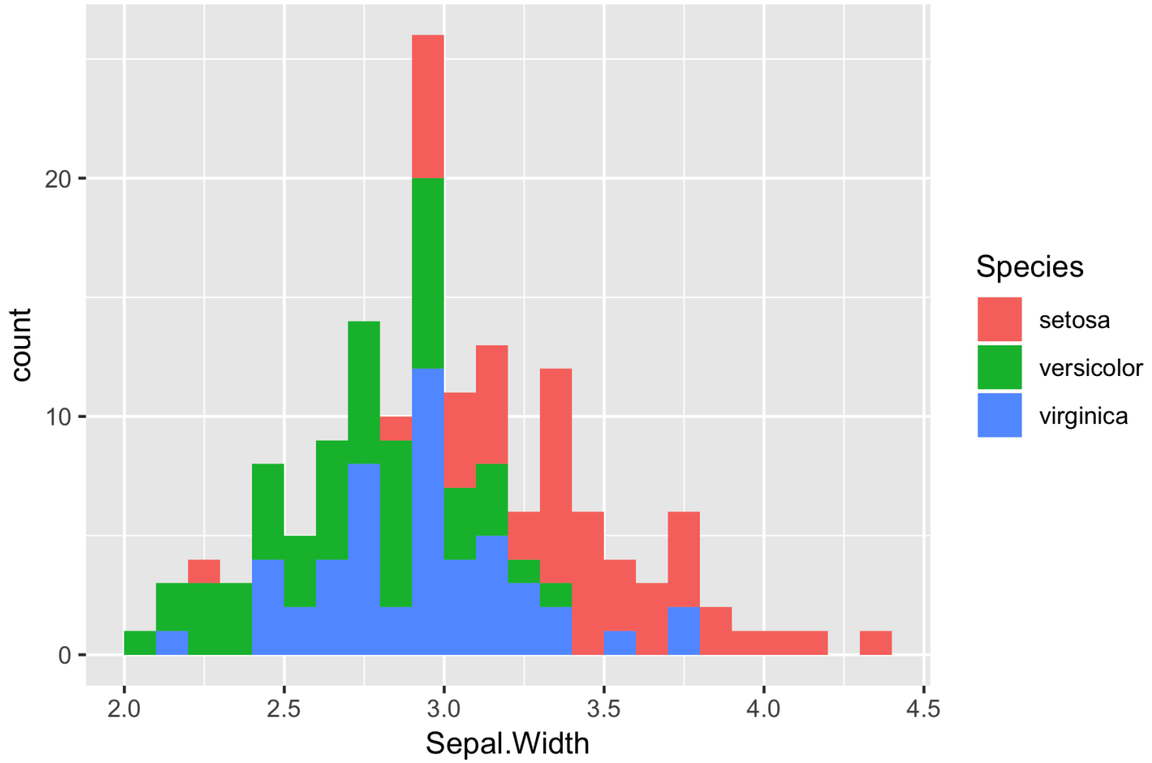
```
ggplot(iris, aes(x = Sepal.Width)) +
  geom_histogram(binwidth = 0.1,
                 center = 0.05)
```

- Always set a meaningful bin widths for your data.
- No spaces between bars.
- X axis labels are between bars.



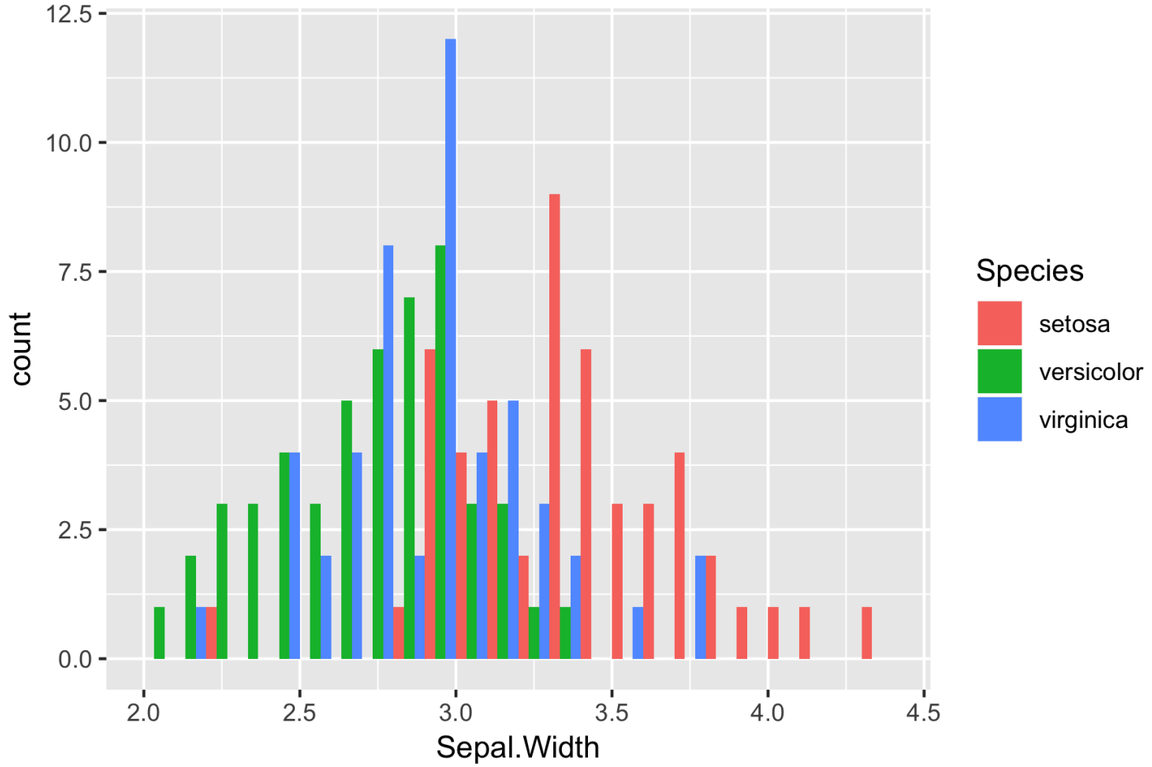
Default position is "stack"

```
ggplot(iris, aes(x = Sepal.Width,
                 fill = Species)) +
  geom_histogram(binwidth = .1,
                 center = 0.05,
                 position = "stack")
```



position = "dodge"

```
ggplot(iris, aes(x = Sepal.Width,
                 fill = Species)) +
  geom_histogram(binwidth = .1,
                 center = 0.05,
                 position = "dodge")
```

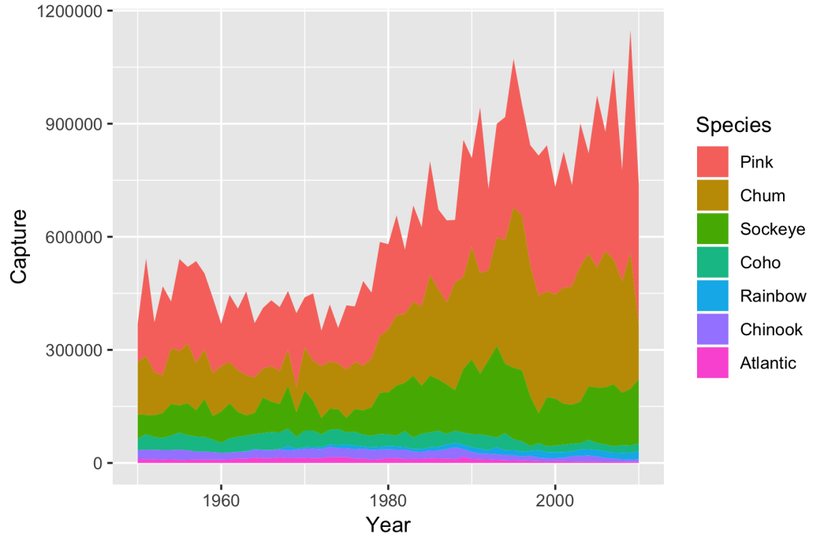


position = "fill"

```
ggplot(iris, aes(x = Sepal.Width,
                 fill = Species)) +
  geom_histogram(binwidth = .1,
                 center = 0.05,
                 position = "fill")
```

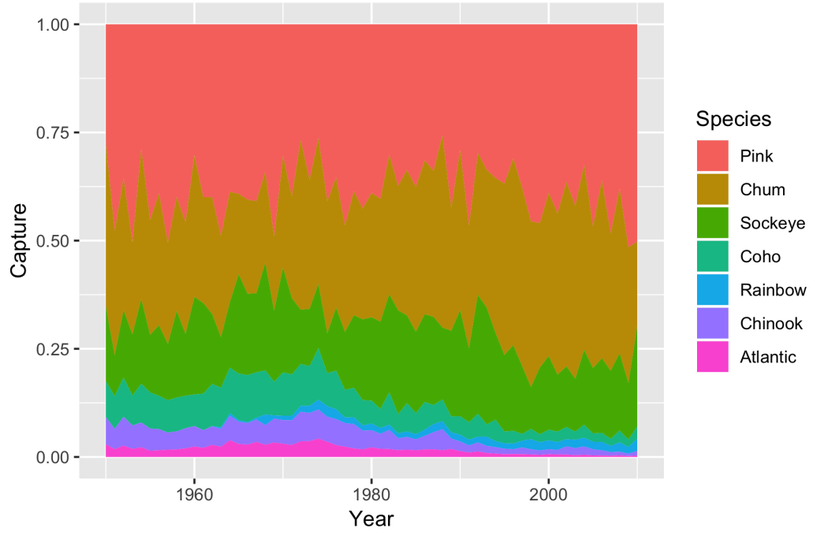
Fill aesthetic with geom_area()

```
ggplot(fish, aes(x = Year,
                 y = Capture,
                 fill = Species)) +
  geom_area()
```



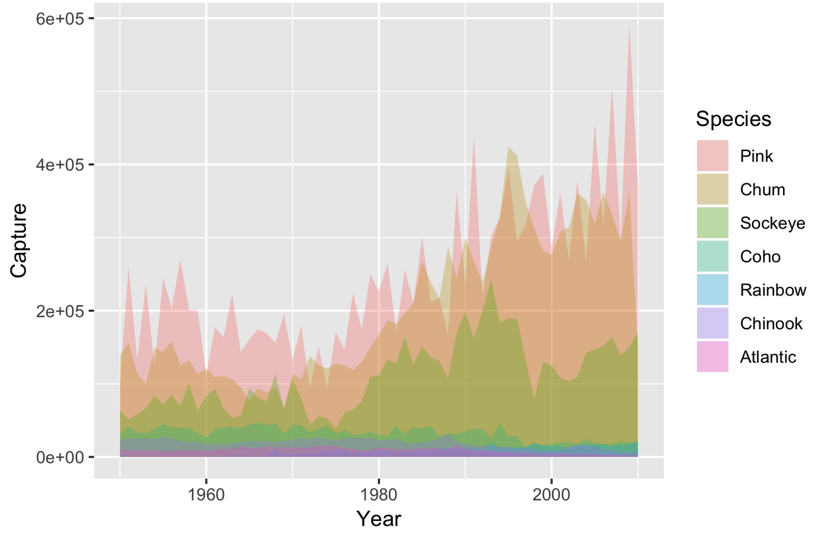
Using position = "fill"

```
ggplot(fish, aes(x = Year,
                 y = Capture,
                 fill = Species)) +
  geom_area(position = "fill")
```

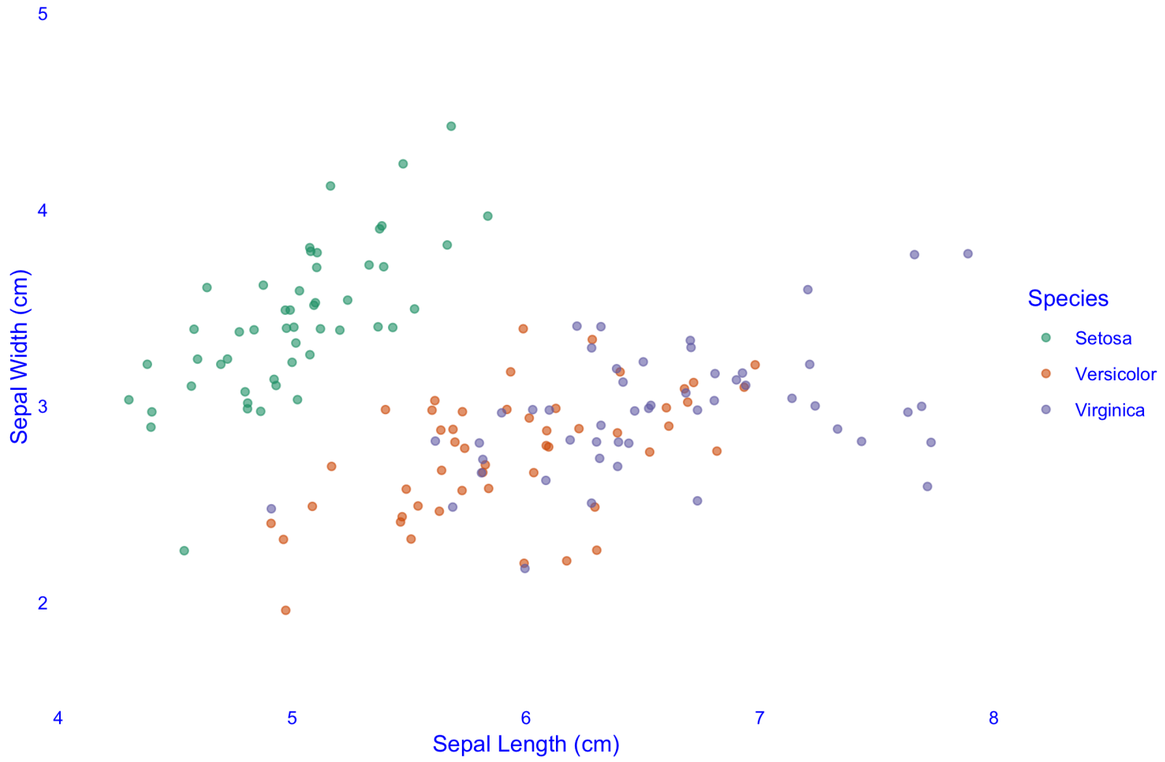


geom_ribbon()

```
ggplot(fish, aes(x = Year,
                 y = Capture,
                 fill = Species)) +
  geom_ribbon(aes(ymax = Capture,
                  ymin = 0),
              alpha = 0.3)
```

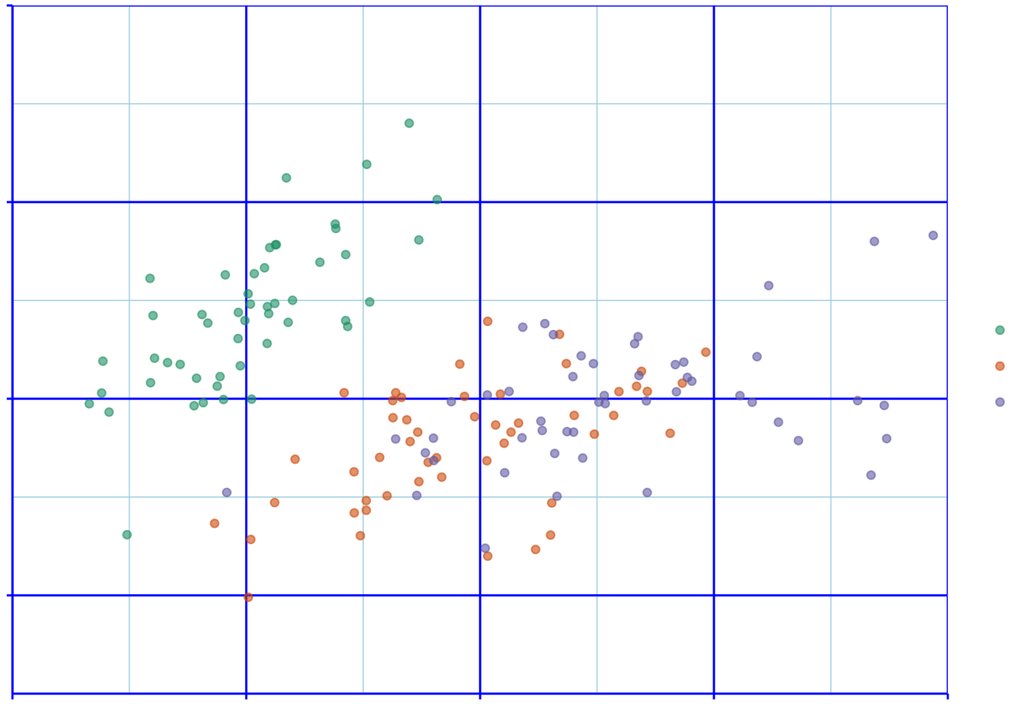


The text elements



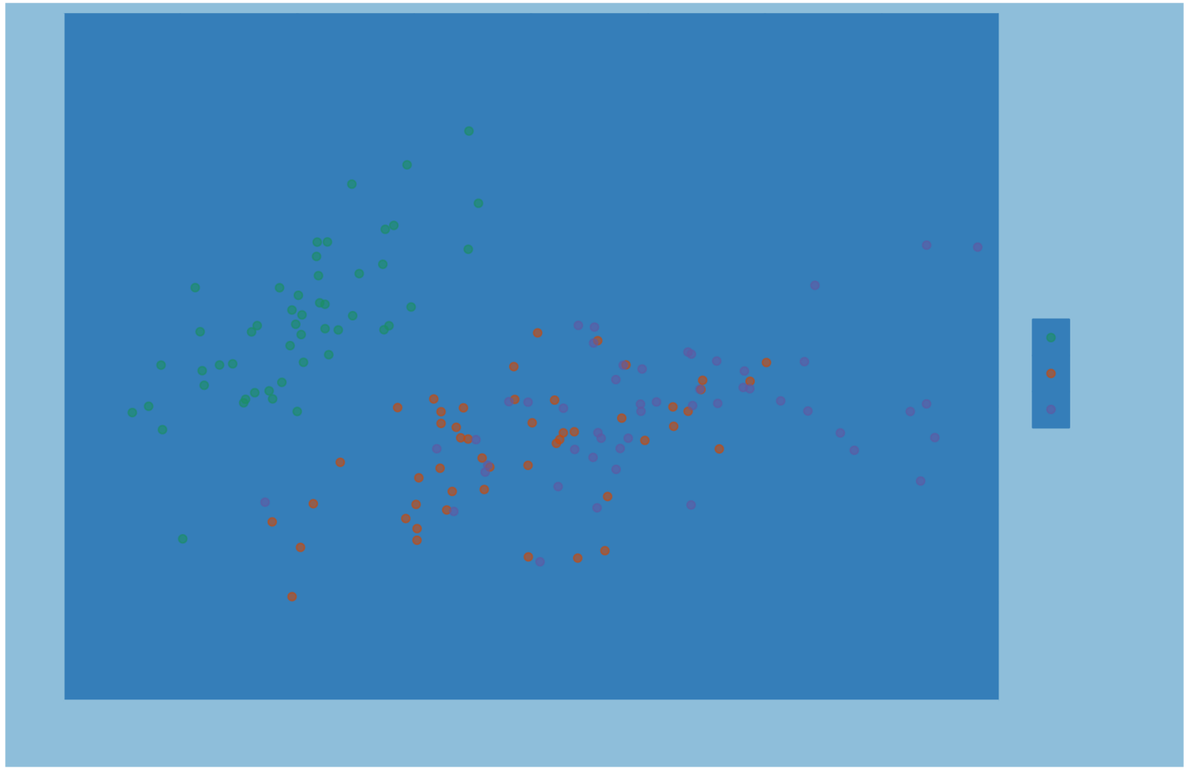

```
theme(
text,
  axis.title,
    axis.title.x,
      axis.title.x.top,
      axis.title.x.bottom,
    axis.title.y,
      axis.title.y.left,
      axis.title.y.right,
  title,
    legend.title,
    plot.title,
    plot.subtitle,
    plot.caption,
    plot.tag,
  axis.text,
    axis.text.x,
      axis.text.x.top,
      axis.text.x.bottom,
    axis.text.y,
      axis.text.y.left,
      axis.text.y.right,
  legend.text,
  strip.text,
    strip.text.x,
    strip.text.y)
```

Line elements



```
theme(
line,
  axis.ticks,
    axis.ticks.x,
      axis.ticks.x.top,
      axis.ticks.x.bottom,
    axis.ticks.y,
      axis.ticks.y.left,
      axis.ticks.y.right,
    axis.line,
      axis.line.x,
        axis.line.x.top,
        axis.line.x.bottom,
      axis.line.y,
        axis.line.y.left,
        axis.line.y.right,
  panel.grid,
    panel.grid.major,
      panel.grid.major.x,
      panel.grid.major.y,
    panel.grid.minor,
      panel.grid.minor.x,
      panel.grid.minor.y)
```

Rect elements



```
theme(
rect,
  legend.background,
  legend.key,
  legend.box.background,
  panel.background,
  panel.border,
  plot.background,
  strip.background,
    strip.background.x,
    strip.background.y)
```

Modifying whitespace

Whitespace means all the non-visible margins and spacing in the plot.

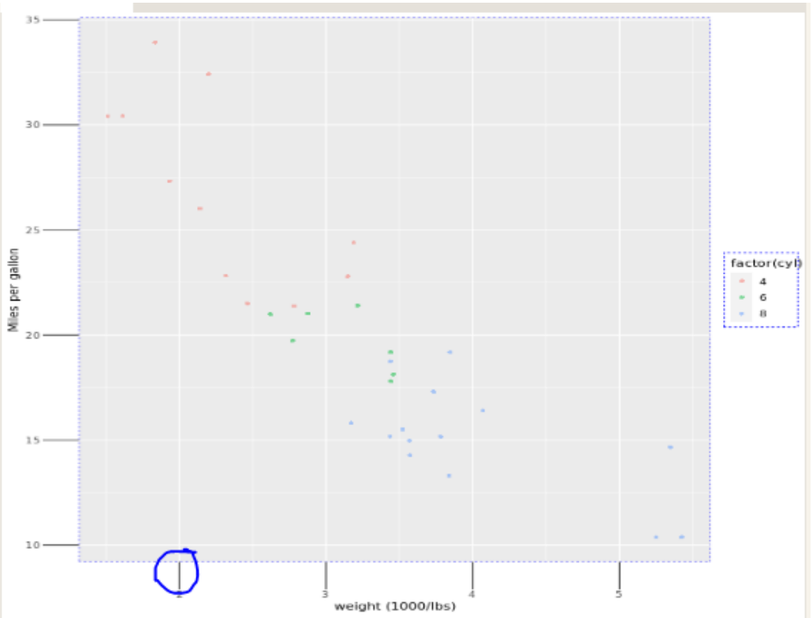
To set a single whitespace value, use `unit(x, unit)`, where `x` is the amount and `unit` is the unit of measure.

Borders require you to set 4 positions, so use `margin(top, right, bottom, left, unit)`. To remember the margin order, think **TRouBLe**.

The default unit is `"pt"` (points), which scales well with text. Other options include "cm", "in" (inches) and "lines" (of text).

`plt_mpg_vs_wt_by_cyl` is available. The panel and legend are wrapped in blue boxes so you can see how they change.

```r
# View the original plot
plt_mpg_vs_wt_by_cyl

plt_mpg_vs_wt_by_cyl +
  theme(
    # Set the axis tick length to 2 lines
    axis.ticks.length = unit(2,"lines")
  )
```



Run Code | Submit Answer | ← Previous Plot | 2/2 | → Next Plot

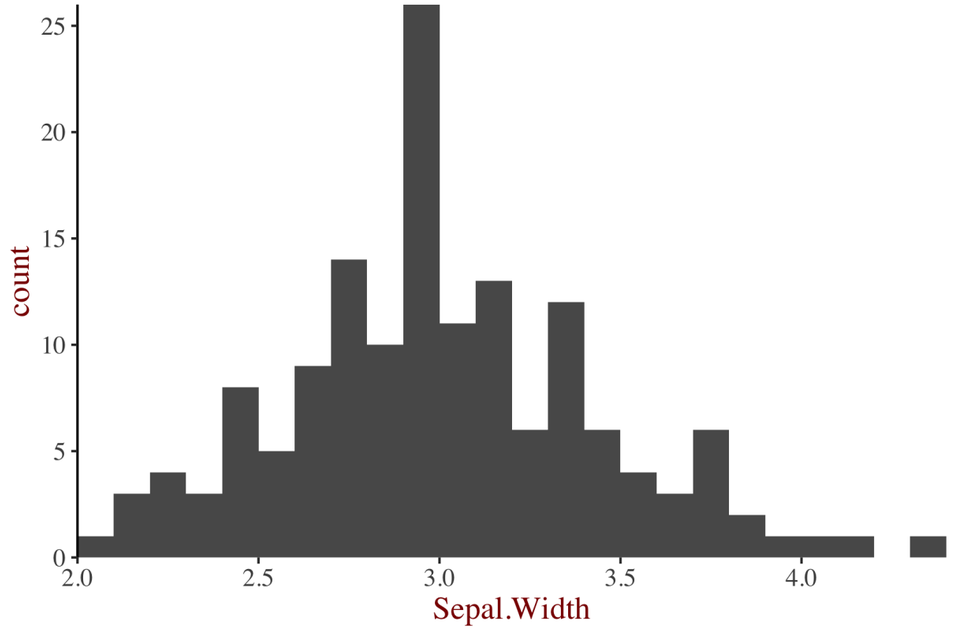
- Give the axis tick length, `axis.ticks.length`, a unit of `2` `"lines"`.
- Give the legend key size, `legend.key.size`, a unit of `3` centimeters (`"cm"`).
- Set the `legend.margin` to `20` points (`"pt"`) on the top, `30` pts on the right, `40` pts on the bottom, and `50` pts on the left.
- Set the plot margin, `plot.margin`, to `10`, `30`, `50`, and `70` millimeters (`"mm"`).

Defining theme objects

```
theme_iris <- theme(text = element_text(family = "serif", size = 14),
          rect = element_blank(),
          panel.grid = element_blank(),
          title = element_text(color = "#8b0000"),
          axis.line = element_line(color = "black"))
```

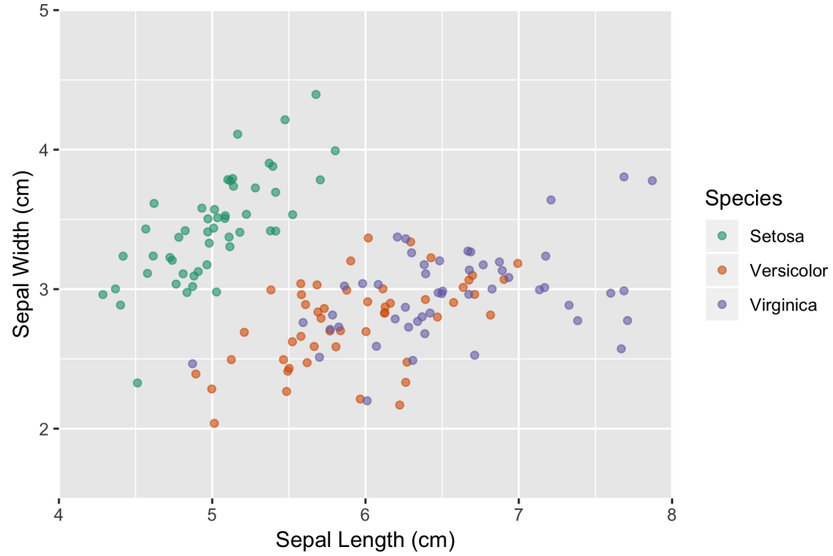
Reusing theme objects

```
m +
  theme_iris +
  theme(axis.line.x = element_blank())
```

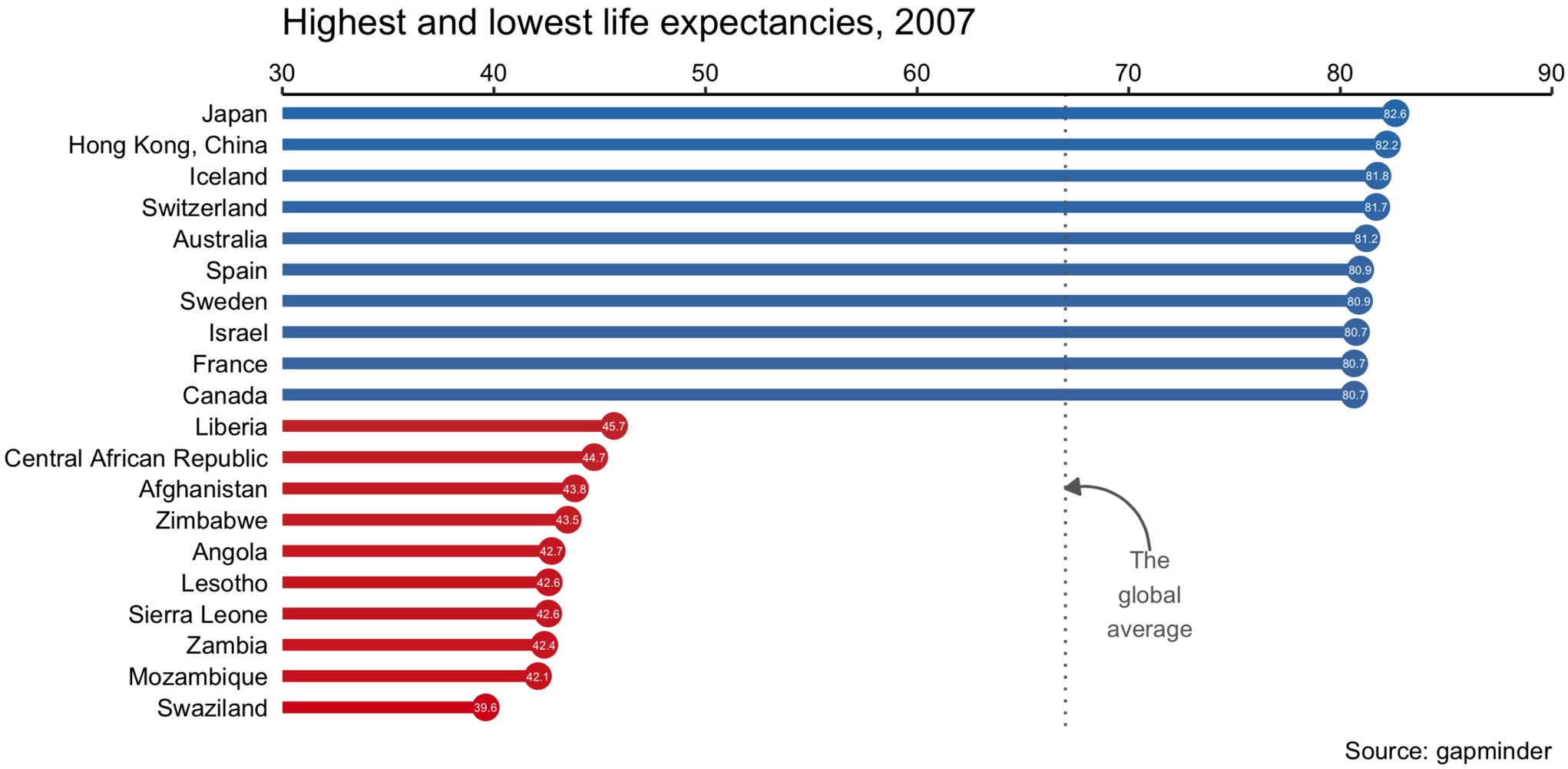


Setting themes

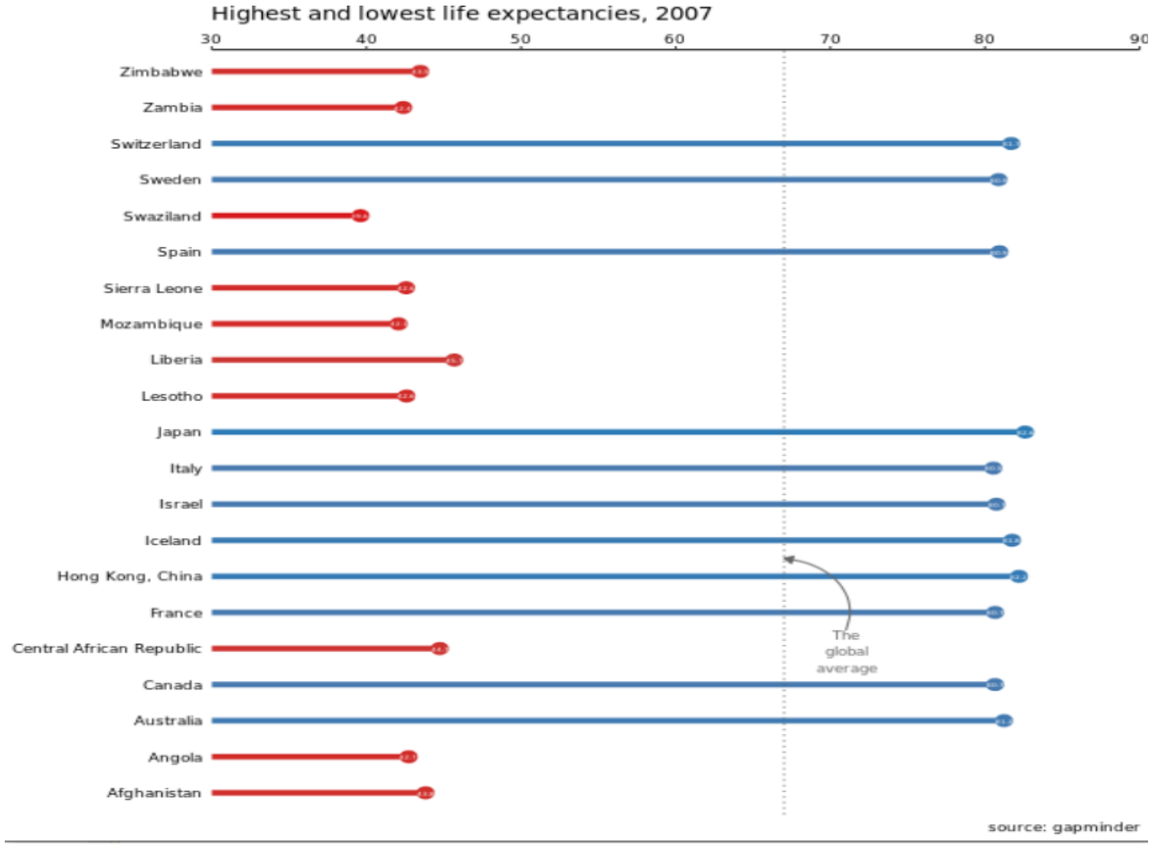
```
theme_set(original)


# Alternatively
# theme_set(theme_grey())
```



Add embellishments



```
# Add a curve
plt_country_vs_lifeExp +
  step_1_themes +
  geom_vline(xintercept = global_mean, color = "grey40", linetype = 3) +
  step_3_annotation +
  annotate(
    "curve",
    x = x_start, y = y_start,
    xend = x_end, yend = y_end,
    arrow = arrow(length = unit(0.2, "cm"), type = "closed"),
    color = "grey40"
  )
```



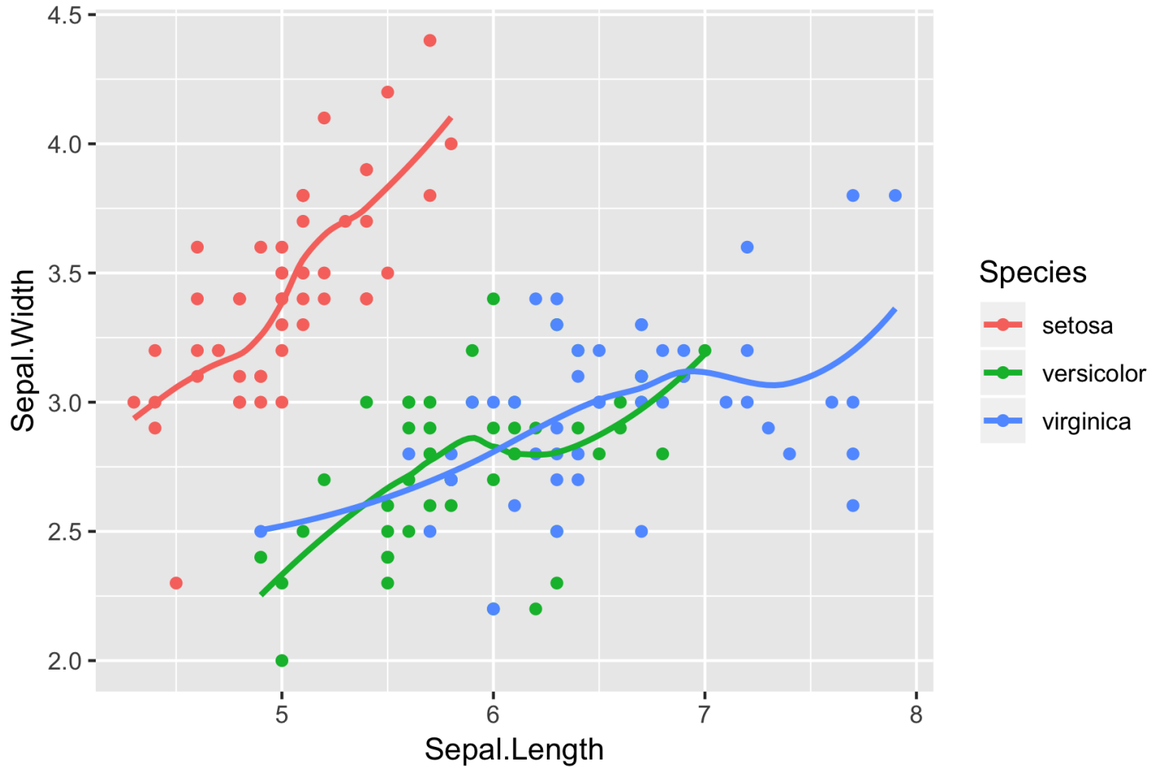
The geom_/stat_ connection

stat_	geom_
`stat_bin()`	`geom_histogram()`, `geom_freqpoly()`
`stat_count()`	`geom_bar()`

stat_smooth(se = FALSE)

```
ggplot(iris, aes(x = Sepal.Length,
                 y = Sepal.Width,
                 color = Species)) +
  geom_point() +
  geom_smooth(se = FALSE)
```

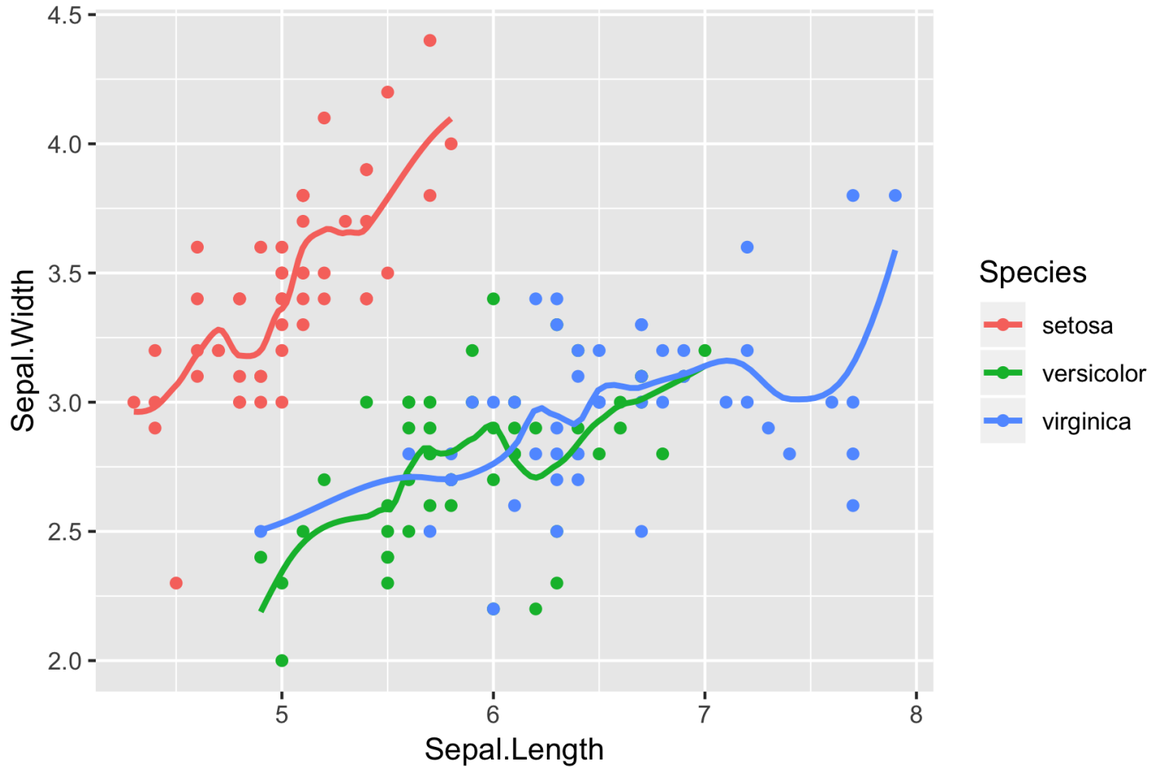
```
geom_smooth() using method = 'loess' and
formula 'y ~ x'
```



geom_smooth(span = 0.4)

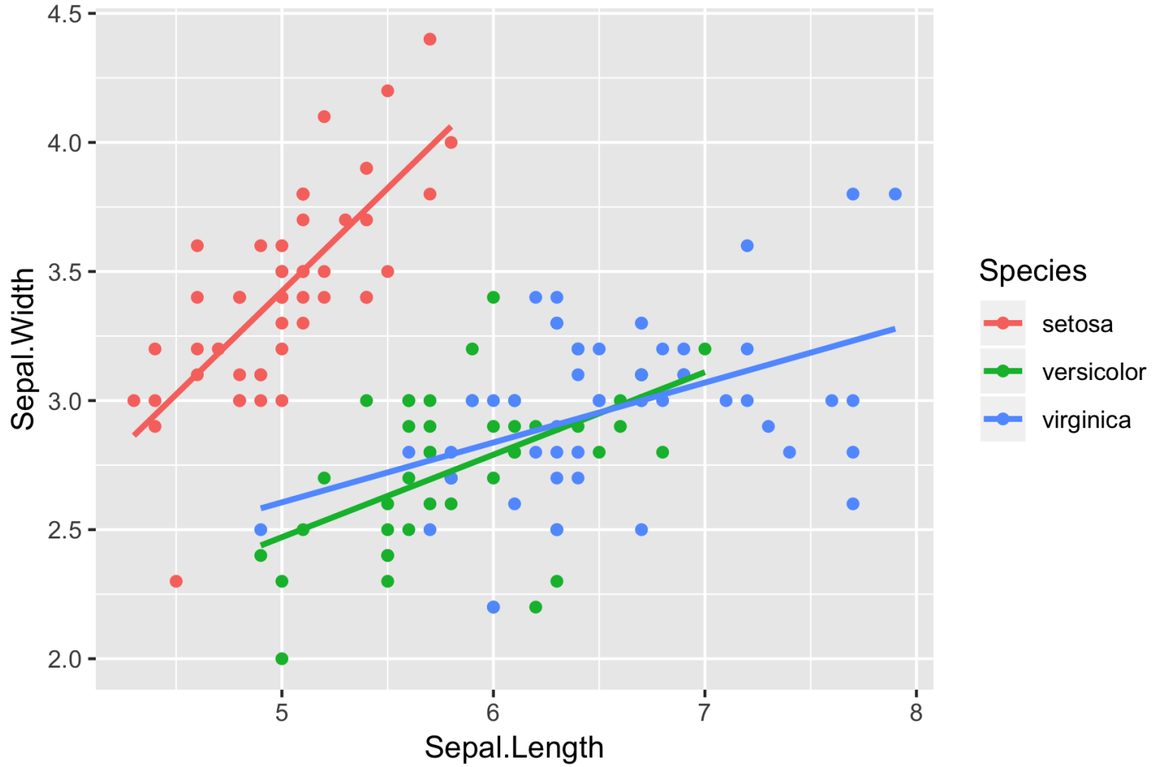
```
ggplot(iris, aes(x = Sepal.Length,
                 y = Sepal.Width,
                 color = Species)) +
  geom_point() +
  geom_smooth(se = FALSE, span = 0.4)
```

```
geom_smooth() using method = 'loess' and
formula 'y ~ x'
```



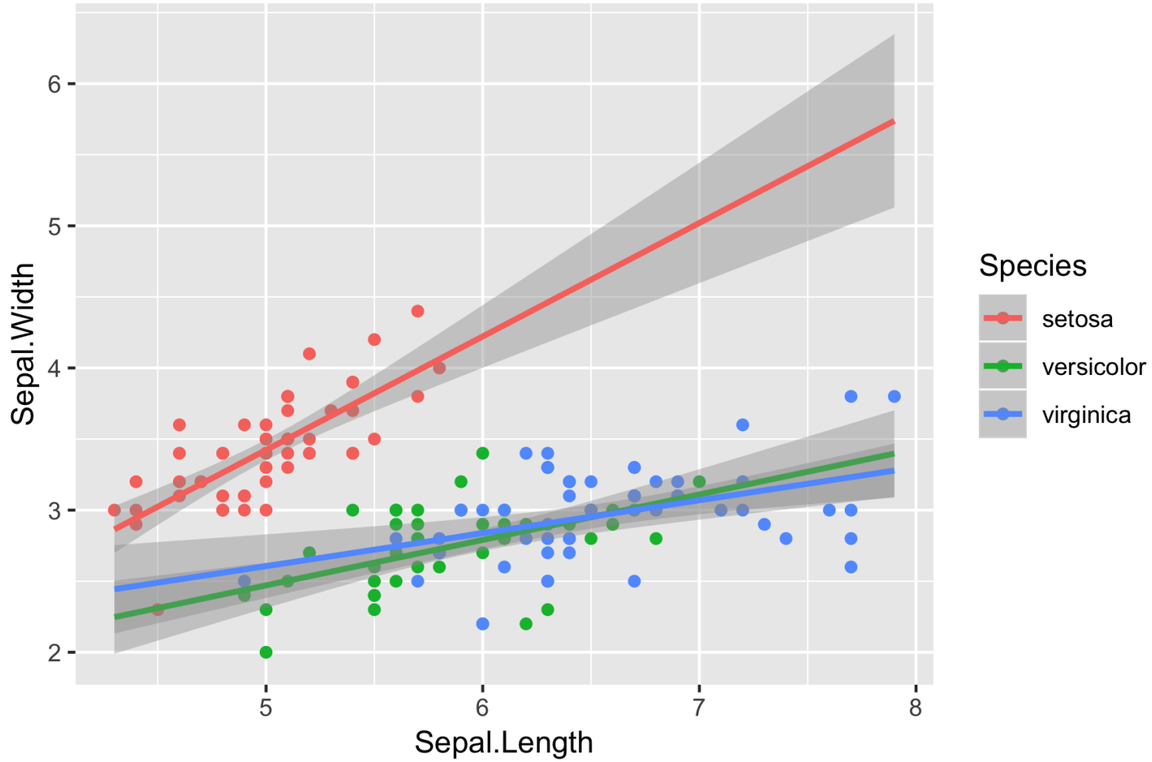
geom_smooth(method = "lm")

```
ggplot(iris, aes(x = Sepal.Length,
                 y = Sepal.Width,
                 color = Species)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```

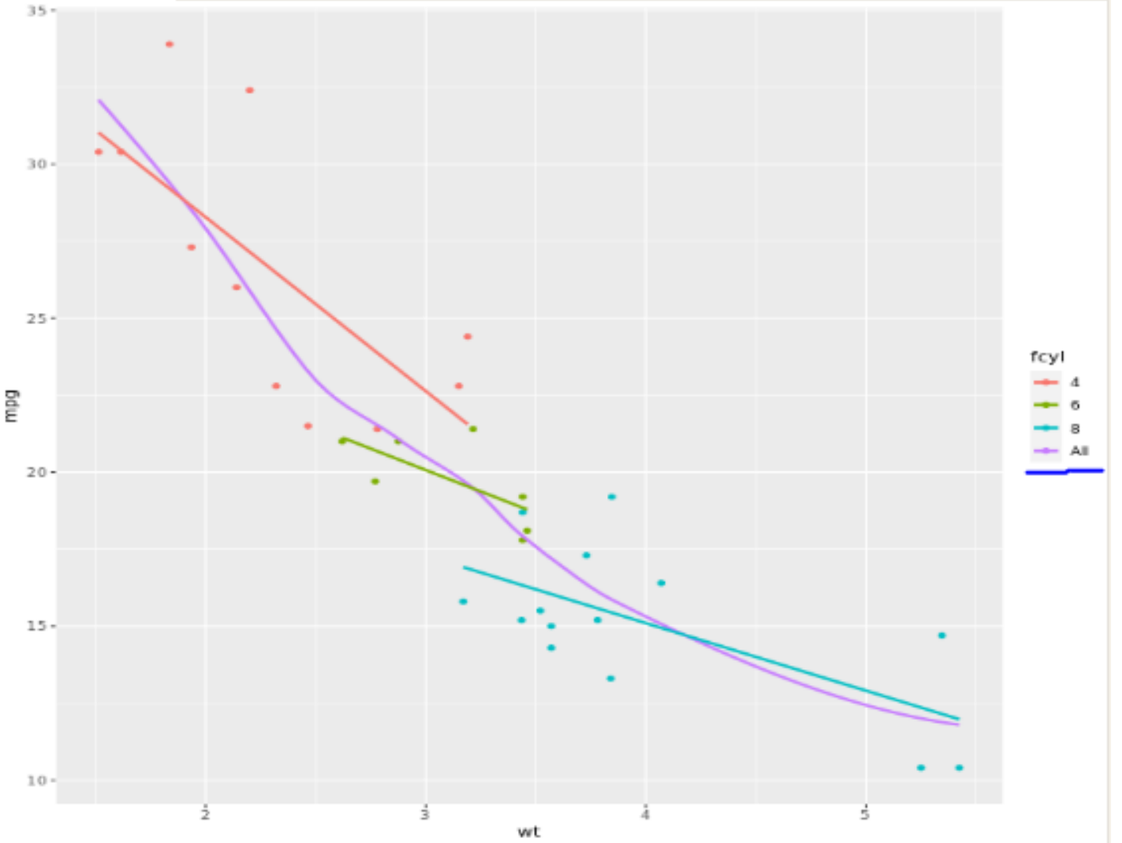


geom_smooth(fullrange = TRUE)

```
ggplot(iris, aes(x = Sepal.Length,
                 y = Sepal.Width,
                 color = Species)) +
  geom_point() +
  geom_smooth(method = "lm",
              fullrange = TRUE)
```



```r
# Amend the plot
ggplot(mtcars, aes(x = wt, y = mpg,
                   color = fcyl)) +
  geom_point() +
  # Map color to dummy variable "All"
  stat_smooth(aes(color = "All"),
              se = FALSE) +
  stat_smooth(method = "lm", se = FALSE)
```



Run Code

Submit Answer

← Previous Plot

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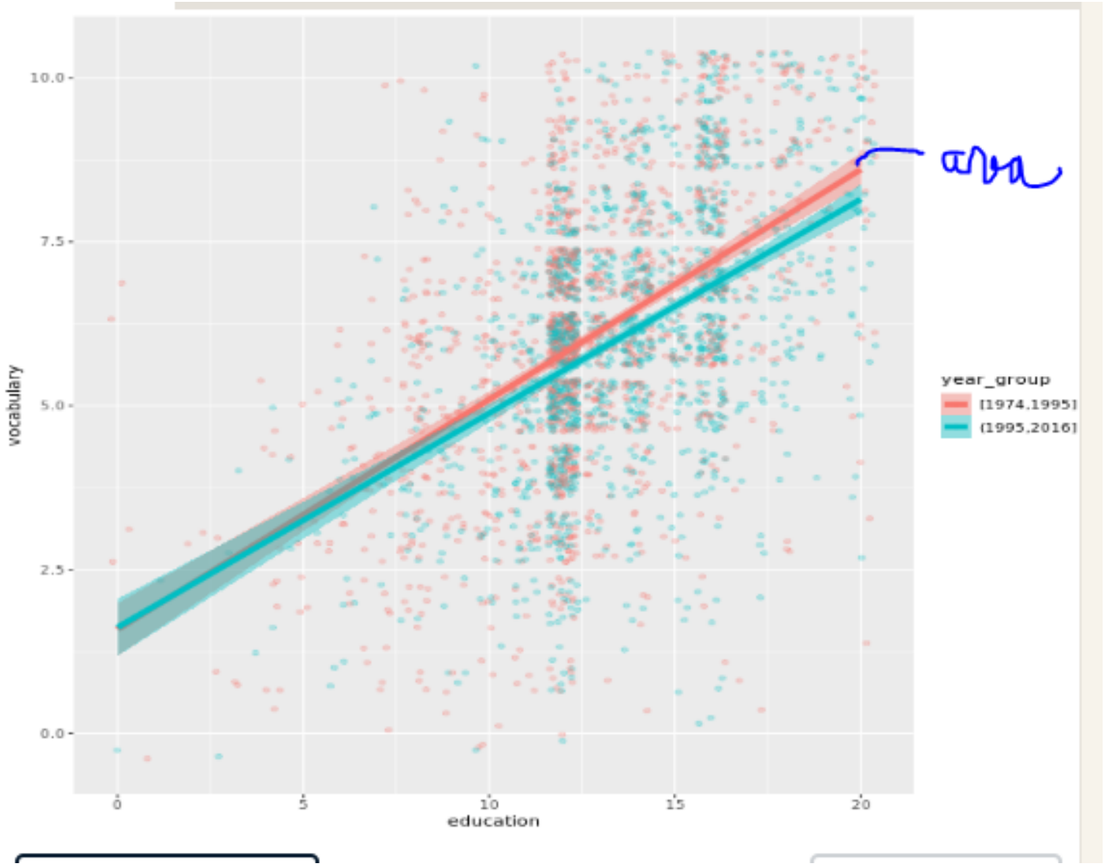
→ Next Plot

```r
# Amend the plot
ggplot(Vocab, aes(x = education, y = vocabulary, color = year_group)) +
  geom_jitter(alpha = 0.25) +
  # Map the fill color to year_group, set the line size to 2
  stat_smooth(aes(fill = year_group), method = "lm", size = 2)
```



Other stat_ functions

stat_	geom_
`stat_boxplot()`	`geom_boxplot()`
`stat_bindot()`	`geom_dotplot()`
`stat_bin2d()`	`geom_bin2d()`
`stat_binhex()`	`geom_hex()`

Other stat_ functions

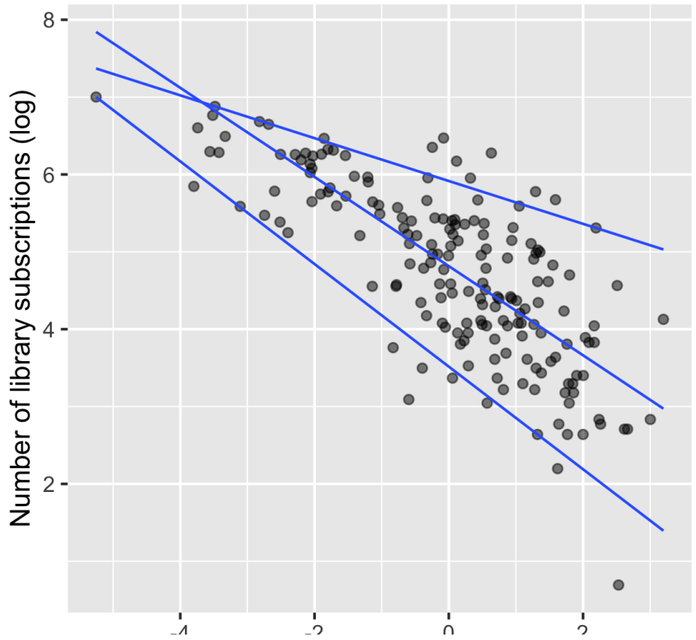
stat_	geom_
`stat_boxplot()`	`geom_boxplot()`
`stat_bindot()`	`geom_dotplot()`
`stat_bin2d()`	`geom_bin2d()`
`stat_binhex()`	`geom_hex()`
`stat_contour()`	`geom_contour()`
`stat_quantile()`	`geom_quantile()`
`stat_sum()`	`geom_count()`

Dealing with heteroscedasticity

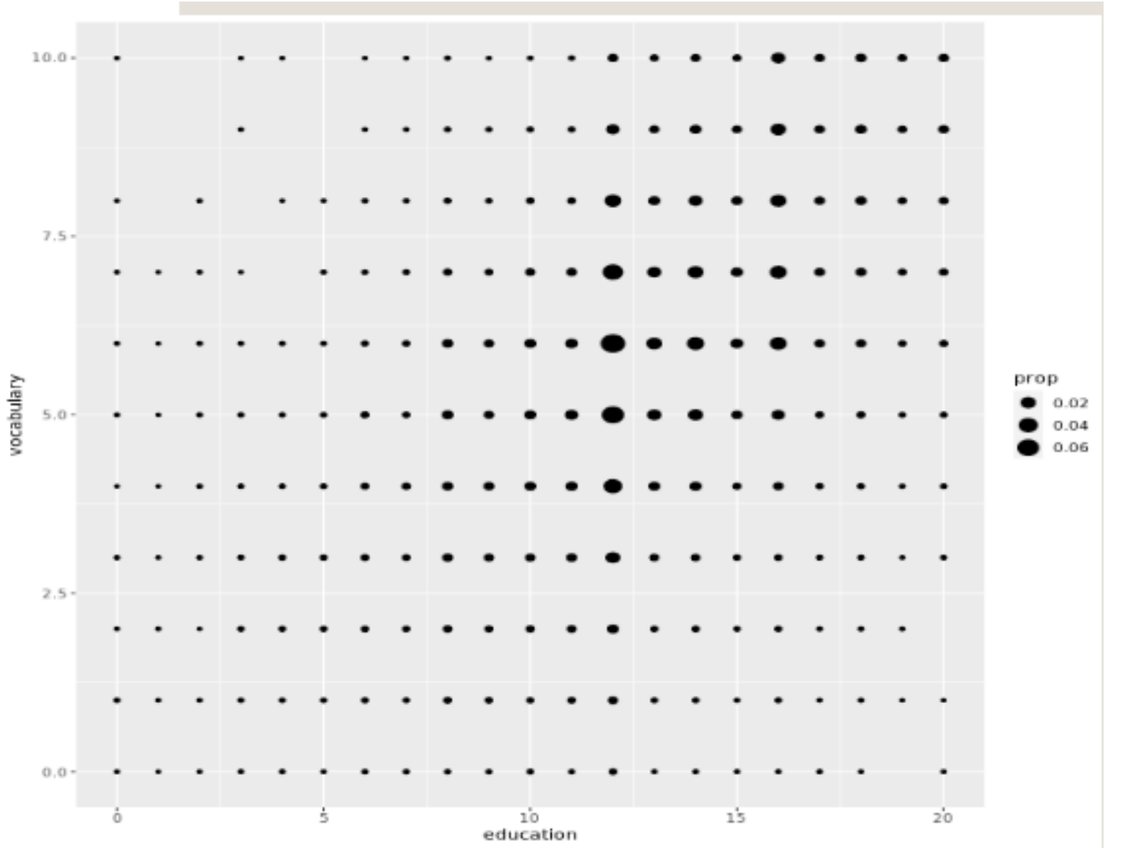
```
library(AER)
data(Journals)

p <- ggplot(Journals,
            aes(log(price/citations),
                log(subs))) +
  geom_point(alpha = 0.5) +
  labs(...)
```

```
p +
  geom_quantile(quantiles =
                c(0.05, 0.50, 0.95))
```

geom_	stat_
`geom_count()`	`stat_sum()`
`geom_quantile()`	`stat_quantile()`



```r
# Amend the stat to use proportion sizes
ggplot(Vocab, aes(x = education, y =
vocabulary)) +
  stat_sum(aes(size = ..prop..))
```



Calculating statistics

```
set.seed(123)
xx <- rnorm(100)

# Hmisc
library(Hmisc)
smean.sdl(xx, mult = 1)
```

```
      Mean       Lower       Upper
 0.09040591 -0.82240997  1.00322179
```

stat_summary()

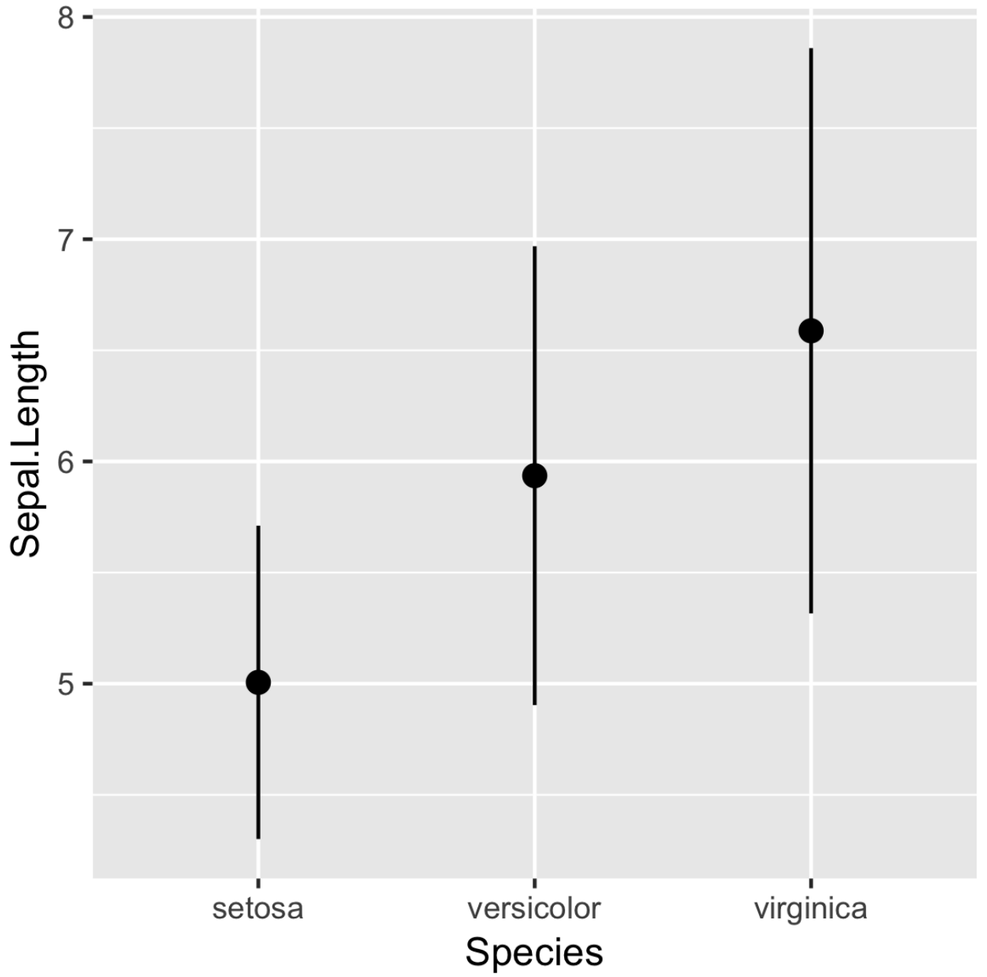
```
# ggplot2
mean_sdl(xx, mult = 1)
```

```
          y     ymin     ymax
1 0.09040591 -0.82241 1.003222
```

A data.frame with this columns

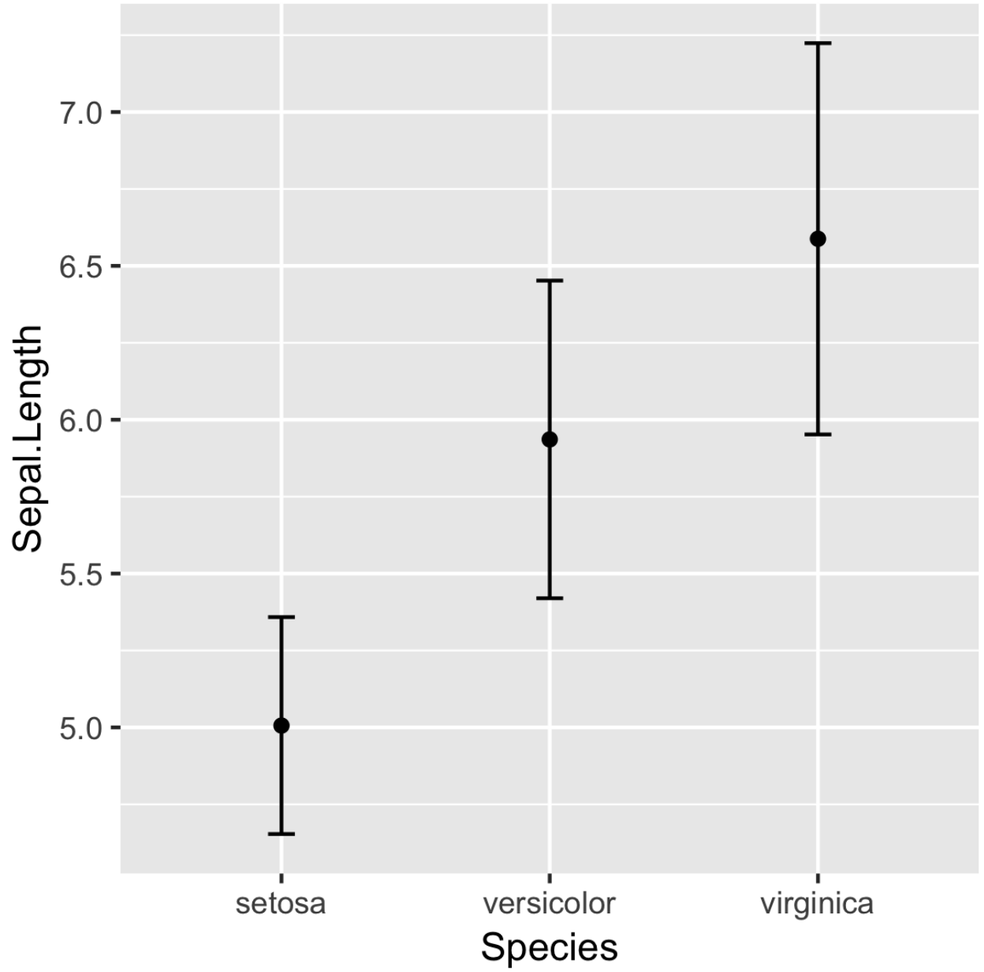
```
ggplot(iris, aes(x = Species,
                 y = Sepal.Length)) +
 stat_summary(fun.data = mean_sdl,
              fun.args = list(mult = 1))
```

- Uses `geom_pointrange()` by default



stat_summary()

```
ggplot(iris, aes(x = Species,
                 y = Sepal.Length)) +
  stat_summary(fun.y = mean,
               geom = "point") +
  stat_summary(fun.data = mean_sdl,
               fun.args = list(mult = 1),
               geom = "errorbar",
               width = 0.1)
```



95% confidence interval

```
ERR <- qt(0.975, length(xx) - 1) * (sd(xx) / sqrt(length(xx)))
mean(xx)
```

```
0.09040591
```

```
mean(xx) + (ERR * c(-1, 1)) # 95% CI
```

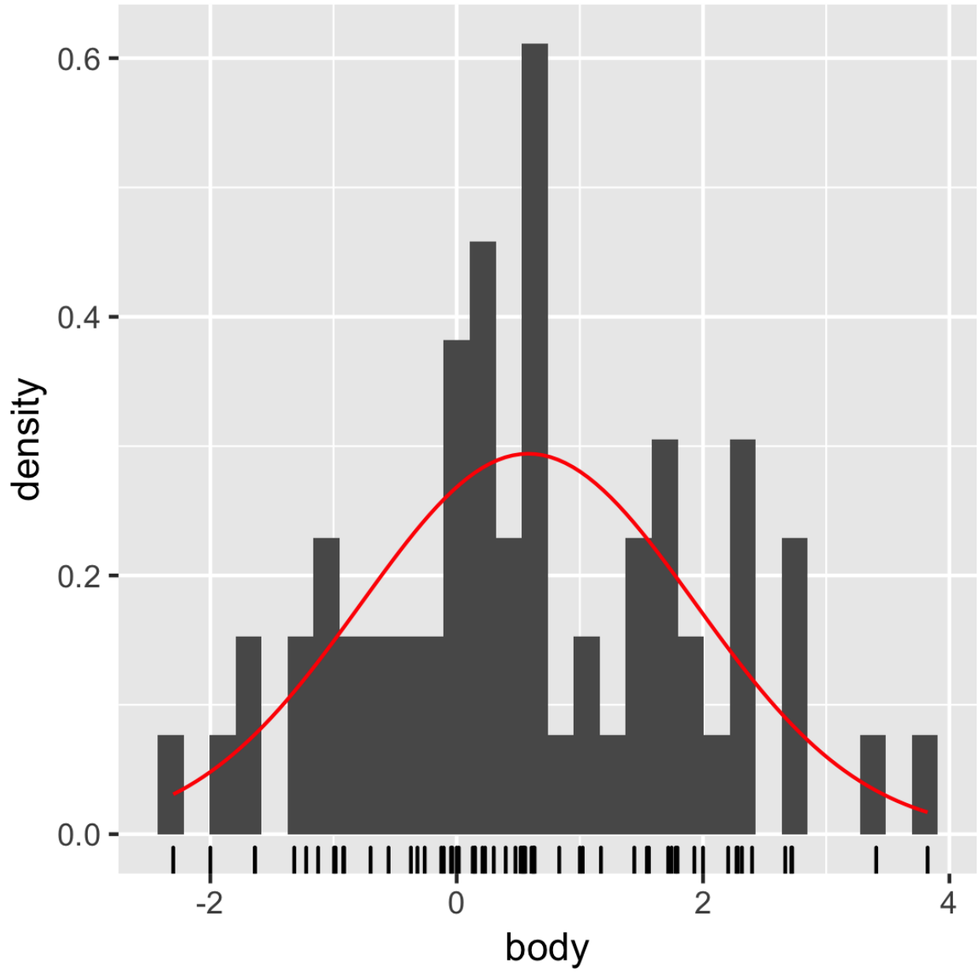
```
-0.09071657  0.27152838
```

```
mean_cl_normal(xx)
```

```
           y        ymin      ymax
0.09040591 -0.09071657 0.2715284
```

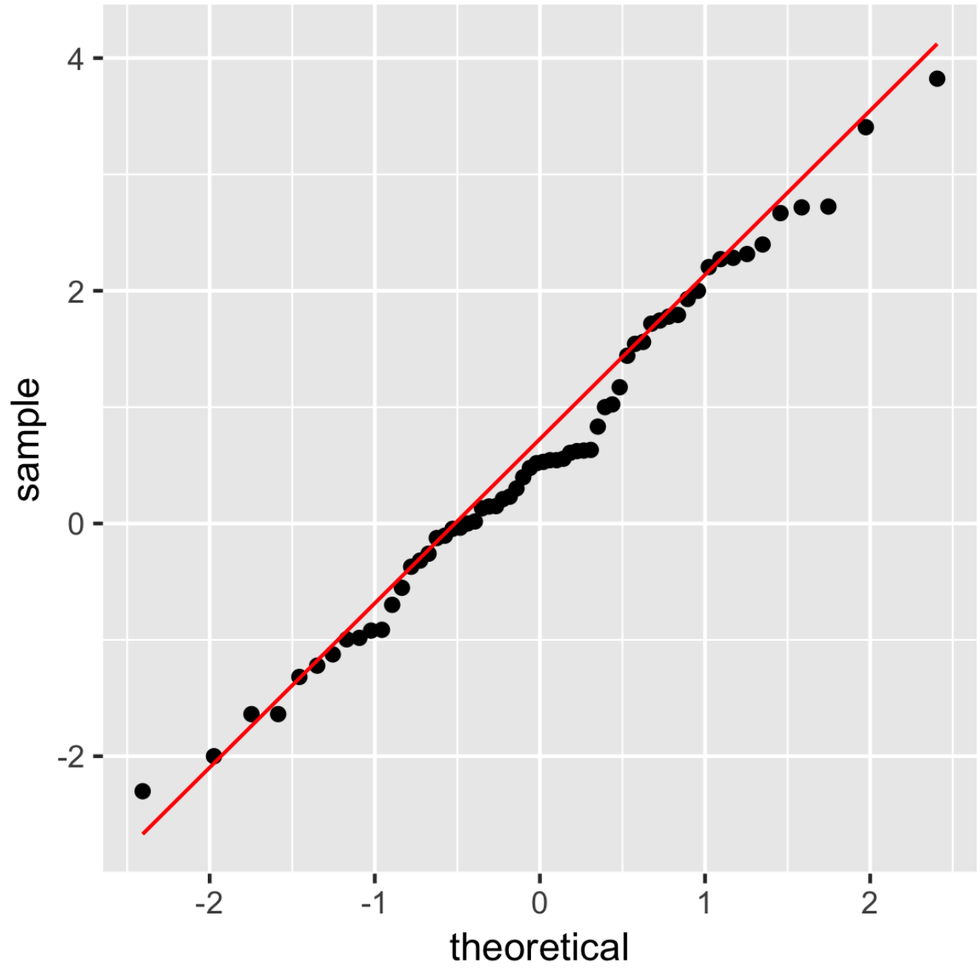
Normal distribution

```
mam.new <- data.frame(body = log10(mammals$body))

ggplot(mam.new, aes(x = body)) +
  geom_histogram(aes( y = ..density..)) +
  geom_rug() +
  stat_function(fun = dnorm, color = "red",
                args = list(mean = mean(mam.new$body),
                            sd = sd(mam.new$body)))
```



QQ plot

```
ggplot(mam.new, aes(sample = body)) +
  stat_qq() +
  geom_qq_line(col = "red")
```



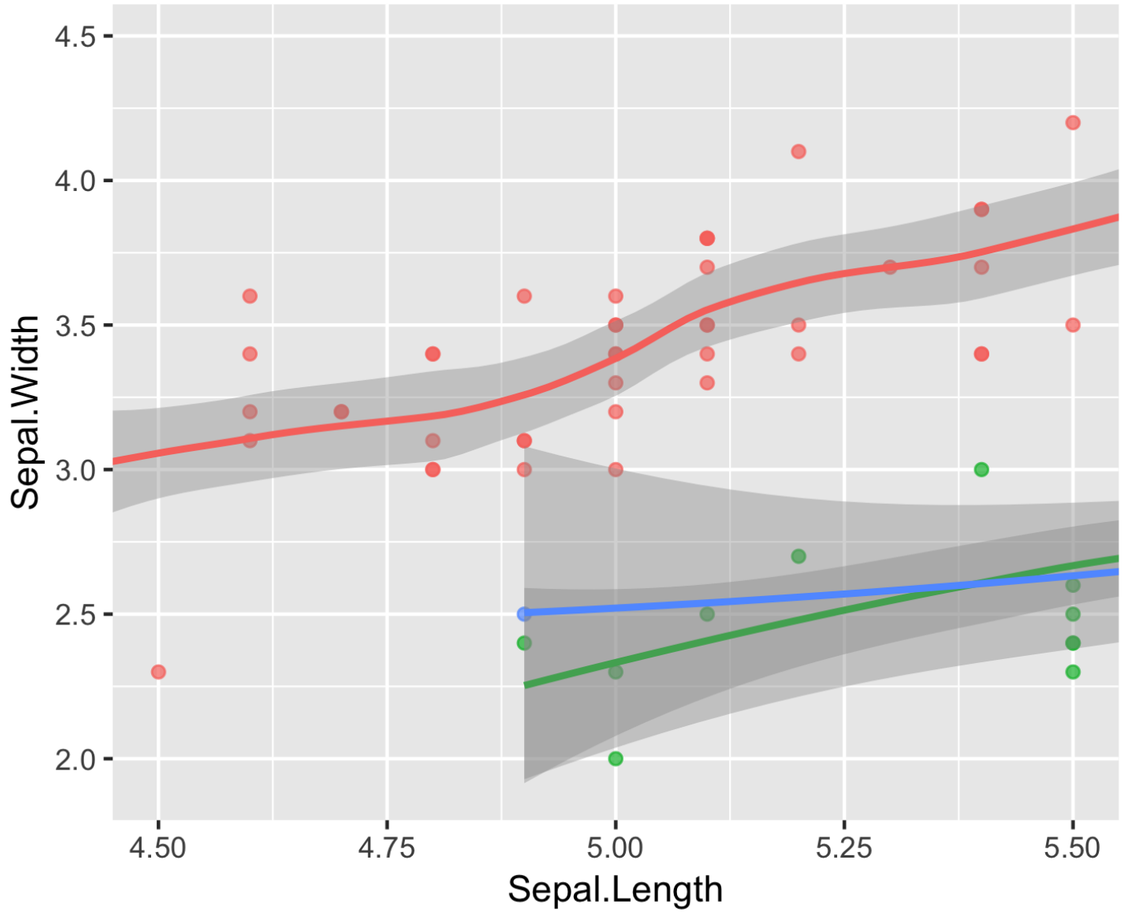
Plot counts to overcome over-plotting

	Cause of Over-plotting	Solutions	Here...
1.	Large datasets	Alpha-blending, hollow circles, point size	alpha = 0.5, shape = "." shape = 16
2.	Aligned values on a single axis	As above, plus change position	position_jitter position_jitterdodge
3.	Low-precision data	Position: jitter geom_jitter(alpha = 0.5, width = 0.1)	`geom_count()`
4.	Integer data	Position: jitter geom_jitter(alpha = 0.2, shape = 1)	`geom_count()`

geom_	stat_
`geom_count()`	`stat_sum()`

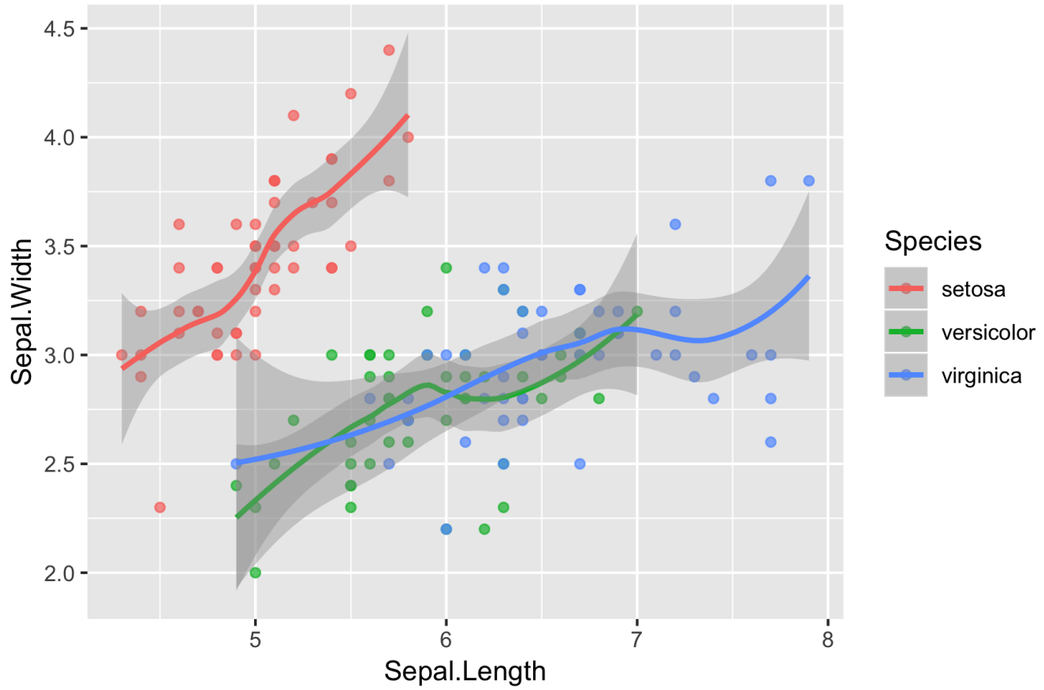
coord_cartesian()

```
iris.smooth +
  coord_cartesian(xlim = c(4.5, 5.5))
```

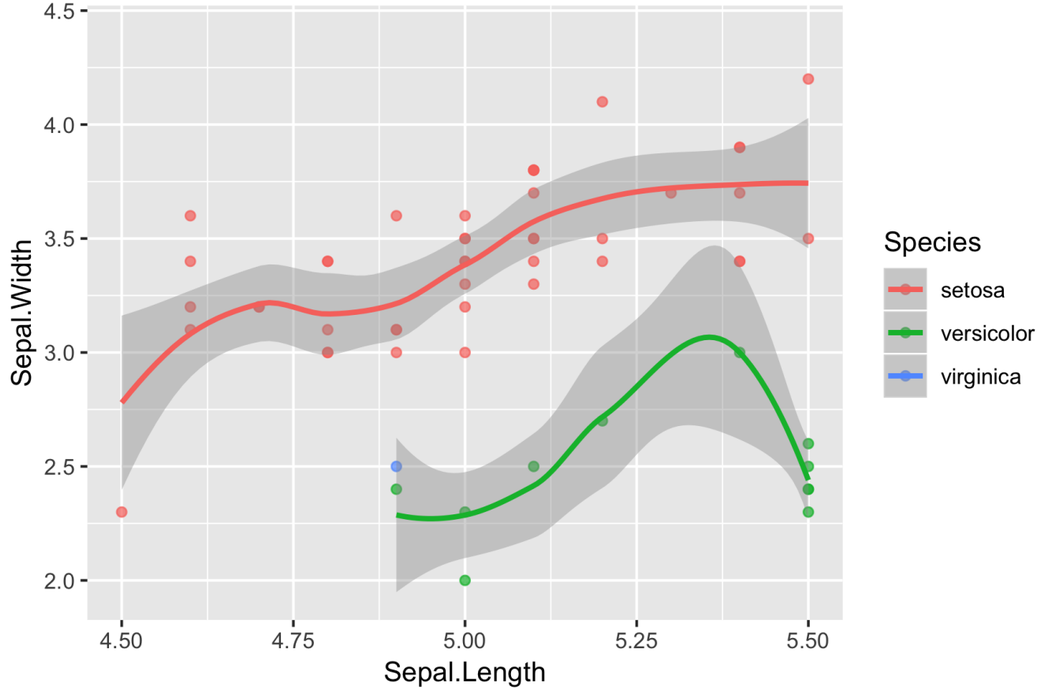


scale_x_continuous()

Original plot



Zoom in with `scale_x_continuous()`

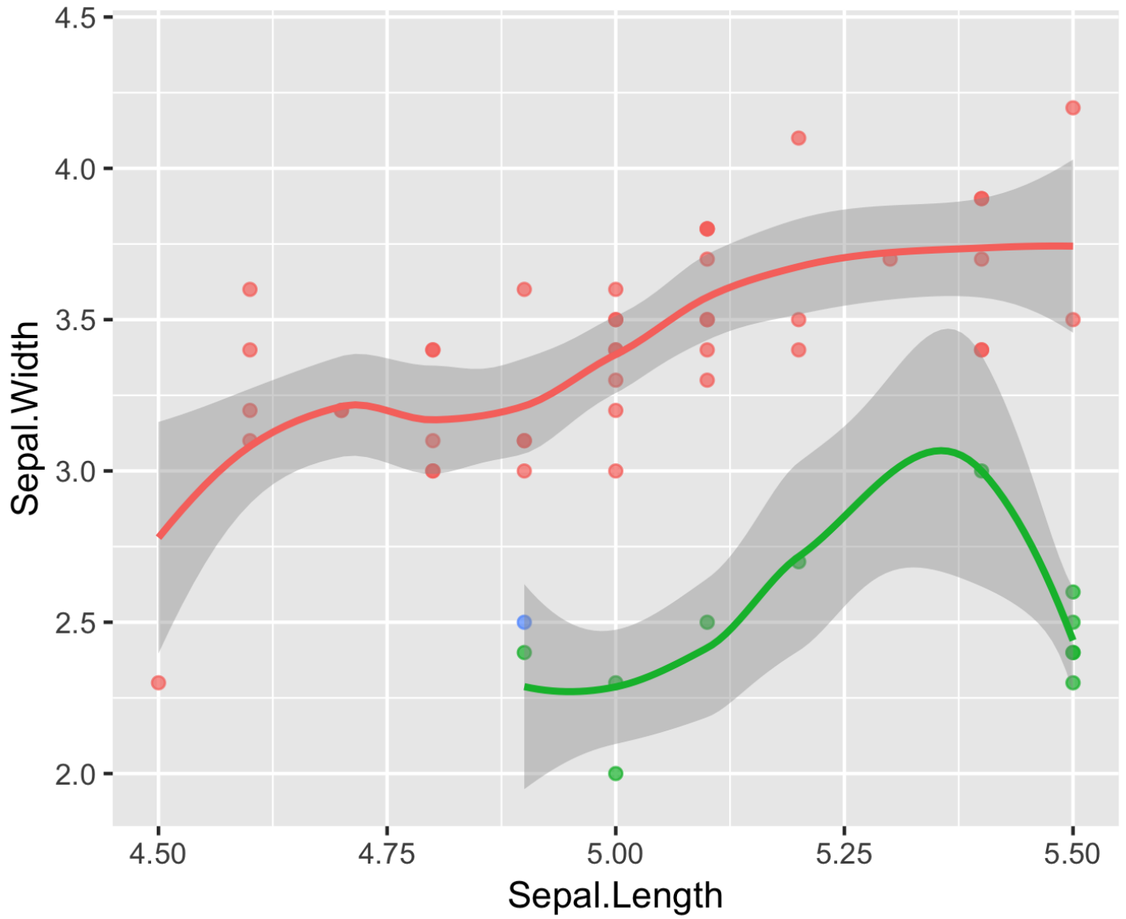


Part of original data is filtered out!

xlim()

```
iris.smooth +
  xlim(c(4.5, 5.5))
```

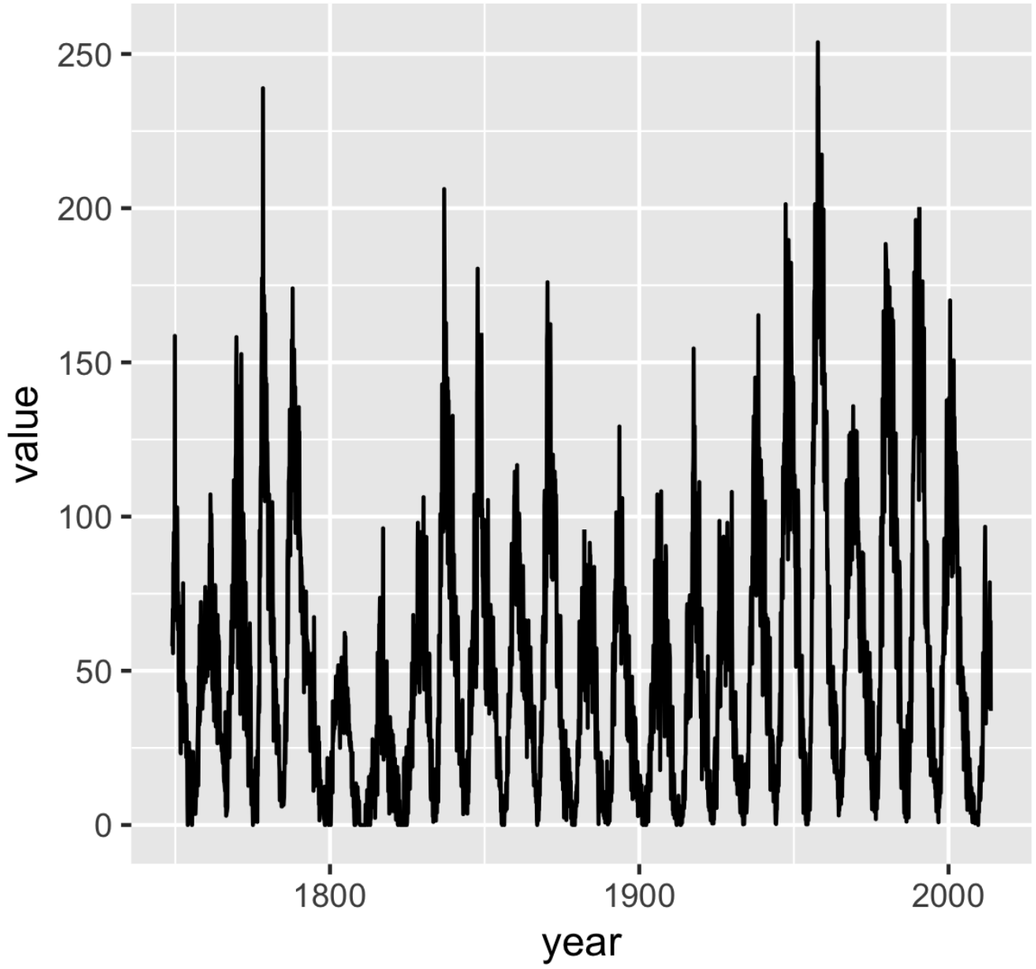
```
Removed 95 rows containing non-finite values
(stat_smooth).
Removed 95 rows containing missing values
(geom_point).
```



Sunspots

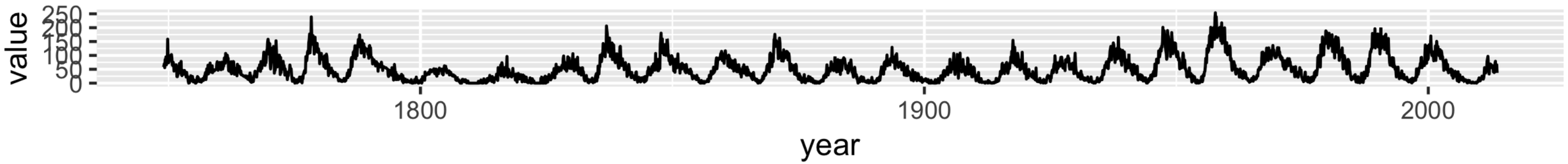
```
library(zoo)
sunspots.m <- data.frame(
    year = index(sunspot.month),
    value = reshape2::melt(sunspot.month)$value)
)

ggplot(sunspots.m, aes(x = year, y = value)) +
  geom_line() +
  coord_fixed() # default to 1:1 aspect ratio
```

- Typically use 1:1 if data is on the same scale



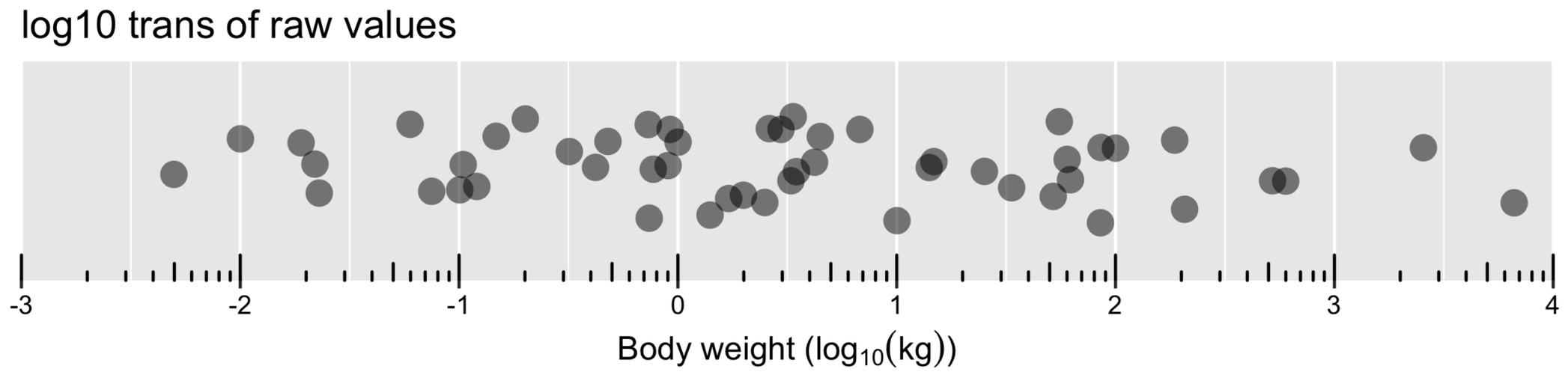
Sunspots

```
ggplot(sunspots.m, aes(x = year, y = value)) +
  geom_line() +
  coord_fixed(0.055)
```



Add logtick annotation

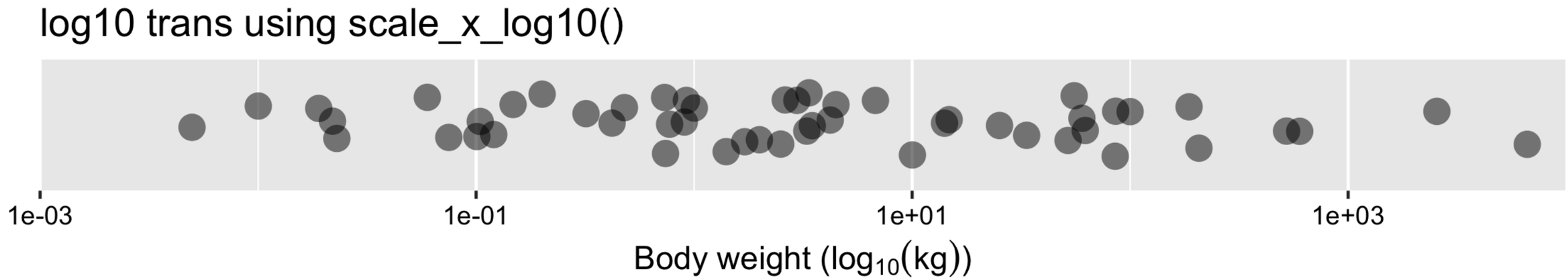
```
ggplot(msleep, aes(log10(bodywt), y = 1)) +
  geom_jitter() +
  scale_x_continuous(limits = c(-3, 4),
                     breaks = -3:4) +
  annotation_logticks(sides = "b")
```



Use scale_*_log10()

```
ggplot(msleep, aes(bodywt, y = 1)) +
  geom_jitter() +
  scale_x_log10(limits = c(1e-03, 1e+04))
```

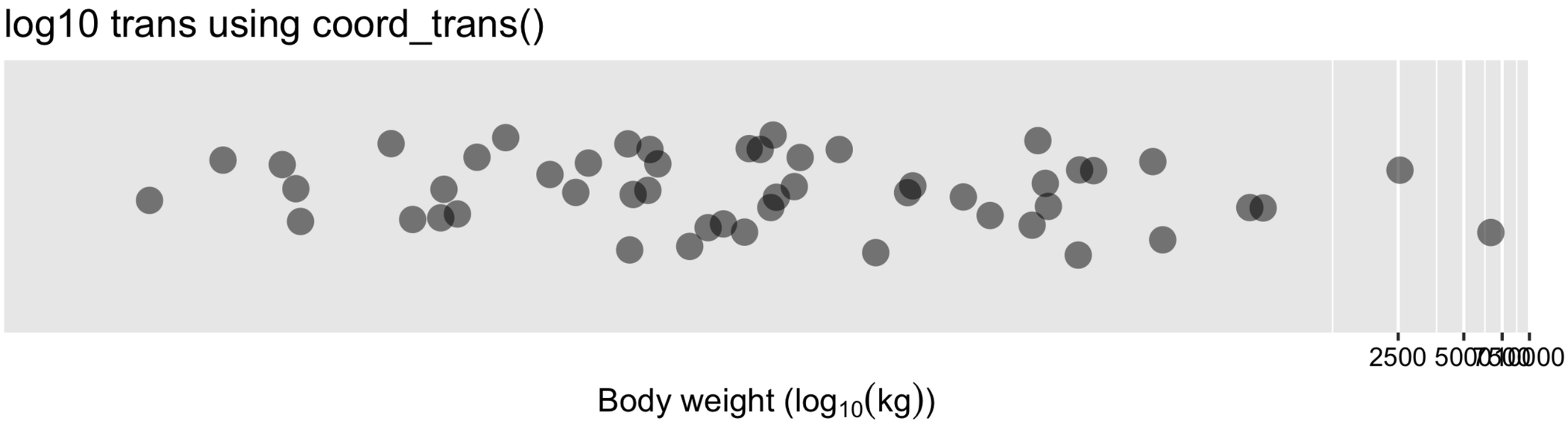
It is equivalent to transforming our actual dataset before getting to ggplot2



Use coord_trans()

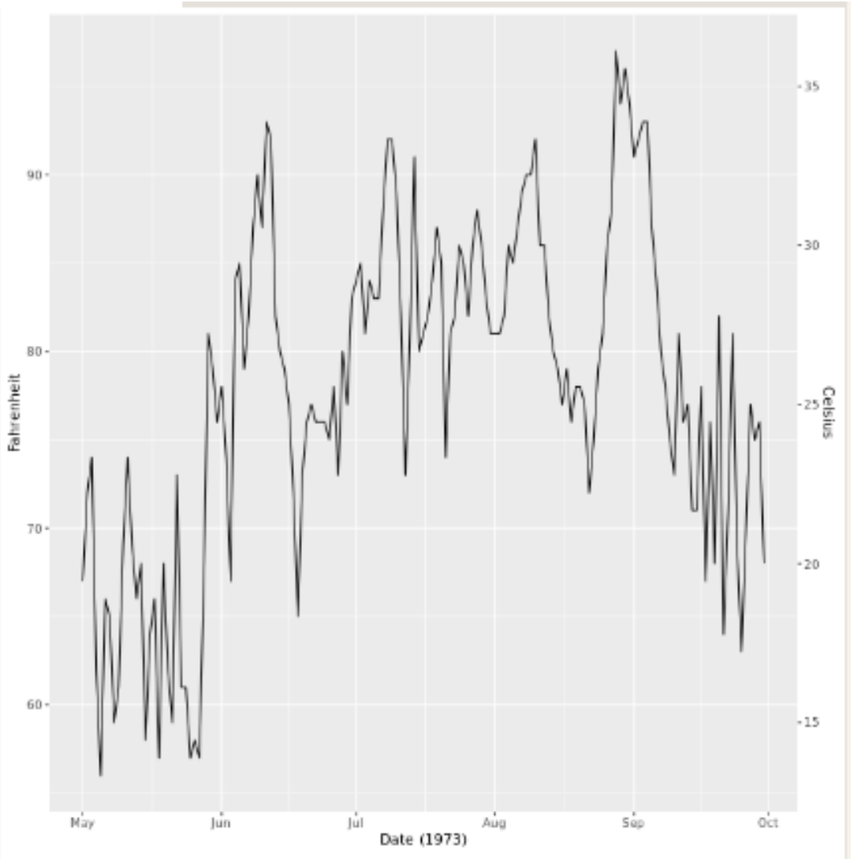
```
ggplot(msleep, aes(bodywt, y = 1)) +
  geom_jitter() +
  coord_trans(x = "log10")
```

It transforms the data after statistics have been calculated, a lm doesn't work with this method.



Double Axis with a vector of values

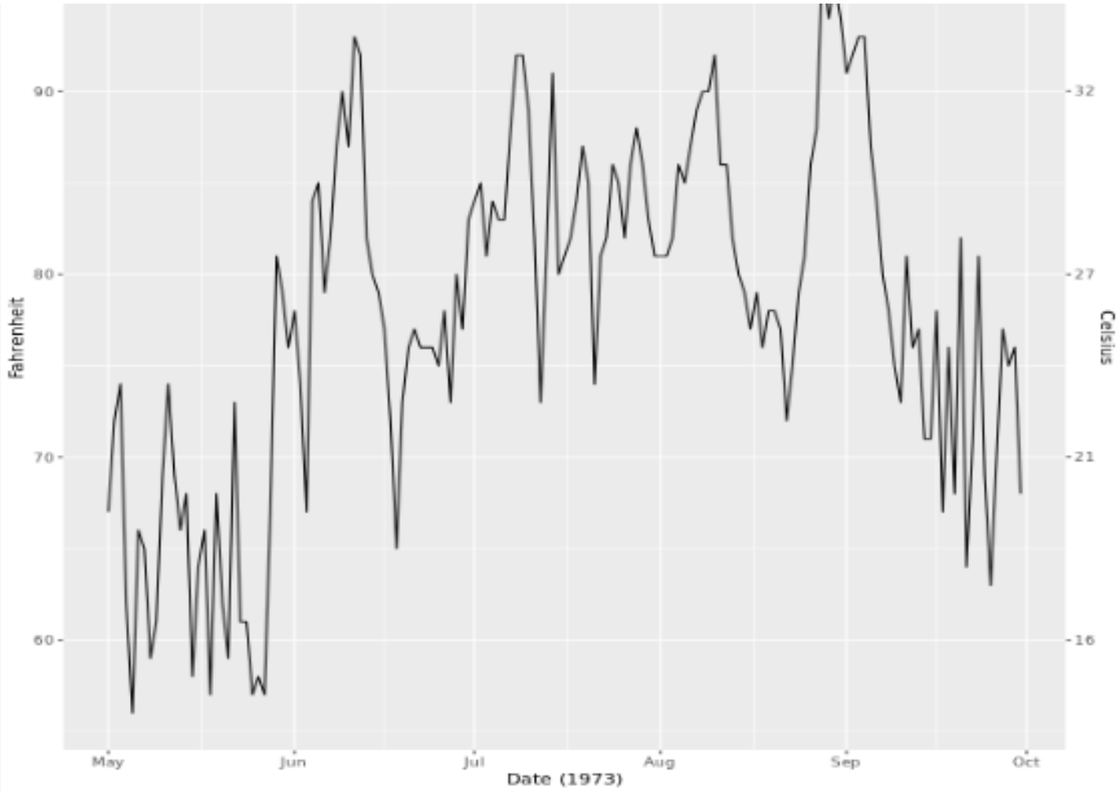
```r
# From previous step
y_breaks <- c(59, 68, 77, 86, 95, 104)
y_labels <- (y_breaks - 32) * 5 / 9
secondary_y_axis <- sec_axis(
  trans = identity,
  name = "Celsius",
  breaks = y_breaks,
  labels = y_labels
)

# Update the plot
ggplot(airquality, aes(Date, Temp)) +
  geom_line() +
  # Add the secondary y-axis
  scale_y_continuous(sec.axis = secondary_y_axis) +
  labs(x = "Date (1973)", y = "Fahrenheit")
```



Double axes are most useful when you want to display the same value in two different units. log10 vs exponent values, count vs proportions, physical magnitudes in different systems.

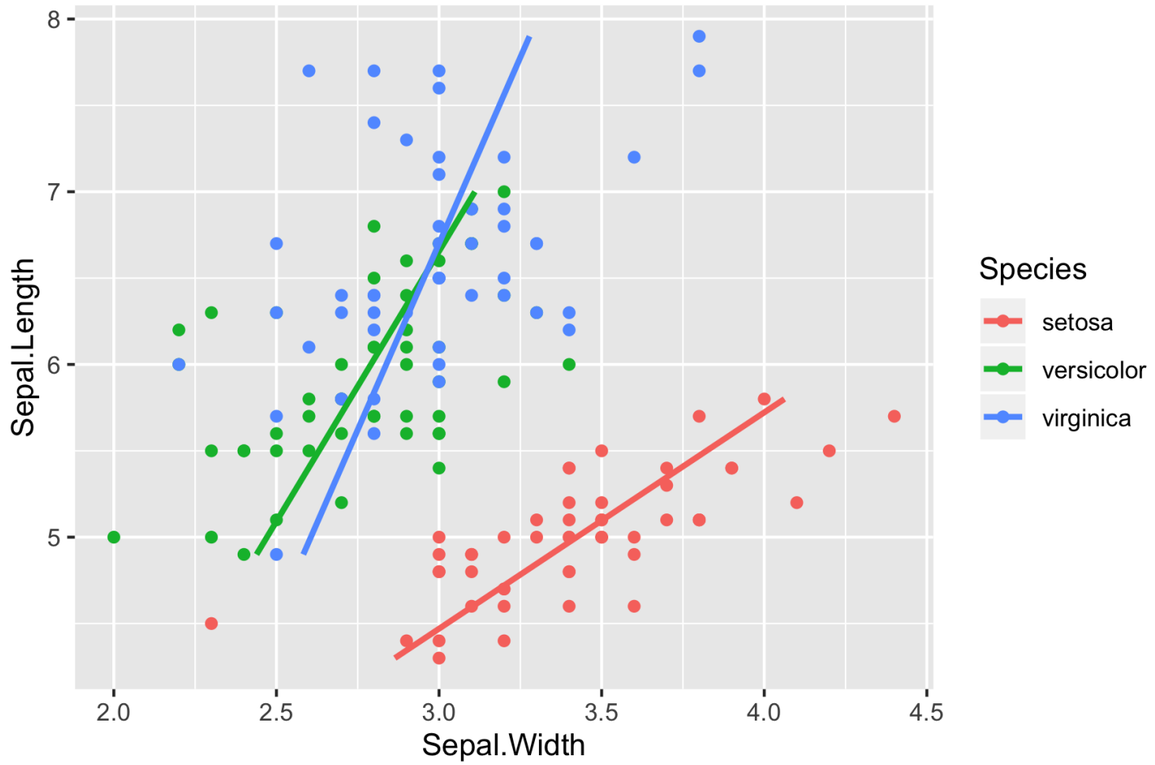
Double Axis with a function

```r
celsius_trans <- function(x){
  round((x - 32) * 5 / 9,0)
}

secondary_y_axis <- sec_axis(
  trans = identity,
  name = "Celsius",
  labels = celsius_trans
)

# Update the plot
ggplot(airquality, aes(Date, Temp)) +
  geom_line() +
  # Add the secondary y-axis
  scale_y_continuous(sec.axis =
secondary_y_axis) +
  labs(x = "Date (1973)", y = "Fahrenheit")
```



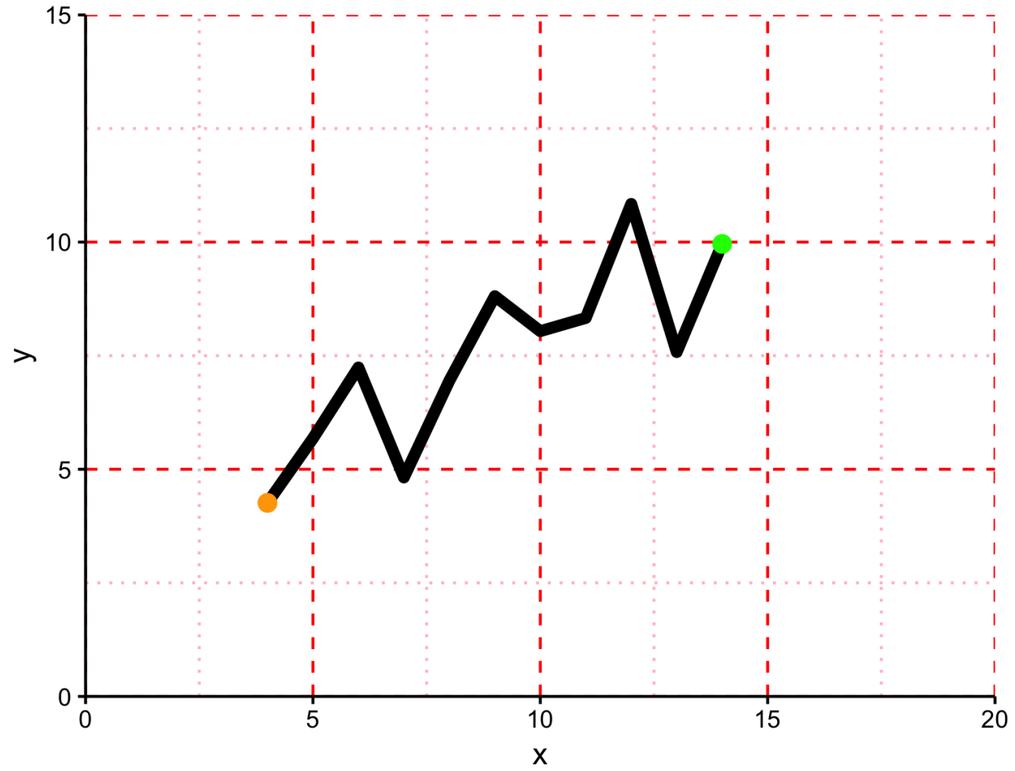
coord_flip()

```
ggplot(iris, aes(x = Sepal.Length,
                 y = Sepal.Width,
                 color = Species)) +
  geom_point() +
  geom_smooth(method = "lm",
              se = FALSE) +
  coord_flip()
```

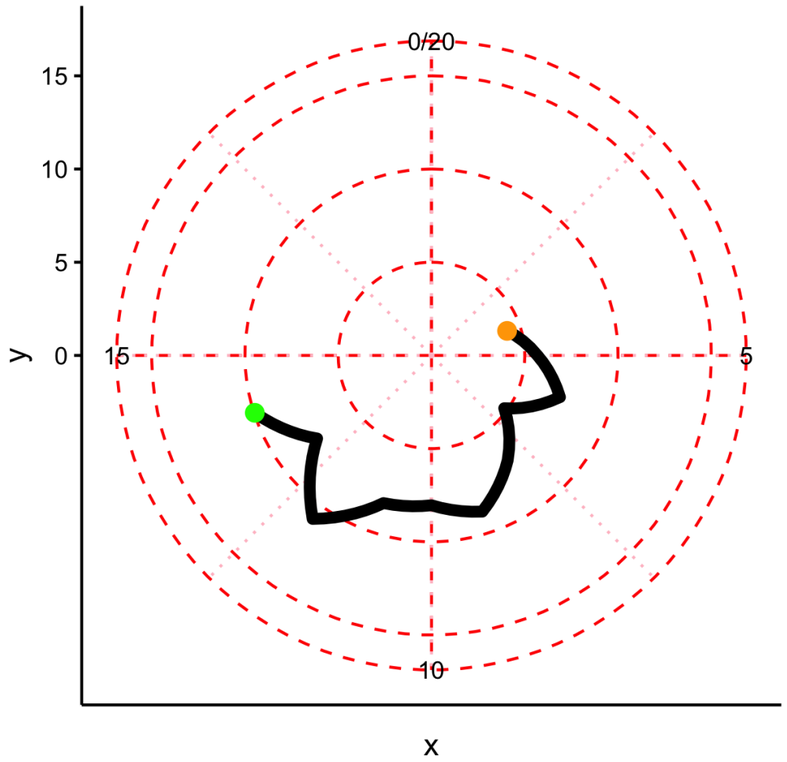


coord_polar()

```
p + coord_fixed()
```

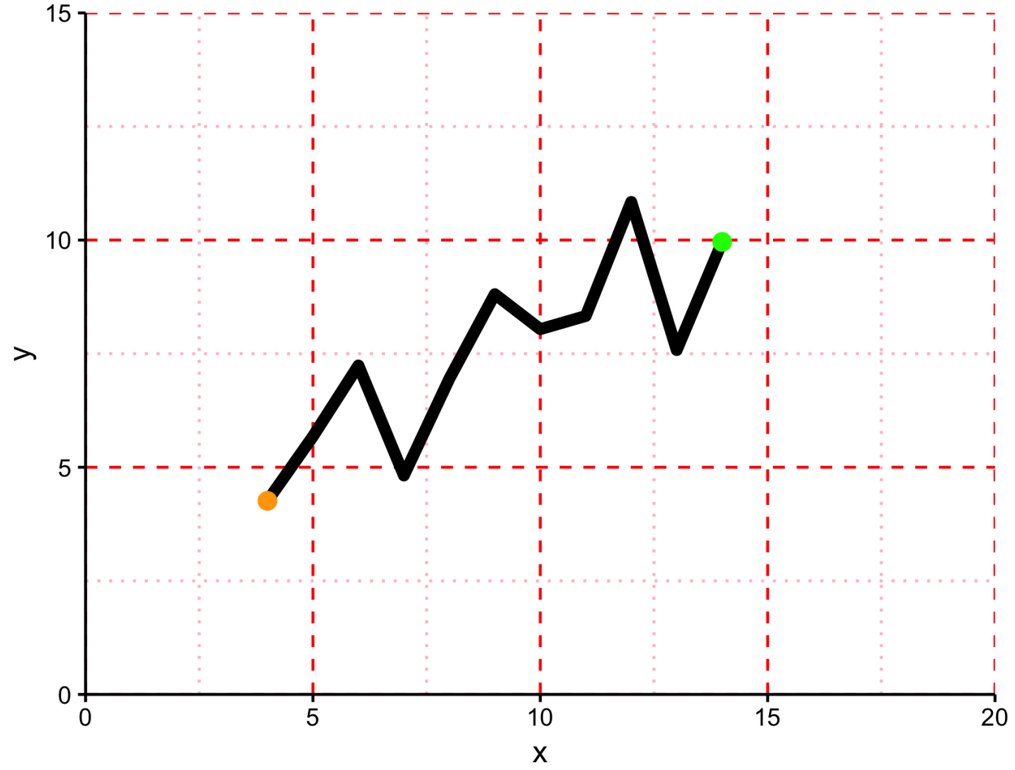



```
p + coord_polar()
```

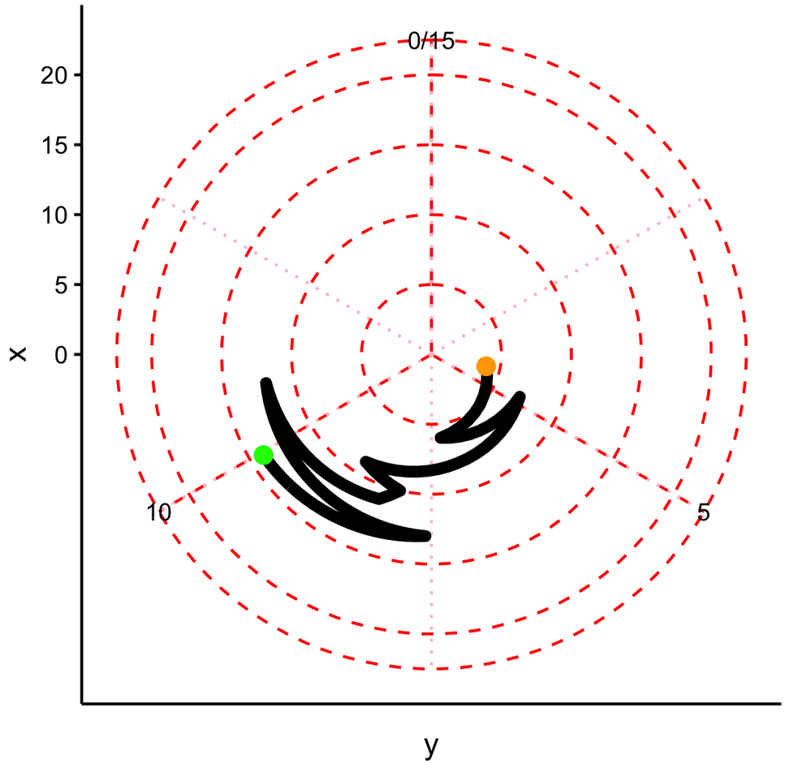


coord_polar(theta = "y")

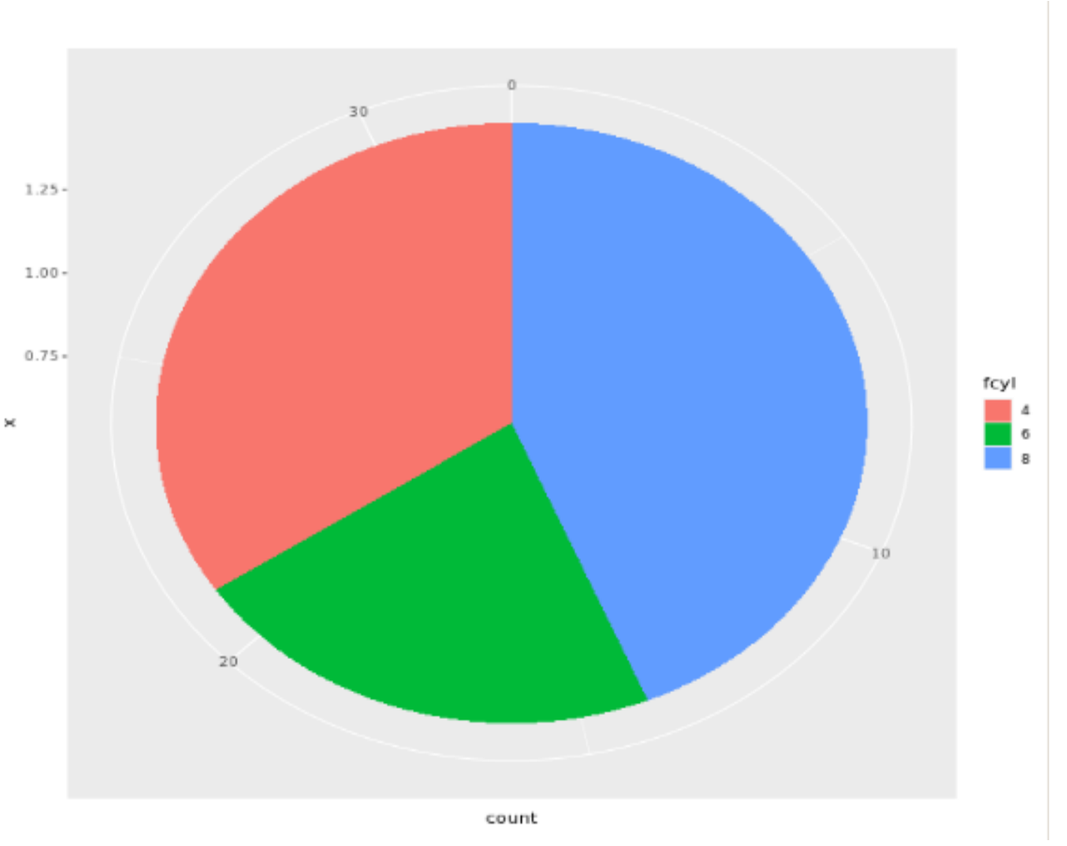
```
p + coord_fixed()
```




```
p + coord_polar(theta = "y")
```

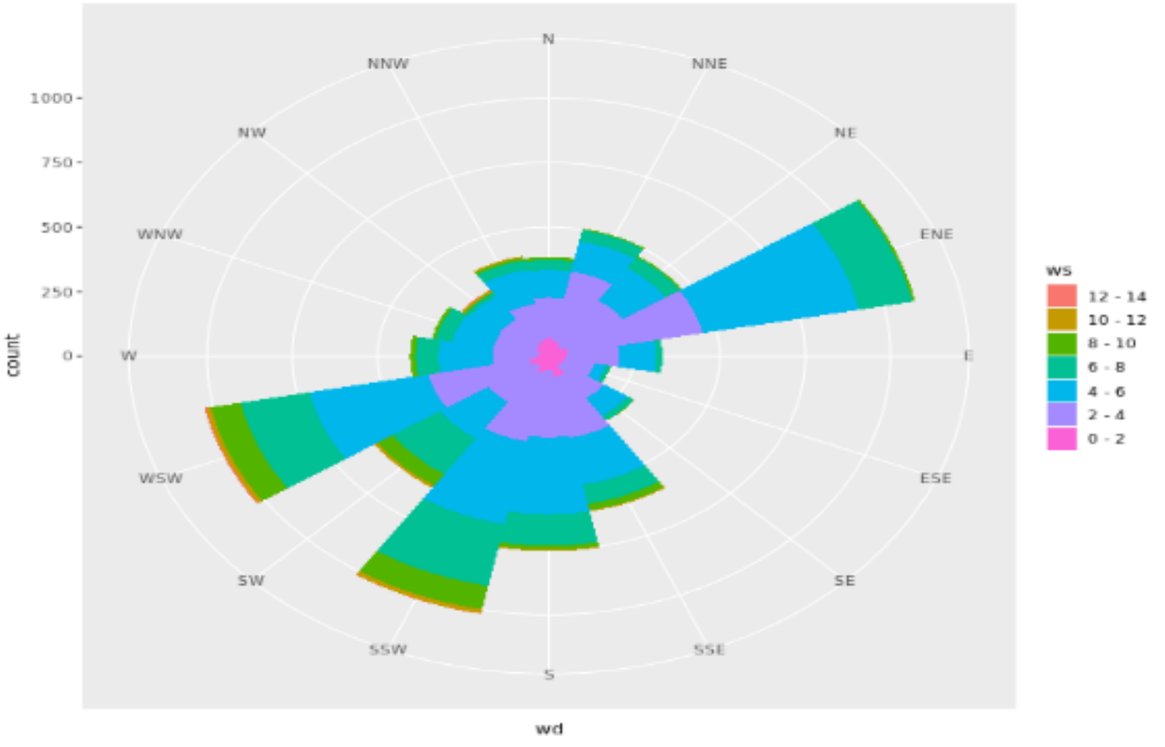


```r
# Run the code, view the plot, then update
it
ggplot(mtcars, aes(x = 1, fill = fcyl)) +
  geom_bar()+
  # Add a polar coordinate system
  coord_polar(theta = "y")
```



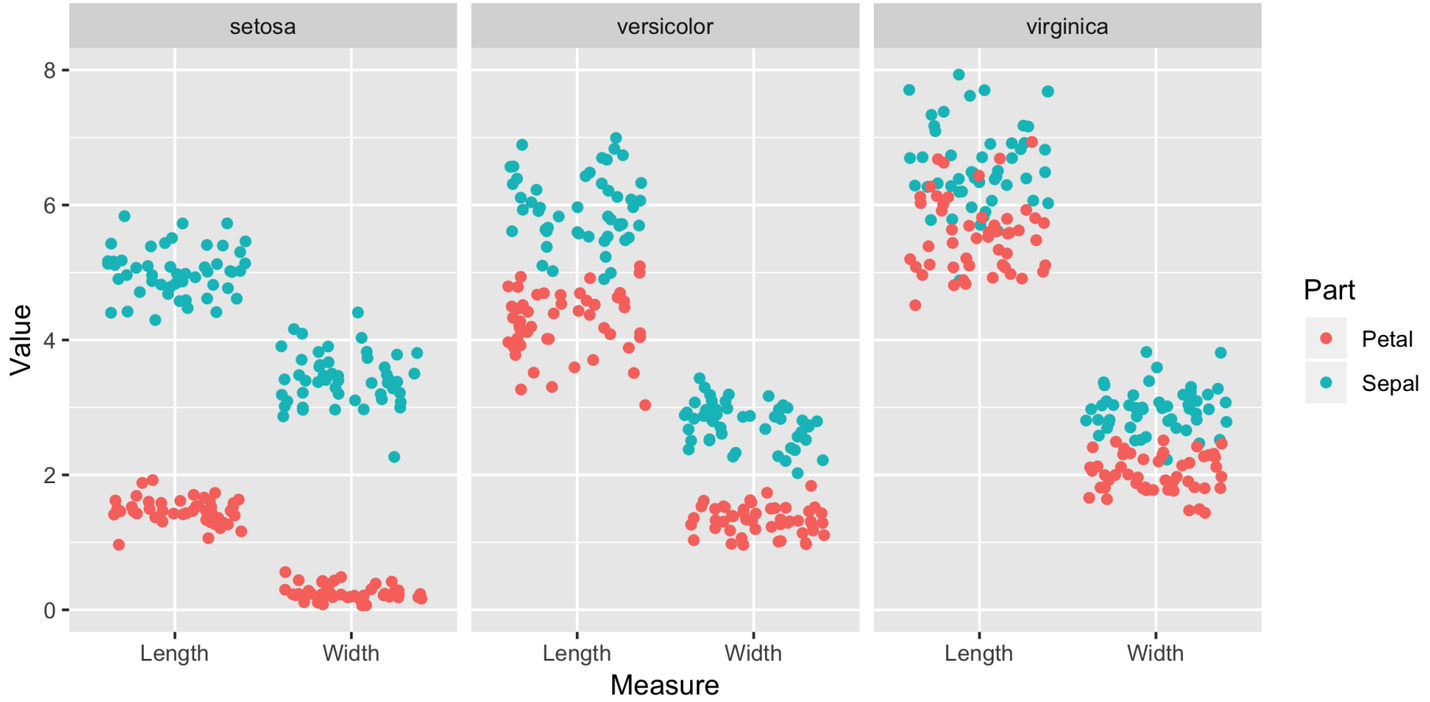
```r
ggplot(mtcars, aes(x = 1, fill = fcyl)) +
  # Reduce the bar width to 0.1
  geom_bar(width = 0.1) +
  coord_polar(theta = "y") +
  # Add a continuous x scale from 0.5 to 1.5
  scale_x_continuous(limits = c(0.5,1.5))
```

```r
# Convert to polar coordinates:
ggplot(wind, aes(wd, fill = ws)) +
  geom_bar(width = 1) +
  coord_polar(start = -pi/16)
```



iris.tidy

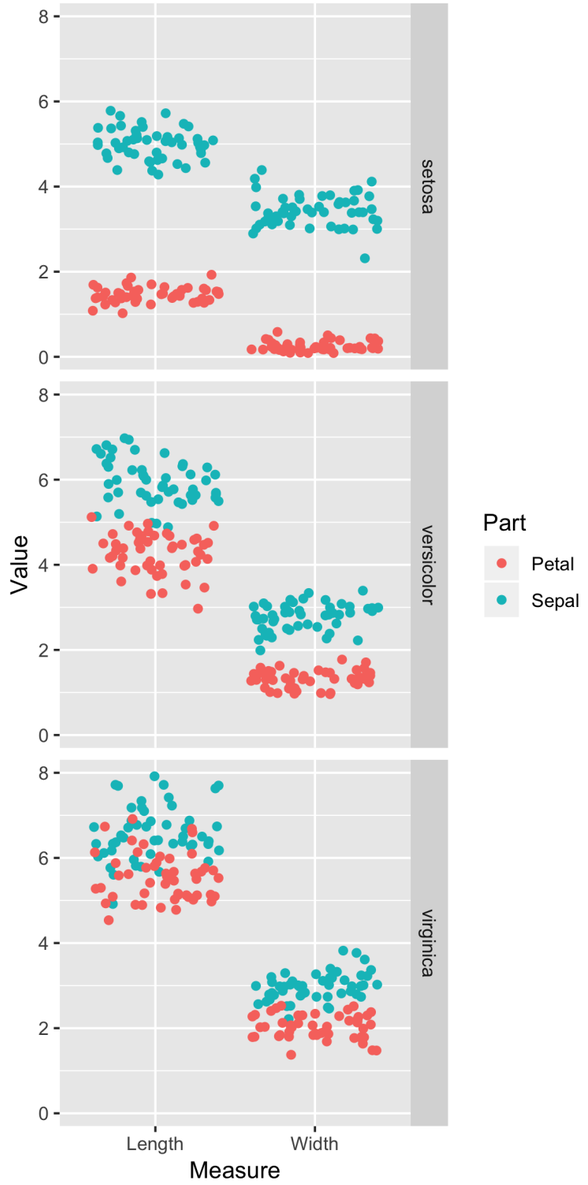
```
ggplot(iris.tidy, aes(x = Measure, y = Value, color = Part)) +
  geom_jitter() +
  facet_grid(cols = vars(Species))
```



`iris.tidy` faceting done wrong:

```
ggplot(iris.tidy, aes(x = Measure,
                      y = Value,
                      color = Part)) +
  geom_jitter() +
  facet_grid(rows = vars(Species))
```

Modern notation	Formula notation
facet_grid(rows = vars(A))	facet_grid(A ~ .)
facet_grid(cols = vars(B))	facet_grid(. ~ B)
facet_grid(rows = vars(A), cols = vars(B))	facet_grid(A ~ B)

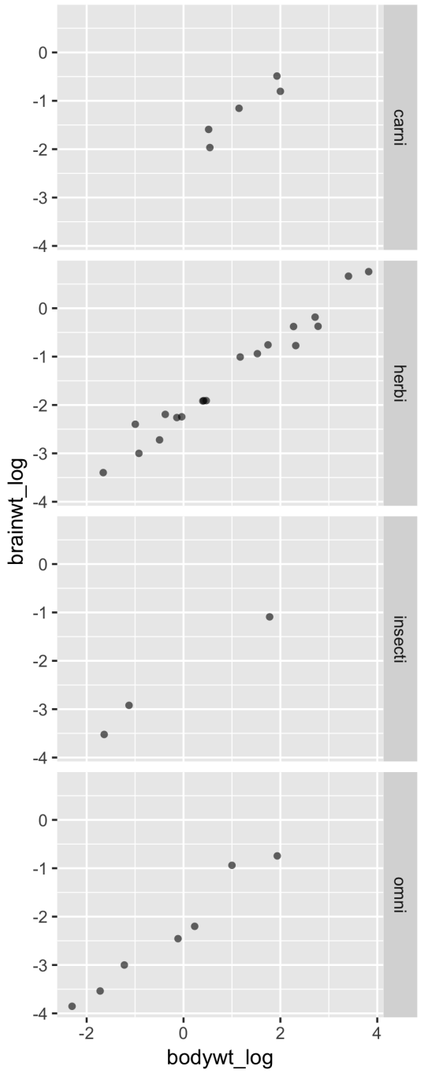


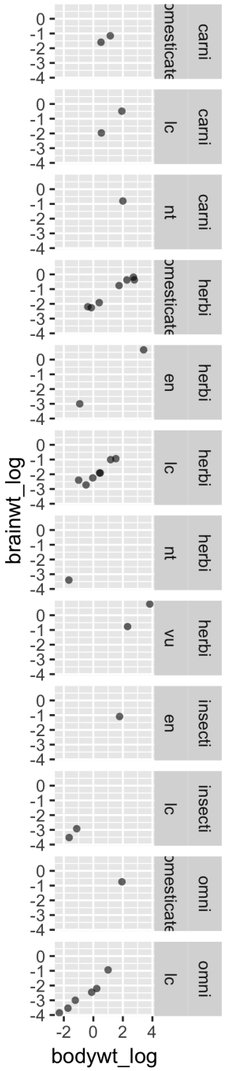
The labeller argument

```
# Default is to label the value
p +
  facet_grid(rows = vars(vore),
             labeller = label_value)
```

This option just shows the category value

```
p +
  facet_grid(rows = vars(vore,
                         conservation))
```



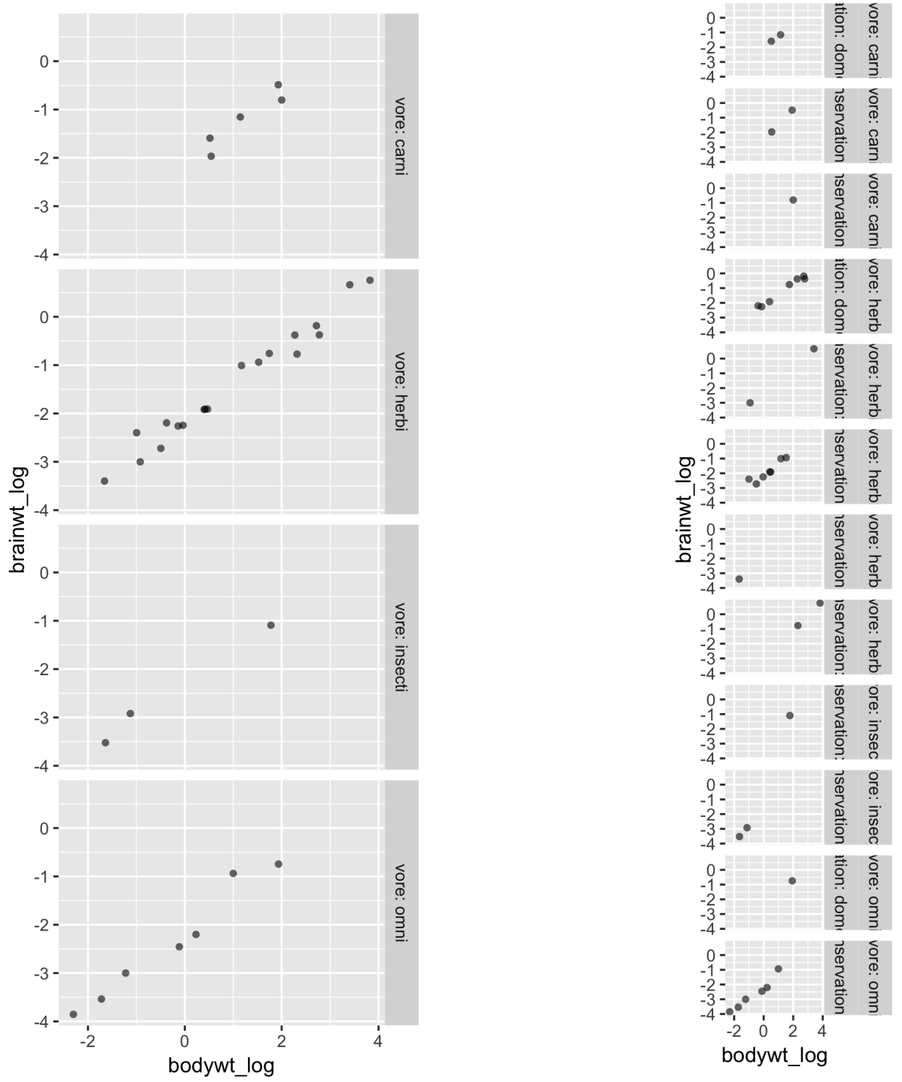


Using label_both adds the variable name

```
# Print variable name also
p +
  facet_grid(rows = vars(vore),
                    labeller = label_both)
```

This option just shows the category name and value

```
p +
  facet_grid(rows = vars(vore,
                         conservation),
                  labeller = label_context)
```

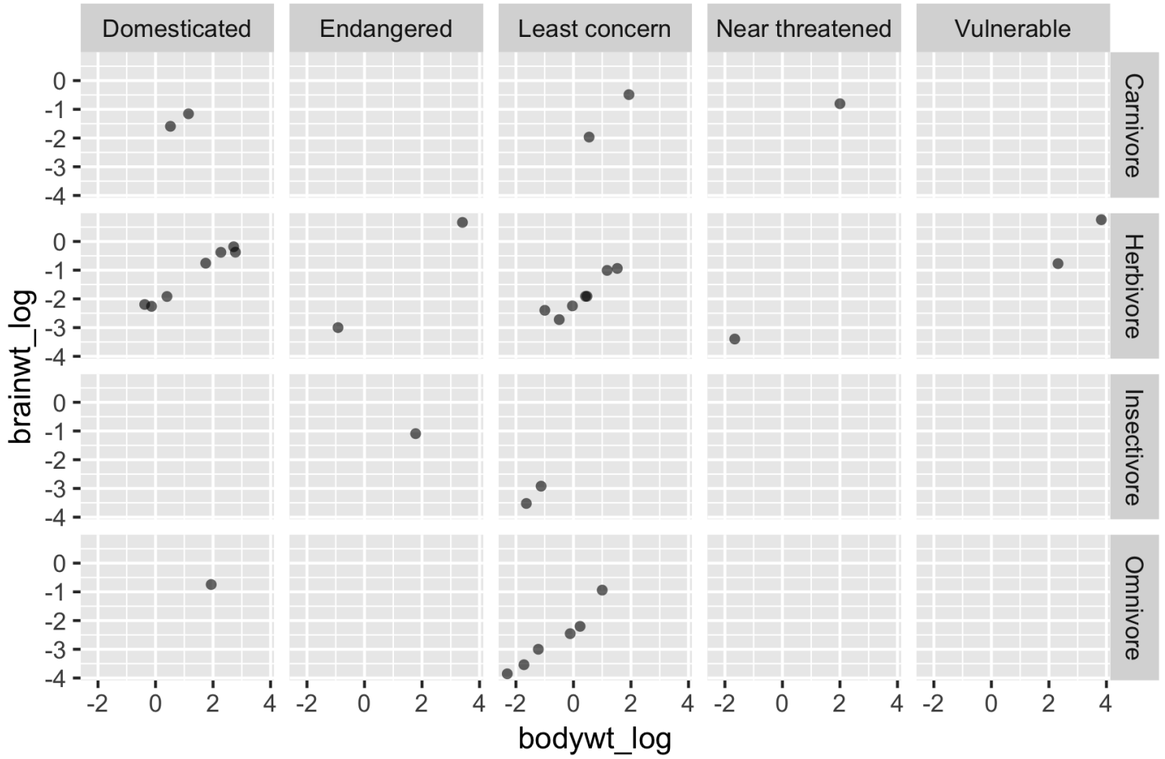


Relabeling and reordering factors

```
msleep2$conservation <- fct_recode(msleep2$conservation,
                                   Domesticated = "domesticated",
                                   `Least concern` = "lc",
                                   `Near threatened` = "nt",
                                   Vulnerable = "vu",
                                   Endangered = "en")

msleep2$vore = fct_recode(msleep2$vore,
                          Carnivore = "carni",
                          Herbivore = "herbi",
                          Insectivore = "insecti",
                          Omnivore = "omni")
```

Reinitialize plot with new labels

```
# Plot
p <- ggplot(msleep2, aes(bodywt_log,
                         brainwt_log)) +
  geom_point(alpha = 0.6, shape = 16) +
  coord_fixed()

p +
  facet_grid(rows = vars(vore),
             cols = vars(conservation))
```

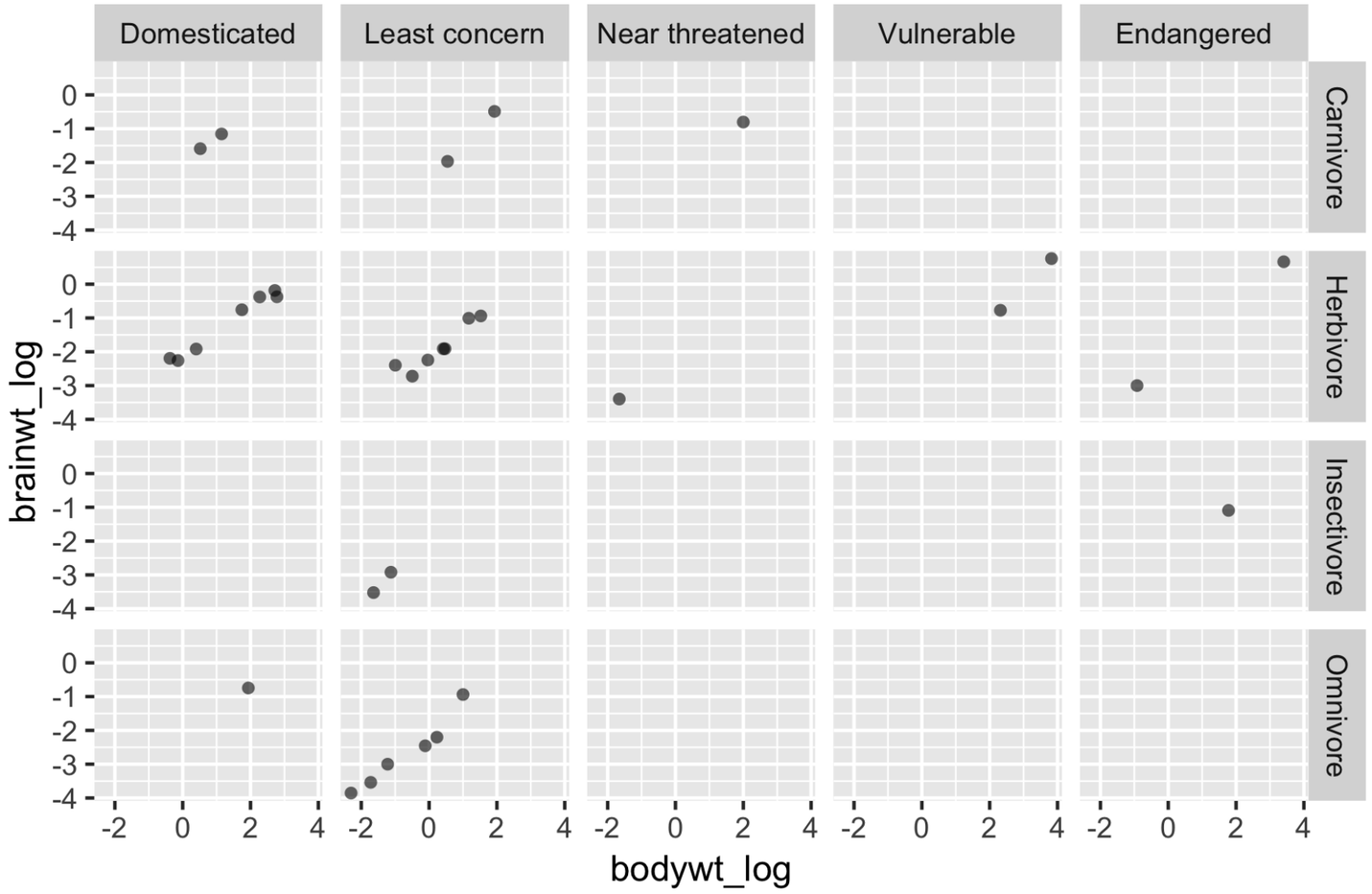


Changing the order of levels

```
# Change order of levels:
msleep2$conservation = fct_relevel(msleep2$conservation,
                                   c("Domesticated",
                                     "Least concern",
                                     "Near threatened",
                                     "Vulnerable",
                                     "Endangered"))
```

```
msleep2 <- msleep2 %>%
  # Arrange from lo to hi weight
  arrange(-bodywt_log) %>%
  # Redefine factor levels in order
  mutate(name = as_factor(name))
```

Reinitialize plot with new order



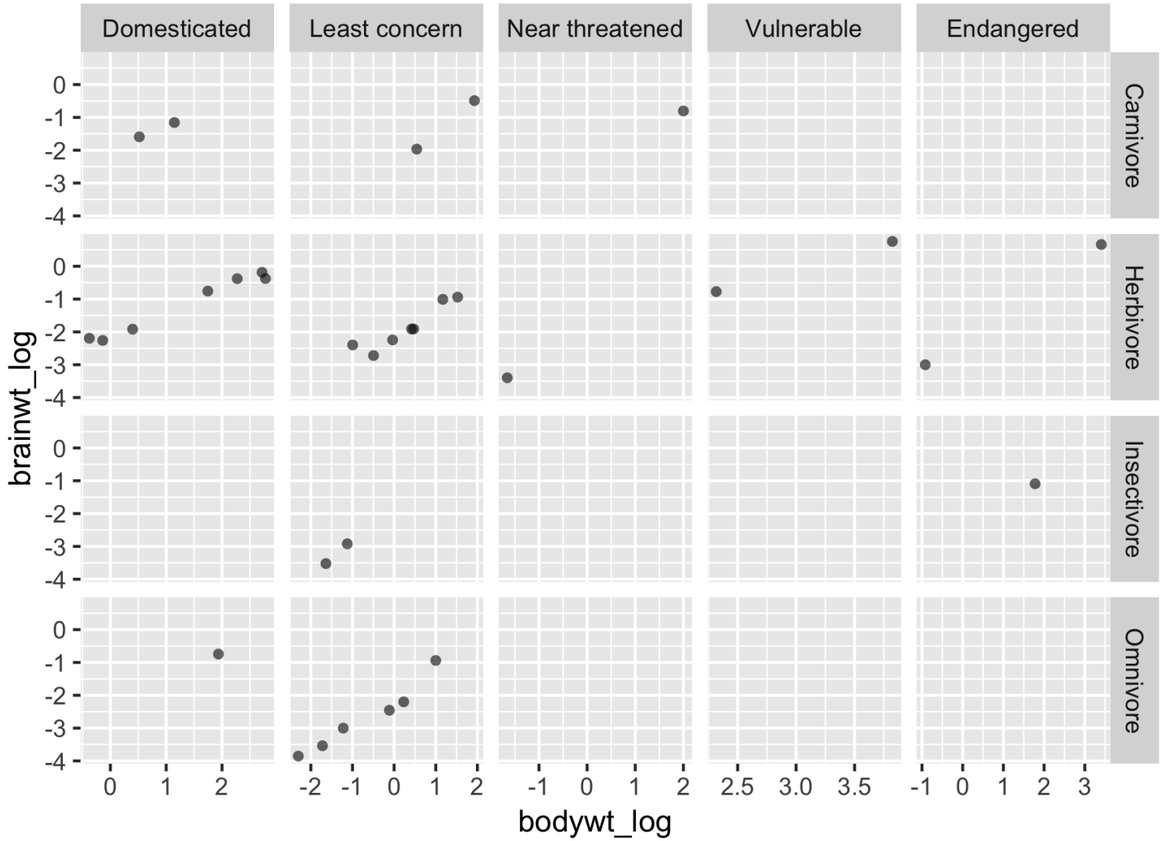
... but not with fixed scales

```
ggplot(msleep2, aes(bodywt_log,
                    brainwt_log)) +
  geom_point(alpha = 0.6, shape = 16) +
  coord_fixed() +
  facet_grid(rows = vars(vore),
             cols = vars(conservation),
             scales = "free_x")
```

```
Error: coord_fixed doesn't support free scales
```

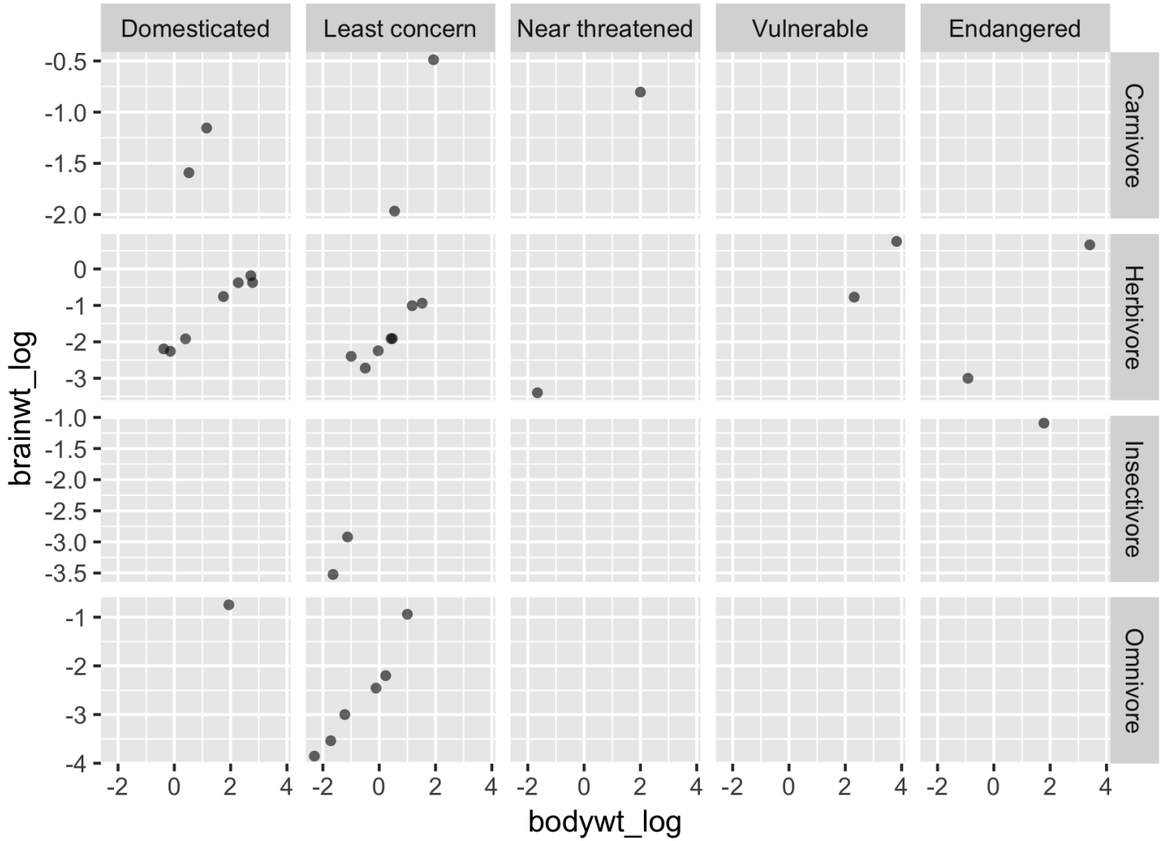
Adjusting the plotting space

```
ggplot(msleep2, aes(bodywt_log,
                    brainwt_log)) +
  geom_point(alpha = 0.6, shape = 16) +
  facet_grid(rows = vars(vore),
             cols = vars(conservation),
             scales = "free_x")
```



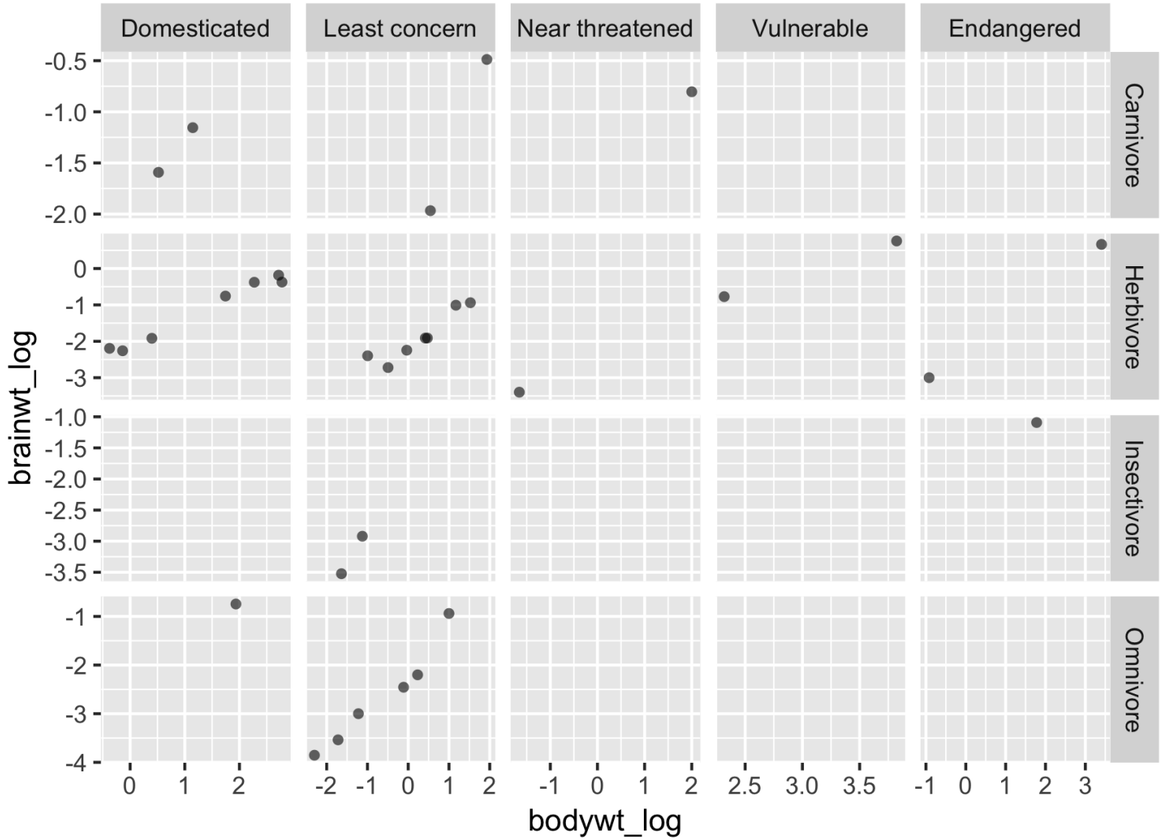
Adjusting the plotting space

```
ggplot(msleep2, aes(bodywt_log,
                    brainwt_log)) +
  geom_point(alpha = 0.6, shape = 16) +
  facet_grid(rows = vars(vore),
             cols = vars(conservation),
             scales = "free_y")
```



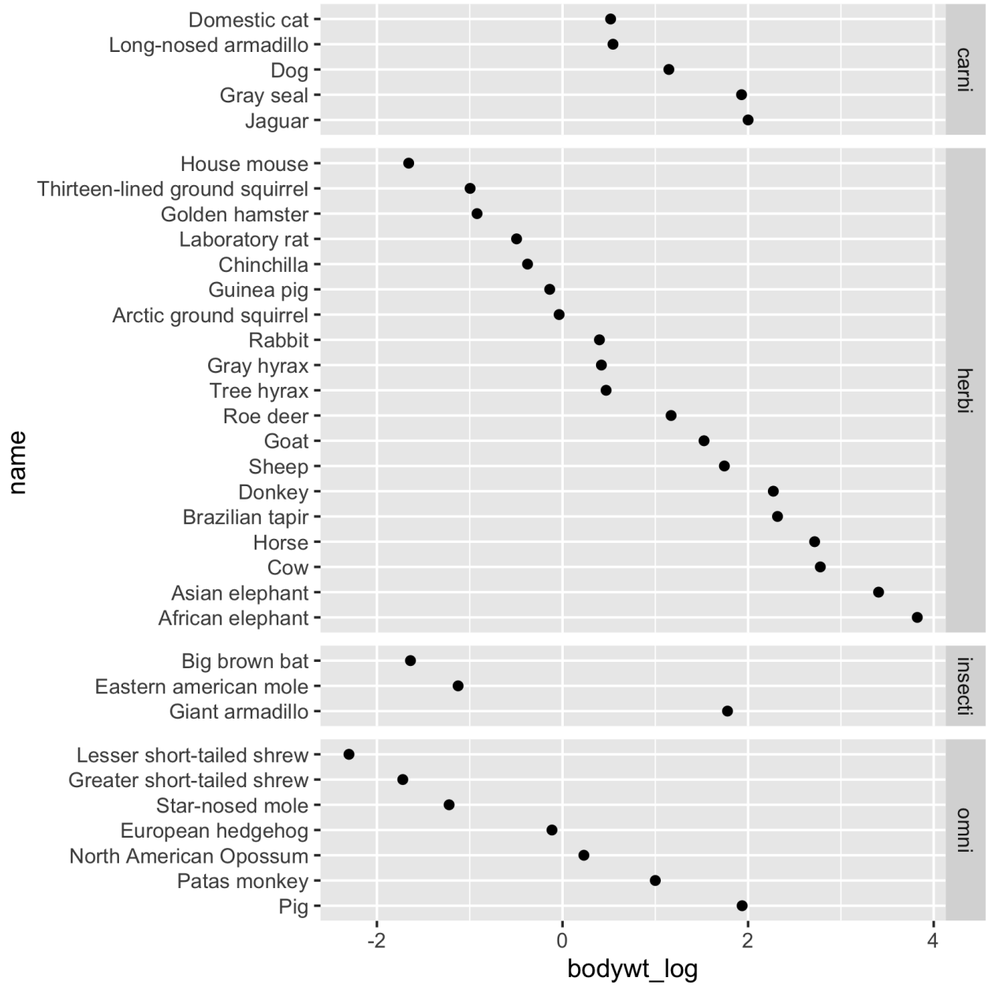
Adjusting the plotting space

```
ggplot(msleep2, aes(bodywt_log,
                    brainwt_log)) +
  geom_point(alpha = 0.6, shape = 16) +
  facet_grid(rows = vars(vore),
             cols = vars(conservation),
             scales = "free")
```



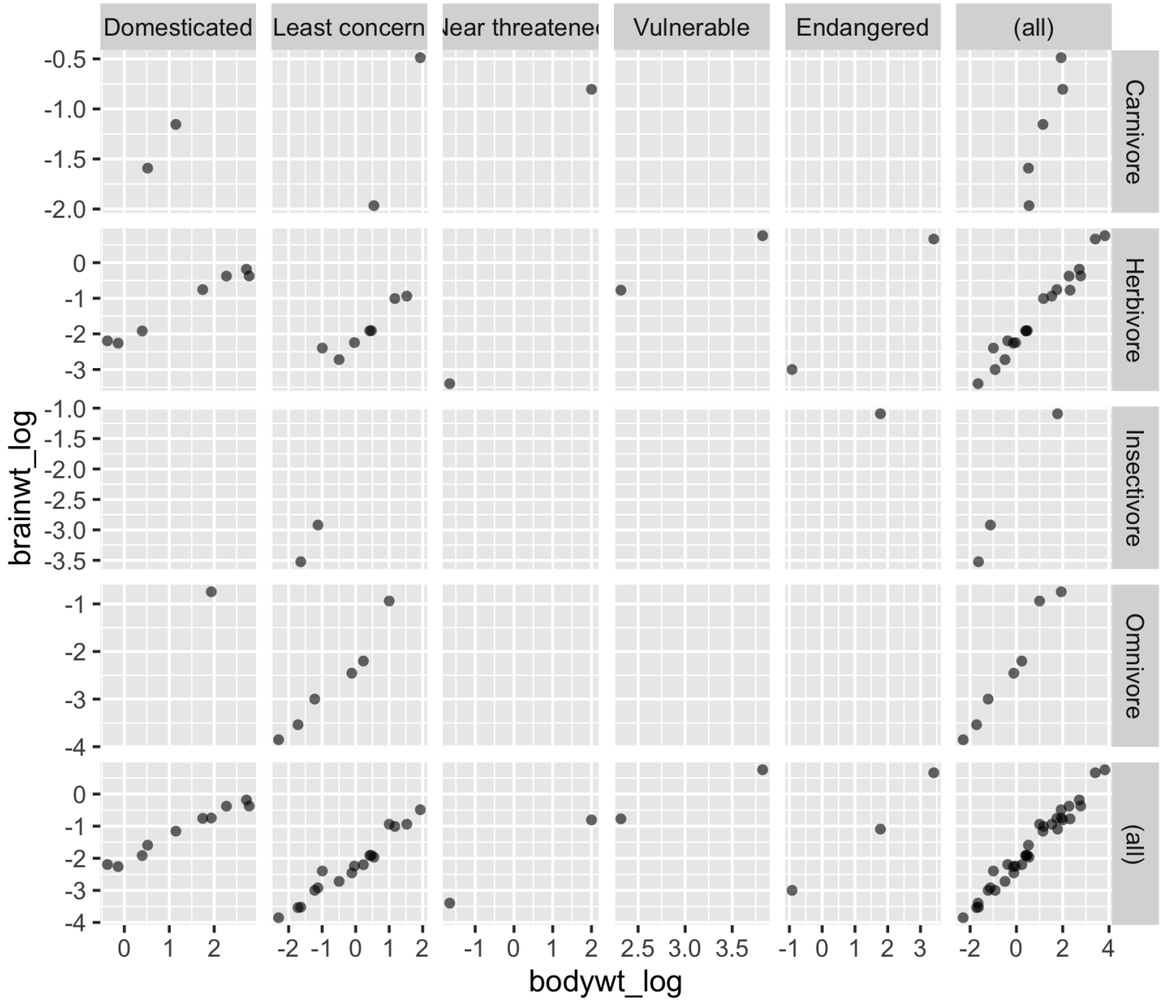
Final adjustments

```
msleep2 <- msleep2 %>%
  # Arrange from lo to hi weight
  arrange(-bodywt_log) %>%
  # Redefine factor levels in order
  mutate(name = as_factor(name))

# New order is reflected in y axis
ggplot(msleep2, aes(x = bodywt_log,
                    y = name)) +
  geom_point() +
  # Free the y scales and space
  facet_grid(rows = vars(vore),
             scales = "free_y",
             space = "free_y")
```



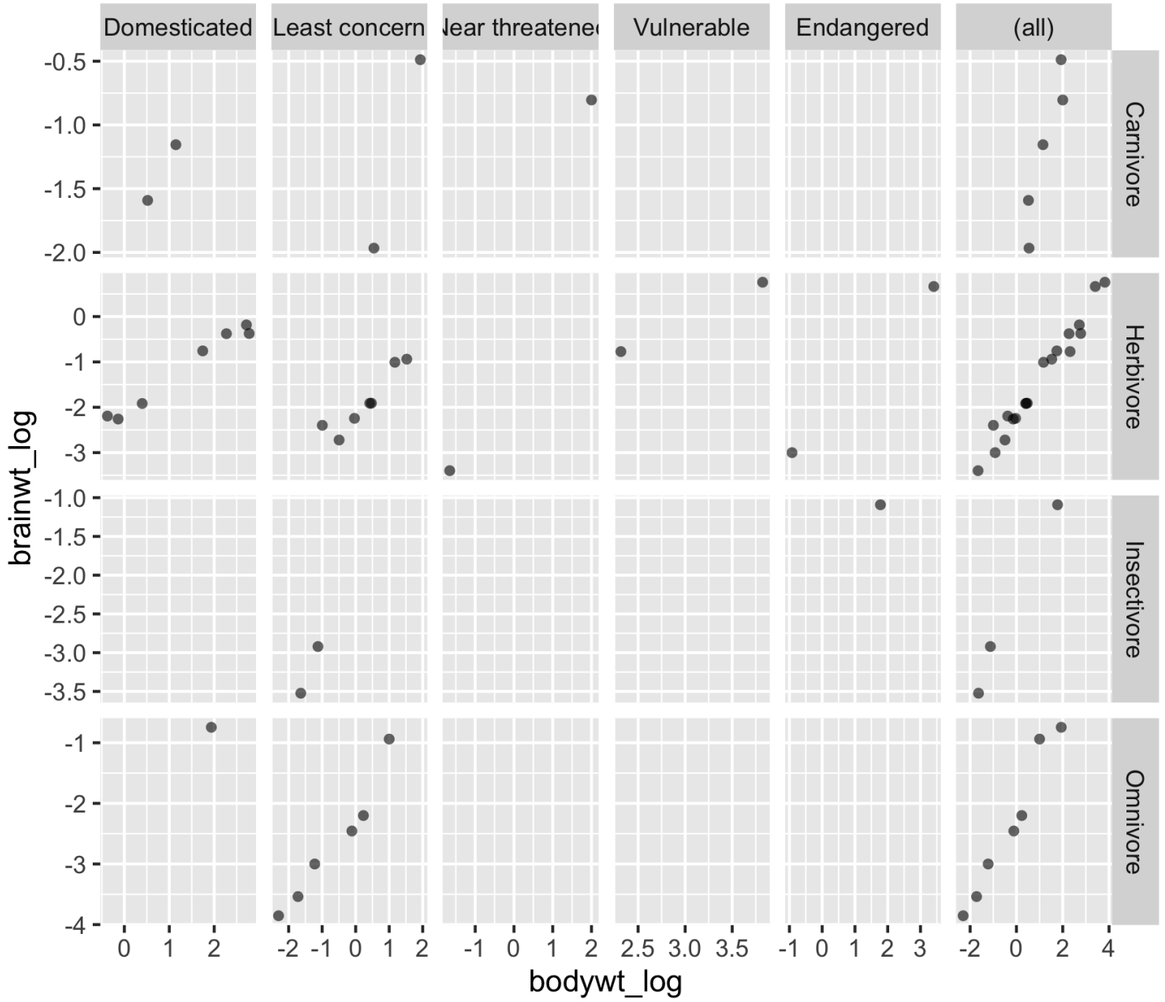
Using margin plots

```
ggplot(msleep2, aes(bodywt_log,
                    brainwt_log)) +
  geom_point(alpha = 0.6, shape = 16) +
  facet_grid(rows = vars(vore),
             cols = vars(conservation),
             scales = "free",
             margins = TRUE)
```



Using margin plots

```
ggplot(msleep2, aes(bodywt_log,
                    brainwt_log)) +
  geom_point(alpha = 0.6, shape = 16) +
  facet_grid(rows = vars(vore),
             cols = vars(conservation),
             scales = "free",
             margins = "conservation")
```



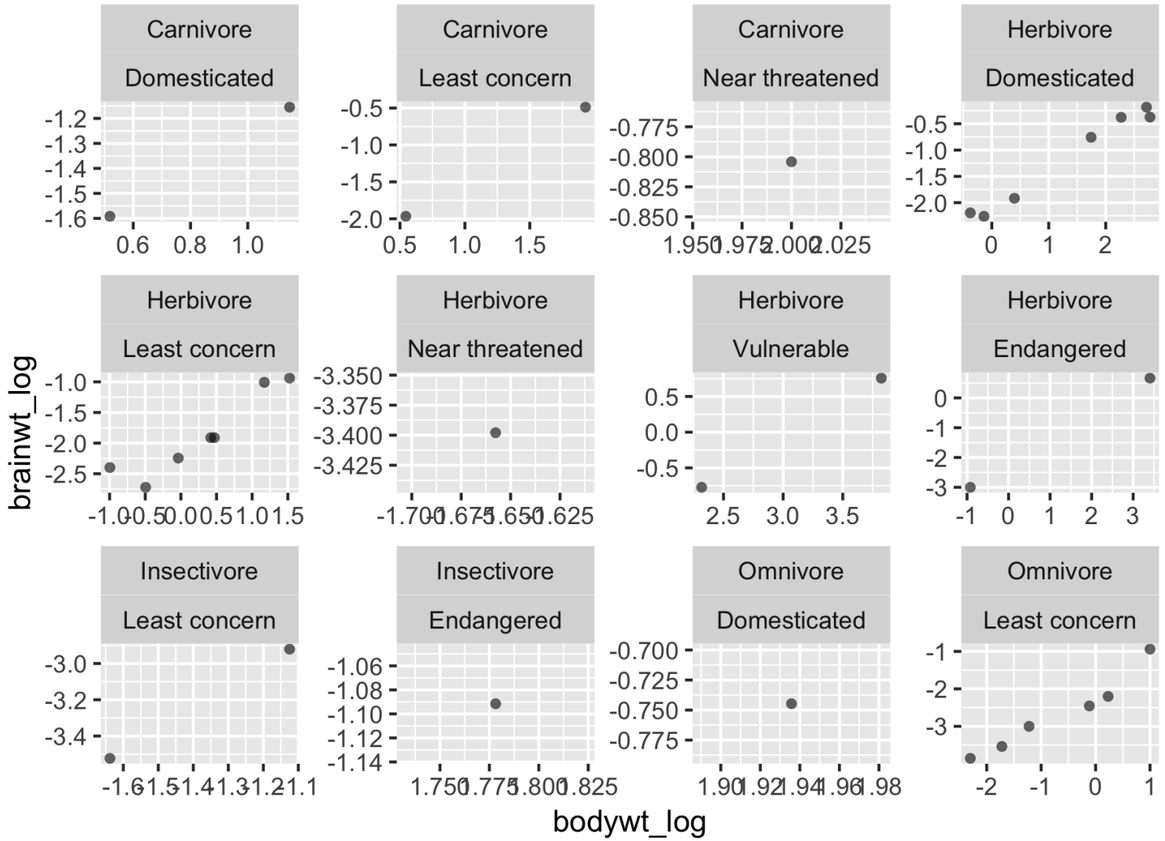
Using facet_wrap()

Use cases:

1. When you want both x and y axes to be free on every individual plot
   - i.e. Not just per row or column as per `facet_grid()`
2. When your categorical (factor) variable has many groups (levels)
   - i.e. too many sub plots for column or row-wise faceting
   - A more typical scenario

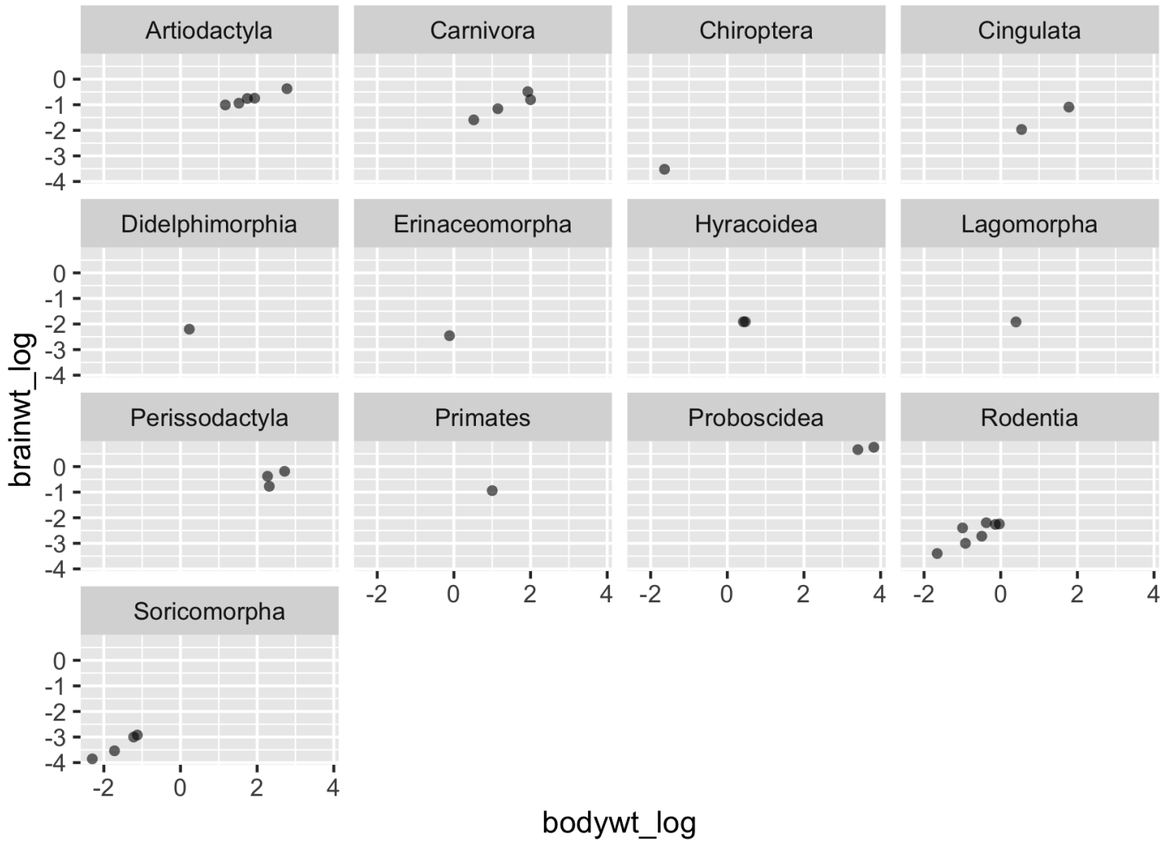
Using facet_wrap() - Scenario 1

```
ggplot(msleep2, aes(bodywt_log,
                    brainwt_log)) +
  geom_point(alpha = 0.6, shape = 16) +
  facet_wrap(vars(vore, conservation),
             scales = "free")
```



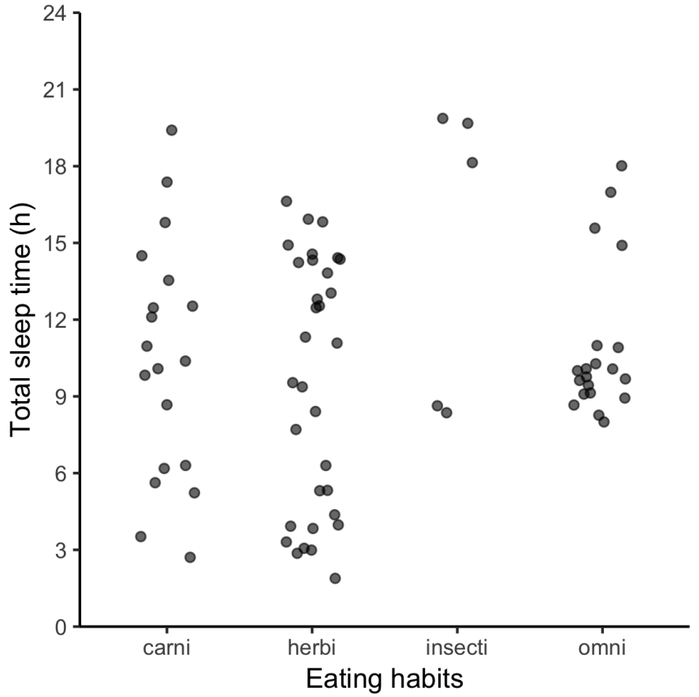
Using facet_wrap() - Scenario 2

```
ggplot(msleep2, aes(bodywt_log,
                    brainwt_log)) +
  geom_point(alpha = 0.6, shape = 16) +
  facet_wrap(vars(order))
```



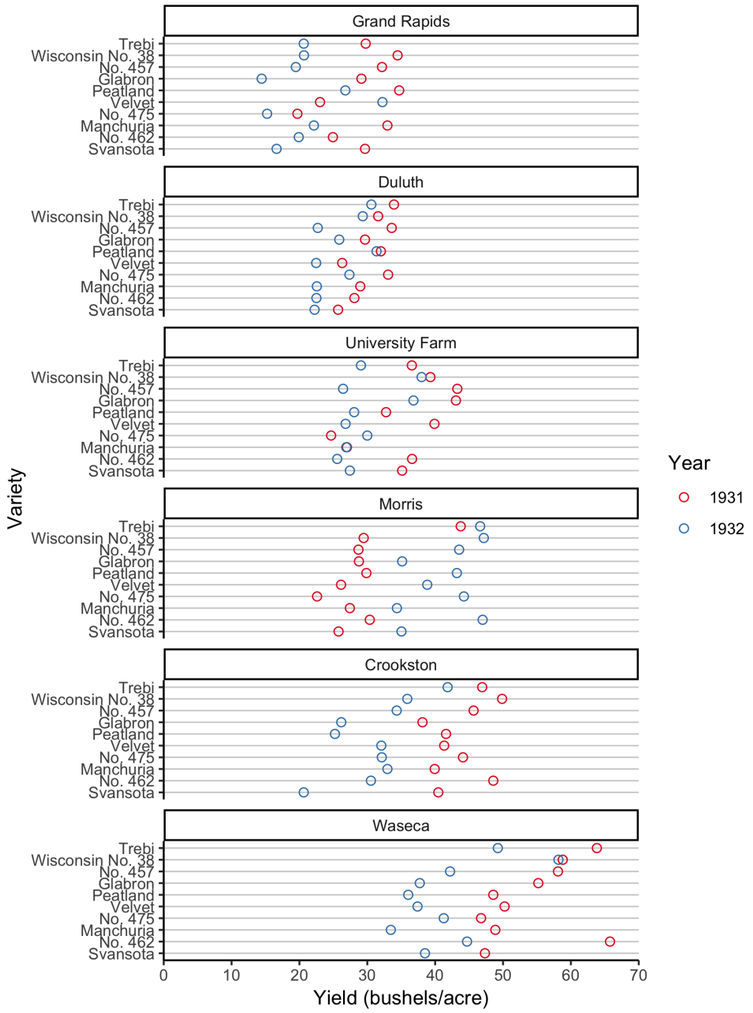
Individual data points

```
# position
posn_j <- position_jitter(width = 0.2)

# plot
d +
  geom_point(alpha = 0.6,
             position = posn_j)
```



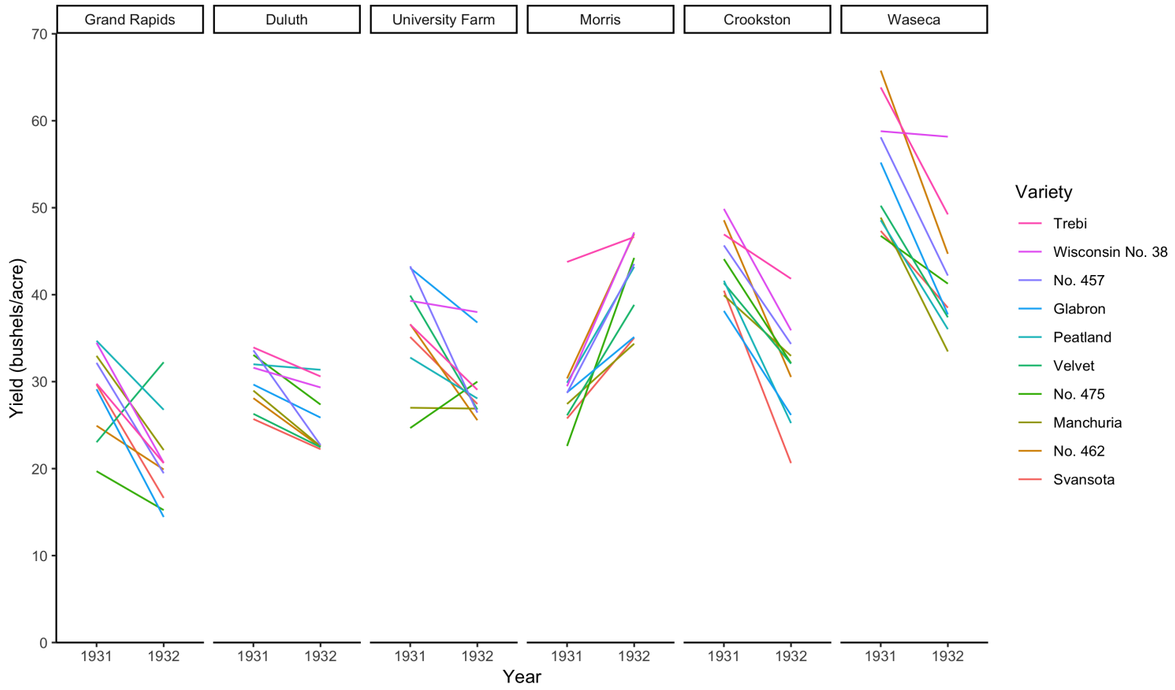
A dot plot

```
ggplot(barley, aes(yield, variety,
                   color = year)) +
  geom_point(...) +
  facet_wrap(vars(site), ncol = 1) +
  ...
```



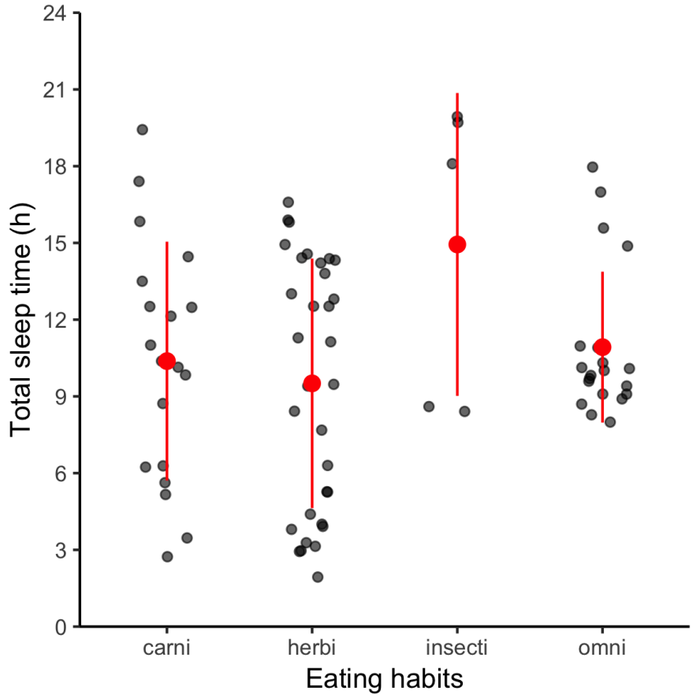
As a time series

```
ggplot(barley, aes(year, yield,
                   group = variety,
                   color = variety)) +
  geom_line() +
  facet_wrap(vars(site), nrow = 1) +
  ...
```



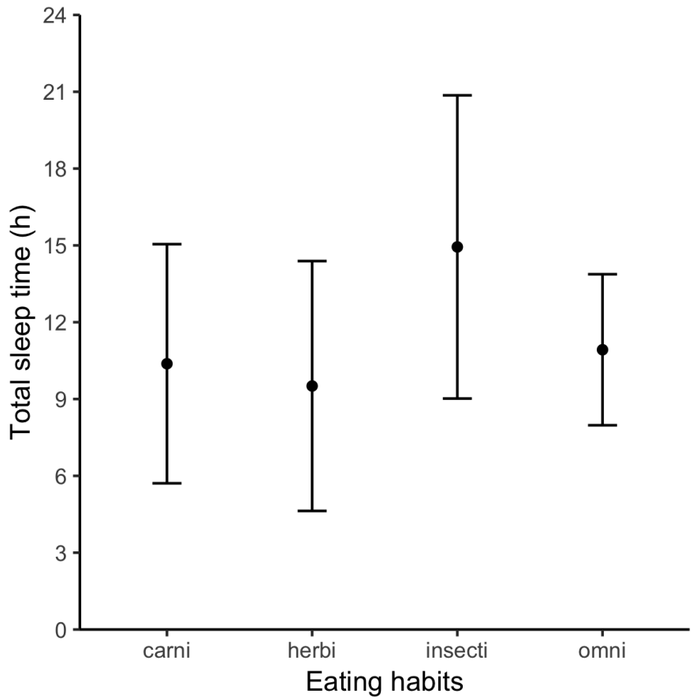
geom_pointrange()

```
d +
  geom_point(...) +
  stat_summary(fun.data = mean_sdl,
               mult = 1,
               width = 0.2,
               color = "red")
```

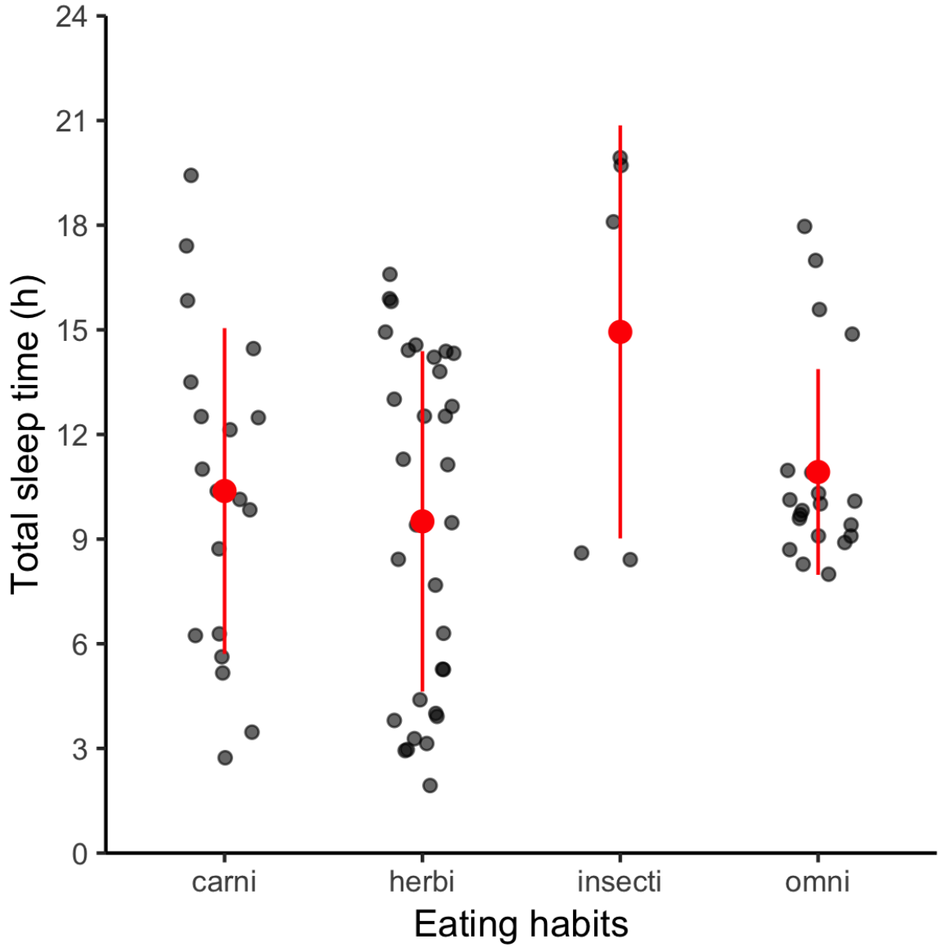


Without data points

```
d +
  stat_summary(fun.y = mean,
               geom = "point") +
  stat_summary(fun.data = mean_sdl,
               fun.args = list(mult = 1),
               geom = "errorbar",
               width = 0.2)
```

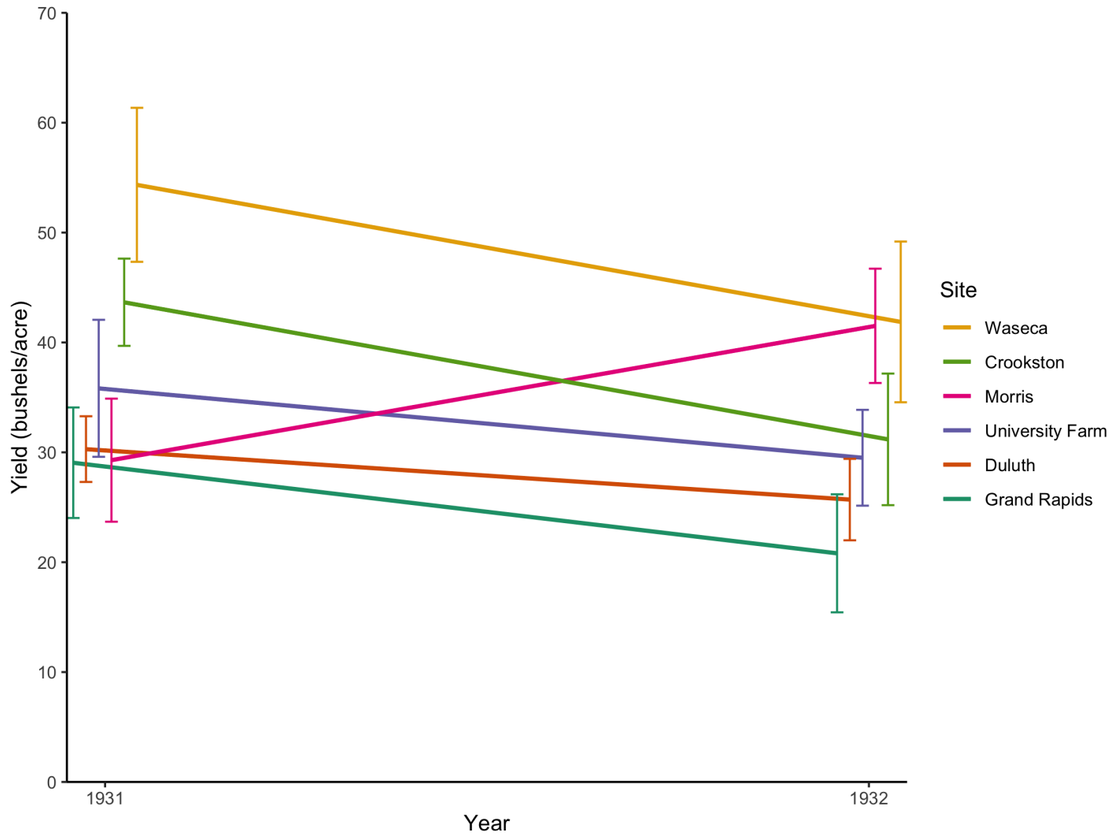


Bars are not necessary



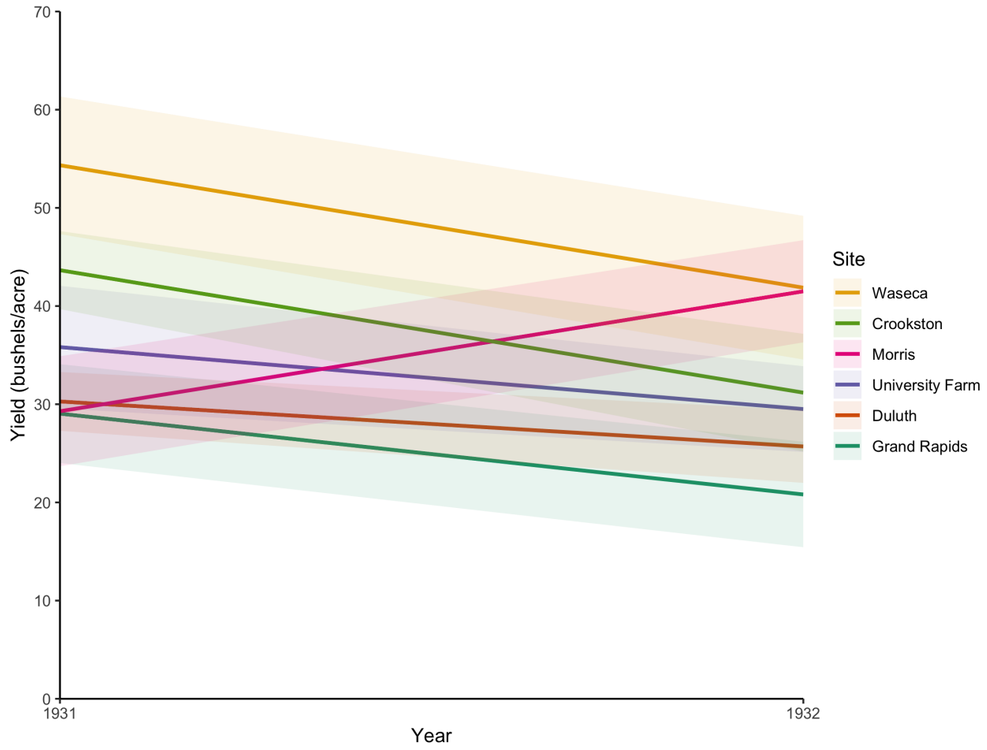
Using dodged error bars

```
ggplot(barley, aes(x = year, y = yield,
                   group = site,
                   color = site)) +
  stat_summary(fun.y = mean,
               geom = "line", ...) +
  stat_summary(fun.data = mean_sdl,
               geom = "errorbar", ...) +
  ...
```

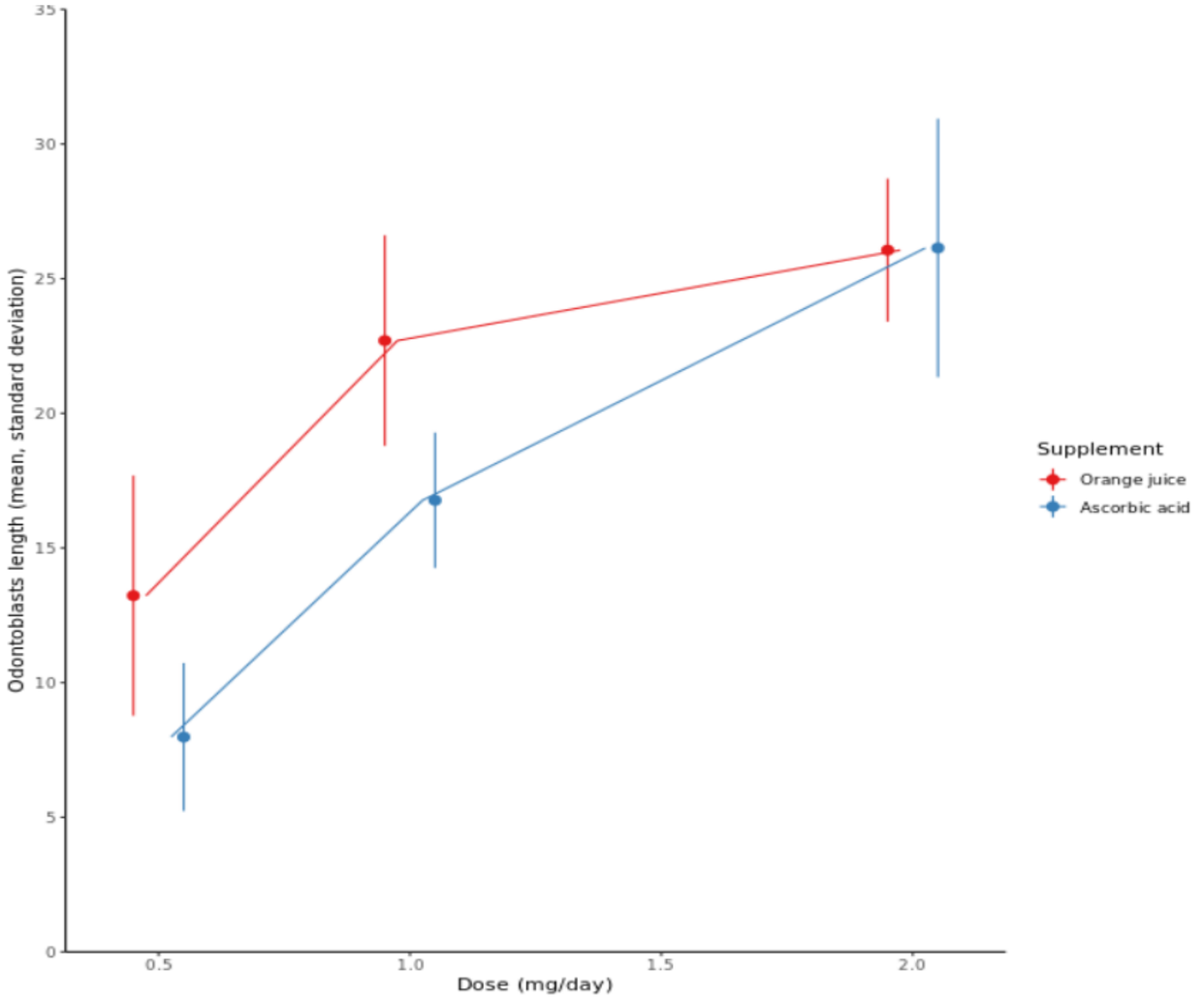


Using ribbons for error

```
# Using barely, plot yield vs. year, colored, grouped, and
filled by site
ggplot(barley, aes(x = year, y = yield,
                   color = site, group = site, fill = site)) +
  # Add a line summary stat aggregated by mean
  stat_summary(fun.y = mean, geom = "line") +
  # Add a ribbon summary stat with 10% opacity, no color
  stat_summary(fun.data = mean_sdl, fun.args = list(mult = 1),
                       geom = "ribbon", alpha = 0.1, color = NA)
```

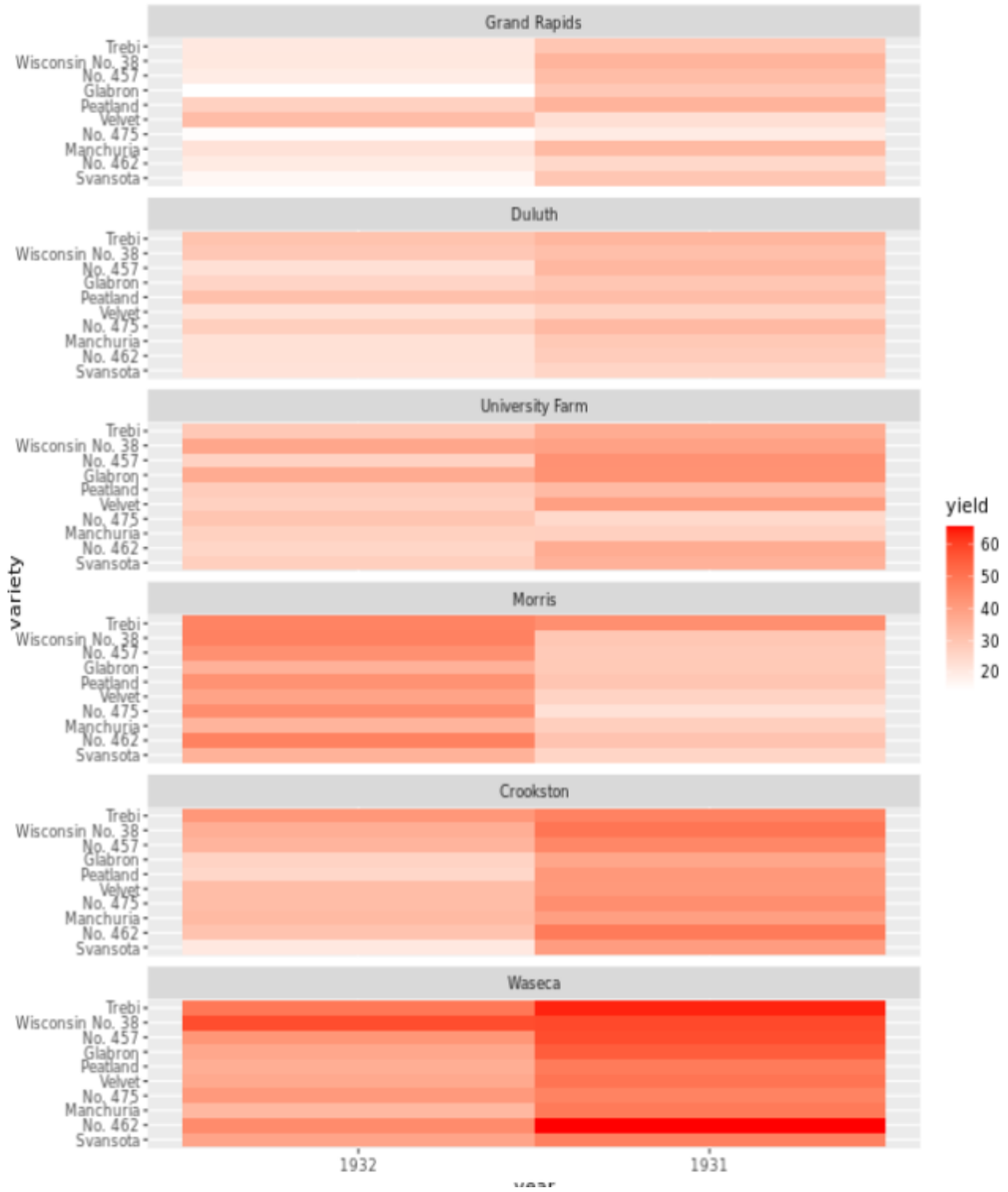


```r
# Change type
TG$dose <- as.numeric(as.character(TG$dose))

# Plot
growth_by_dose <- ggplot(TG, aes(dose, len, color = supp)) +
  stat_summary(fun.data = mean_sdl,
               fun.args = list(mult = 1),
               position = position_dodge(0.2)) +
  stat_summary(fun.y = mean,
               geom = "line",
               position = position_dodge(0.1)) +
  theme_classic() +
  # Adjust labels and colors:
  labs(x = "Dose (mg/day)",
       y = "Odontoblasts length (mean, standard deviation)",
       color = "Supplement") +
  scale_color_brewer(palette = "Set1",
                     labels = c("Orange juice", "Ascorbic acid")) +
  scale_y_continuous(limits = c(0,35),
                     breaks = seq(0, 35, 5),
                     expand = c(0,0))

# View plot
growth_by_dose
```



A basic heat map

```
# Previously defined
ggplot(barley, aes(x = year, y = variety, fill = yield)) +
  geom_tile() +
  # Facet, wrapping by site, with 1 column
  facet_wrap(facets = vars(site), ncol = 1) +
  # Add a fill scale using an 2-color gradient
  scale_fill_gradient(low = "white", high = "red")
```

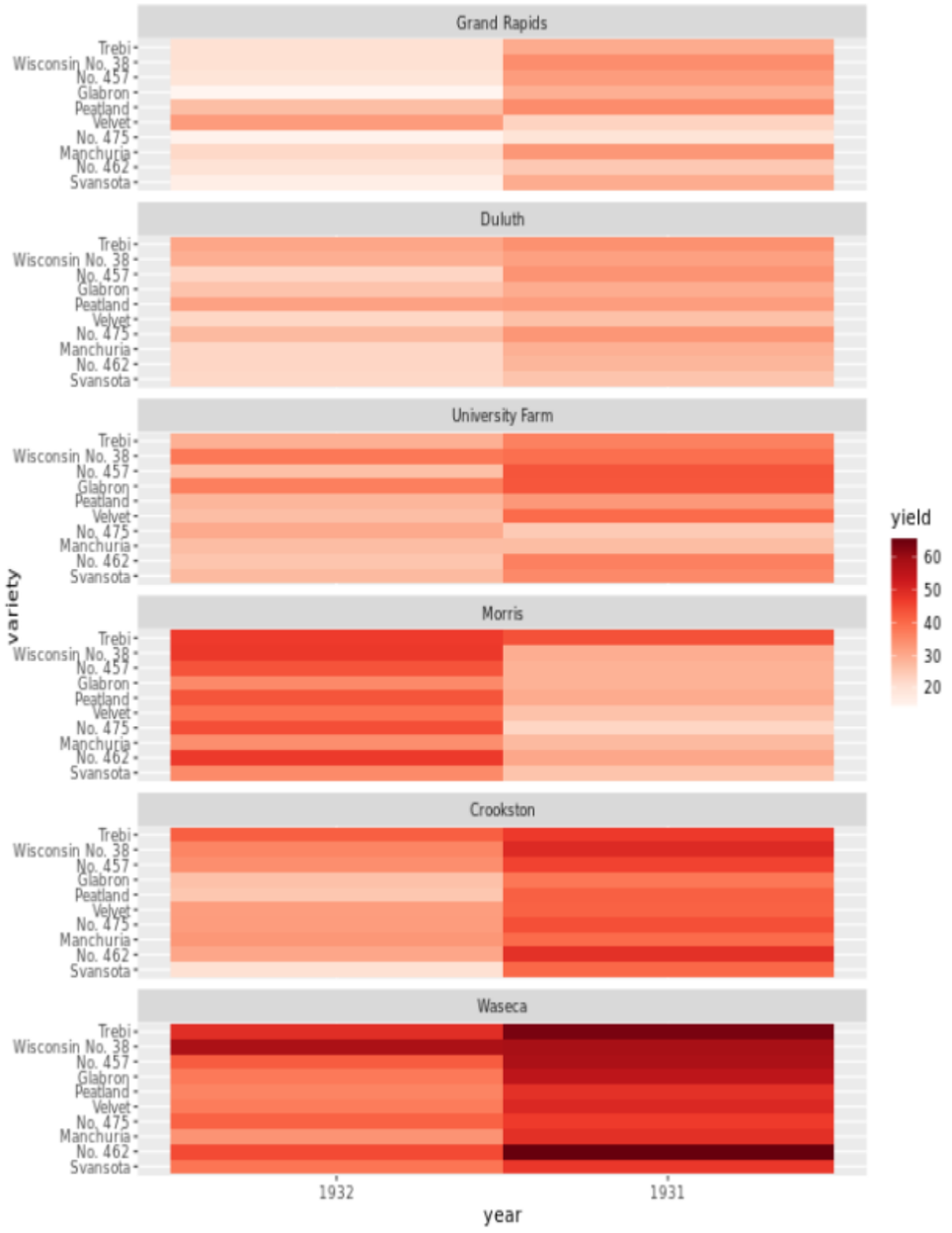


Heat maps are most useful if you have:
* a small number of boxes
* a clear pattern that allows

There are few groups with large differences.

A basic heat map

```
# A palette of 9 reds
red_brewer_palette <- brewer.pal(9, "Reds")

# Update the plot
ggplot(barley, aes(x = year, y = variety, fill = yield)) +
  geom_tile() +
  facet_wrap(facets = vars(site), ncol = 1) +
  # Update scale to use n-colors from red_brewer_palette
  scale_fill_gradientn(colors = red_brewer_palette)
```



Heat maps are most useful if you have:
* a small number of boxes
* a clear pattern that allows

There are few groups with large differences.

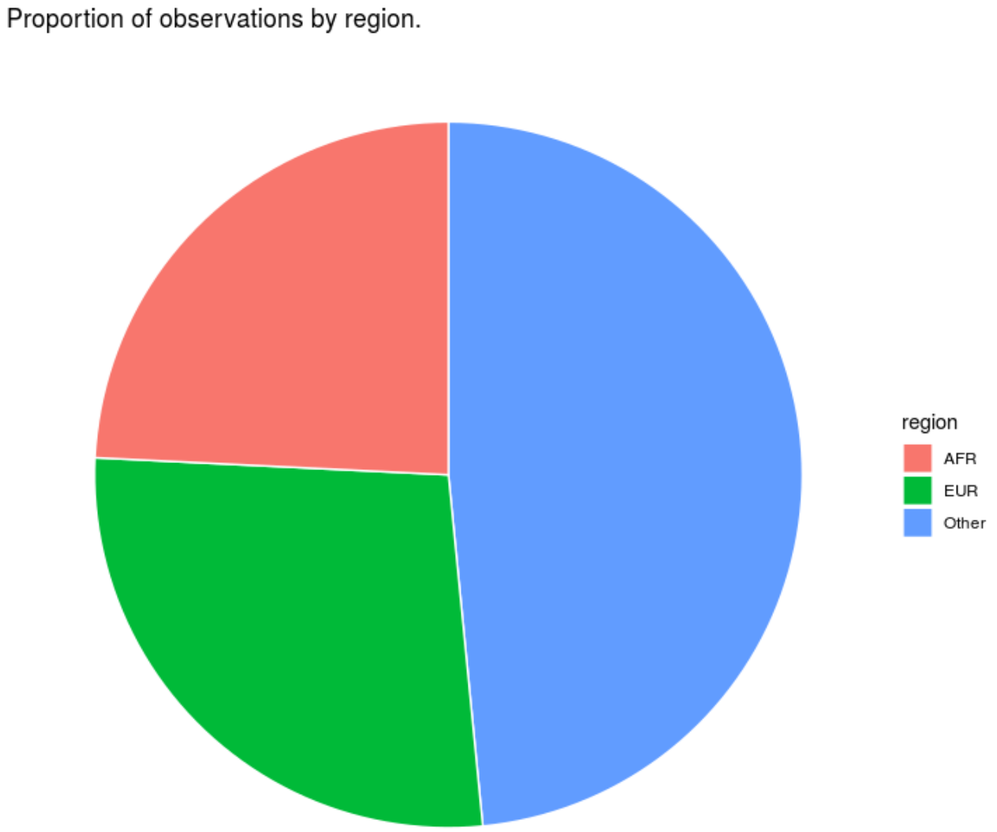
A sour pie

- Pie charts are not very precise
  - Data encoded in angles
- Doesn't handle lots of classes well
  - After three slices it becomes hard to compare

A sweet pie

- Intuitive and compact

```
who_disease %>%
  mutate(
    region = ifelse(
      region %in% c('EUR', 'AFR'),
      region, 'Other')
  ) %>%
  ggplot(aes(x = 1, fill = region)) +
    geom_bar(color = 'white') +
    coord_polar(theta = "y") +
    theme_void()
```

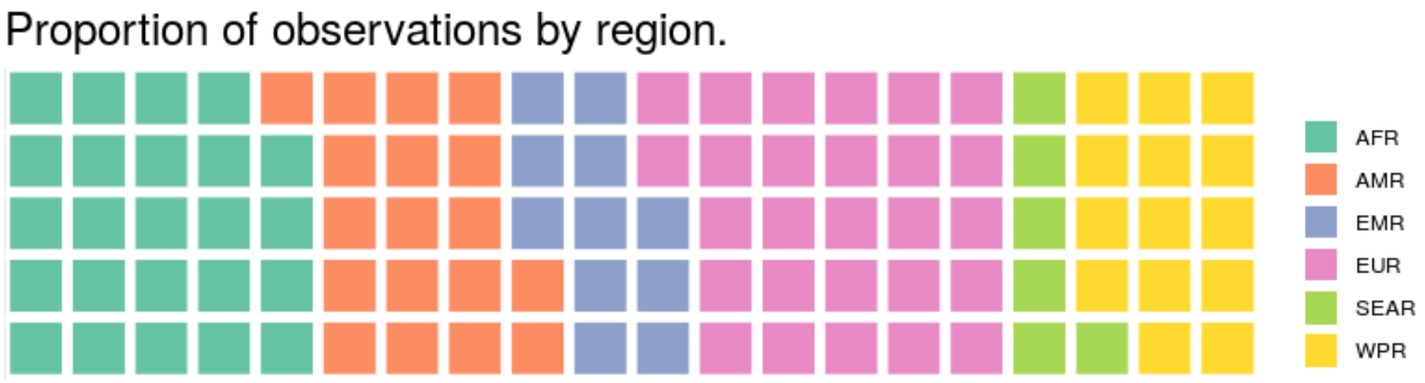


The waffle chart

- More precise than pie charts
- Encode data in area, not angles

```
obs_by_region <- who_disease %>%
  group_by(region) %>% summarise(num_obs = n()) %>%
  mutate(percent = round(num_obs/sum(num_obs)*100))

# Array of rounded percentages
percent_by_region <- obs_by_region$percent
names(percent_by_region) <- obs_by_region$region

# Send array of percentages to waffle plot function
waffle::waffle(percent_by_region, rows = 5)
```

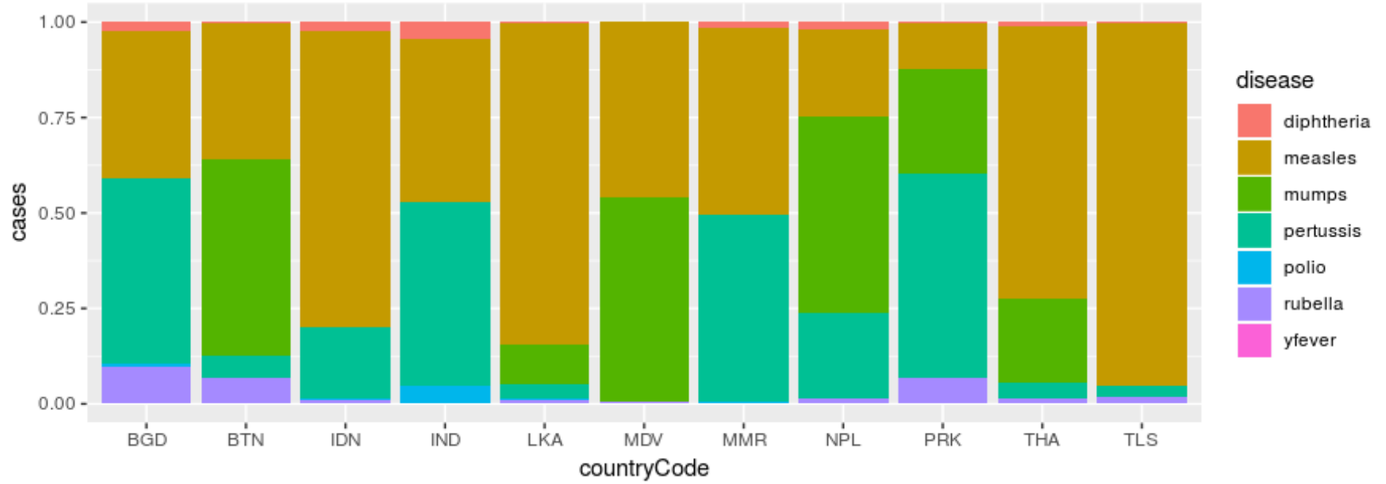
The waffle chart



The stacked bar chart

- Allow each population to share the same y-axis
- Enables easier comparisons based on vertical position/size

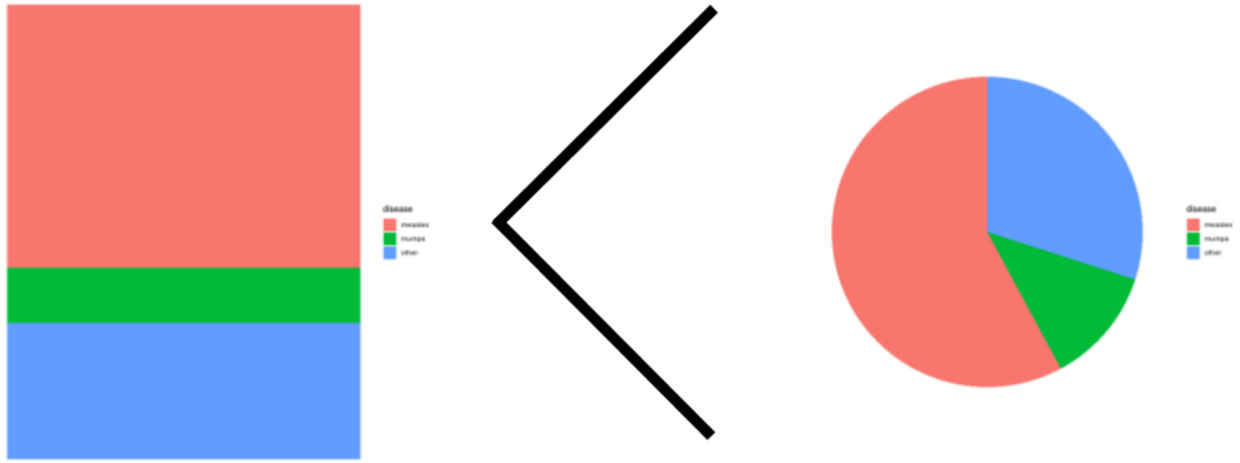
```
who_disease %>%
  filter(region == 'SEAR') %>%
  ggplot(aes(x = countryCode, y = cases, fill = disease)) +
    geom_col(position = 'fill')
```



Your goal should be to compare lots of populations makeups to each other

Caveats

- Worse in isolation than pie or waffle charts
- Accuracy degrades rapidly after 3 classes

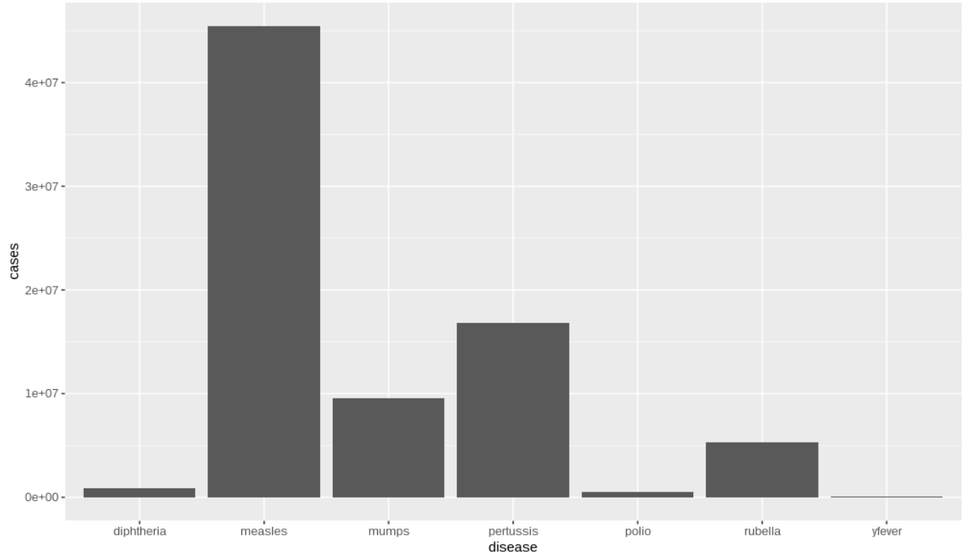


The bar chart

- Popular
- Simple
- Accurate

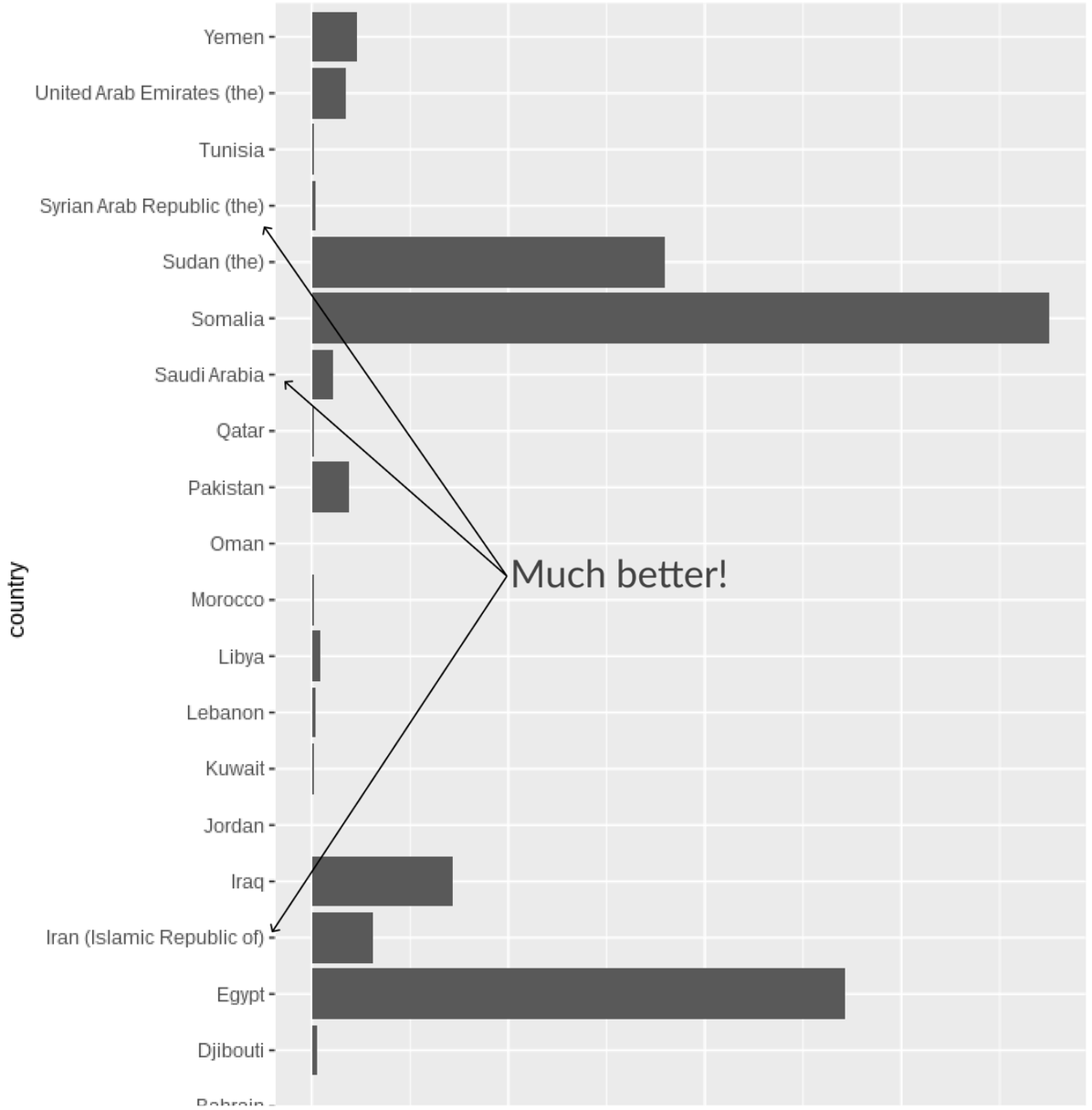
They should be used to describe totals

```
ggplot(who_disease) +
  geom_col(aes(x = disease, y = cases))
```



NOT:Some common types of data that aren't stackable are percentiles, ratios, or sensor readings like temperature as they don't go to 0.

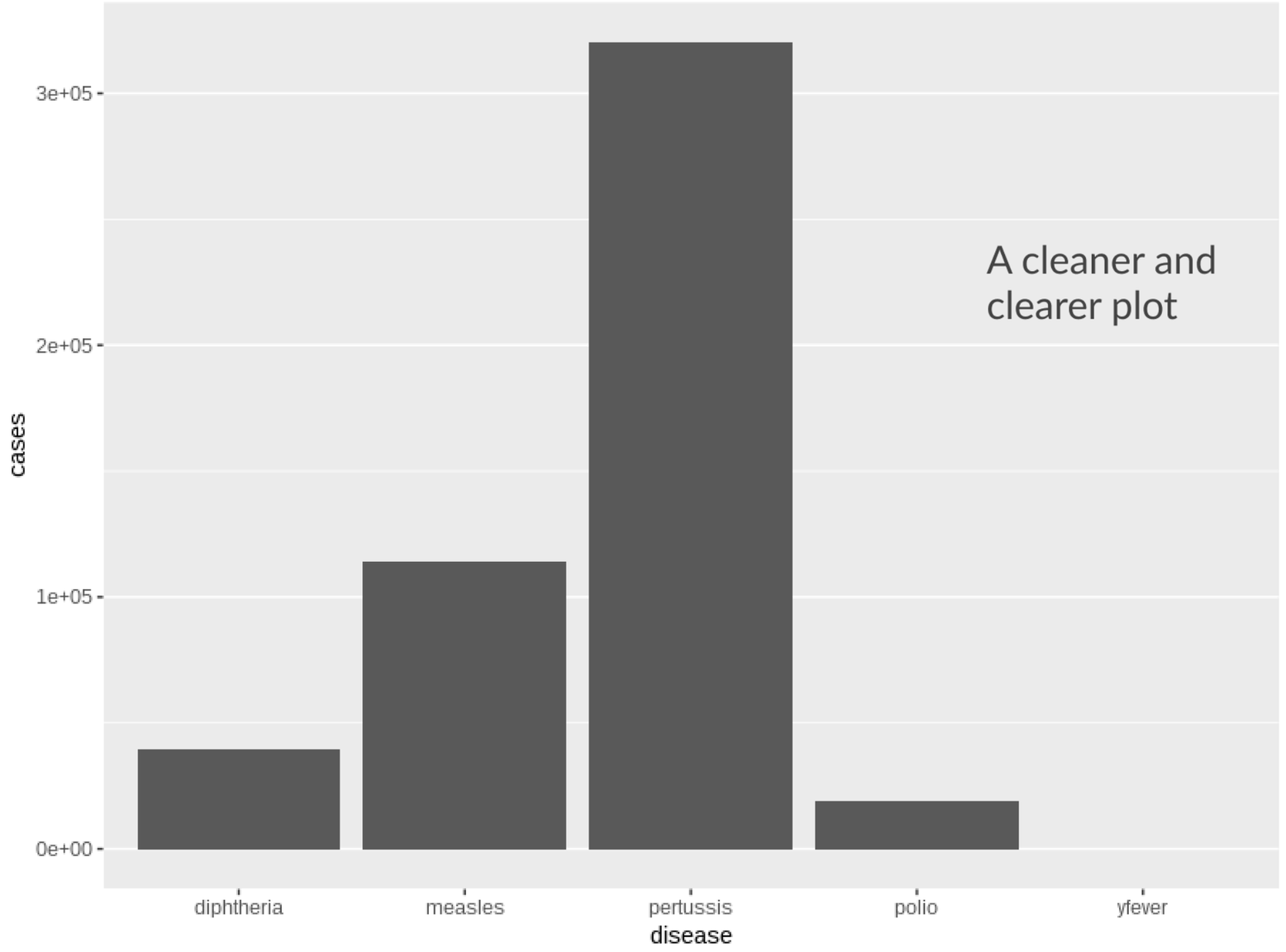
When data have a non-linear transformation such as the log, square root, or exponentiation.


Yemen
United Arab Emirates (the)
Tunisia
Syrian Arab Republic (the)
Sudan (the)
Somalia
Saudi Arabia
Qatar
Pakistan
Oman
Morocco
Libya
Lebanon
Kuwait
Jordan
Iraq
Iran (Islamic Republic of)
Egypt
Djibouti
country
Much better!

Removing vertical grid

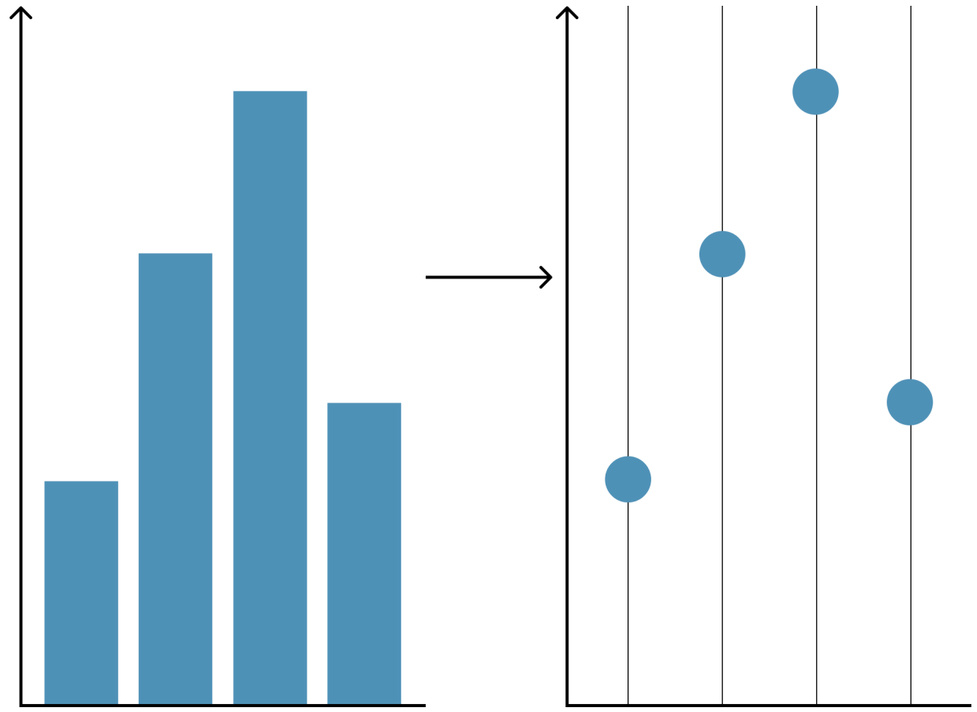
```
plot <- who_disease %>%
  filter(country == "India", year == 1980) %>%
  ggplot(aes(x = disease, y = cases)) +
    geom_col()
```

```
# Remove vertical grid lines
 plot + theme(
    panel.grid.major.x = element_blank()
  )
```


A cleaner and clearer plot
3e+05
2e+05
1e+05
0e+00
cases
diphtheria
measles
pertussis
polio
yfever
disease

Point charts

- Simply replace bar with a point
- Sometimes called point charts or dot plots

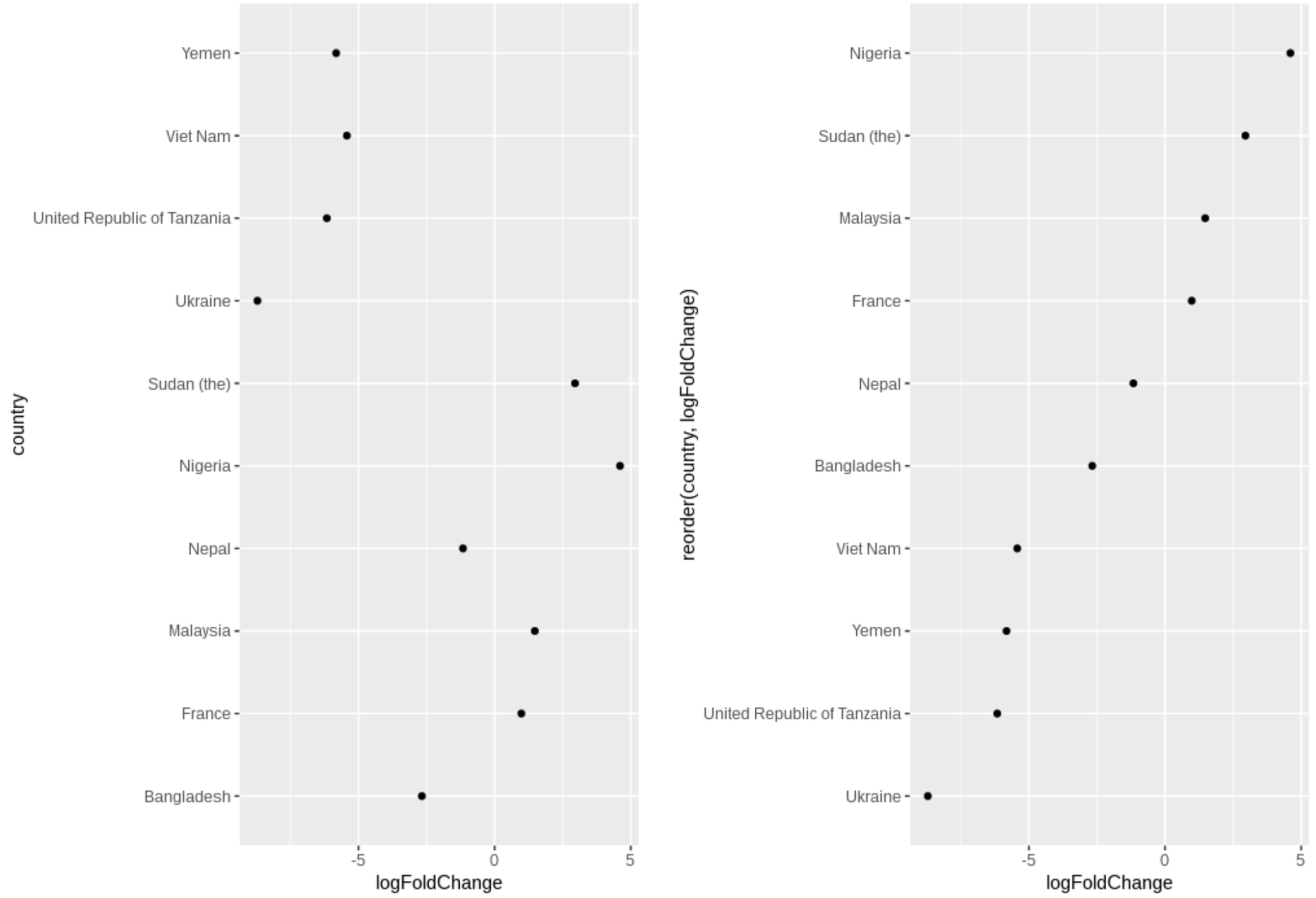


Ordering your point charts

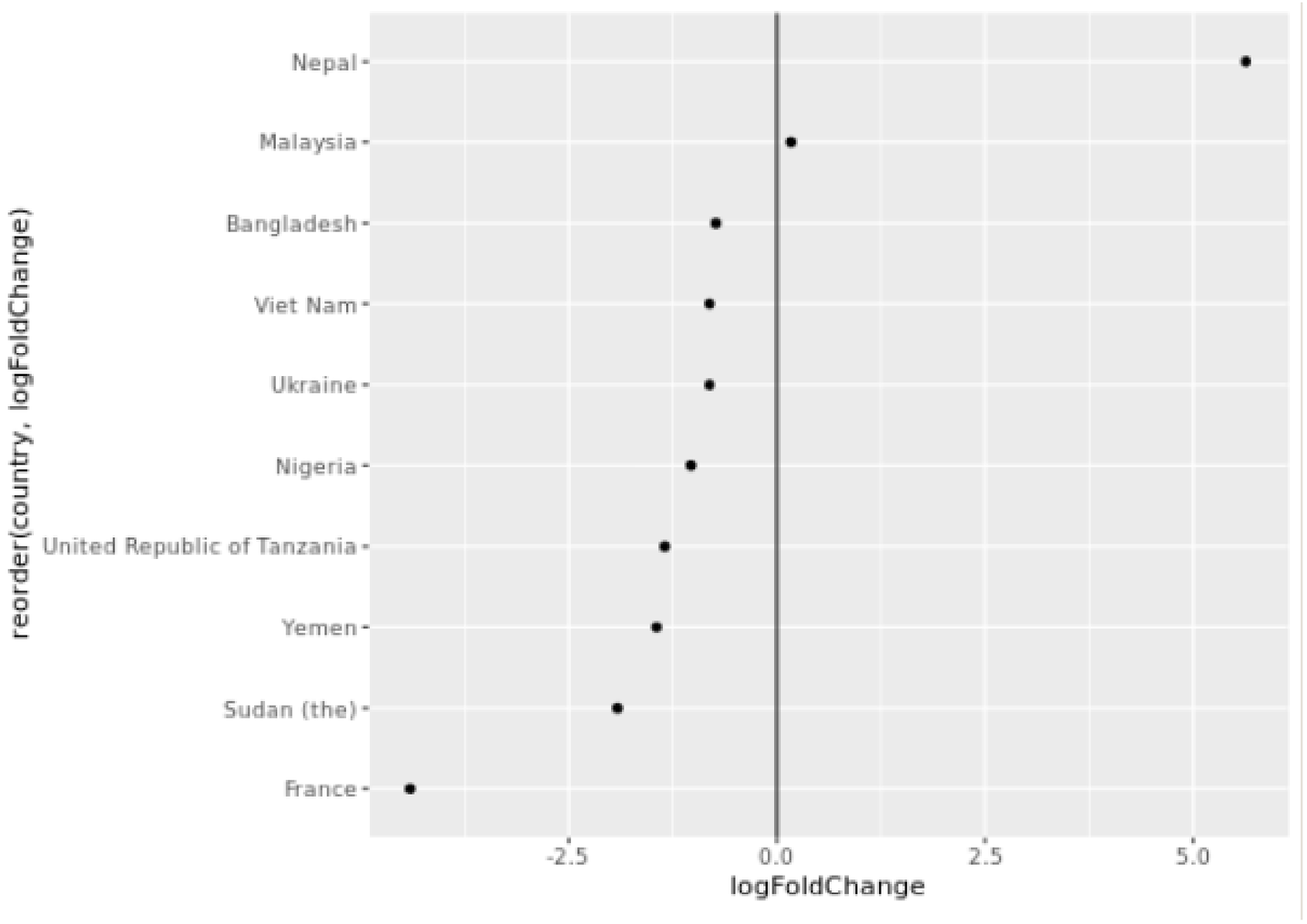
- Ordering can vastly help legibility
- Use the `reorder()` function in the aesthetic assignment

```
who_subset %>%
  # calculate the log fold change between 2016 and 2006
  mutate(logFoldChange = log2(cases_2016/cases_2006)) %>%
  ggplot(aes(x = logFoldChange, y = reorder(country, logFoldChange))) +
  geom_point()
```

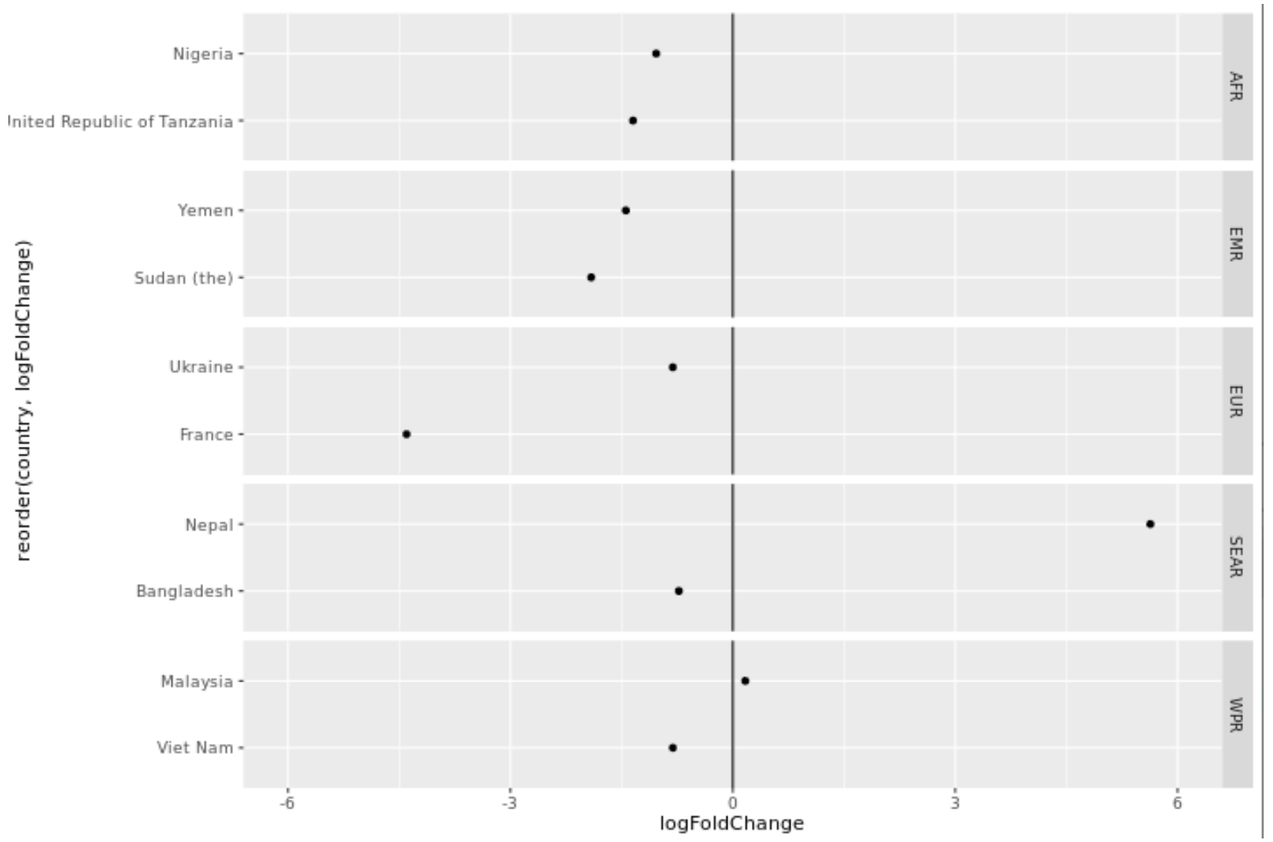
reorder


Yemen
Viet Nam
United Republic of Tanzania
Ukraine
Sudan (the)
Nigeria
Nepal
Malaysia
France
Bangladesh
country
-5
0
5
logFoldChange
Nigeria
Sudan (the)
Malaysia
France
Nepal
Bangladesh
Viet Nam
Yemen
United Republic of Tanzania
Ukraine
reorder(country, logFoldChange)
-5
0
5
logFoldChange

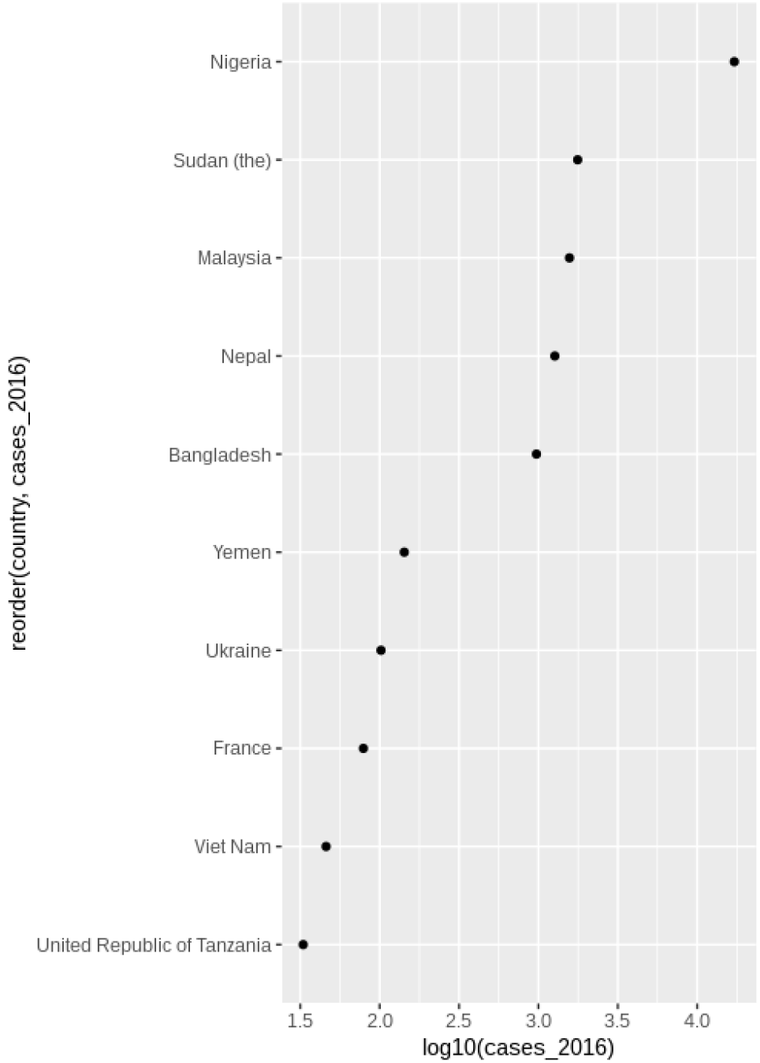
Adding simple visual cues to orient the reader like a line at a neural value can greatly improve the legibility to the chart, especially for non-experts in the data you are visualizing.

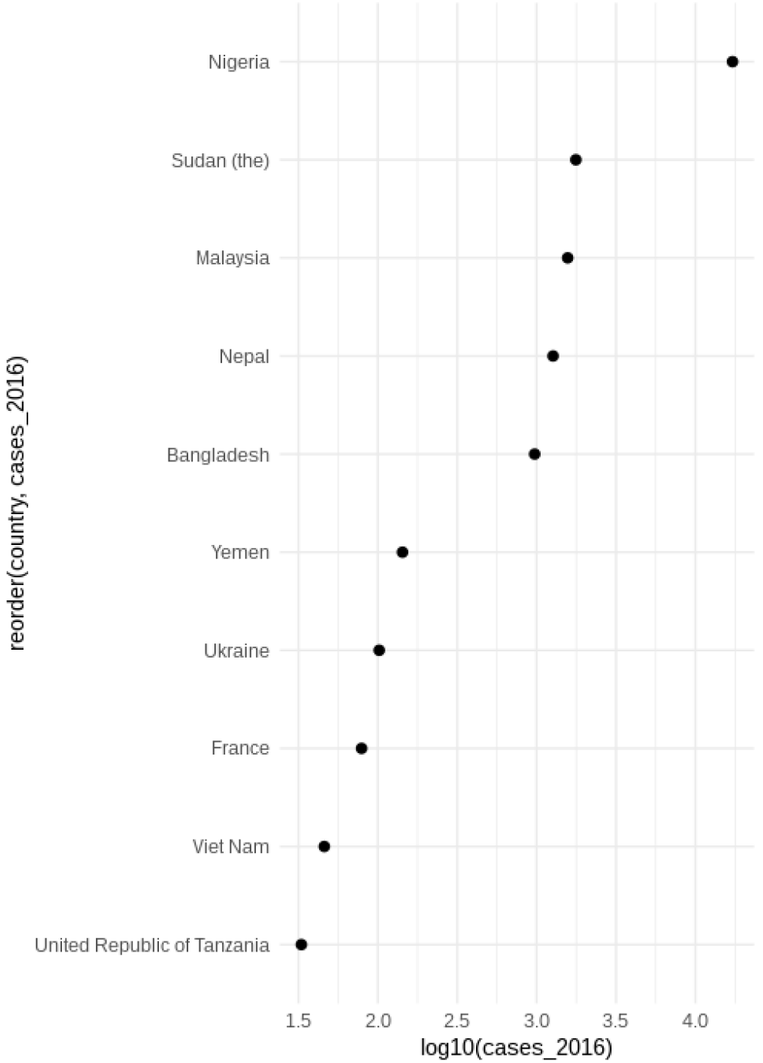


Facing can add more information



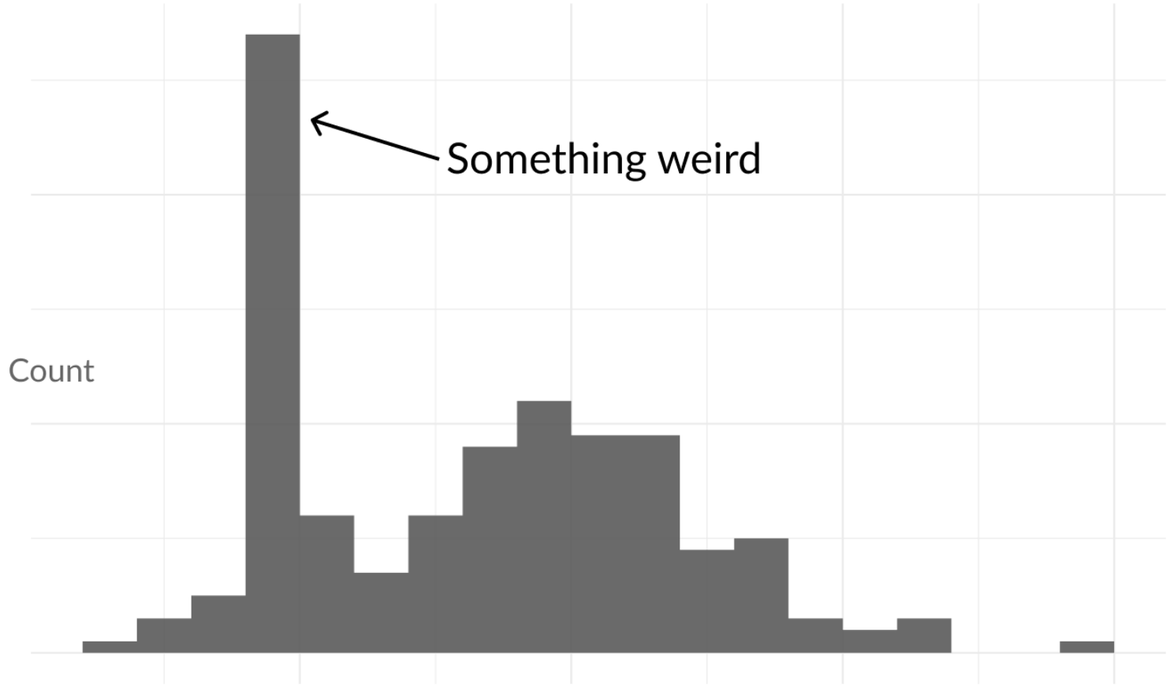
```
size=2 +
theme_minimal()
```





Why distributions are important

- Data collection or cleaning errors can become apparent
- Could indicate the need to control for a variable in a model
- Being true to the data

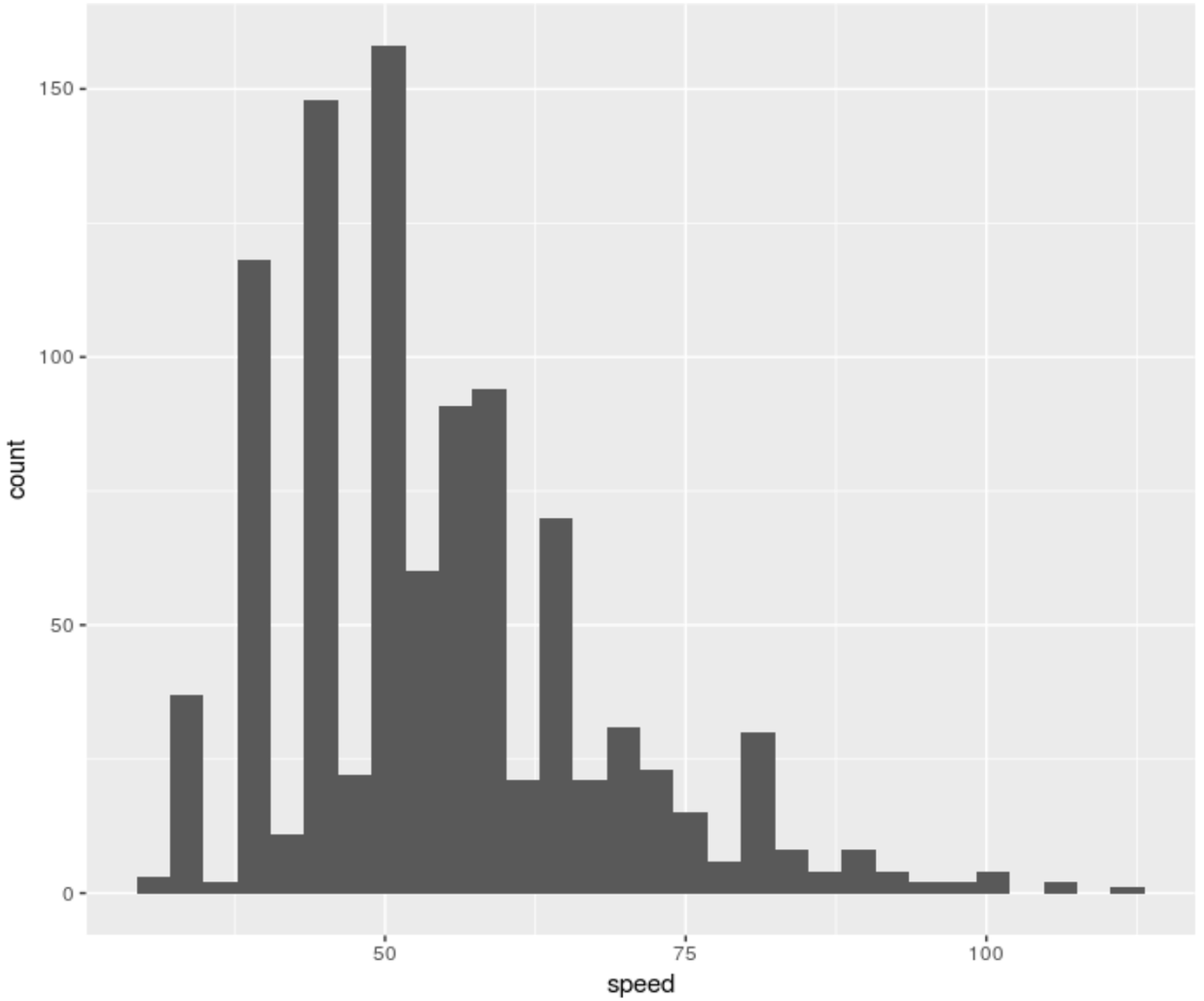


Making a histogram in ggplot2

- `geom_histogram()`
- Automatically bins data for you
- Just supply `x` `aes` thetic

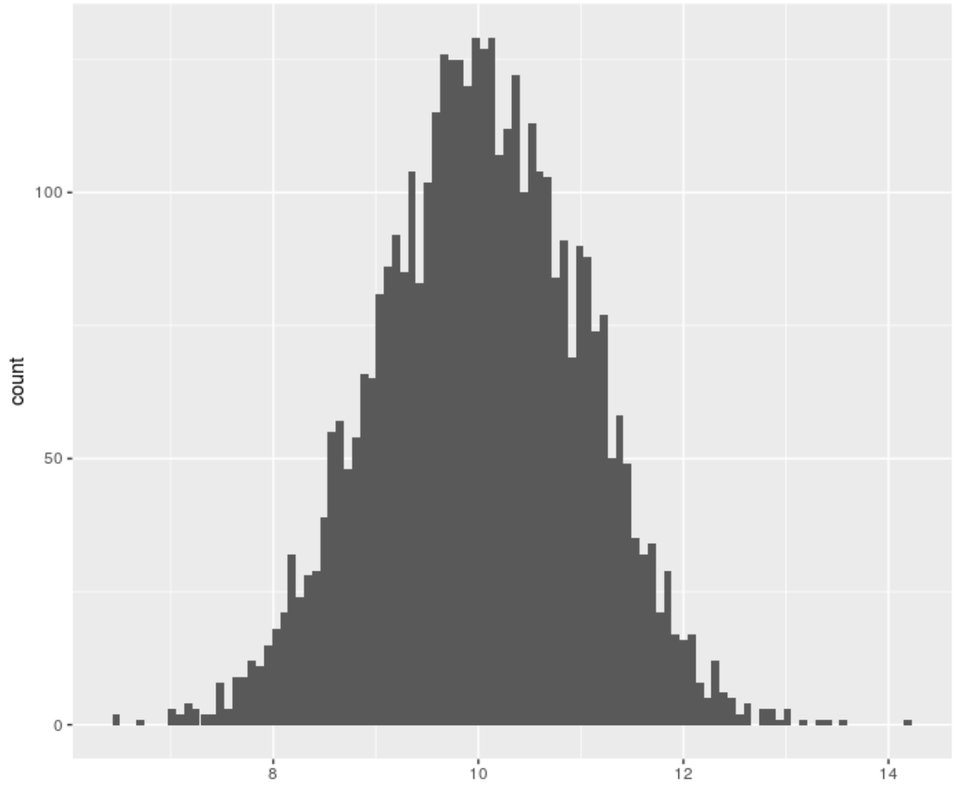
```
md_speeding %>%
  filter(vehicle_color == 'BLUE') %>%
  ggplot(aes(x = speed)) +
  geom_histogram()
```

```
# Load md_speeding into ggplot
ggplot(md_speeding) +
  # add a geom_histogram with x mapped to percentage_over_limit
    geom_histogram(
        aes(percentage_over_limit),
        bins = 40,     # set bin number to 40
        alpha = 0.8)    # reduce alpha to 0.8
```



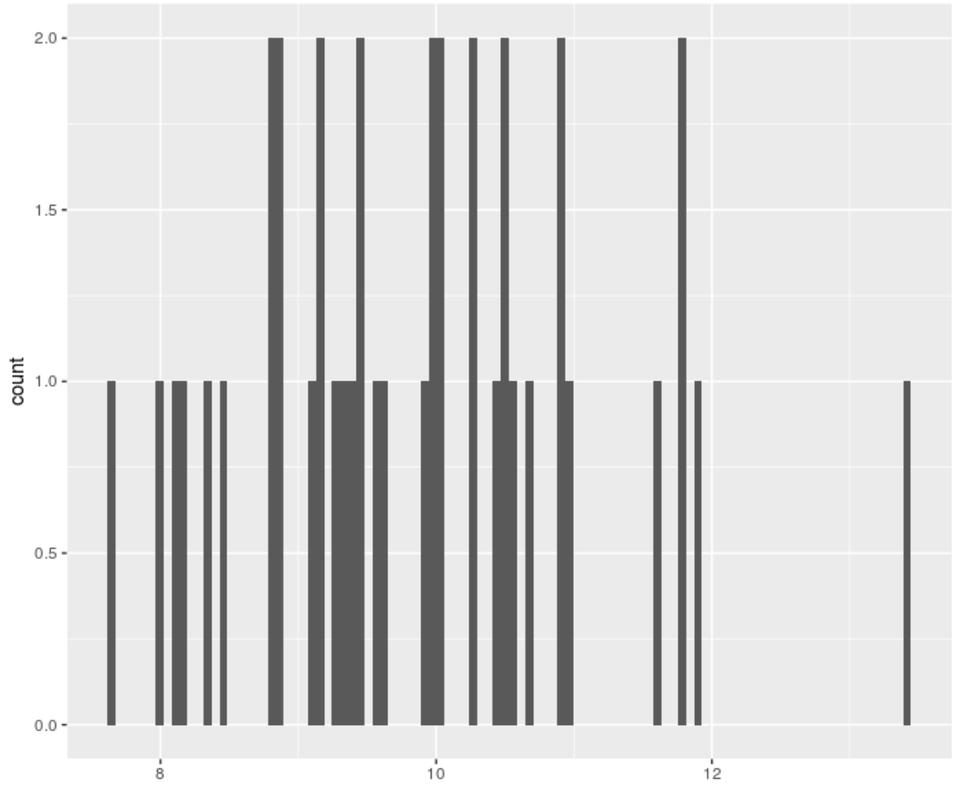
Histogram positives

- Intuitive
- Interpretable



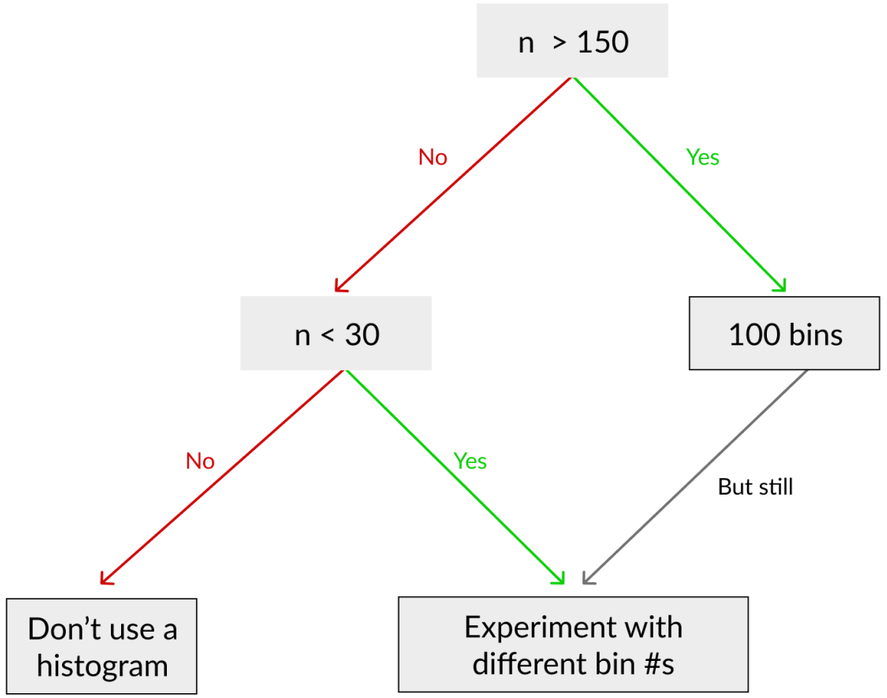
Histogram negatives

- Sensitive to bin placements
- Iffy with small amounts of data

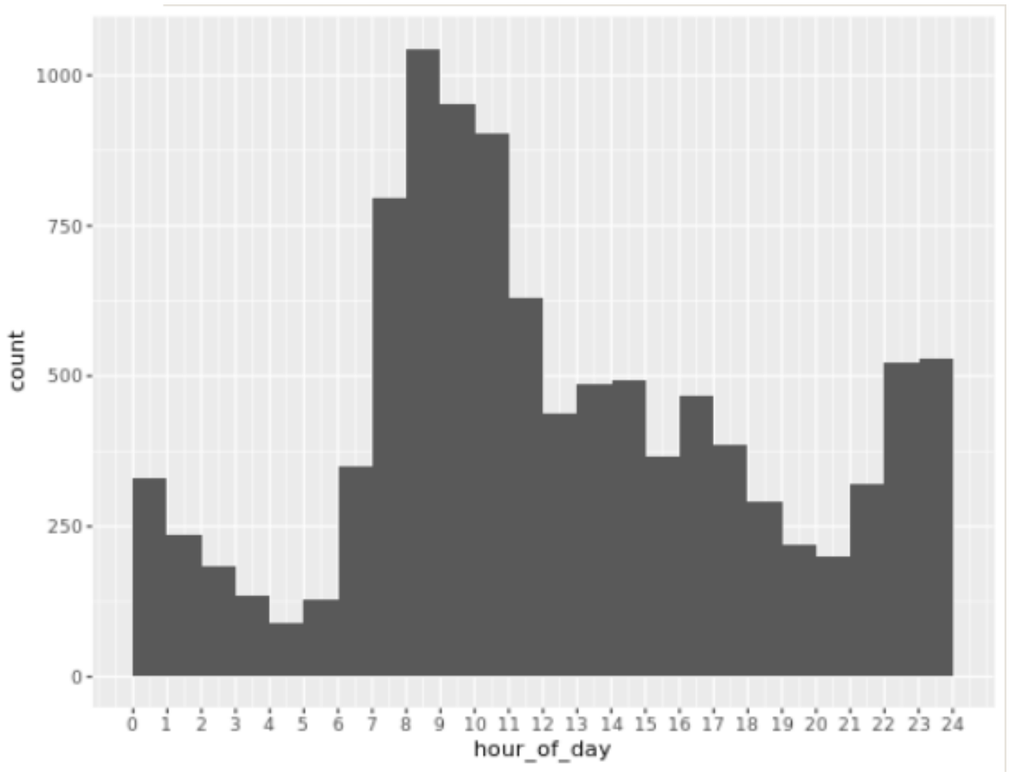


Bin number best practices

- If `length(data$x) > 150` → `bins = 100`
- Otherwise, play around to get a good sense of the data



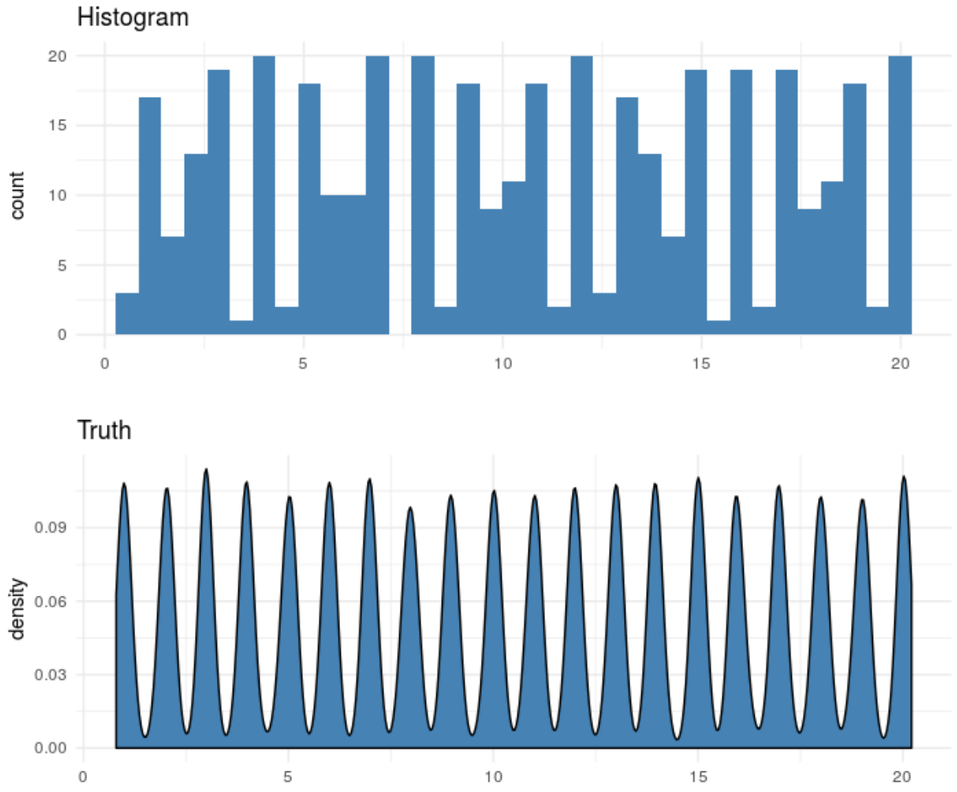
```r
ggplot(md_speeding,aes(x = hour_of_day)) +
    geom_histogram(
        binwidth = 1,
        center = 0.5
    ) +
    scale_x_continuous(breaks = 0:24)
```



When your data has natural breakpoints like this, you should exploit them. In this case, we can set our breaks to fall on the hour boundaries.

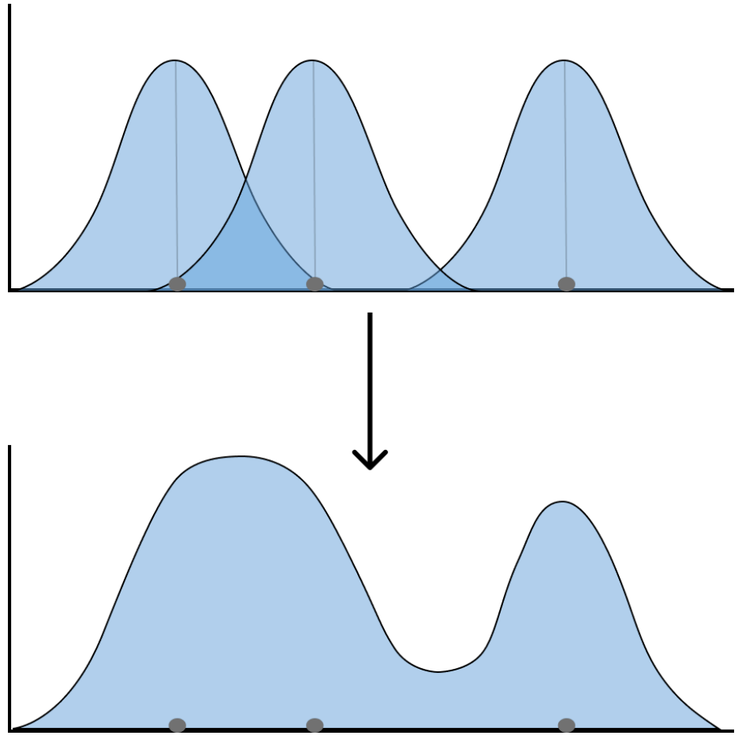
Where histograms struggle

- Data with multiple strong peaks
- Small data



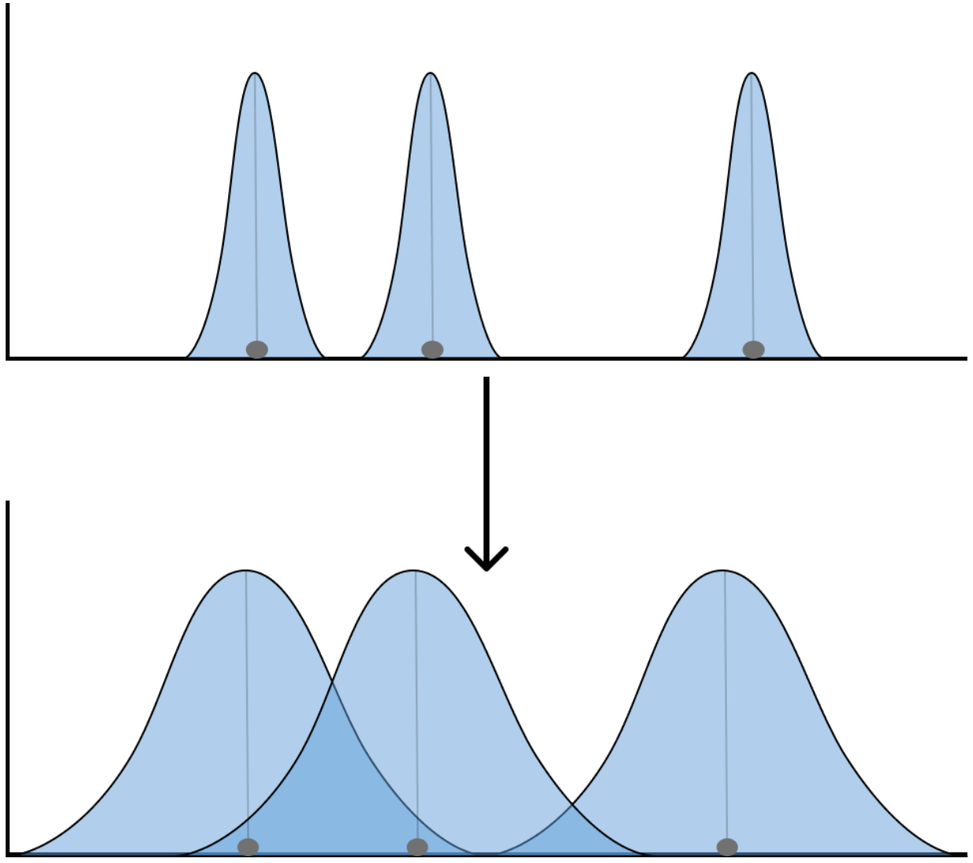
Kernel density plots

- Place "kernel" on top of every data point
- Add up heights of all overlapping kernels



A new width to worry about

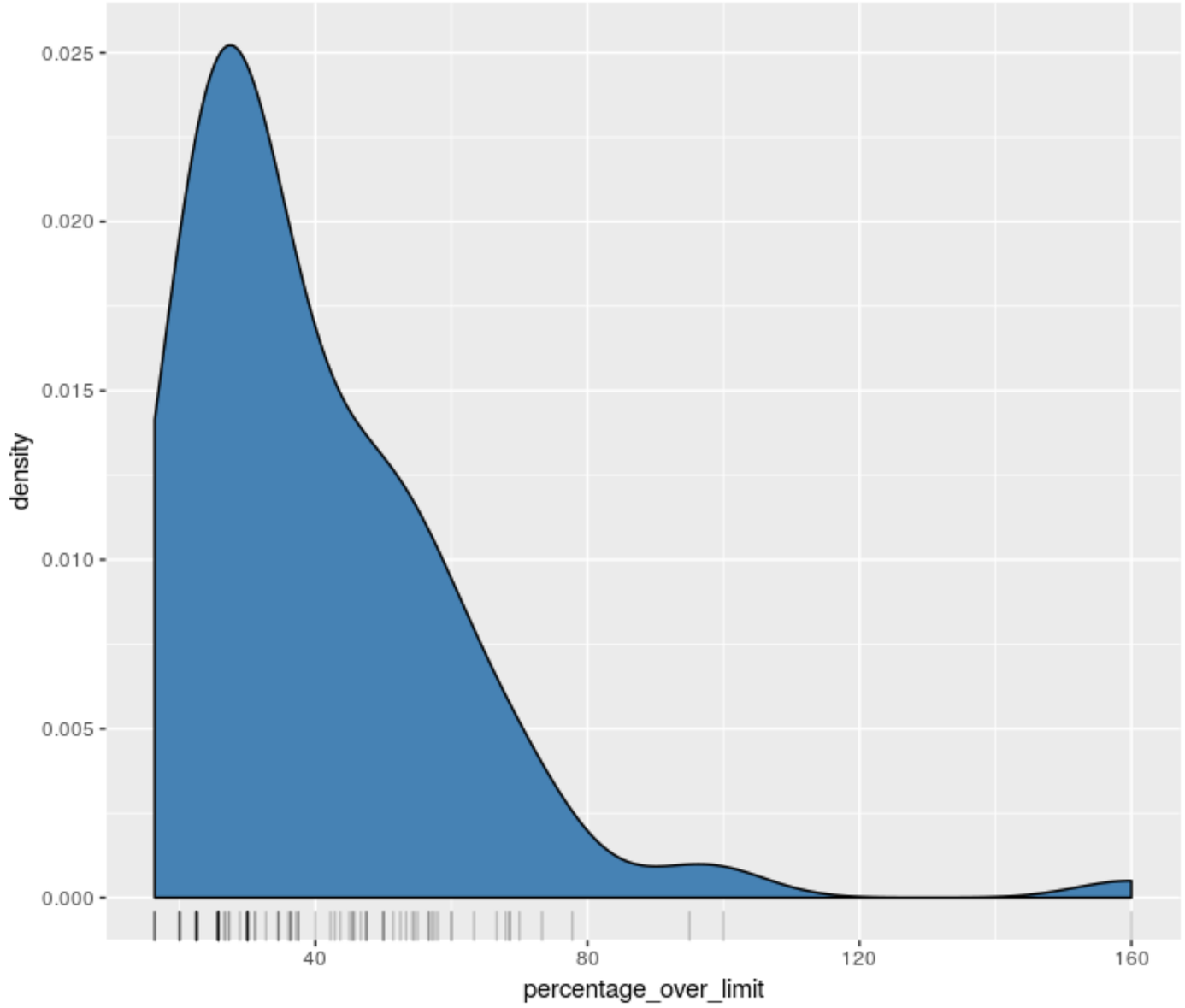
- Need to adjust the standard deviation of the kernel placed on each point



Show all the data

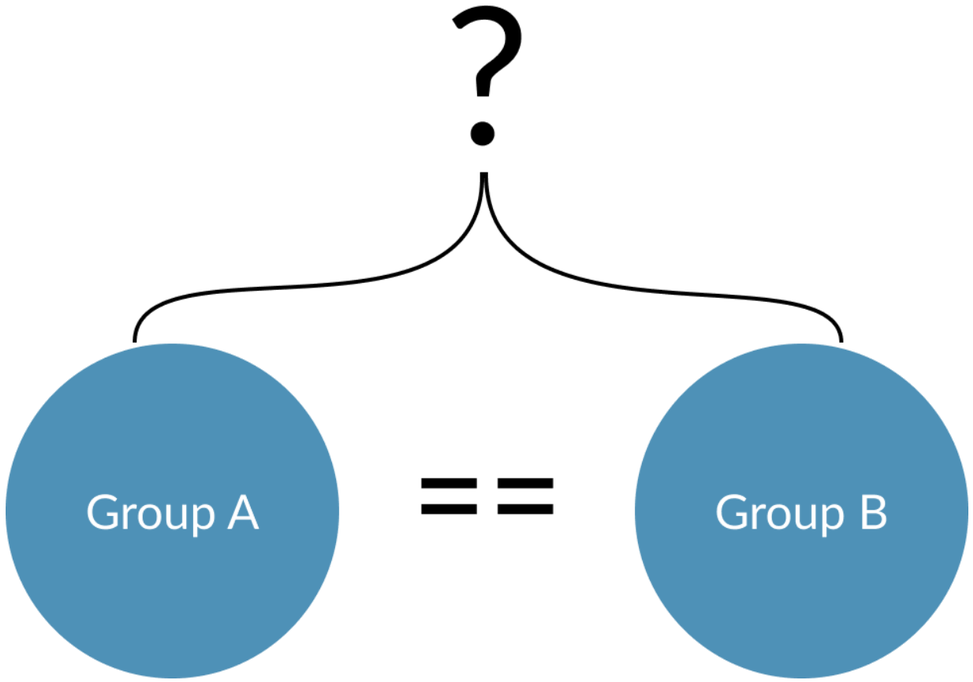
Use `geom_rug()` to show all data below KDE with lines

```
p <-sample_n(md_speeding, 100) %>%
  ggplot(aes(x = percentage_over_limit)) +
  geom_density(alpha = 0.7,
    fill = 'steelblue', # fill in curve with color
    bw = 8 # standard deviation of kernel
  )
p + geom_rug(alpha = 0.4)
```


0.025
0.020
0.015
0.010
0.005
0.000
density
40
80
120
160
percentage_over_limit

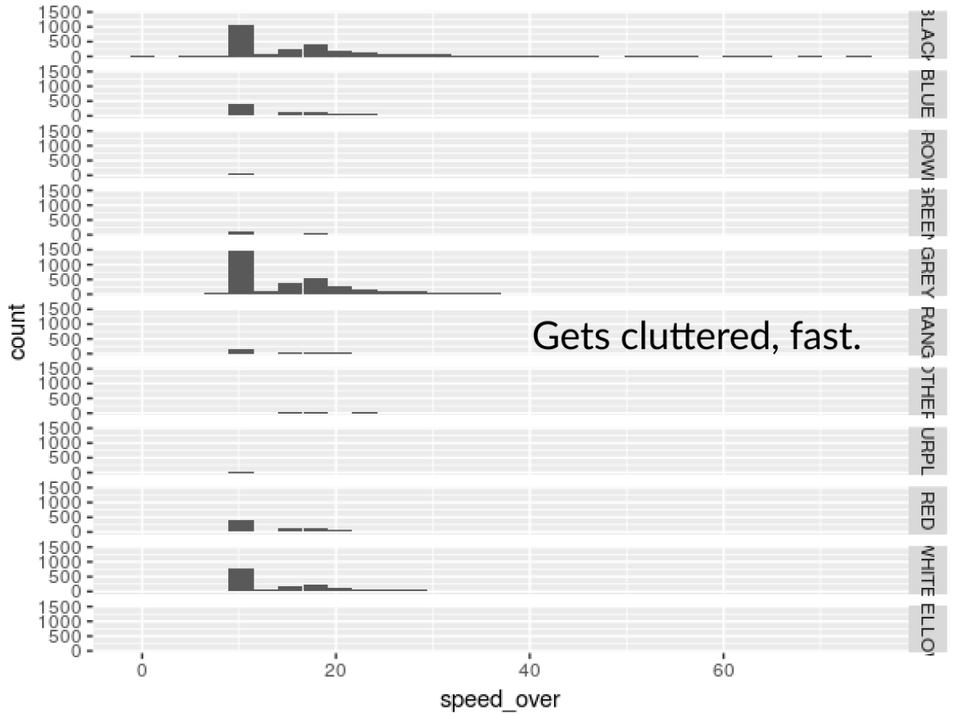
Why compare distributions?

- Verify balanced groups
- For comparison's sake

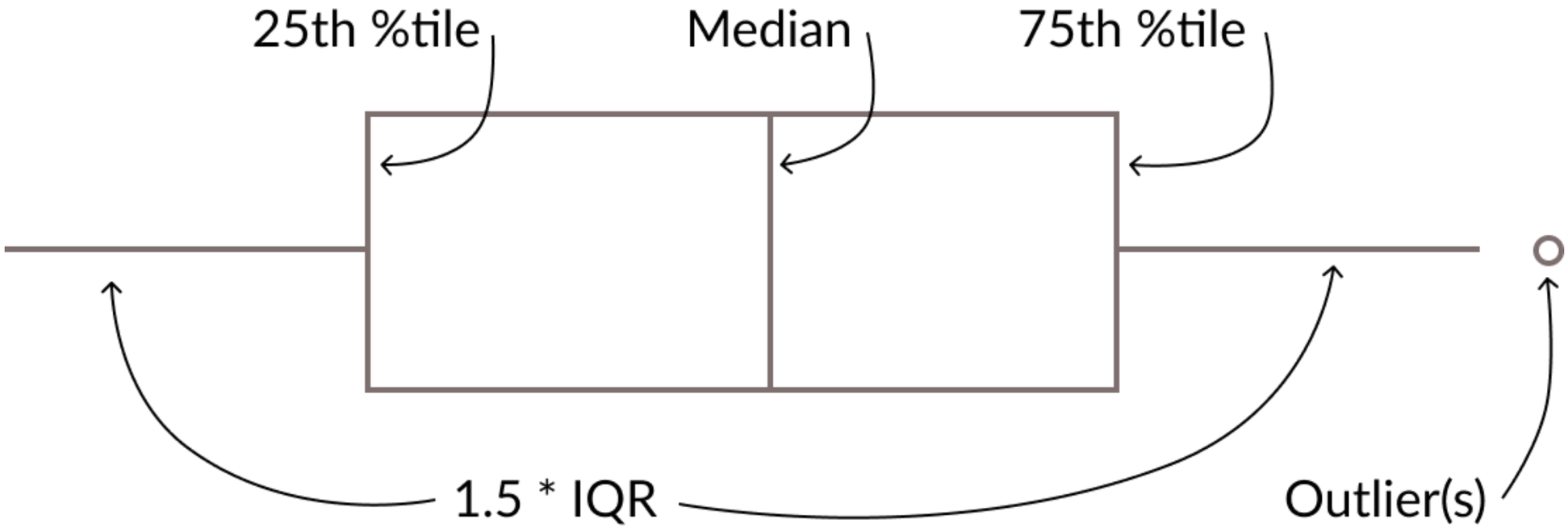


Why not facet histogams?

```
ggplot(md_speeding, aes(x = speed_over)) +
  geom_histogram() +
  facet_grid(vehicle_color ~ .)
```



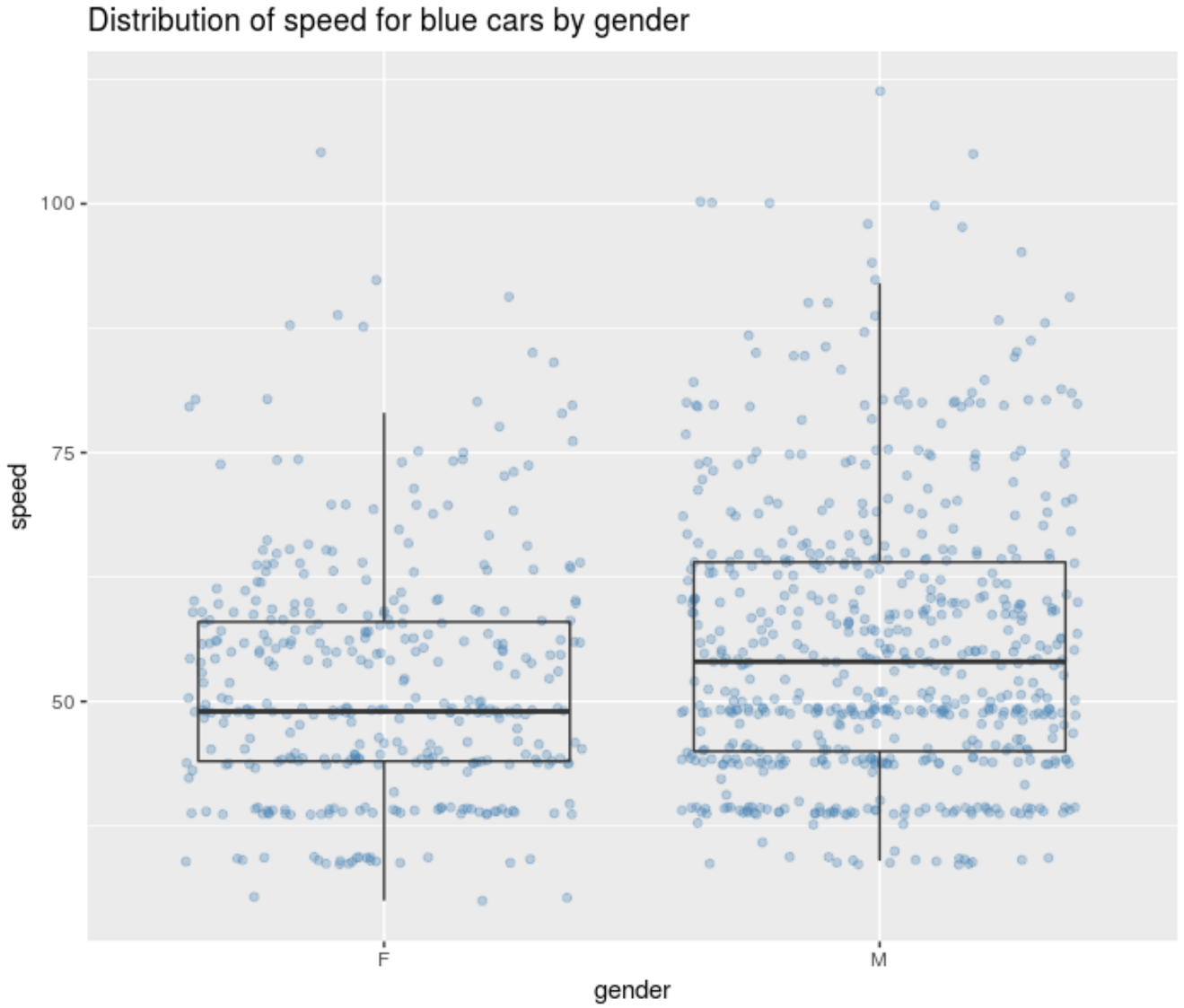
The boxplot



A simple addition

- `geom_jitter()` shows raw points jostled to avoid overlap.
- Layer under your `geom_boxplot()`.

```
md_speeding %>%
  filter(vehicle_color == 'BLUE') %>%
  ggplot(aes(x = gender, y = speed)) +
    # Draw points behind
    geom_jitter(alpha = 0.3, color = 'steelblue') +
    # Make transparent
    geom_boxplot(alpha = 0) +
    labs(title = 'Distribution of speed for blue cars by gender')
```


Distribution of speed for blue cars by gender
speed
100
75
50
F
M
gender

Beeswarm plots

- 'Smart' jittering
- Individual points are clumped together as close to the axis as possible
- Handily included as `geom_beeswarm()` in the `ggbeeswarm` package.

```
library(ggbeeswarm)
ggplot(data, aes(y = y, x =  group)) +
  geom_beeswarm(color = 'steelblue')
```

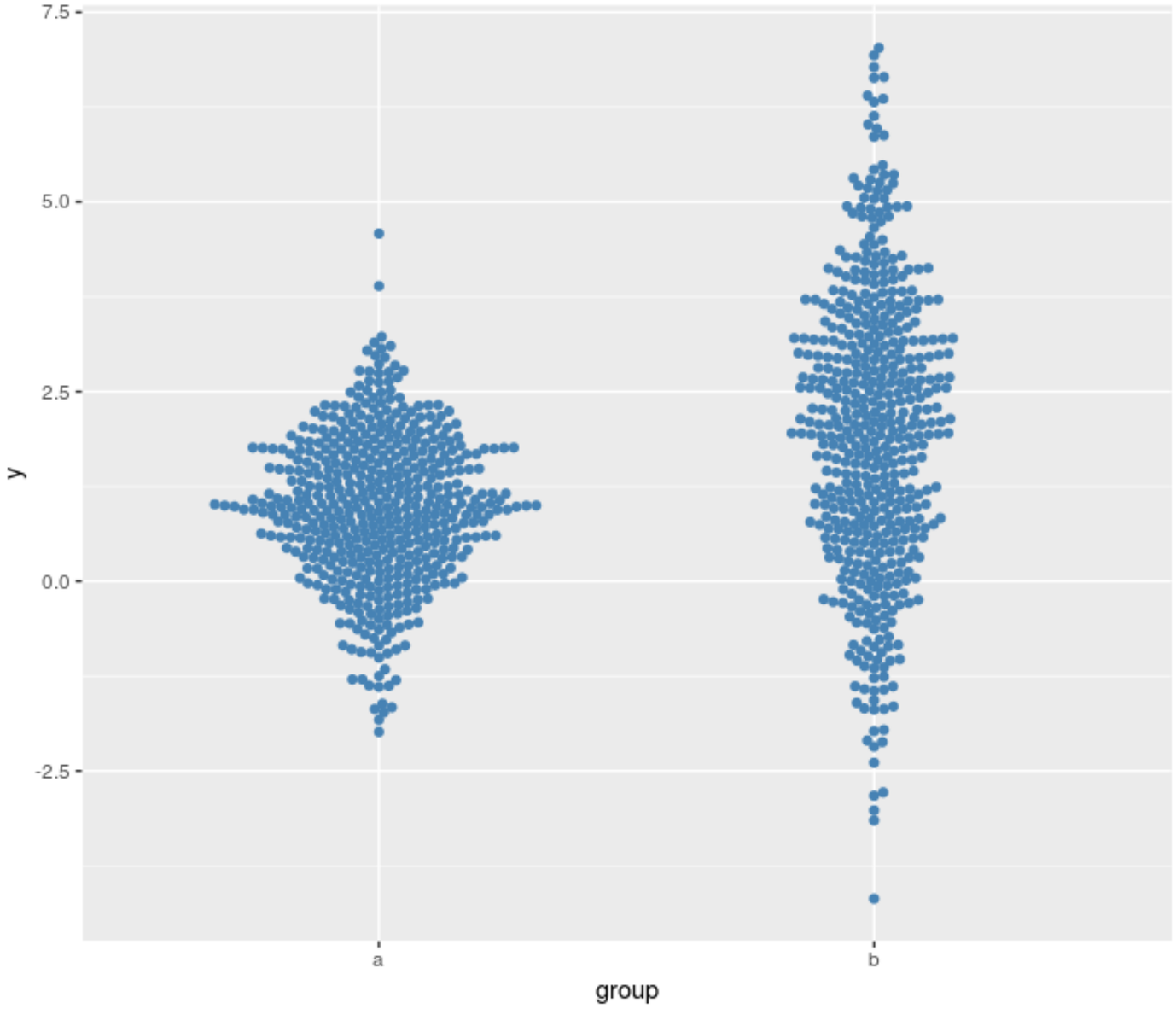
cex: size of the points

Beeswarm pros

- Individual data points
- Distributional shape

Beeswarm cons

- Get hard with lots of data
- Poor placement of points can cause artificially inflated widths of the plot


7.5
5.0
2.5
0.0
-2.5
y
a
b
group

Violin plots

- KDE reflected to be symmetric
- Just replace `geom_boxplot()` with `geom_violin()`.

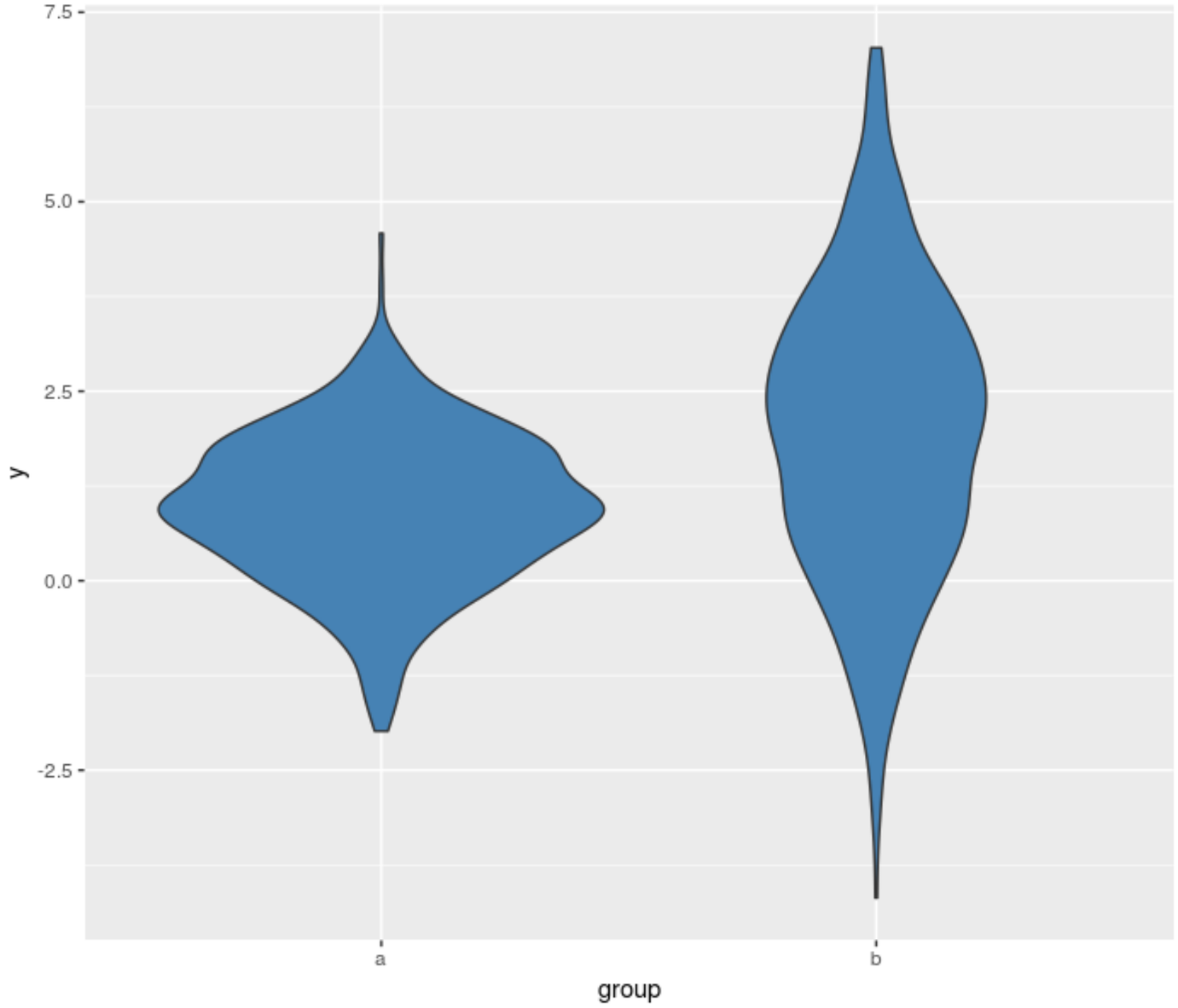
```
ggplot(data, aes(y = y, x = group)) +
  geom_violin(fill = 'steelblue')
```

Violin pros

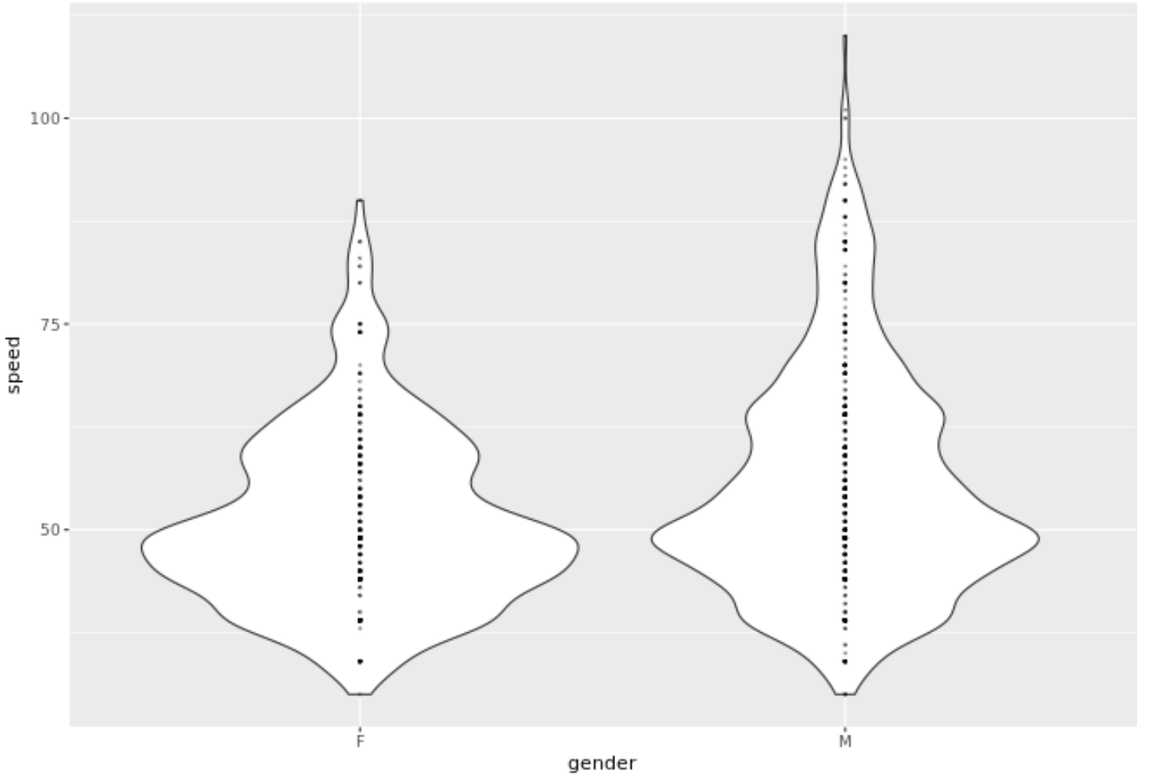
- Every data point is heard
- Not every data point is seen, so good for lots of data.

Violin cons

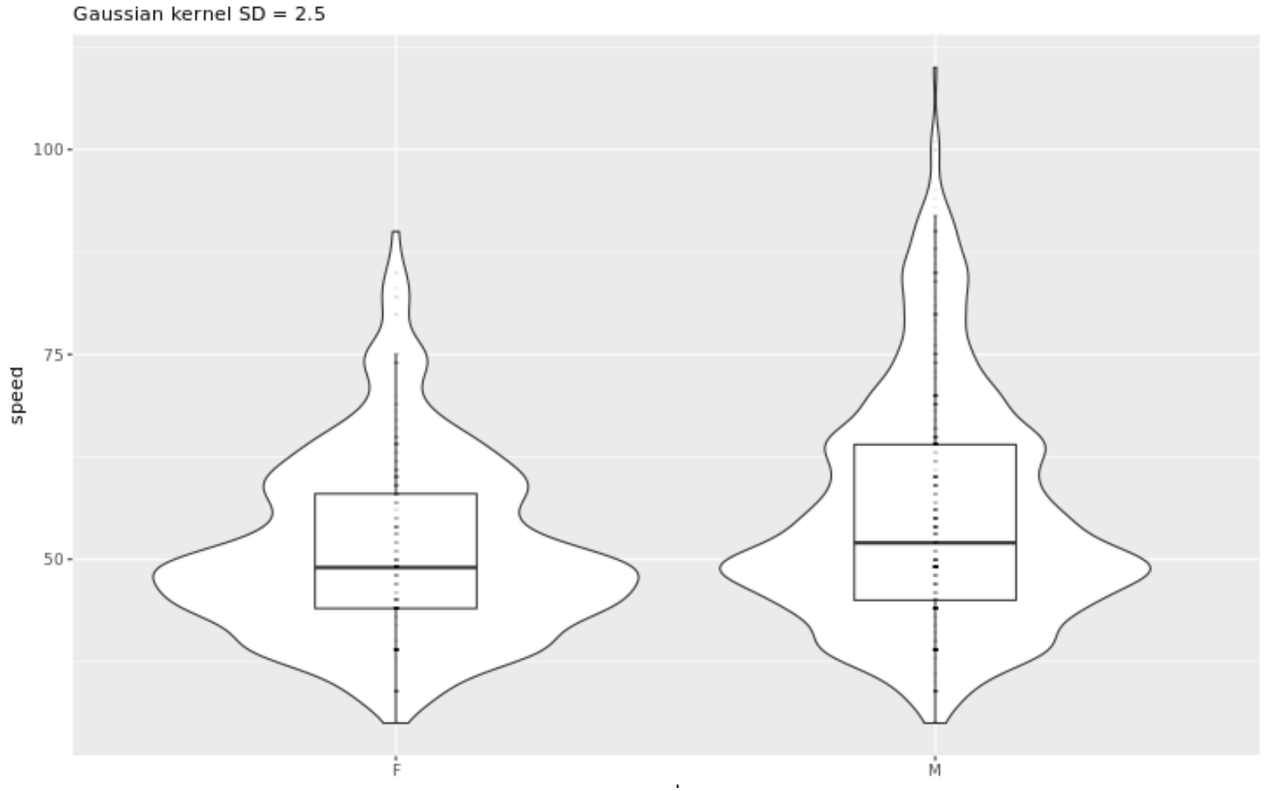
- Kernel width choice
- Not every data point is seen


7.5
5.0
2.5
0.0
-2.5
y
a
b
group

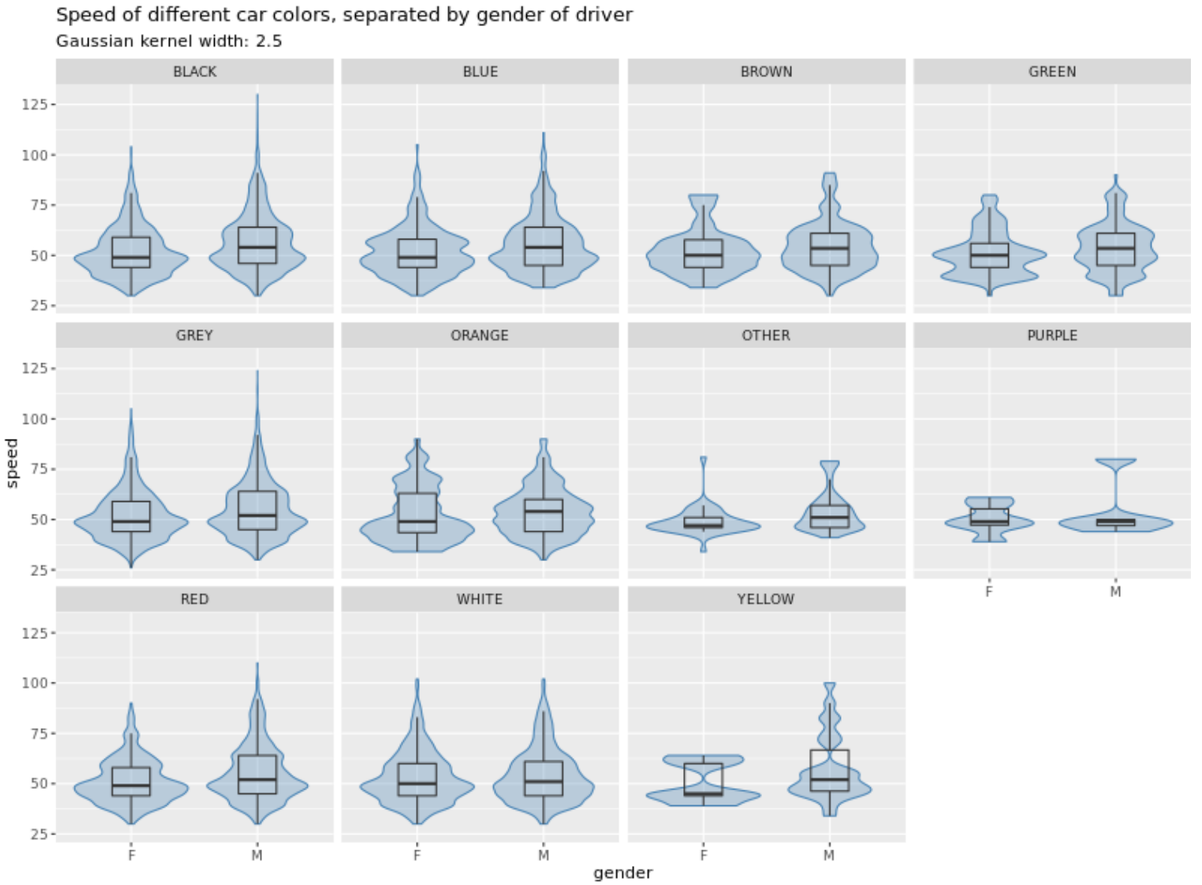
```r
md_speeding %>%
    filter(vehicle_color == 'RED') %>%
    ggplot(aes(x = gender, y = speed)) +
    # Replace beeswarm geometry with a violin geometry
with kernel width of 2.5
    geom_violin(bw = 2.5) +
    # add individual points on top of violins
    geom_point(alpha = 0.3, size = 0.5)
```



```r
md_speeding %>%
    filter(vehicle_color == 'RED') %>%
    ggplot(aes(x = gender, y = speed)) +
    geom_violin(bw = 2.5) +
    # add a transparent boxplot and shrink its width to 0.3
    geom_boxplot(alpha = 0, width = 0.3) +
    # Reset point size to default and set point shape to 95
    geom_point(alpha = 0.3, shape = 95) +
    # Supply a subtitle detailing the kernel width
    labs(subtitle = 'Gaussian kernel SD = 2.5')
```

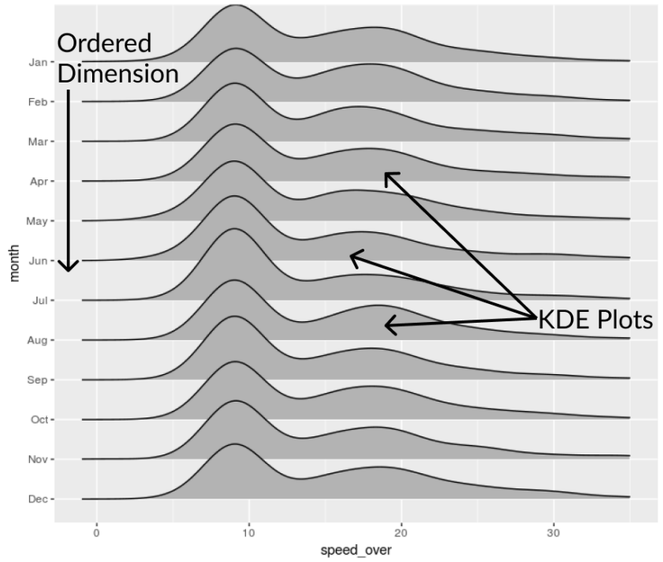


```r
md_speeding %>%
    ggplot(aes(x = gender, y = speed)) +
    # replace with violin plot with kernel width of 2.5, change color argument
to fill
    geom_violin(alpha = 0.3, color = 'steelblue', fill = 'steelblue', bw = 2.5) +
    # reduce width to 0.3
    geom_boxplot(alpha = 0, width = 0.3) +
    facet_wrap(~vehicle_color) +
    labs(
        title = 'Speed of different car colors, separated by gender of driver',
        subtitle = 'Gaussian kernel width: 2.5'

    )
```

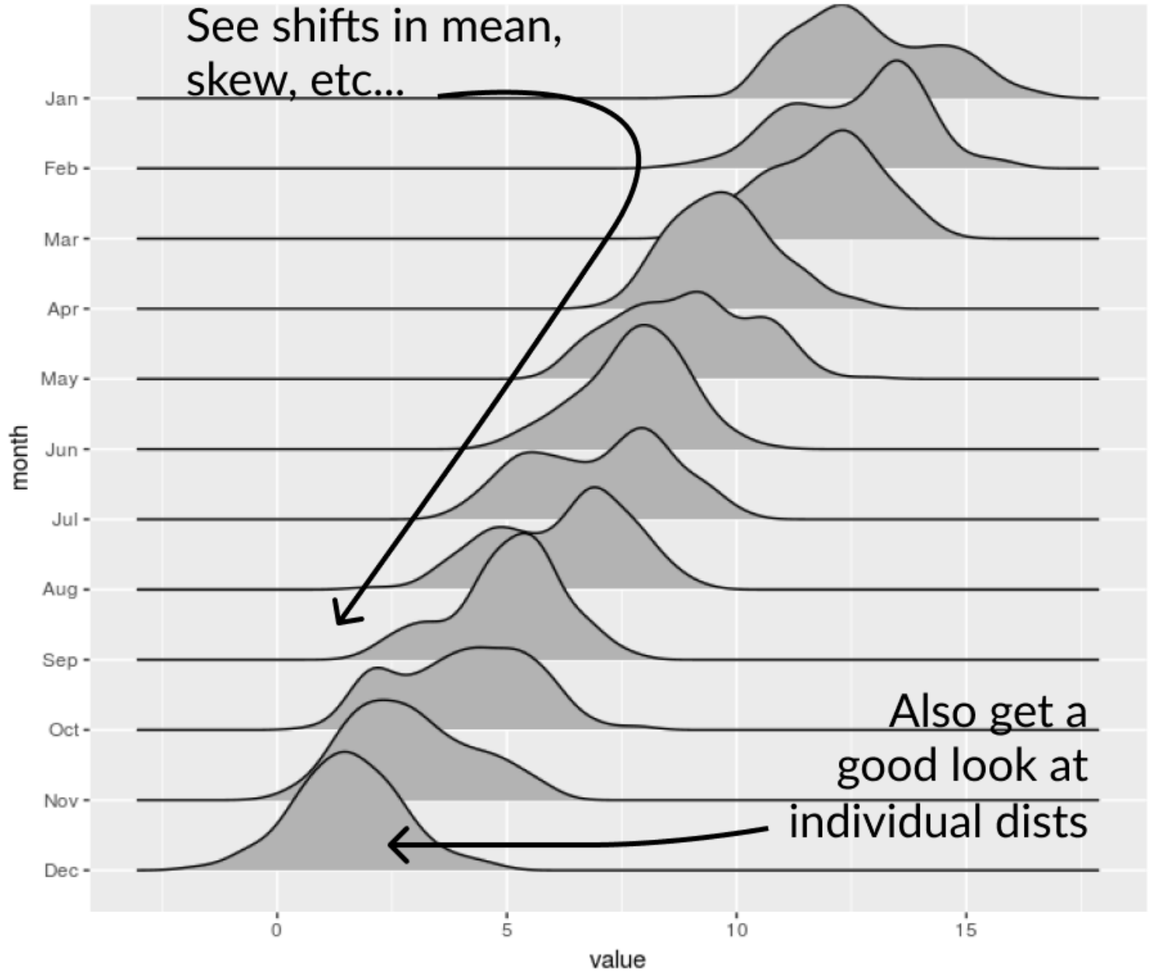


The ridgeline plot

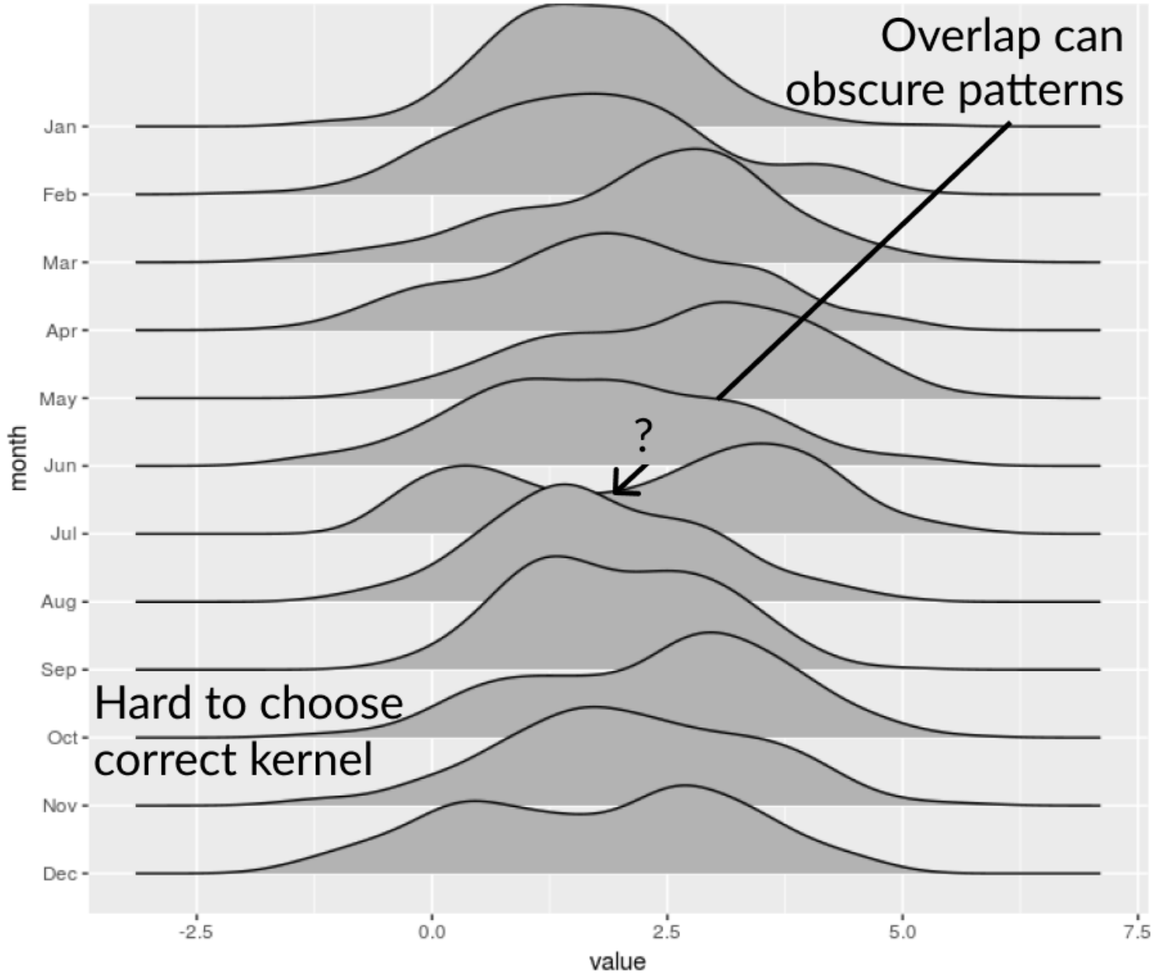
```
library(ggridges) # Gives us geom_density_ridges()
ggplot(md_speeding, aes(x = speed_over, y = month)) +
  geom_density_ridges(bandwidth = 2) +
  xlim(1, 35)
```



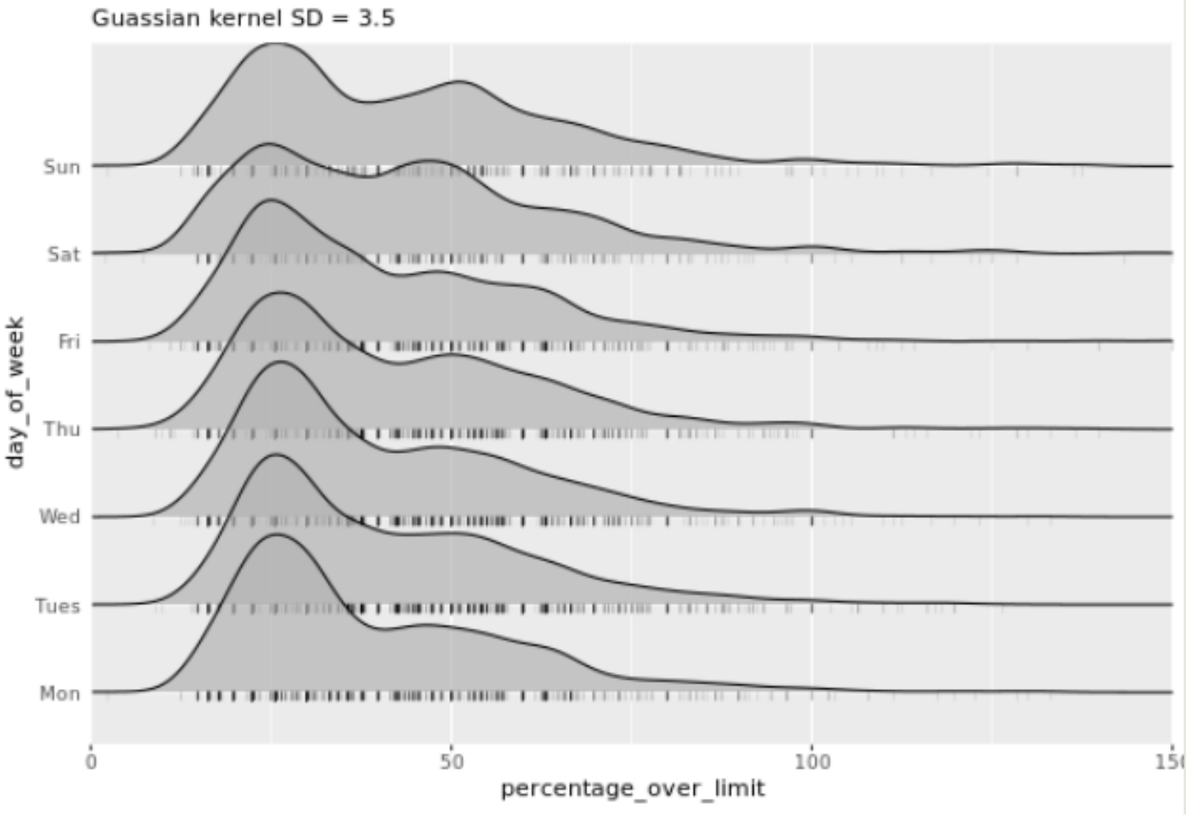
Ridgeline pros



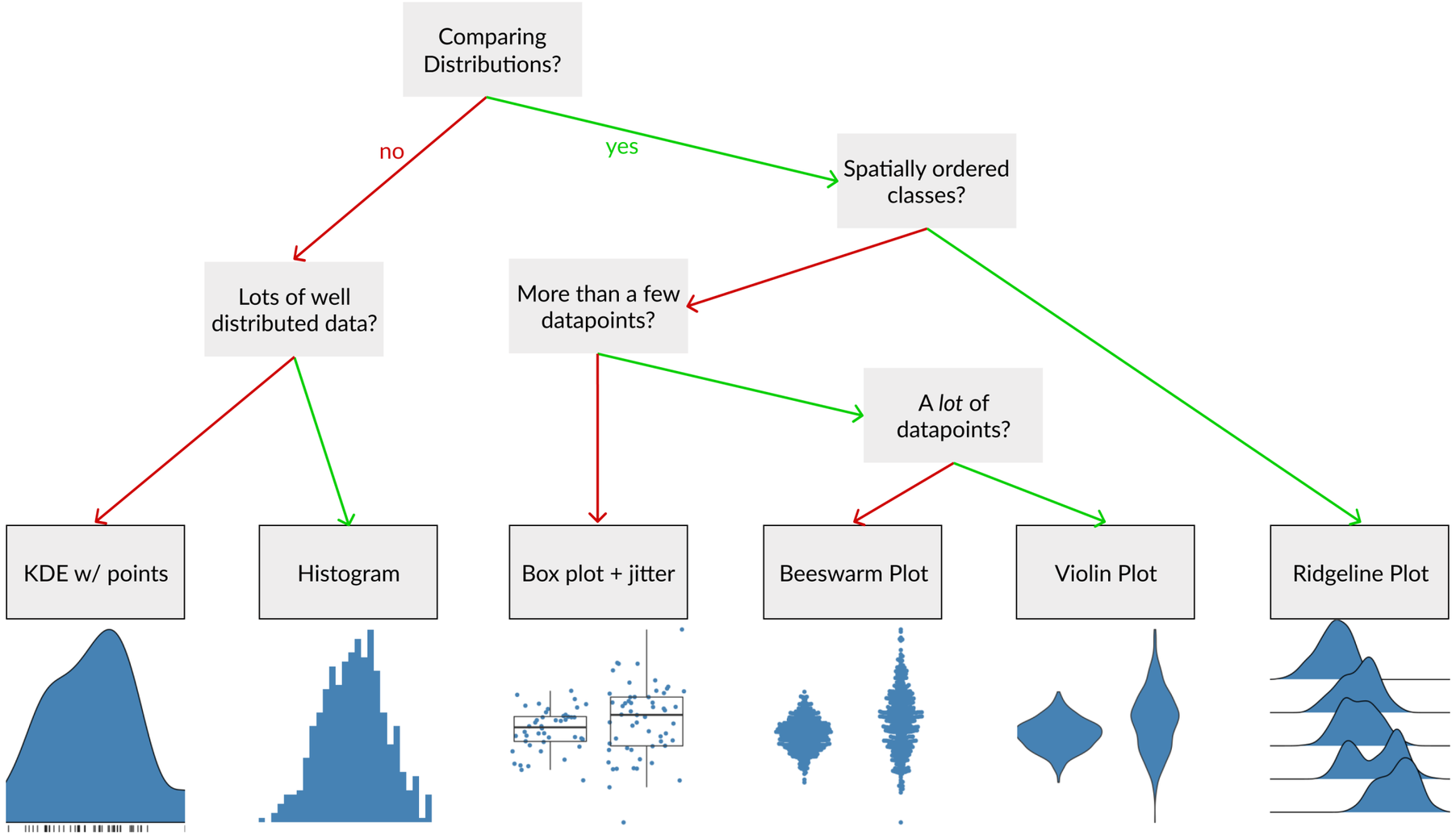
Ridgeline cons



```r
md_speeding %>%
    mutate(day_of_week = factor(day_of_week,
    levels = c("Mon","Tues","Wed","Thu","Fri","Sat","Sun") )) %>%
    ggplot(aes( x = percentage_over_limit, y = day_of_week)) +
    geom_point(
        alpha = 0.2,
        shape = '|',
        position = position_nudge(y = -0.05)
    ) +
    geom_density_ridges(bandwidth = 3.5, alpha = 0.7) +
    scale_x_continuous(limits = c(0,150), expand  = c(0,0)) +
    labs(subtitle = 'Guassian kernel SD = 3.5') +
    theme( axis.ticks.y = element_blank() )
```



Overview of distribution visualizations

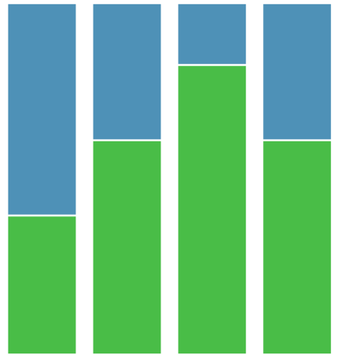


Chapter 1: Proportions

Three or less classes and precision not important?

Need more precision and have the space?

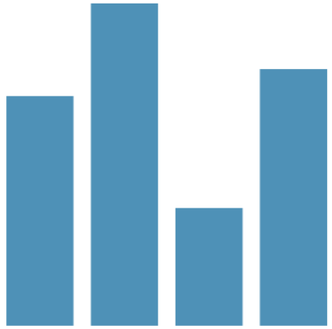
Good for comparing values *across* populations....



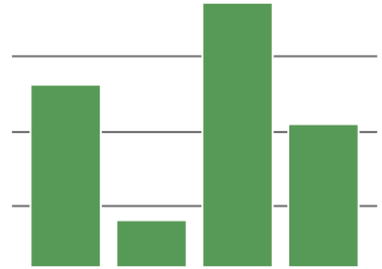
... bad for comparing values *within* populations

Chapter 2: Point data

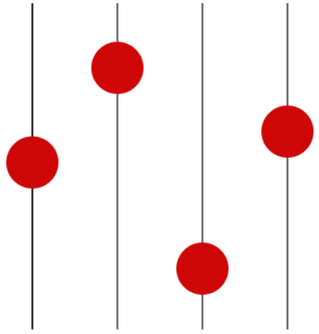
Data is a stackable quantity? E.g. dollars, counts...



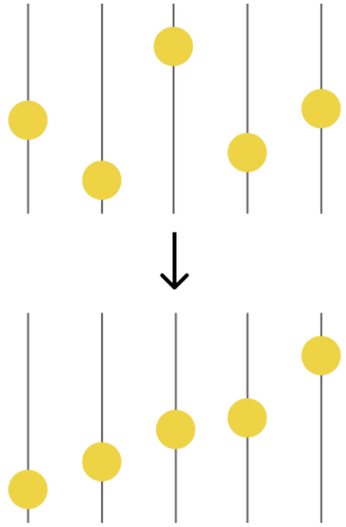
No need for vertical grid lines on bars.



Not stackable? E.g. percents, ratio...

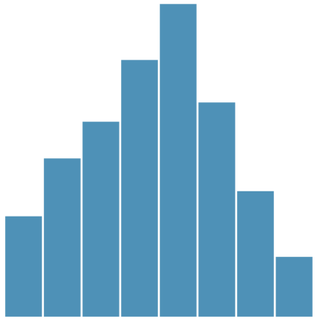


Ordering is almost always a good idea.

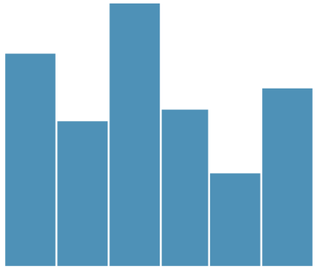


Chapter 3: Single distributions

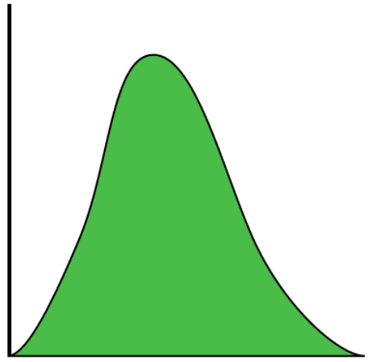
Histograms are simple and intuitive...



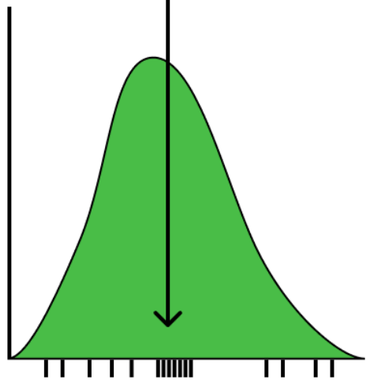
... but are sensitive to bin width and placement choices.



Kernel Density Estimators work with small data and produce nice smooth plots.

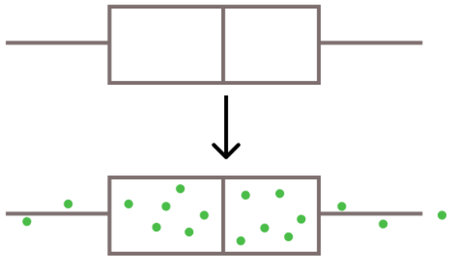


But always try and show raw data if possible to see gaps the KDE may be filling.

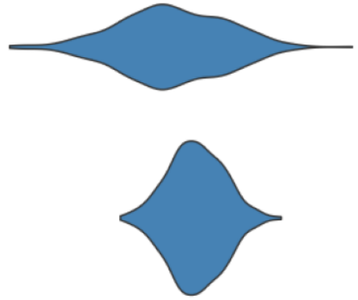


Chapter 4: Comparing distributions

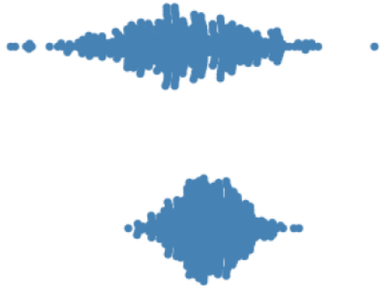
Boxplots hide a lot of data, so augment them with jittered points



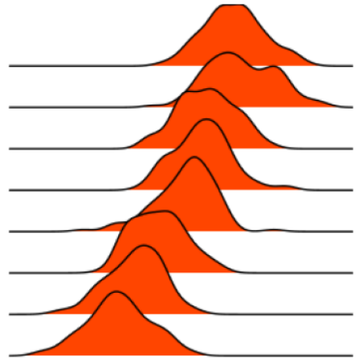
Violin plots are symmetric KDEs that work well when you have lots of points.



Beeswarm plots are an alternative 'smart' jittering that shows density.



If you have spatially ordered groups, consider the ridgeline plot.



Going further

Flowing data

Curated list of data visualizations and R-based tutorials.

Datawrapper Blog

Articles that dig deep into visualization techniques and mistakes.

Twitter (#datavis)

An ongoing stream of cool projects and inspiration.

Books!

- **Data Visualization**, Andy Kirk
- **The Functional Art and The Truthful Art** by Alberto Cairo

Thank you!

VISUALIZATION BEST PRACTICES IN R