Data visualization with ggplot2

Day 2 - Introduction to Data Analysis with R

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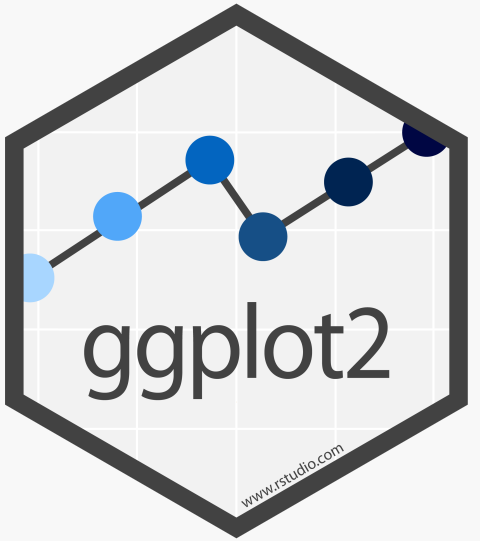
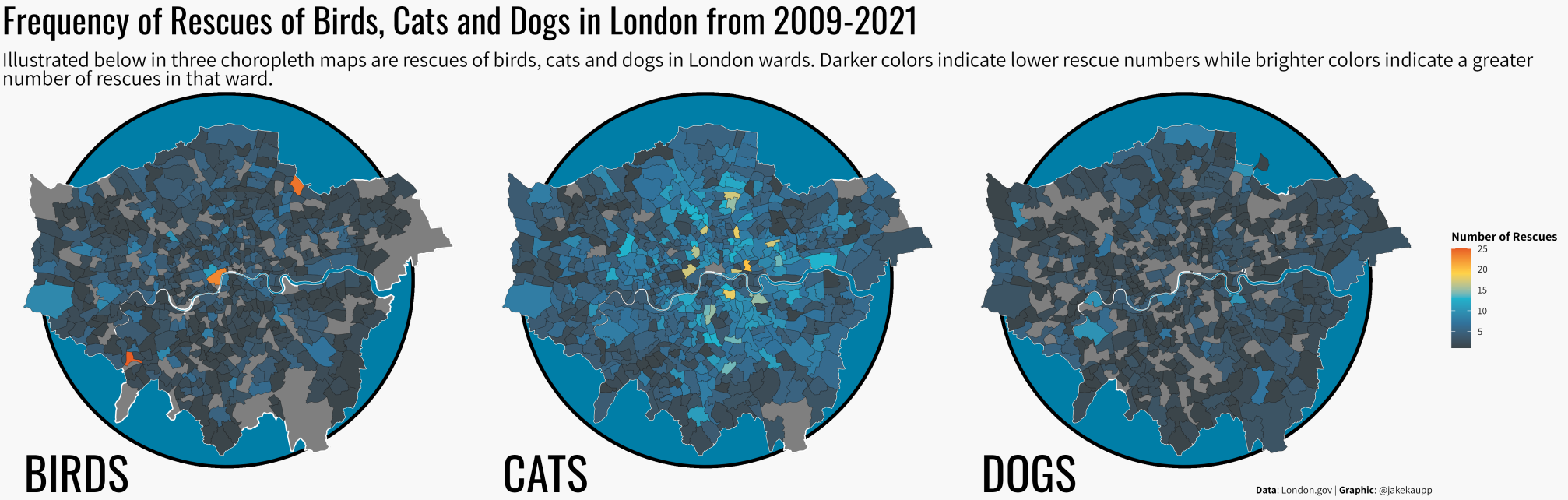


A ggplot showcase

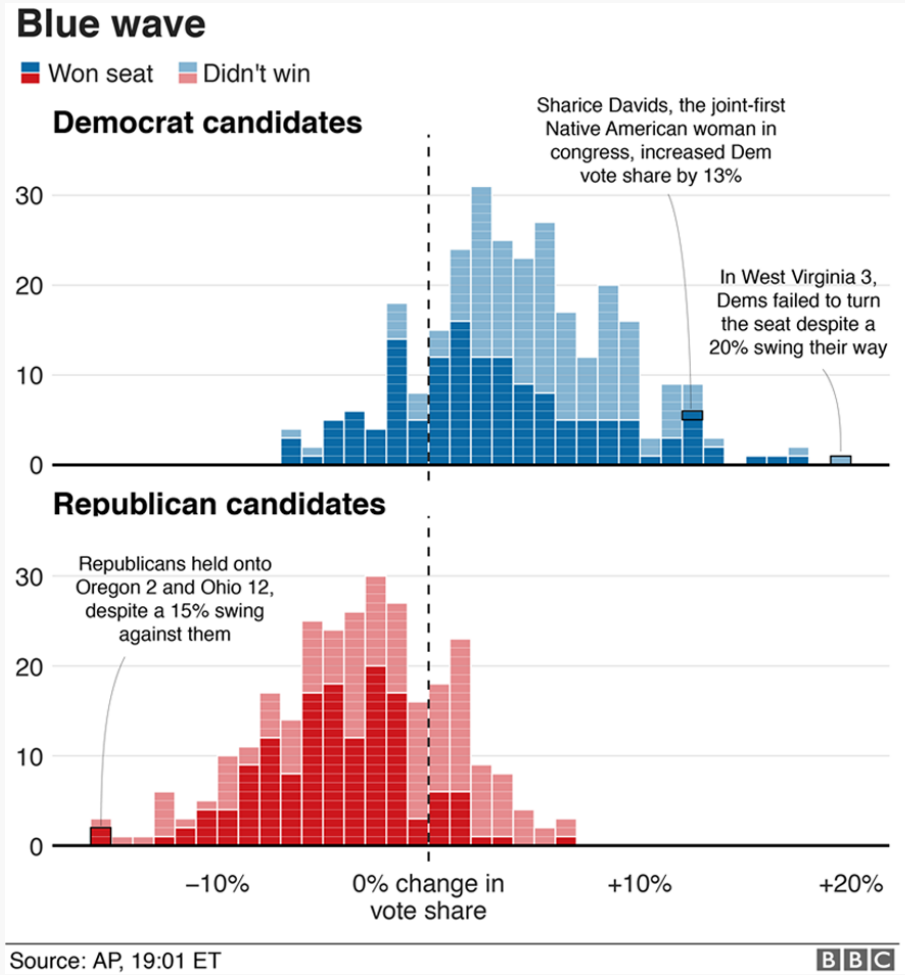
> Example plots you can create with ggplot

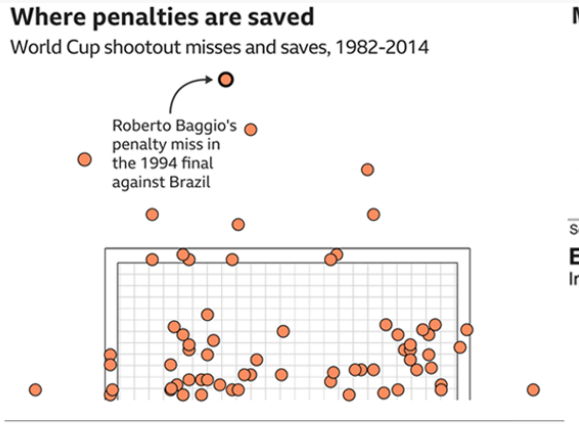
A ggplot showcase

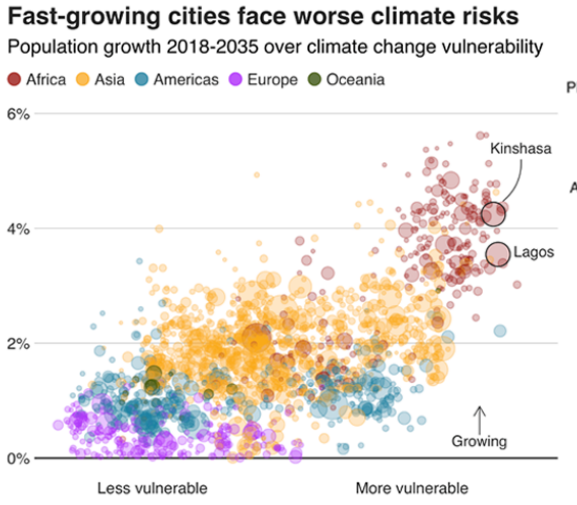


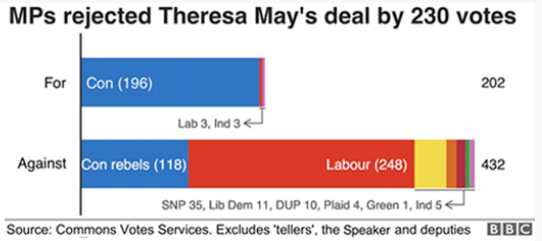
Visualization by Jake Kaupp, code available on Github

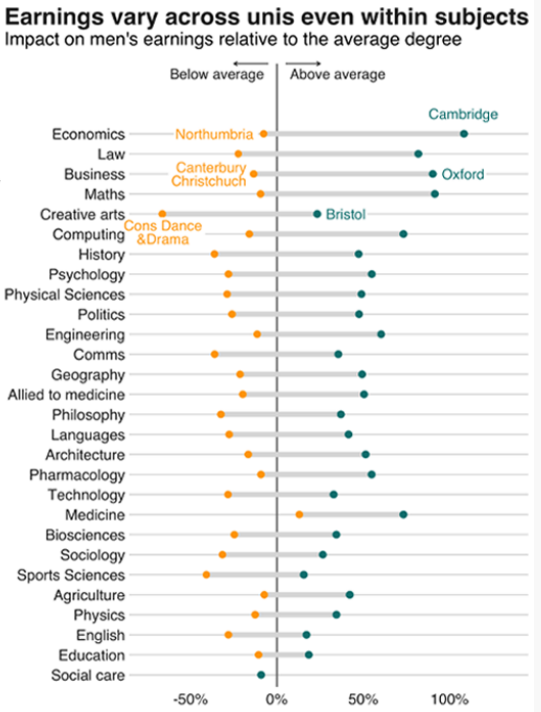
A ggplot showcase





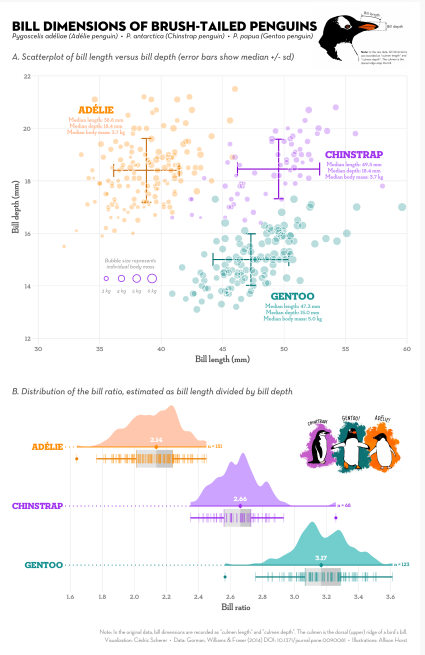






Visualizations produced by the BBC News data team

A ggplot showcase



Visualization by Cédric Scherer, code available on Github

Advantages of ggplot

- **Consistent** grammar/structure
- **Flexible** structure allows you to produce any type of plots
- Highly **customizable appearance** (themes)

- Many **extension packages** that provide
  - Additional plot types
    - Additional themes and colors
    - Animation
    - Composition of multiple plots
    - ...

- Active community that provides help and inspiration
- Perfect package for **exploratory data analysis** and **beautiful plots**

The data

Data set `and_vertebrates` with measurements of a trout and 2 salamander species in different forest sections.

- `year`: observation year
- `section`: CC (clear cut forest) or OG (old growth forest)
- `unittype`: channel classification (C = Cascade, P = Pool, ...)
- `species`: Species measured
- `length_1_mm`: body length [mm]
- `weight_g`: body weight [g]

Coastal giant salamander (terrestrial form) Andrews Forest Program by Lina DiGregorio via CC-BY from https://andrewsforest.oregonstate.edu

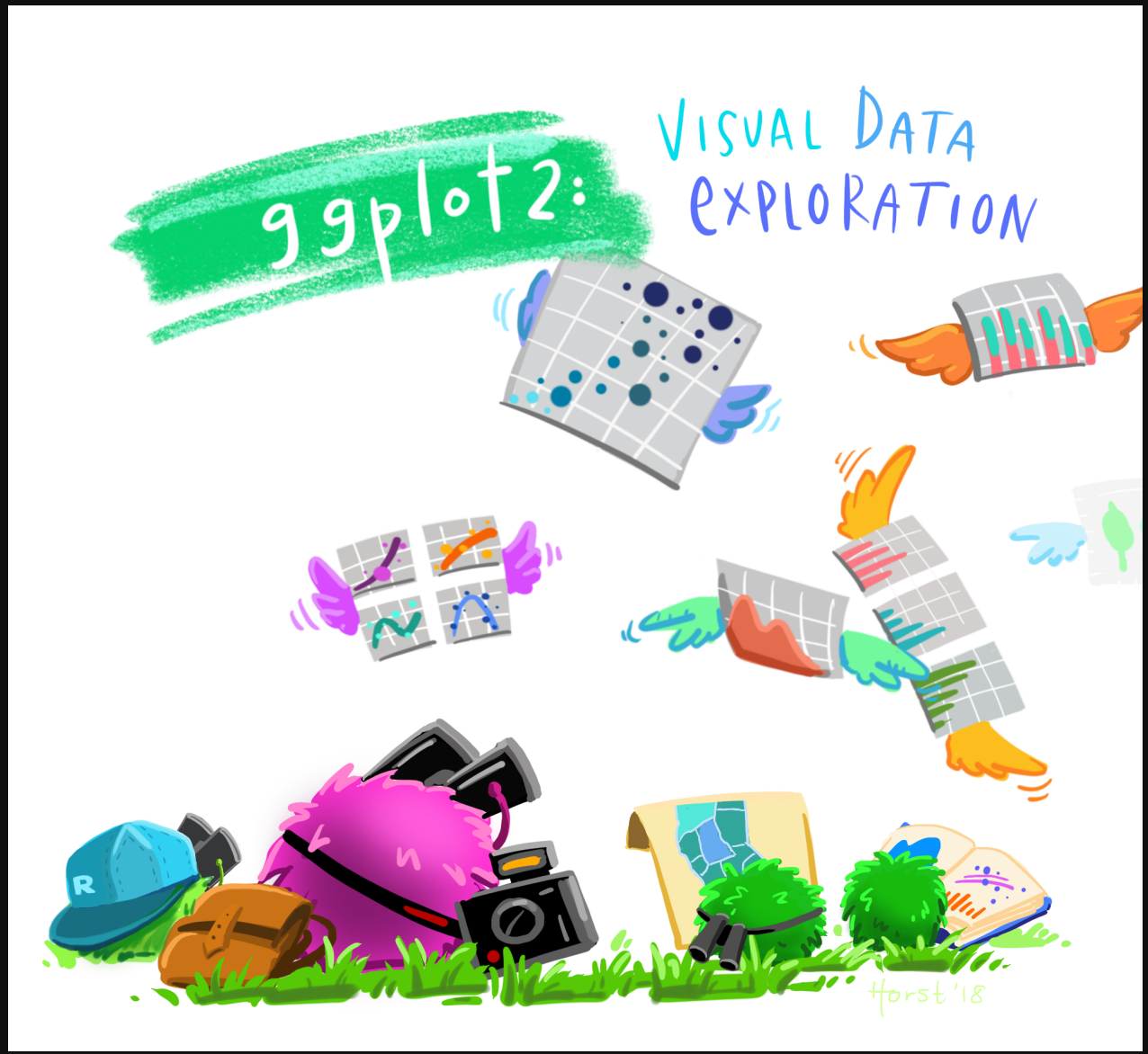
References: Kaylor, M.J. and D.R. Warren. (2017) and Gregory, S.V. and I. Arismendi. (2020) as provided in the

The data

Data set `and_vertebrates` with measurements of a trout and 2 salamander species in different forest sections.

```
1  library(lterdatasampler)
2  and_vertebrates
```

```
#> # A tibble: 32,191 × 6
#>     year section unittype species          length_1_mm weight_g
#>    <dbl> <chr>   <chr>    <chr>                  <dbl>    <dbl>
#>  1  1987 CC      R        Cutthroat trout           58     1.75
#>  2  1987 CC      R        Cutthroat trout           61     1.95
#>  3  1987 CC      R        Cutthroat trout           89     5.6
#>  4  1987 CC      R        Cutthroat trout           58     2.15
#>  5  1987 CC      R        Cutthroat trout           93     6.9
#>  6  1987 CC      R        Cutthroat trout           86     5.9
#>  7  1987 CC      R        Cutthroat trout          107    10.5
#>  8  1987 CC      R        Cutthroat trout          131    20.6
#>  9  1987 CC      R        Cutthroat trout          103     9.55
#> 10  1987 CC      R        Cutthroat trout          117    13
#> # ℹ 32,181 more rows
```



Artwork by Allison Horst

ggplot(data)

The `ggplot()` function initializes a ggplot object. Every ggplot needs this function.

```
1  library(ggplot2) # or library(tidyverse)
2
3  ggplot(data = and_vertebrates)
```

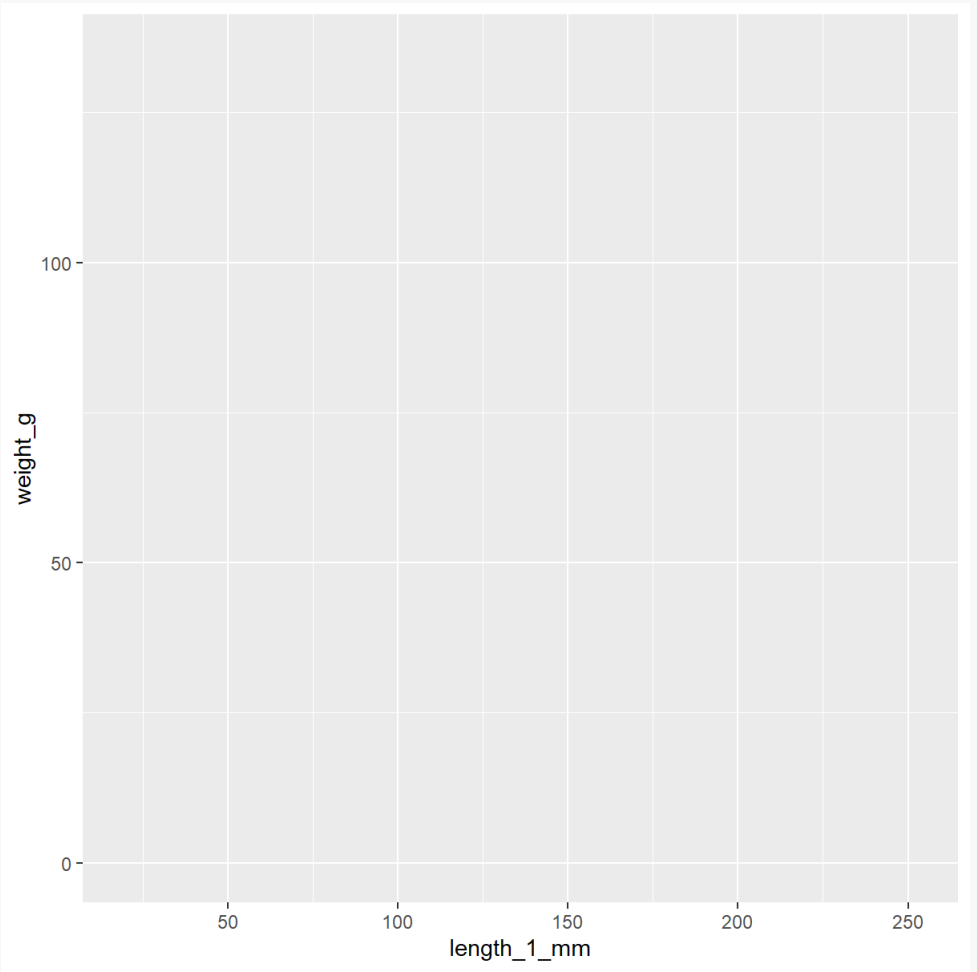
- Empty plot because we did not specify the mapping of data variables

aes(x, y)

The **aes**thetics define how data variables are mapped plot properties.

```
ggplot(data = and_vertebrates,
       mapping = aes(
         x = length_1_mm,
         y = weight_g))
```

- Map variable `length_1_mm` to x-axis and `weight_g` to y-axis
- Default scales are automatically adapted to range of data



This is the same but shorter:

```
ggplot(and_vertebrates,
       aes(x = length_1_mm,
           y = weight_g))
```

Remember argument matching by position?

`geom_*`

`geoms` define how data points are represented. There are many different geoms to chose from

a + geom_blank()
(Useful for expanding limits)

b + geom_curve(aes(yend = lat + 1, xend=long+1),curvature=1) - x, xend, y, yend, alpha, angle, color, curvature, linetype, size

a + geom_path(lineend="butt", linejoin="round", linemitre=1)
x, y, alpha, color, group, linetype, size

a + geom_polygon(aes(group = group))
x, y, alpha, color, fill, group, linetype, size

b + geom_rect(aes(xmin = long, ymin=lat, xmax= long + 1, ymax = lat + 1)) - xmax, xmin, ymax, ymin, alpha, color, fill, linetype, size

a + geom_ribbon(aes(ymin=unemploy - 900, ymax=unemploy + 900)) - x, ymax, ymin, alpha, color, fill, group, linetype, size

LINE SEGMENTS
common aesthetics: x, y, alpha, color, linetype, size

b + geom_abline(aes(intercept=0, slope=1))
b + geom_hline(aes(yintercept = lat))
b + geom_vline(aes(xintercept = long))

b + geom_segment(aes(yend=lat+1, xend=long+1))
b + geom_spoke(aes(angle = 1:1155, radius = 1))

ONE VARIABLE continuous
c <- ggplot(mpg, aes(hwy)); c2 <- ggplot(mpg)

c + geom_area(stat = "bin")
x, y, alpha, color, fill, linetype, size

c + geom_density(kernel = "gaussian")
x, y, alpha, color, fill, group, linetype, size, weight

c + geom_dotplot()
x, y, alpha, color, fill

c + geom_freqpoly() x, y, alpha, color, group, linetype, size

c + geom_histogram(binwidth = 5) x, y, alpha, color, fill, linetype, size, weight

e + geom_label(aes(label = cty), nudge_x = 1, nudge_y = 1, check_overlap = TRUE) x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

e + geom_jitter(height = 2, width = 2)
x, y, alpha, color, fill, shape, size

e + geom_point(), x, y, alpha, color, fill, shape, size, stroke

e + geom_quantile(), x, y, alpha, color, group, linetype, size, weight

e + geom_rug(sides = "bl"), x, y, alpha, color, linetype, size

e + geom_smooth(method = lm), x, y, alpha, color, fill, group, linetype, size, weight

e + geom_text(aes(label = cty), nudge_x = 1, nudge_y = 1, check_overlap = TRUE), x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

discrete x , continuous y
f <- ggplot(mpg, aes(class, hwy))

f + geom_col(), x, y, alpha, color, fill, group, linetype, size

f + geom_boxplot(), x, y, lower, middle, upper, ymax, ymin, alpha, color, fill, group, linetype, shape, size, weight

f + geom_dotplot(binaxis = "y", stackdir = "center"), x, y, alpha, color, fill, group

f + geom_violin(scale = "area"), x, y, alpha, color, fill, group, linetype, size, weight

discrete x , discrete y
g <- ggplot(diamonds, aes(cut, color))

g + geom_count(), x, y, alpha, color, fill, shape, size, stroke

h + geom_bin2d(binwidth = c(0.25, 500))
x, y, alpha, color, fill, linetype, size, weight

h + geom_density2d()
x, y, alpha, colour, group, linetype, size

h + geom_hex()
x, y, alpha, colour, fill, size

continuous function
i <- ggplot(economics, aes(date, unemploy))

i + geom_area()
x, y, alpha, color, fill, linetype, size

i + geom_line()
x, y, alpha, color, group, linetype, size

i + geom_step(direction = "hv")
x, y, alpha, color, group, linetype, size

visualizing error
df <- data.frame(grp = c("A", "B"), fit = 4:5, se = 1:2)
j <- ggplot(df, aes(grp, fit, ymin = fit-se, ymax = fit+se))

j + geom_crossbar(fatten = 2)
x, y, ymax, ymin, alpha, color, fill, group, linetype, size

j + geom_errorbar(), x, ymax, ymin, alpha, color, group, linetype, size, width (also **geom_errorbarh()**)

j + geom_linerange()
x, ymin, ymax, alpha, color, group, linetype, size

j + geom_pointrange()
x, y, ymin, ymax, alpha, color, fill, group, linetype, shape, size

maps
data <- data.frame(murder = USArrests$Murder, state = tolower(rownames(USArrests)))
map <- map_data("state")
k <- ggplot(data, aes(fill = murder))

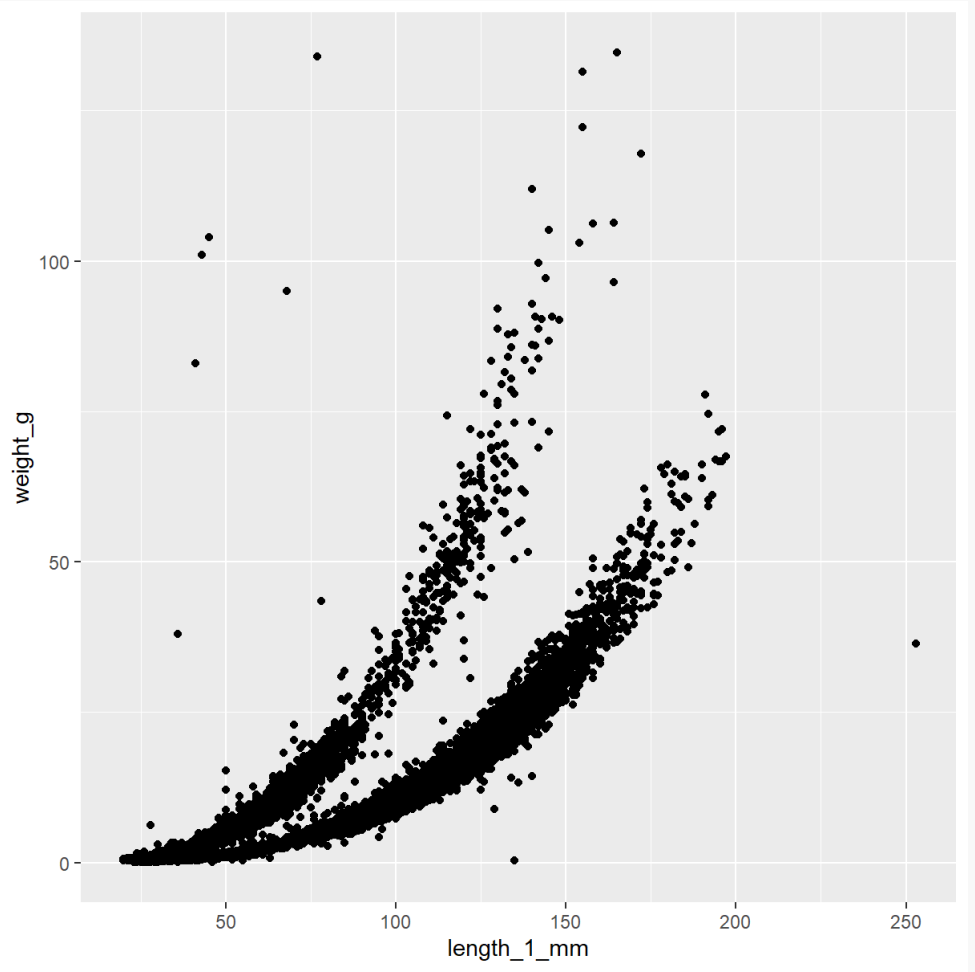
k + geom_map(aes(map_id = state), map = map) **+ expand_limits**(x = map$long, y = map$lat), map_id, alpha, color, fill, linetype, size

{width = 70%}

geom_point

```
1  ggplot(data = and_vertebrates,
2         aes(x = length_1_mm,
3             y = weight_g)) +
4    geom_point()
```

```
#> Warning: Removed 13270 rows containing missing
values (`geom_point()`).
```



- New plot layers added with +
- Warning that points could not be plotted due to missing values
- `data` and `aes` defined in `ggplot` call are inherited to all plot layers
- `data` and `aes` can be local to a layer:

```
1  ggplot() +
2    geom_point(
3      data = and_vertebrates,
4      aes(
5        x = length_1_mm,
6        y = weight_g
7      ))
```

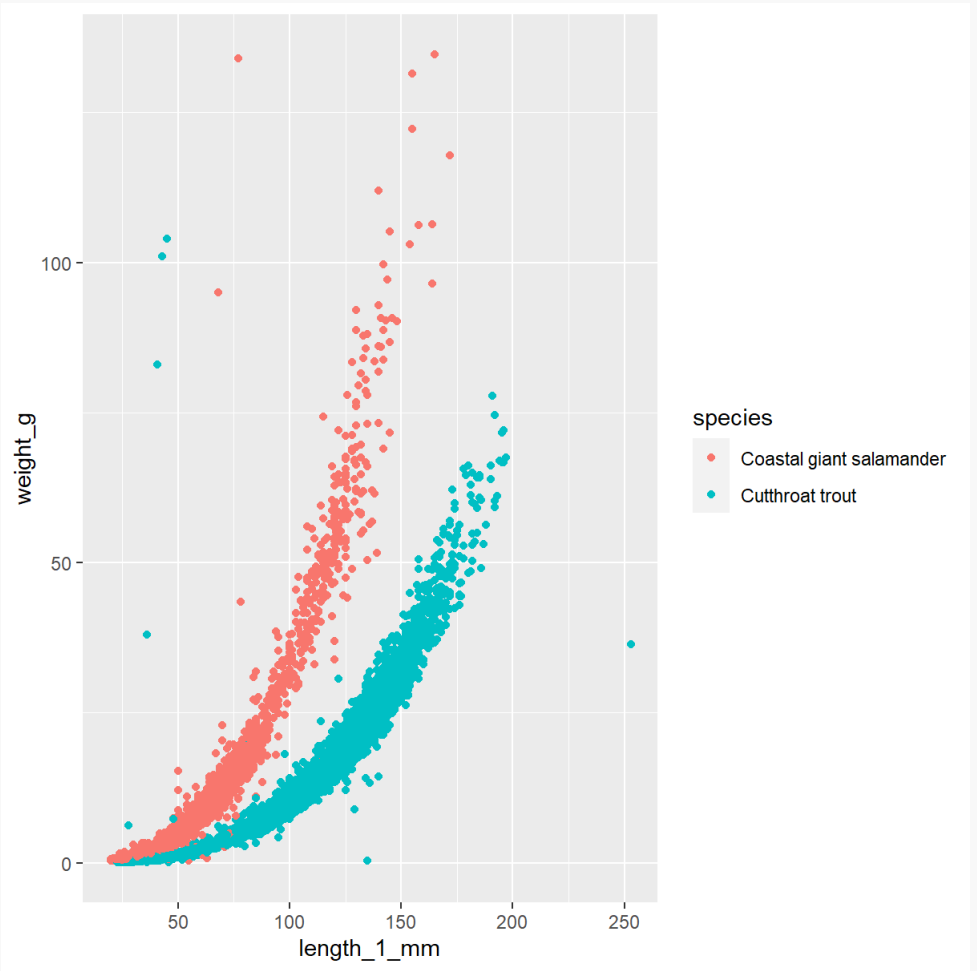
Here, it does not make a difference.

`aes(color)`: mapping color to a variable

Looks like there are two groups of data: **Map color of points to a variable** by adding it to aesthetics:

```
1  ggplot(data = and_vertebrates,
2         aes(x = length_1_mm,
3             y = weight_g,
4             color = species)) +
5    geom_point()
```

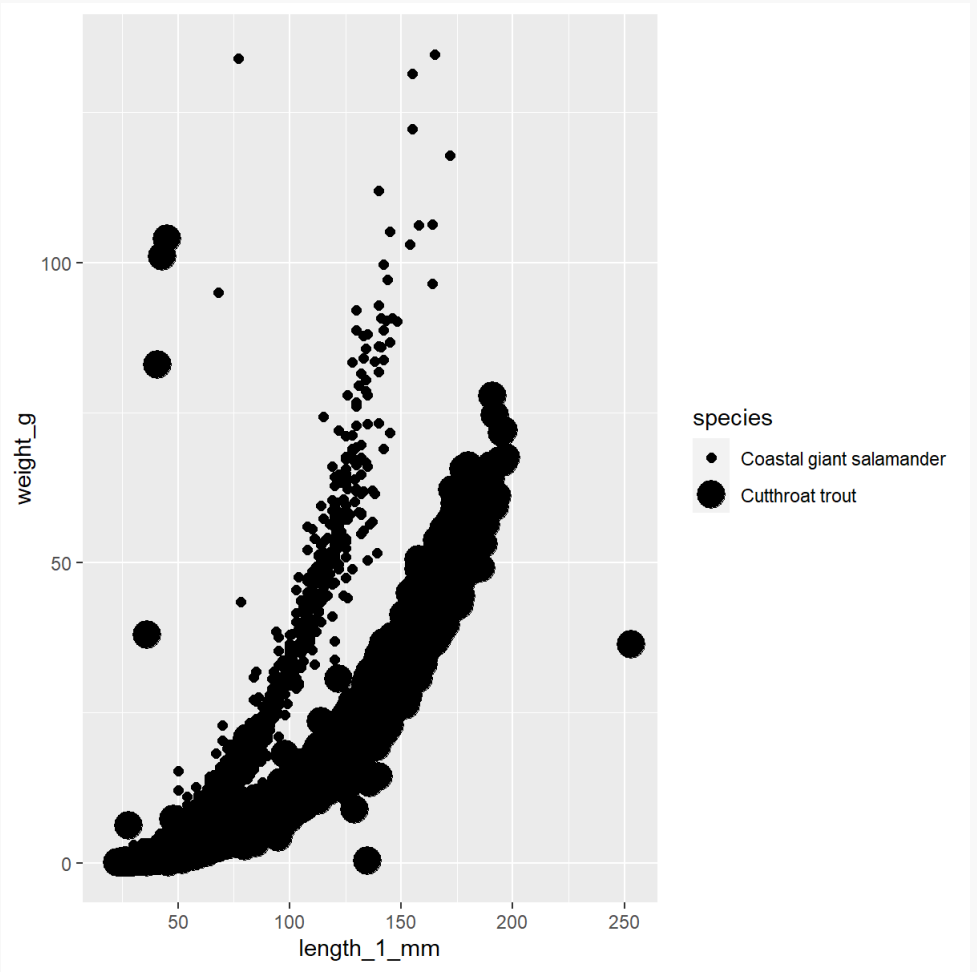
- Map the `species` variable to the color aesthetic of the plot



`aes(size)`: mapping size to a variable

We can do the same with size:

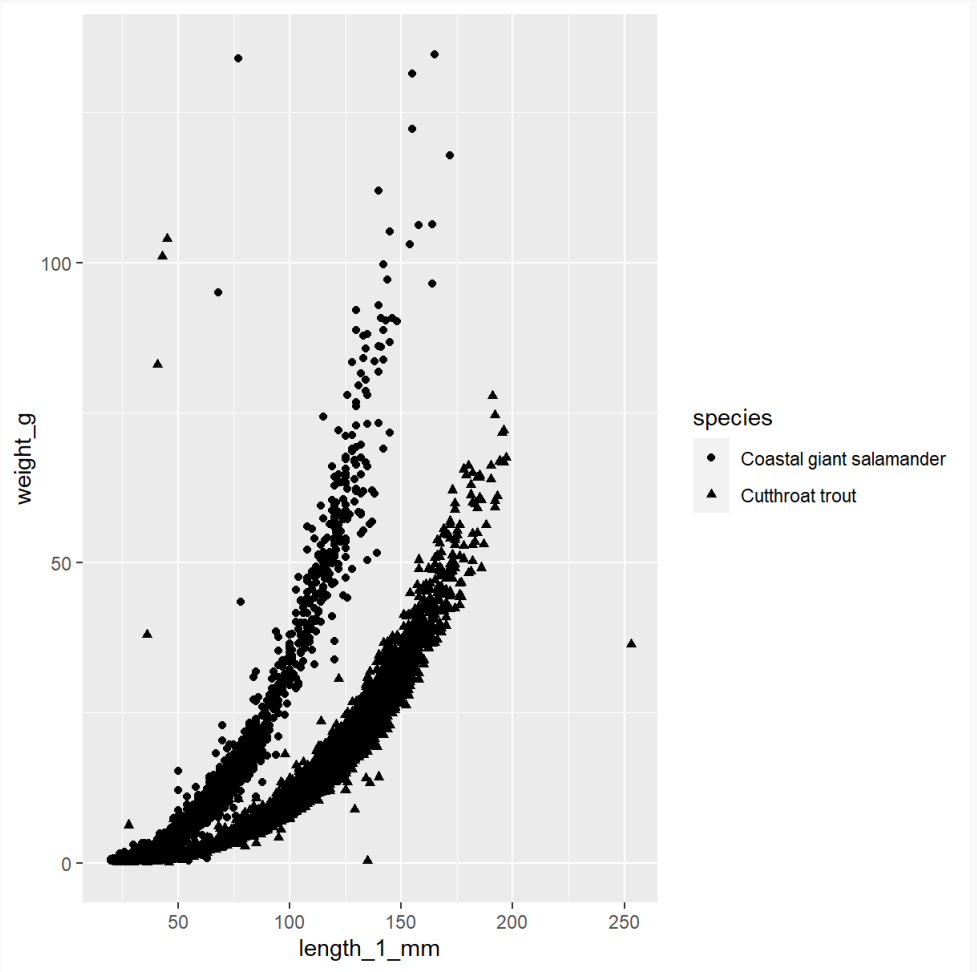
```
1  ggplot(data = and_vertebrates,
2         aes(x = length_1_mm,
3             y = weight_g,
4             size = species)) +
5    geom_point()
```



`aes(shape)`: mapping shape to a variable

We can do the same with shape:

```
1  ggplot(data = and_vertebrates,
2         aes(x = length_1_mm,
3             y = weight_g,
4             shape = species)) +
5    geom_point()
```

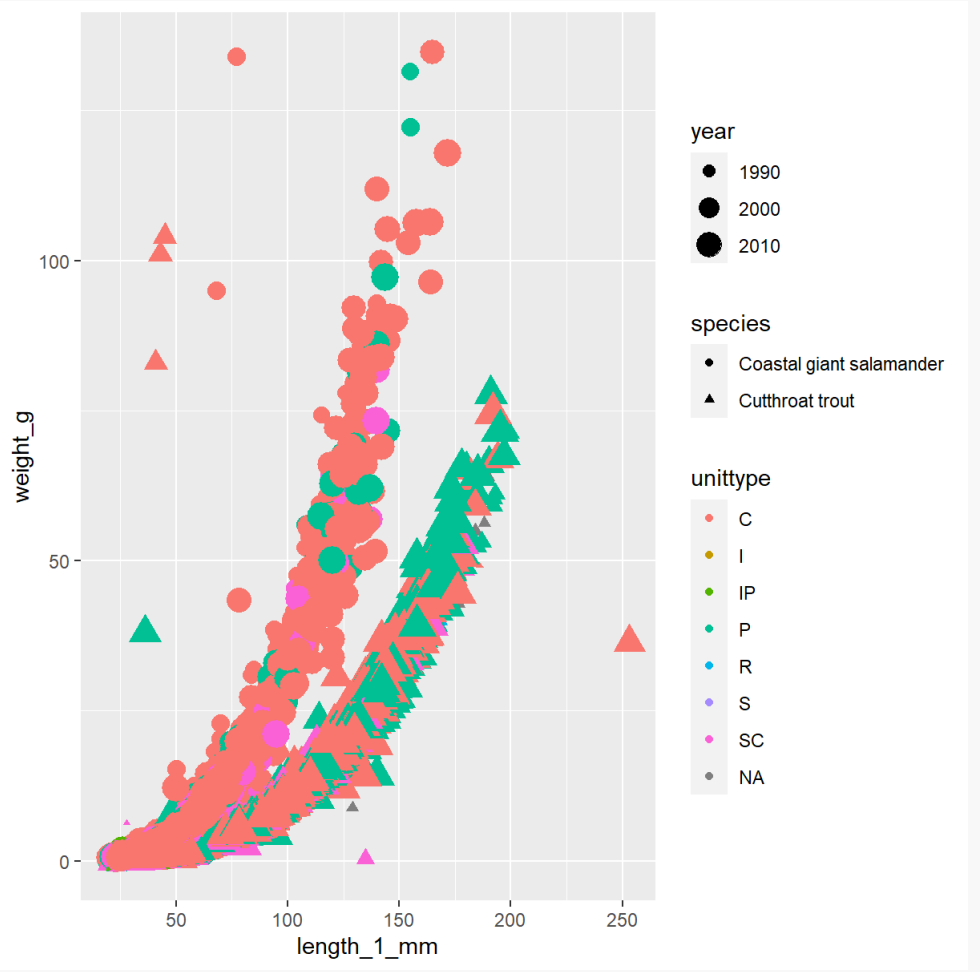


Combine color, size and shape

We can also combine these aesthetics and map different variables

```
ggplot(data = and_vertebrates,
       aes(x = length_1_mm,
           y = weight_g,
           color = unittype,
           shape = species,
           size = year)) +
  geom_point()
```

- This is a bit too much for this plot, but sometimes can be useful

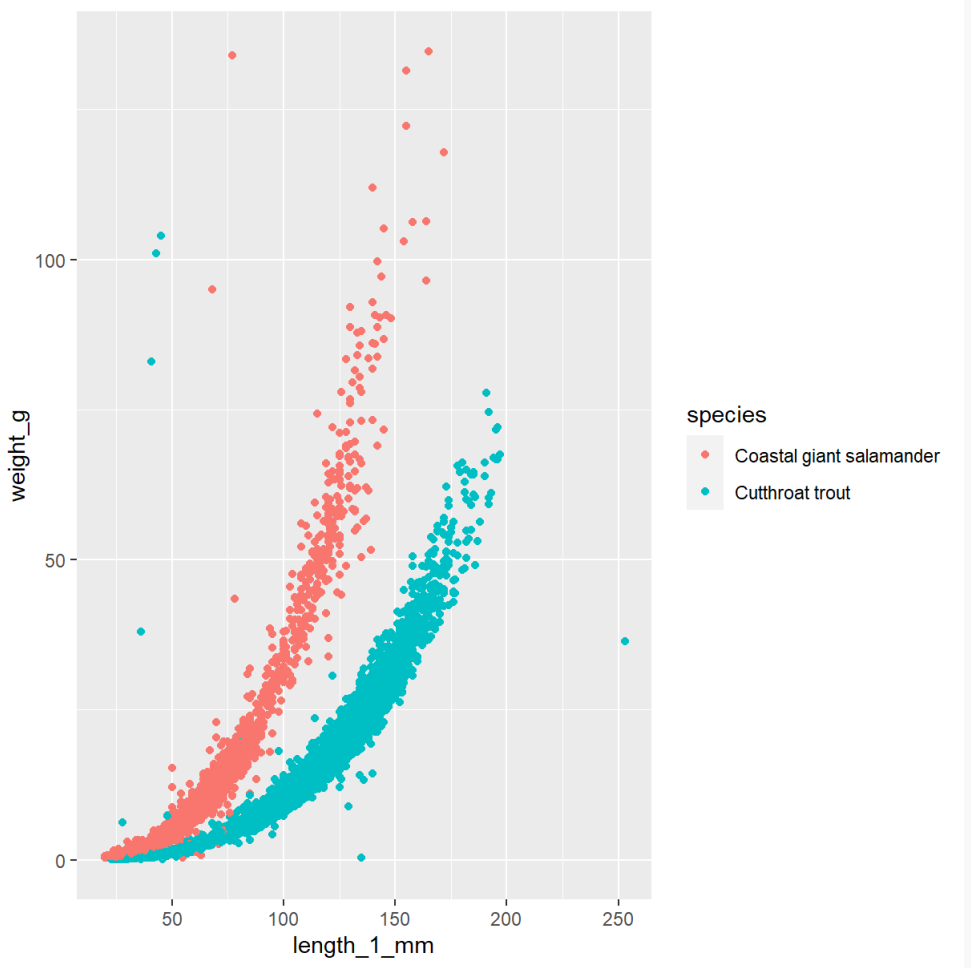


Changing the scales of the aesthetics

The scales onto which the aesthetic elements are mapped can be changed.

```
ggplot(data = and_vertebrates,
       aes(x = length_1_mm,
           y = weight_g,
           color = species)) +
  geom_point()
```

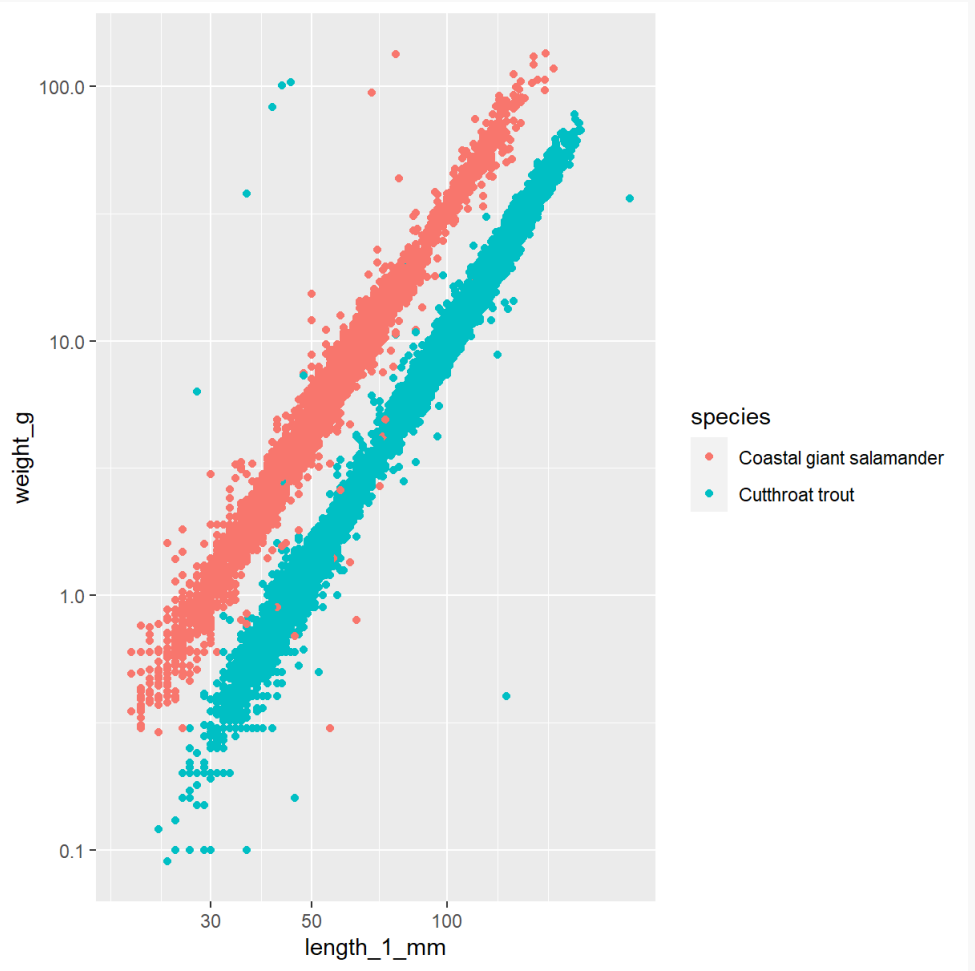
- Exponential relationship?
- How does it look like on the log scale?



scale_x_log10

The scales onto which the aesthetic elements are mapped can be changed.

```
ggplot(data = and_vertebrates,
       aes(x = length_1_mm,
           y = weight_g,
           color = species)) +
  geom_point() +
  scale_x_log10() +
  scale_y_log10()
```



- Scales can be changed for all elements of `aes`
- The general format of scale functions are:

`scale_aes-name_scale-type`

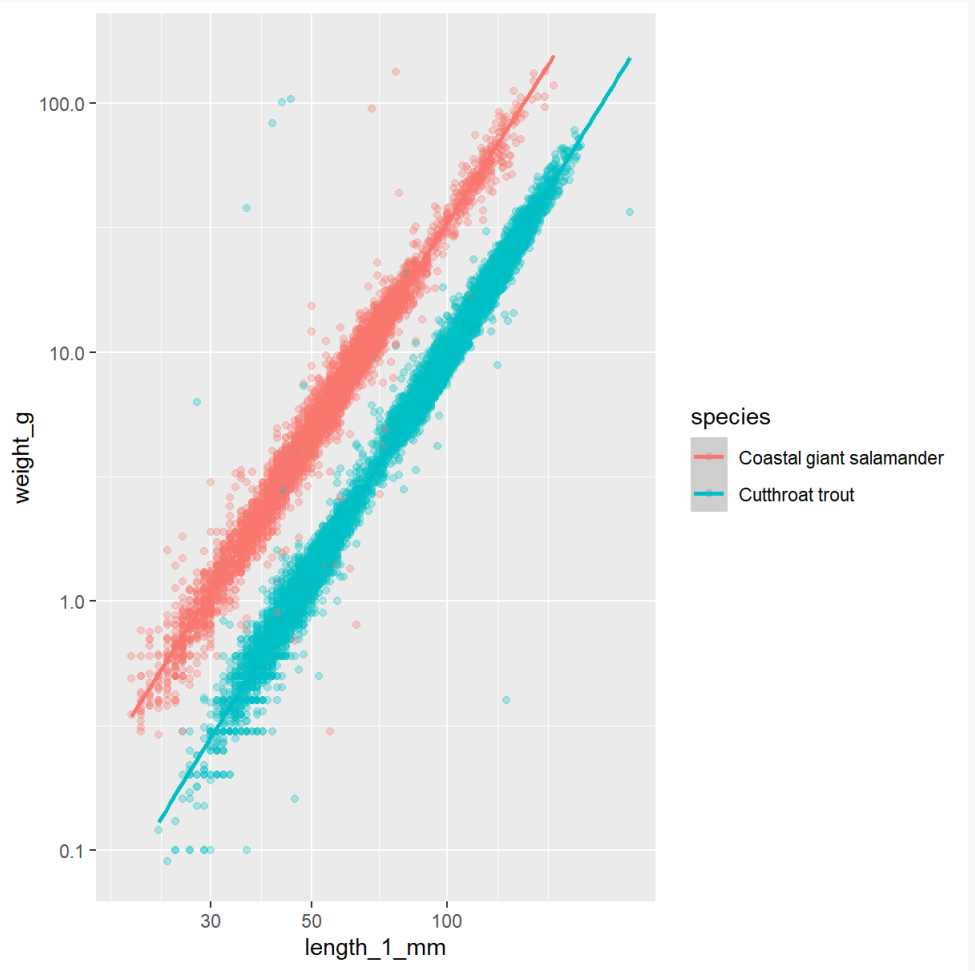
In this example we scale the **x** and the **y** aesthetic to **log10**.

geom_smooth

Add a smoothing line that helps see patterns in the data

```
ggplot(data = and_vertebrates,
       aes(x = length_1_mm,
           y = weight_g,
           color = species)) +
  geom_point(alpha = 0.3) +
  geom_smooth(method = "lm") +
  scale_x_log10() +
  scale_y_log10()
```

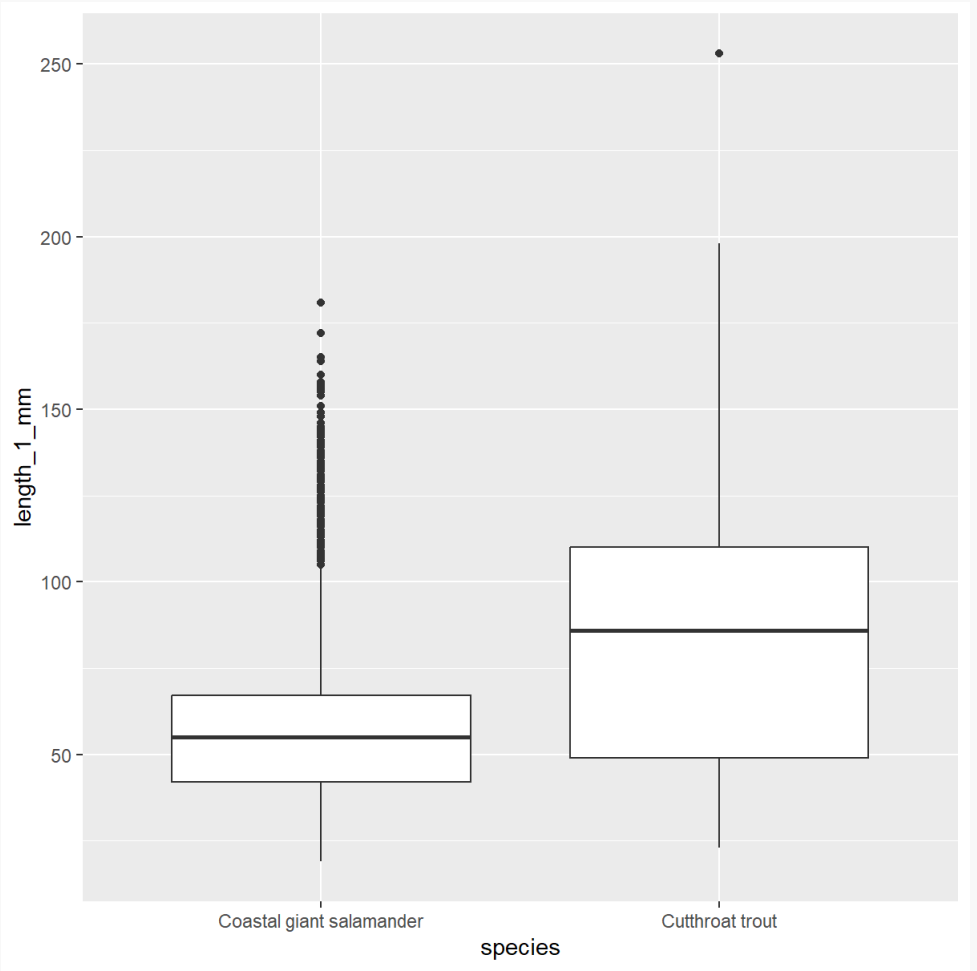
- With `method = "lm"`, a linear regression line is added
- All geoms are done separately for the species because color is defined globally
- Alpha makes the points transparent (0-1 with 0 being invisible)



geom_boxplot

Compare groups using a boxplot

```
1  ggplot(and_vertebrates,
2         aes(x = species,
3             y = length_1_mm)) +
4    geom_boxplot()
```

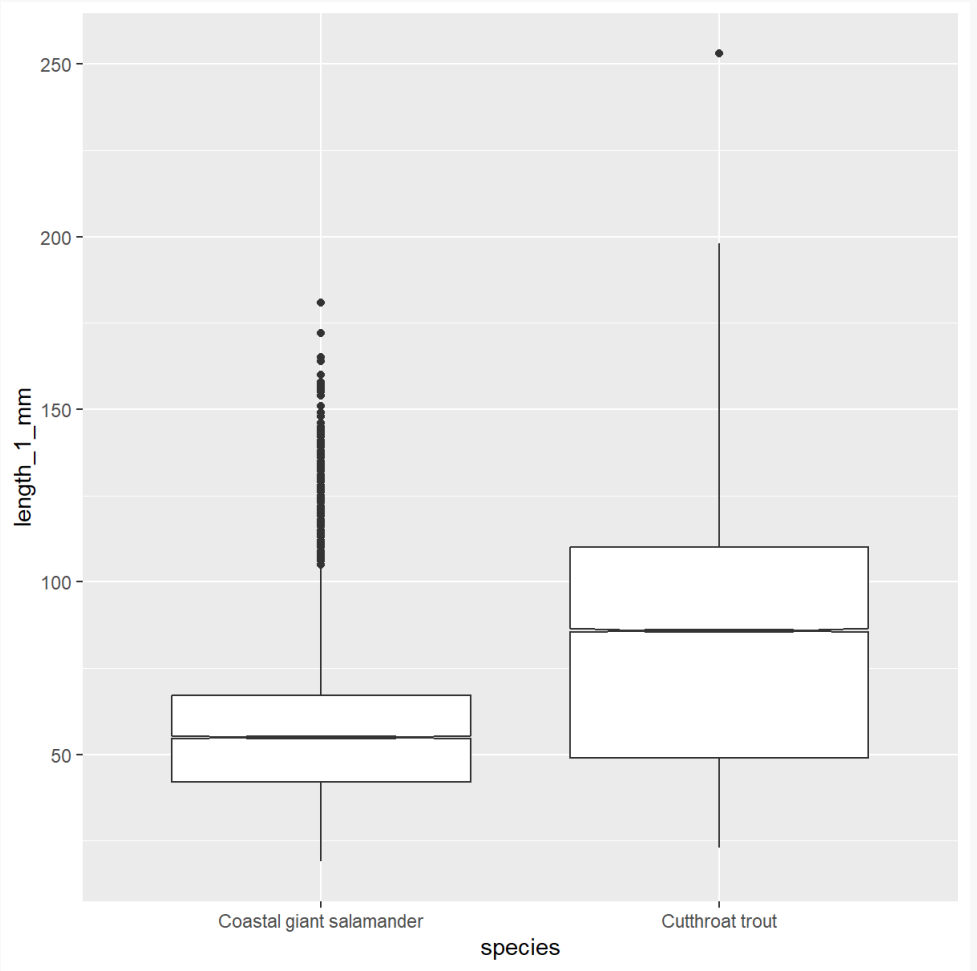


geom_boxplot

Compare groups using a boxplot

```
1  ggplot(and_vertebrates,
2         aes(x = species,
3             y = length_1_mm)) +
4    geom_boxplot(notch = TRUE)
```

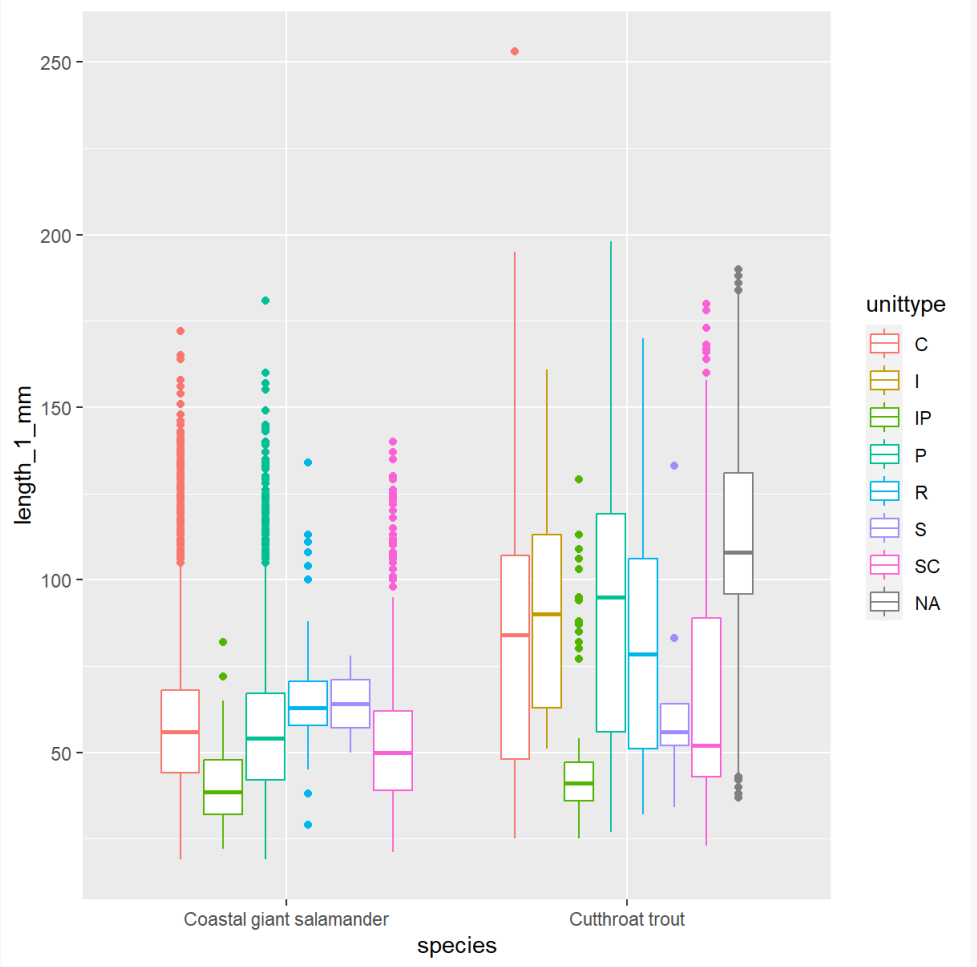
- If notches don't overlap, the medians of the groups are likely different



geom_boxplot

Map the `unittype` to the **color** aesthetic of the boxplot

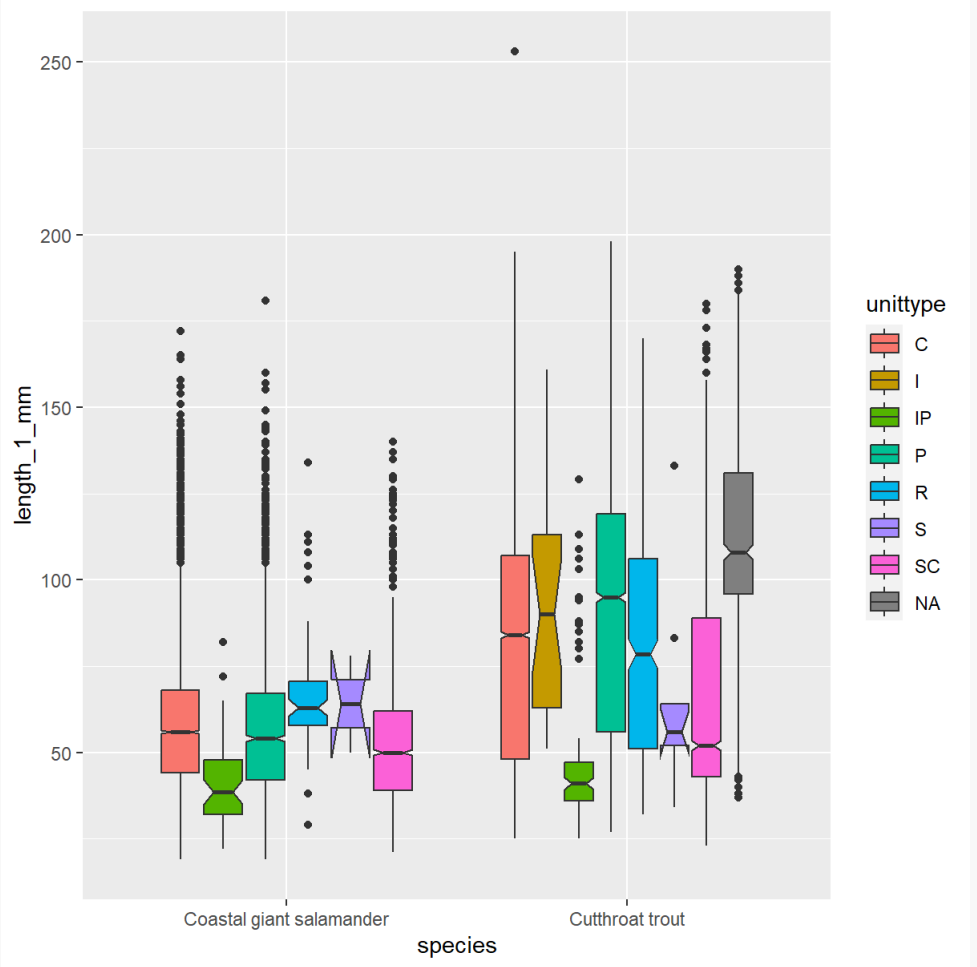
```
1  ggplot(and_vertebrates,
2         aes(x = species,
3             y = length_1_mm,
4             color = unittype)) +
5    geom_boxplot()
```



geom_boxplot

Map the `unittype` to the **fill** aesthetic of the box

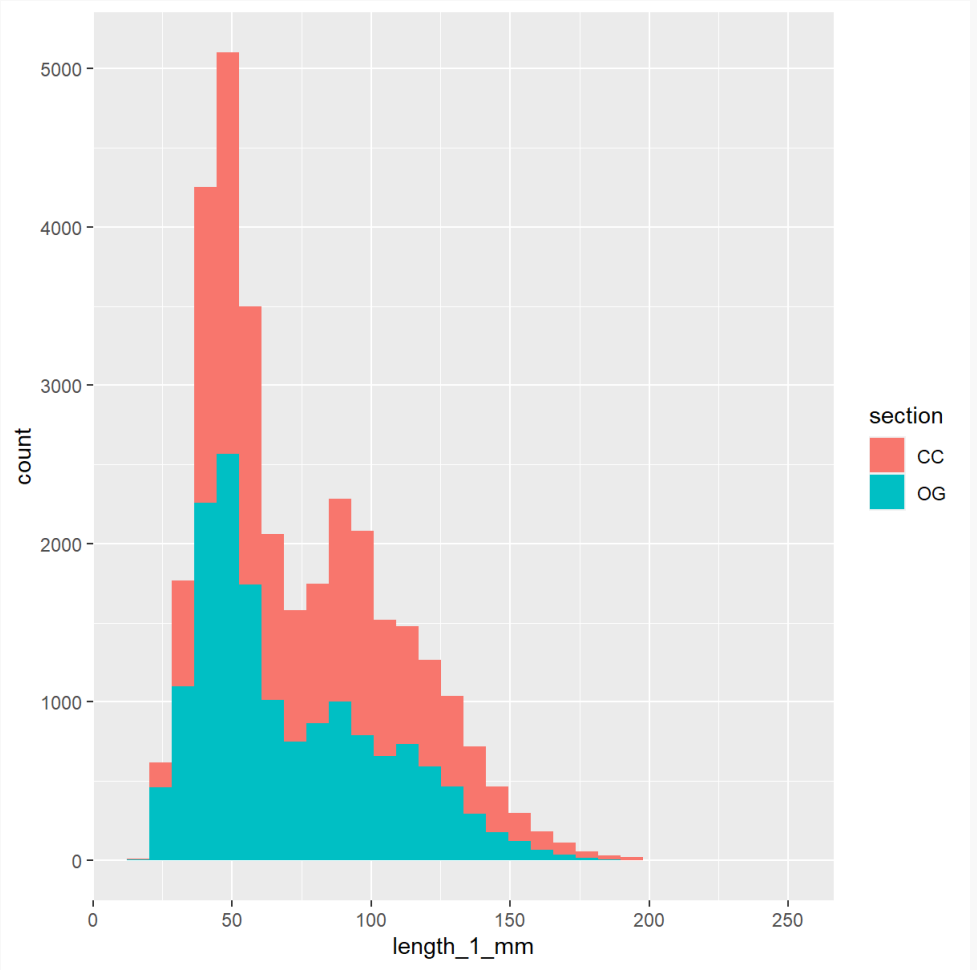
```
1  ggplot(and_vertebrates,
2         aes(x = species,
3             y = length_1_mm,
4             fill = unittype)) +
5    geom_boxplot(notch = TRUE)
```



geom_histogram

```
1  ggplot(and_vertebrates,
2         aes(x = length_1_mm,
3             fill = section)) +
4    geom_histogram()
```

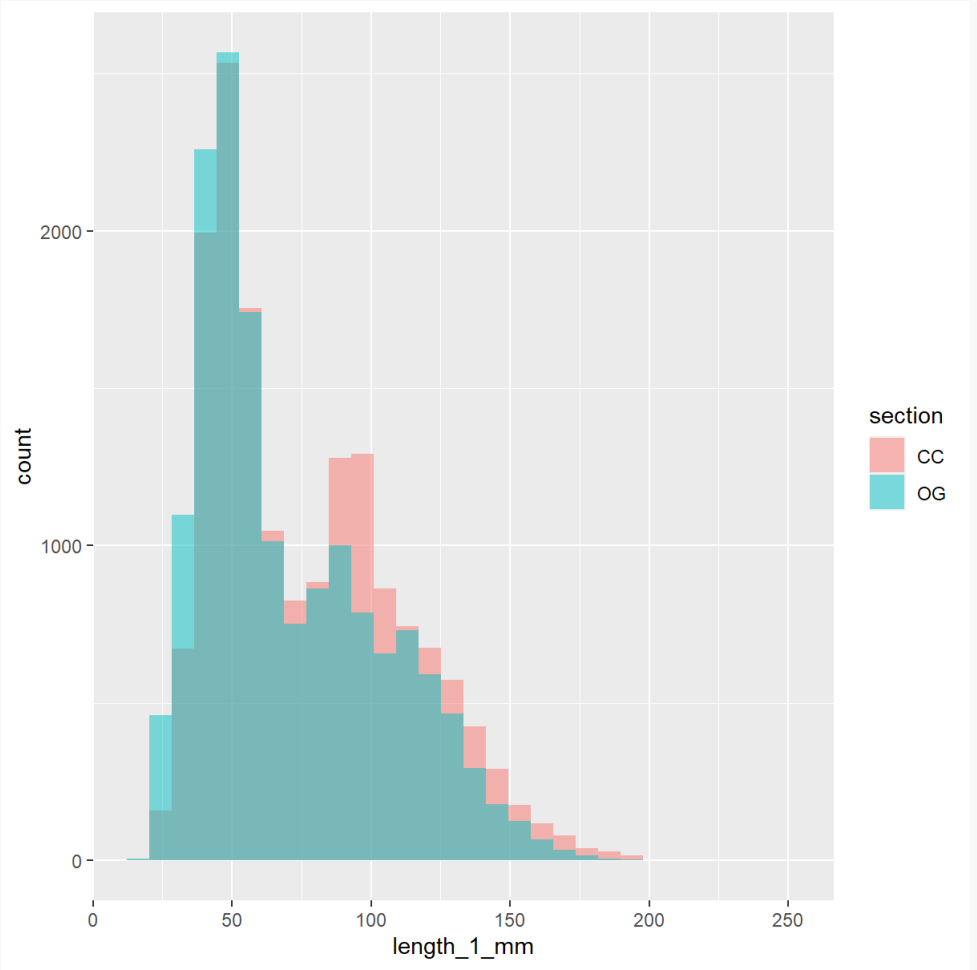
- Careful: By default the histogram is stacked for the different groups!



geom_histogram

```
ggplot(and_vertebrates,
       aes(x = length_1_mm,
           fill = section)) +
  geom_histogram(
    position = "identity",
    alpha = 0.5
    )
```

- Change the position of the histogram to `"identity"`, if you don't want it stacked
- `alpha` makes sure that you see overlapping areas

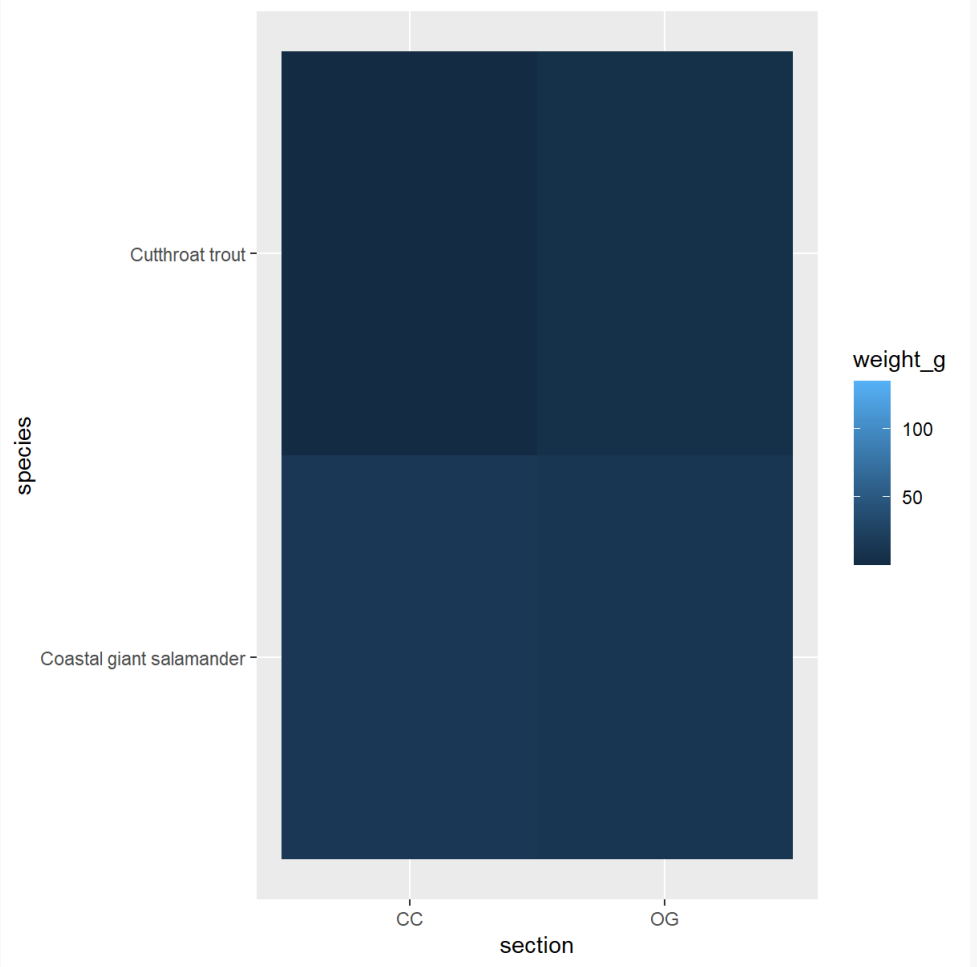


geom_tile

You can create a simple heatmap with `geom_tile`

```
ggplot(and_vertebrates,
       aes(x = section,
           y = species,
           fill = weight_g)) +
  geom_tile()
```

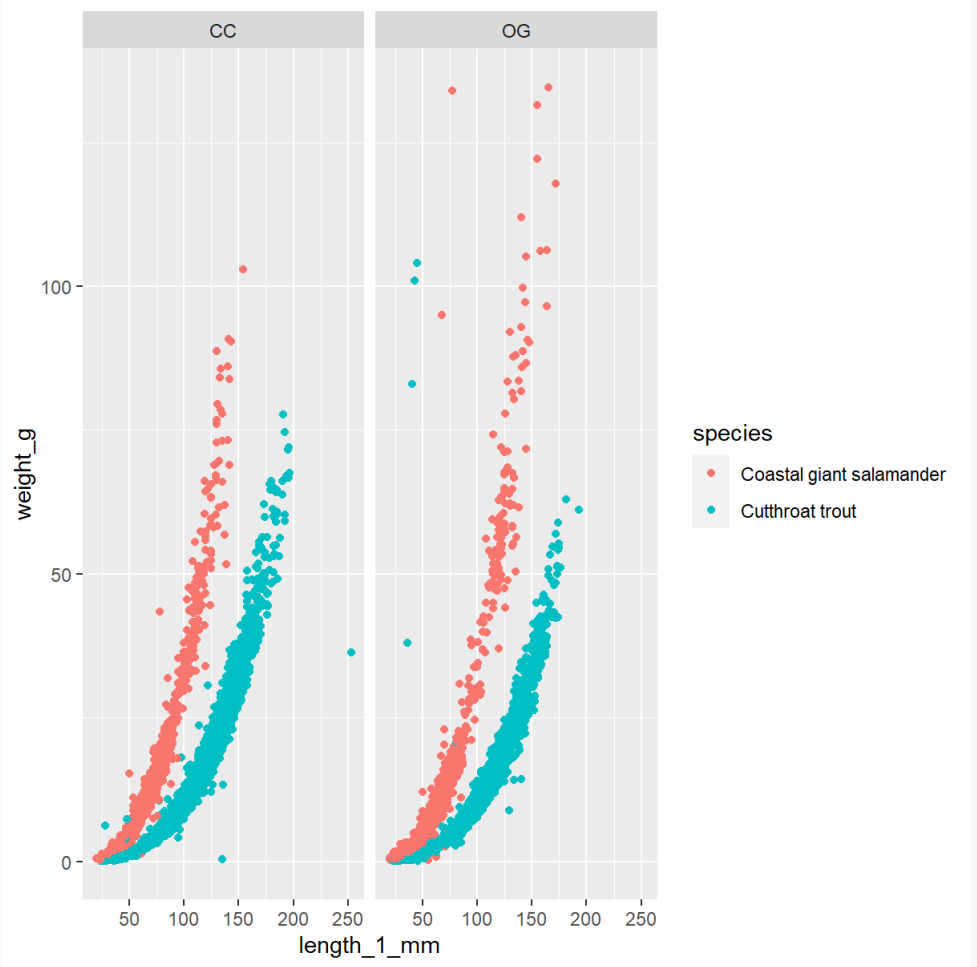
- Here we would have to choose a different color scheme to see differences



Small multiples with `facet_wrap`

Split your plots along one variable with `facet_wrap`

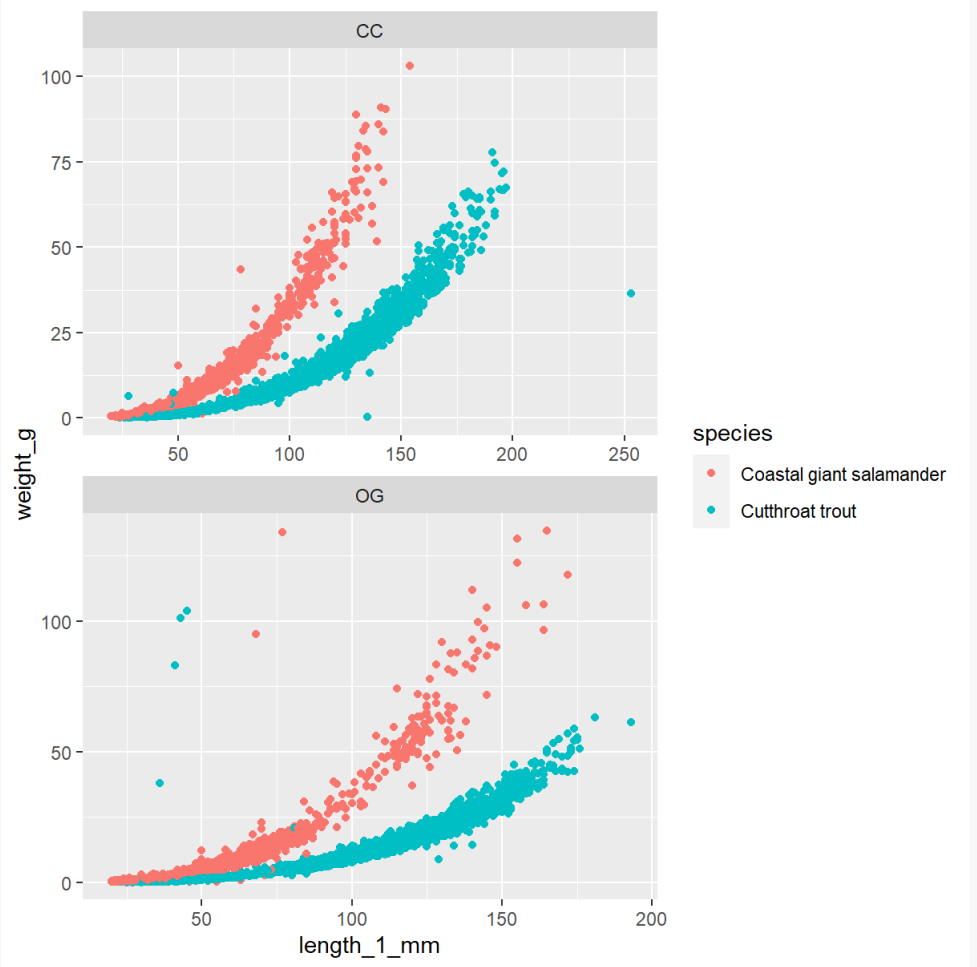
```
ggplot(data = and_vertebrates,
       aes(x = length_1_mm,
           y = weight_g,
           color = species)) +
  geom_point() +
  facet_wrap(~section)
```



Small multiples with `facet_wrap`

Split your plots along one variable with `facet_wrap`

```
ggplot(data = and_vertebrates,
       aes(x = length_1_mm,
           y = weight_g,
           color = species)) +
  geom_point() +
  facet_wrap(~section,
             nrow = 2,
             scales = "free")
```



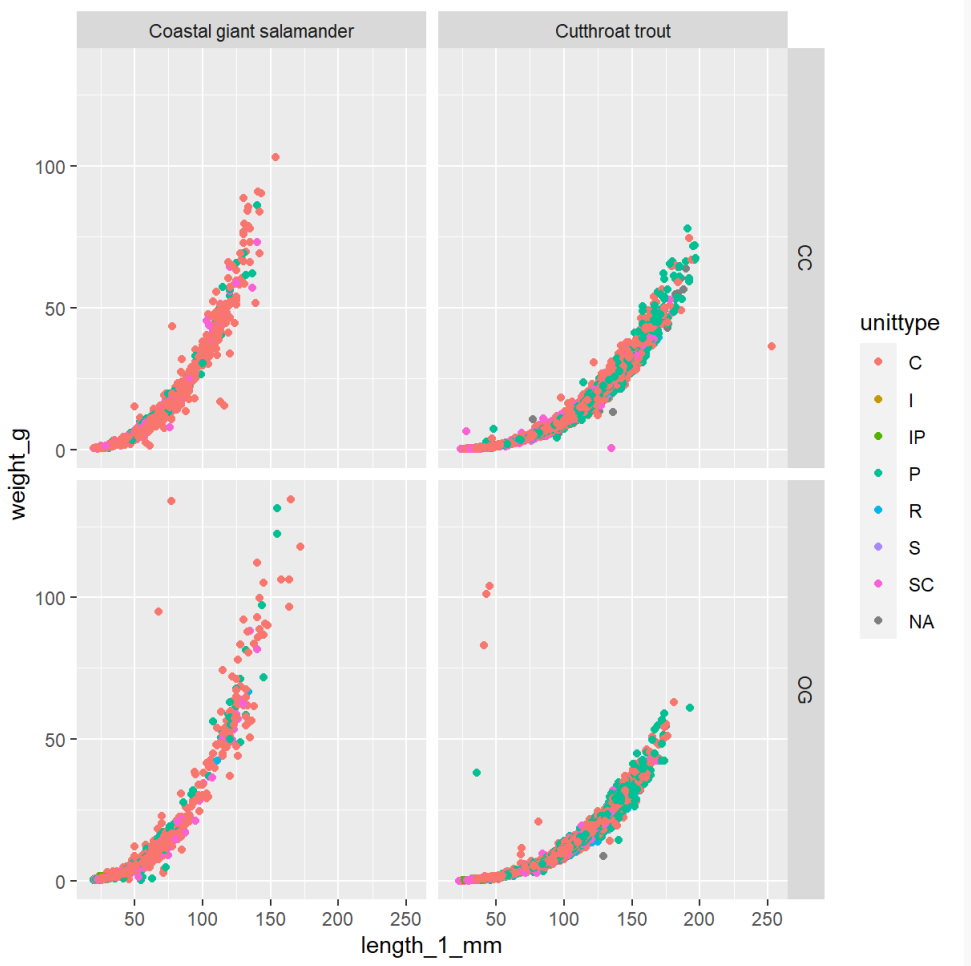
- Specify number of rows and columns with `nrow`/`ncol`
- Set separate scales for x and y with `scales`
  - `"free"`: x and y axis are free
  - `"free_y"`: only y-axis is free
  - `"free_x"`: only x-axis is free

Small multiples with `facet_grid`

Split your plots along two variables with `facet_grid`

```
1  ggplot(data = and_vertebrates,
2         aes(x = length_1_mm,
3             y = weight_g,
4             color = unittype)) +
5    geom_point() +
6    facet_grid(section ~ species)
```

- `facet_grid(rows ~ columns)`



Now you

Task 1.1 - 1.3 (45 min)

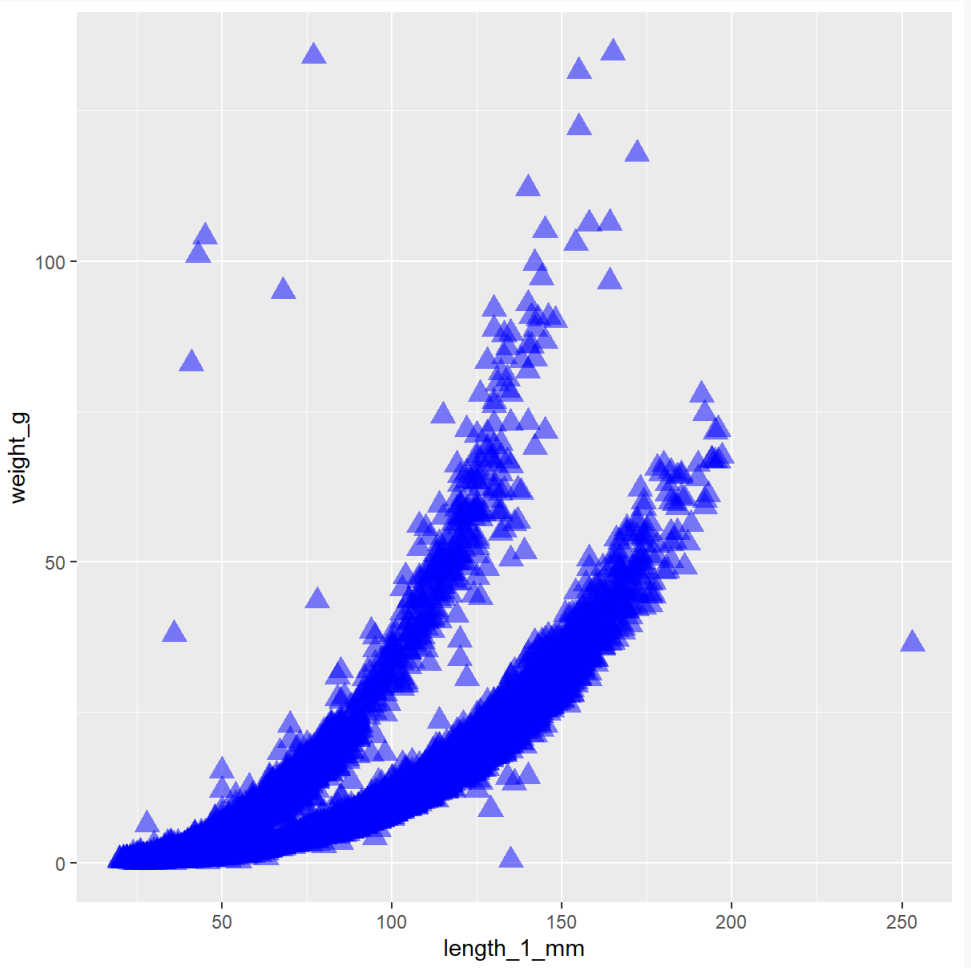
Exploratory data analysis with the penguin data set

Find the task description here

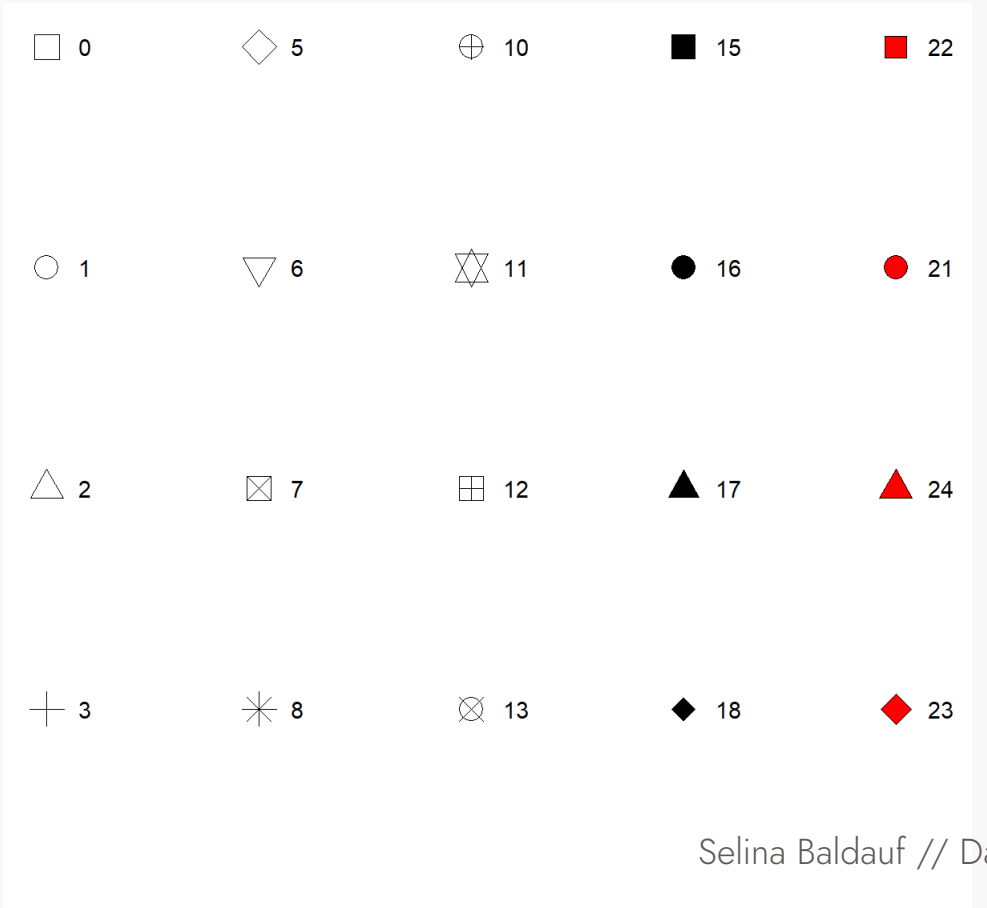
Artwork by Allison Horst

Change appearance of points

```
ggplot(and_vertebrates, aes(
  x = length_1_mm,
  y = weight_g
)) +
  geom_point(
    size = 4,
    shape = 17,
    color = "blue",
    alpha = 0.5
  )
```



- shape and color codes:

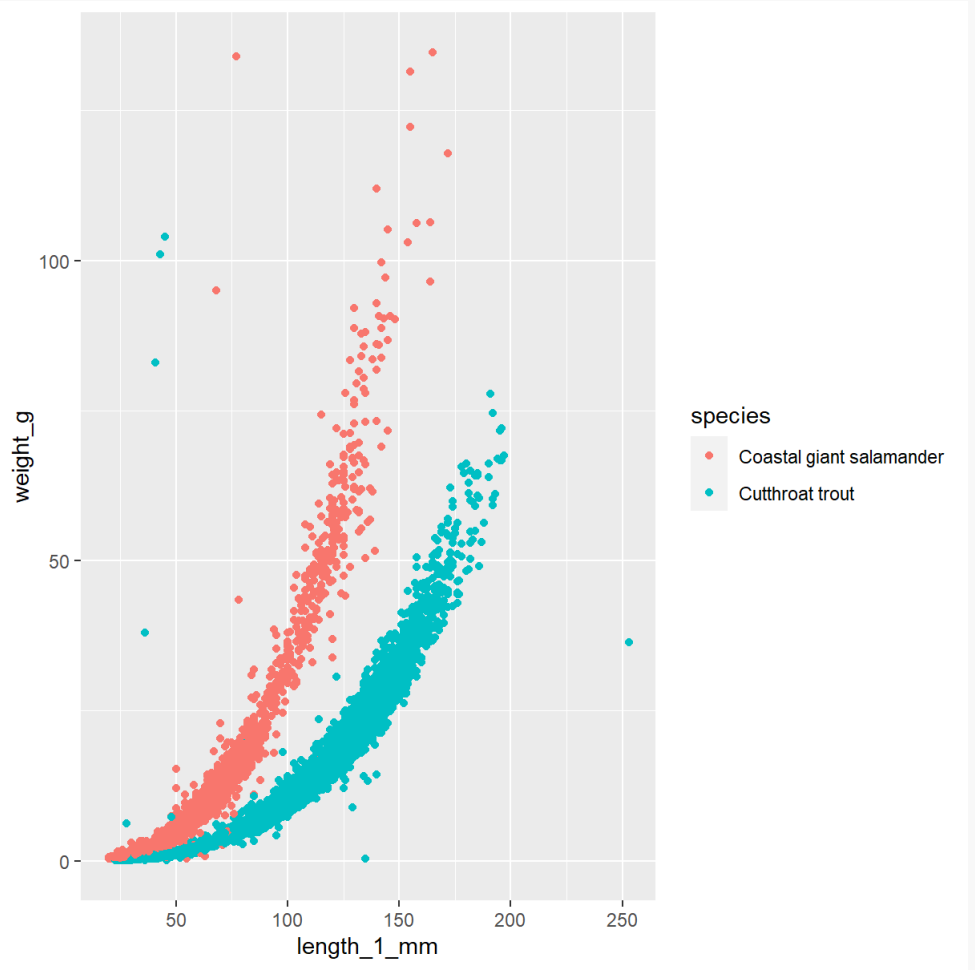


Change color scale

We can also save a plot in a variable

```
g <- ggplot(and_vertebrates, aes(
  x = length_1_mm,
  y = weight_g,
  color = species
)) +
  geom_point()
g
```

- Other plot layers can still be added to `g`

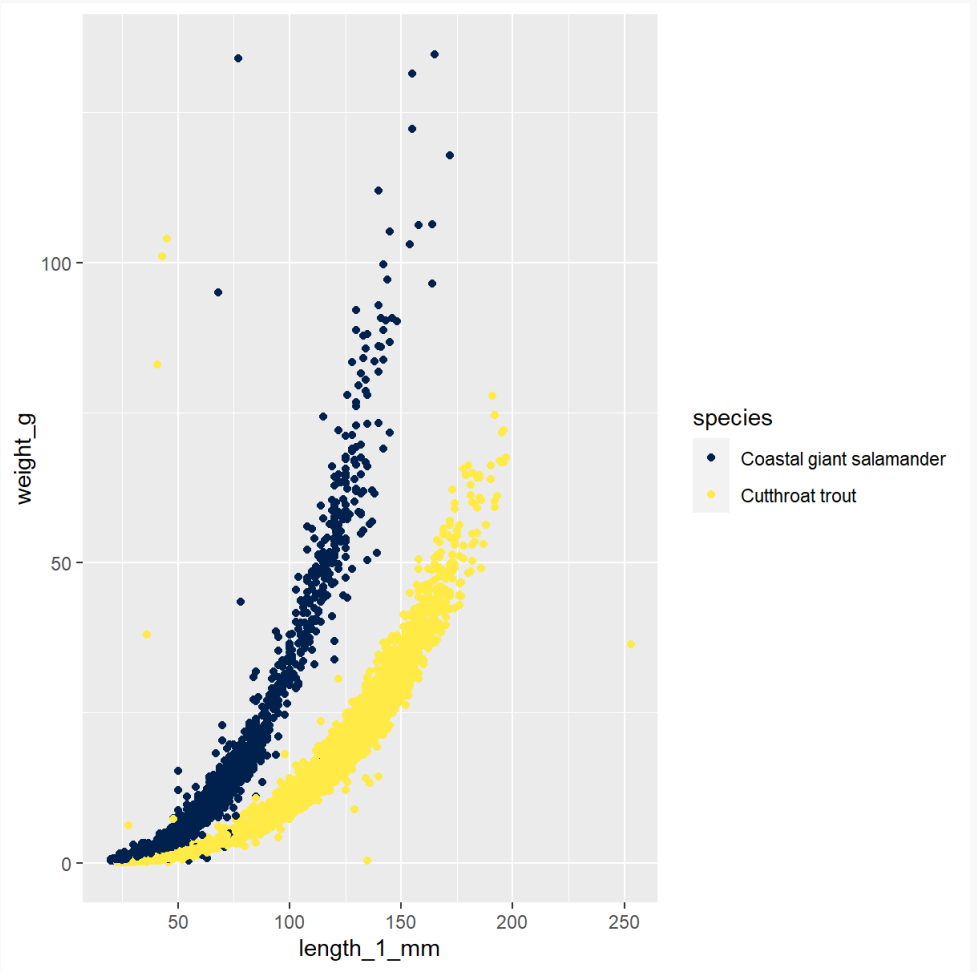


scale_color_viridis_d

Change the colors of the color aesthetic:

```
g +
  scale_color_viridis_d(
    option = "cividis"
  )
```

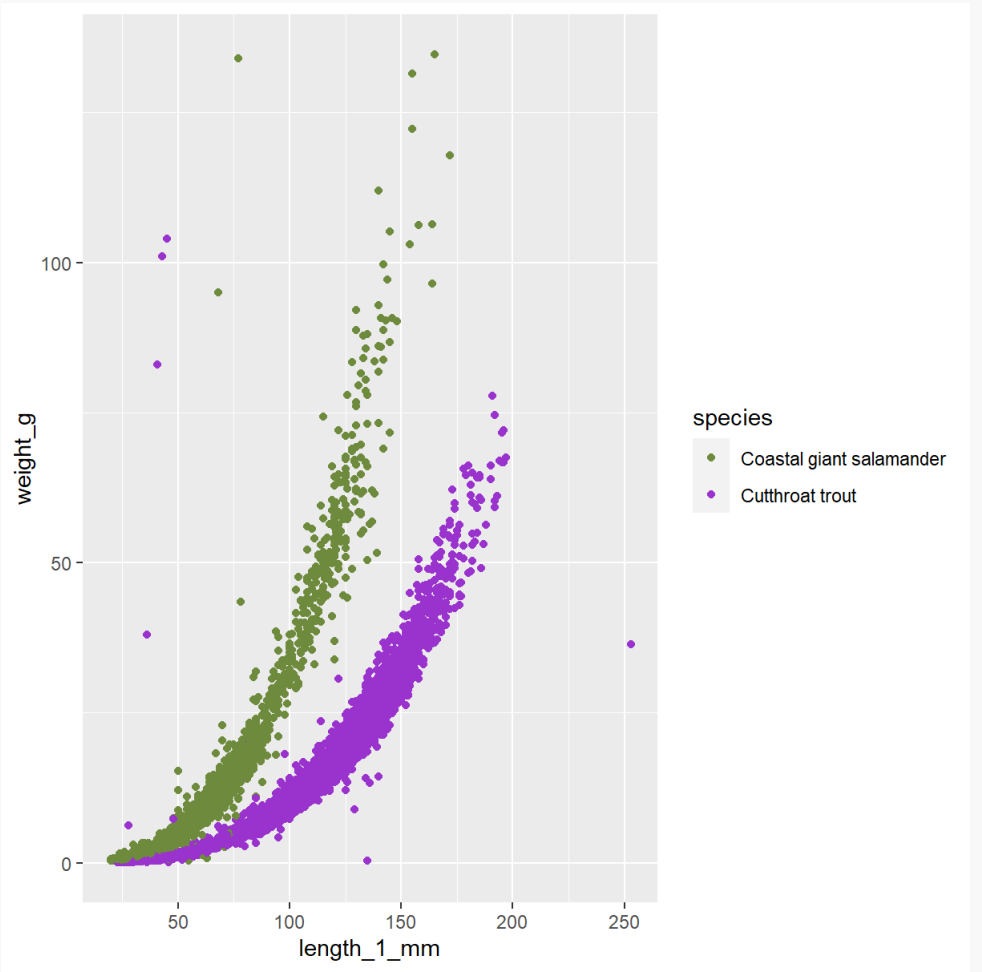
- The viridis color palette is designed for viewers with common forms of color blindness
- Different options of viridis color palettes: `"magma"`, `"inferno"`, `"plasma"`, `"viridis"`, `"cividis"`



scale_color_manual

We can also manually specify colors:

```
g +
  scale_color_manual(
    values = c(
      "darkolivegreen4",
      "darkorchid3"
    )
  )
```



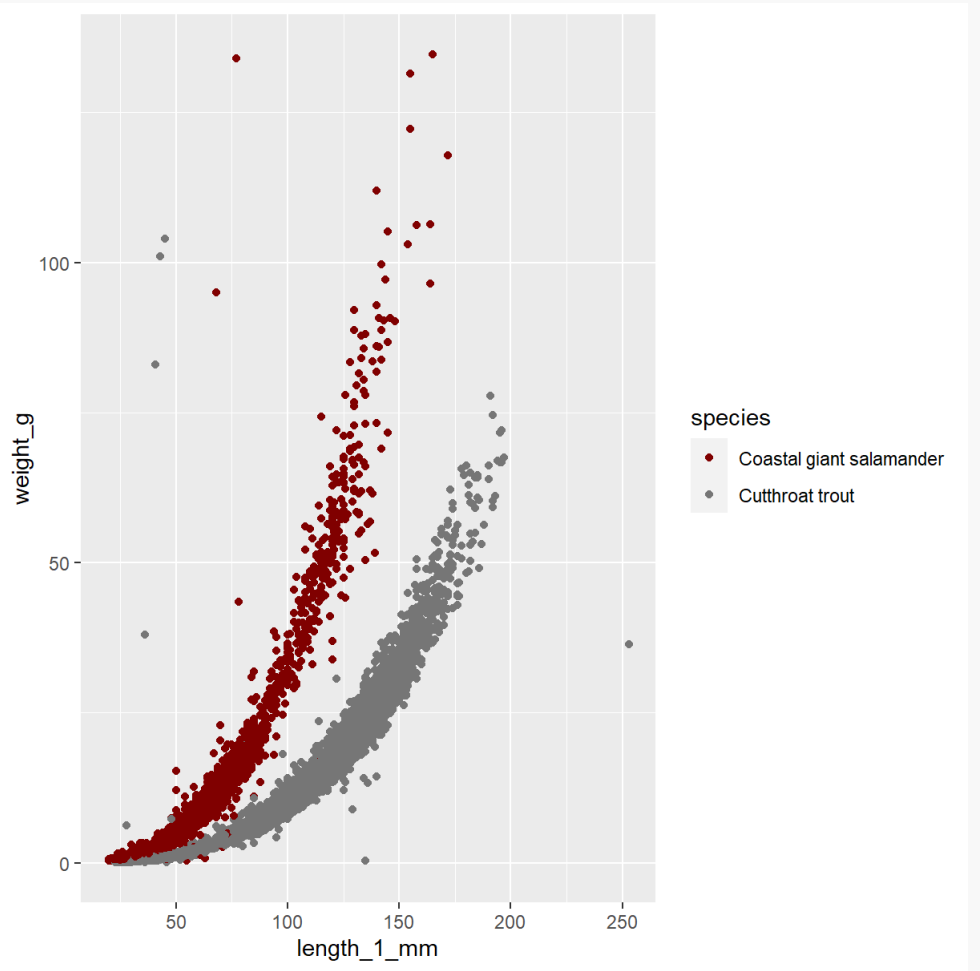
- Length of color vector has to match number of levels in your aesthetic
- Specify colors
  - Via their name
  - Via their Hex color codes (use websites to generate your own color palettes, e.g. here)

Other color scales

You can use the `paletteer` package to access color scales from many packages.

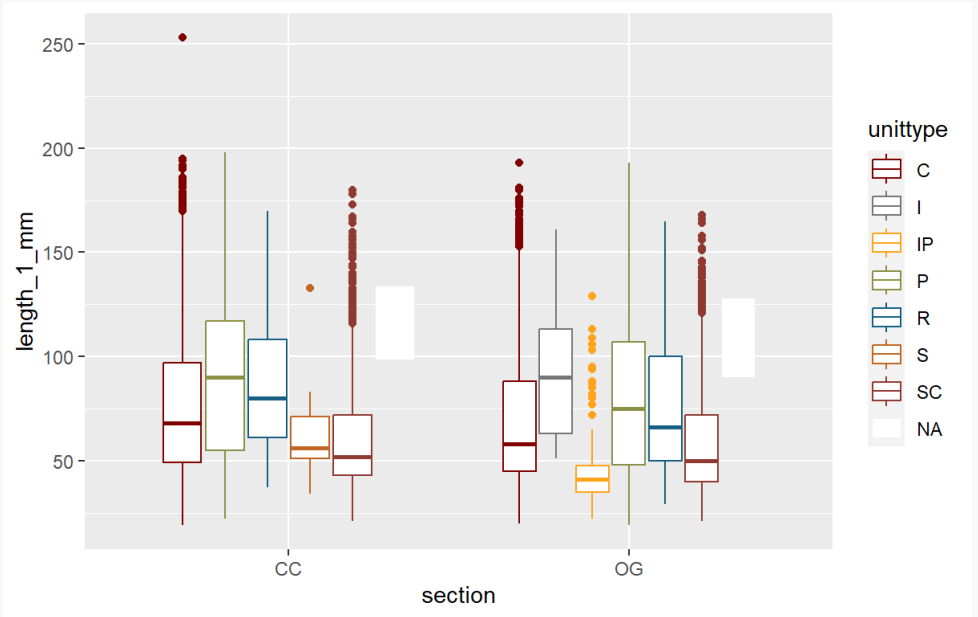
```
1  # install.packages("paletteer")
2  library(paletteer)
3  g <- g +
4    scale_color_paletteer_d(
5      palette = "ggsci::default_uchicago"
6    )
7  g
```

- Use `scale_color_paletteer_d` for discrete and `scale_color_paletteer_c` for continuous color scales
- Check out all palettes available here

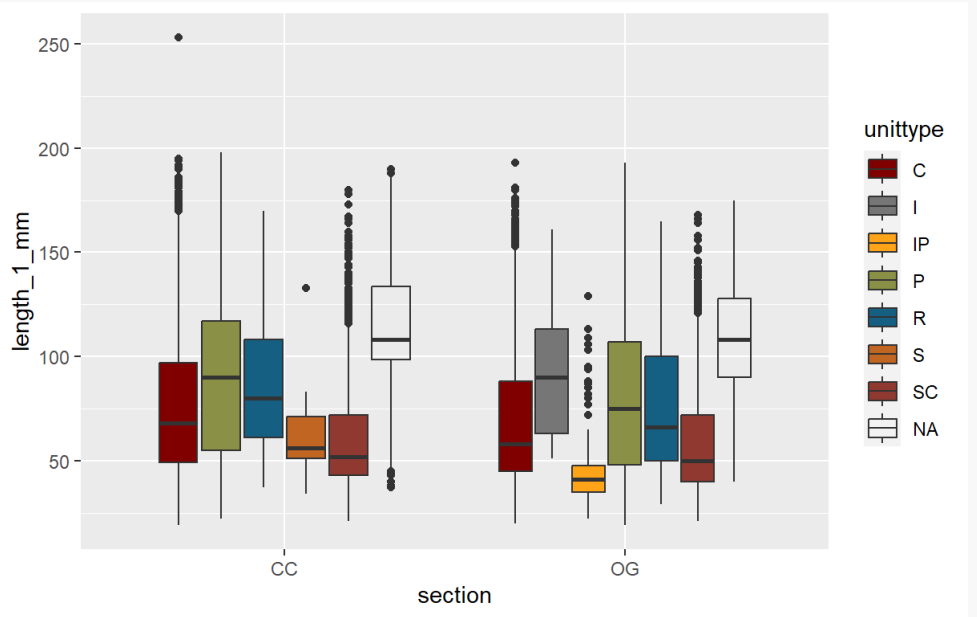


scale_fill_* vs. scale_color_*

```
ggplot(
  and_vertebrates,
  aes(
    x = section,
    y = length_1_mm,
    color = unittype )) +
  geom_boxplot() +
  paletteer::scale_color_paletteer_d(
    palette = "ggsci::default_uchicago"
  )
```

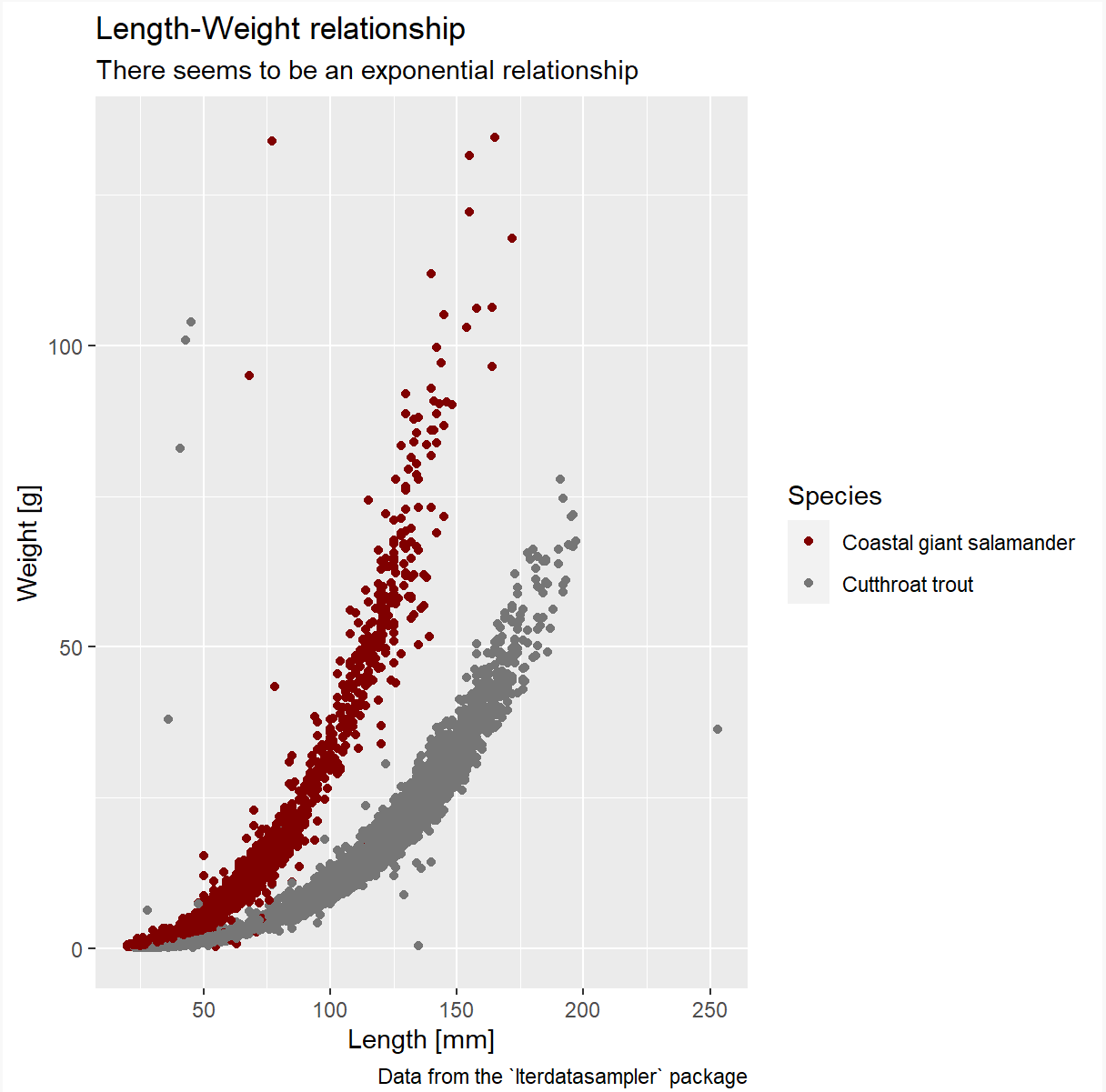



```
ggplot(
  and_vertebrates,
  aes(
    x = section,
    y = length_1_mm,
    fill = unittype )) +
  geom_boxplot() +
  paletteer::scale_fill_paletteer_d(
    palette = "ggsci::default_uchicago"
  )
```



`labs`: Change axis and legend titles and add plot title

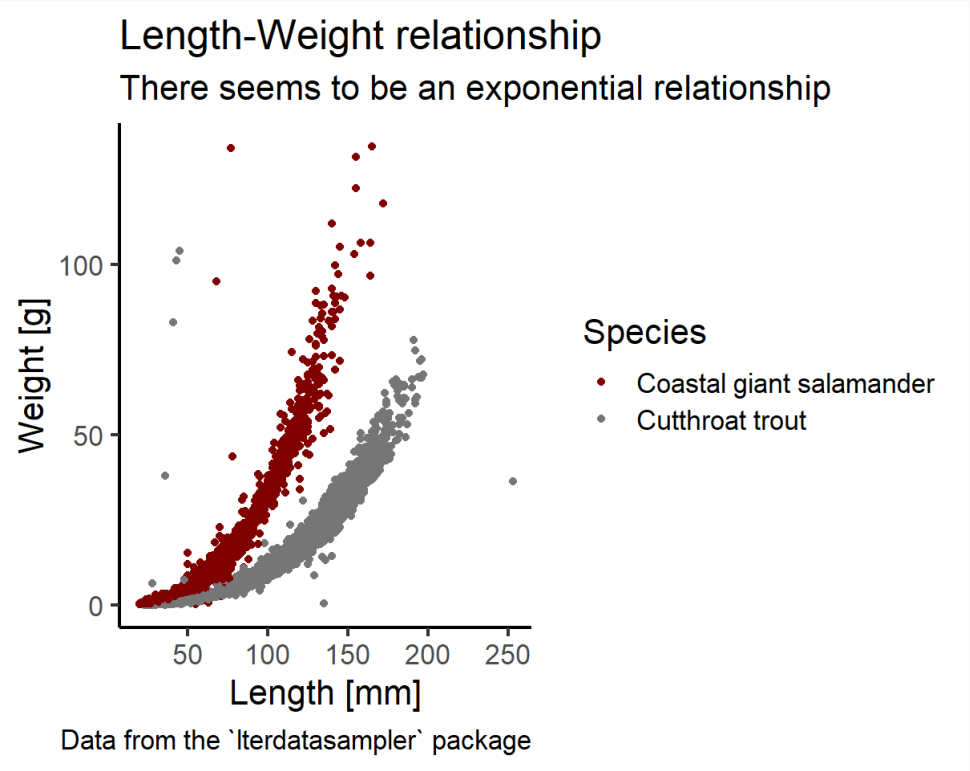
```
g <- g +
  labs(
    x = "Length [mm]",
    y = "Weight [g]",
    color = "Species",
    title = "Length-Weight relationship",
    subtitle = "There seems to be an exponential relationship",
    caption = "Data from the `lterdatasampler` package"
  )
g
```


Length-Weight relationship
There seems to be an exponential relationship
Weight [g]
100
50
0
50
100
150
200
250
Length [mm]
Data from the `lterdatasampler` package
Species
Coastal giant salamander
Cutthroat trout

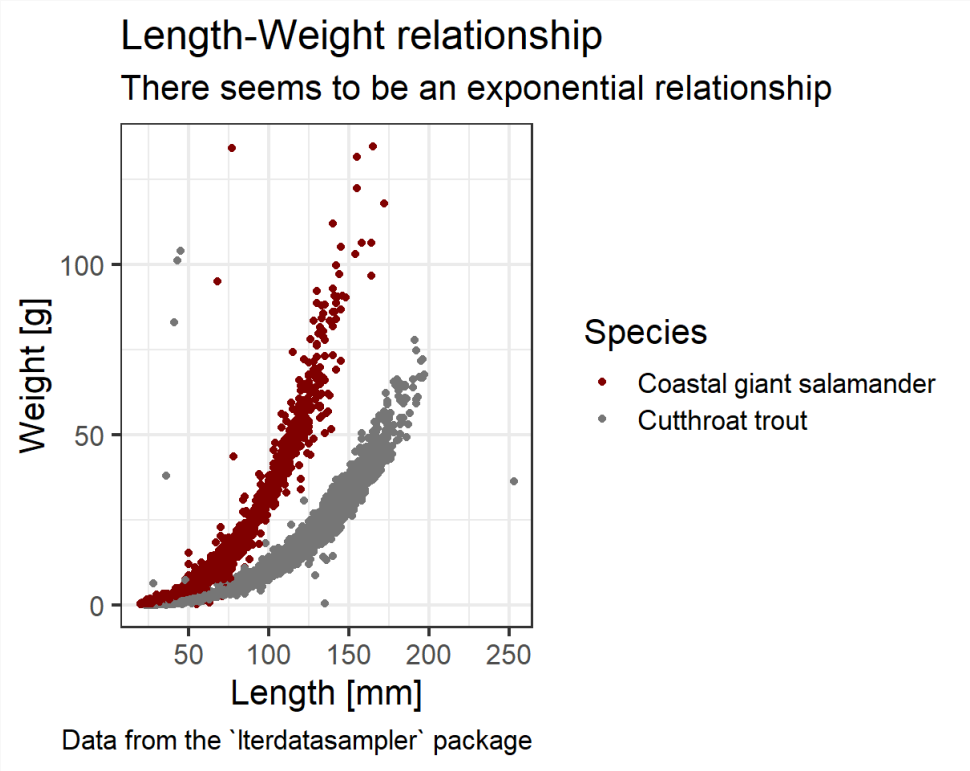
`theme_*`: change appearance

`ggplot2` offers many pre-defined themes that we can apply to change the appearance of a plot.

```
1  g +
2    theme_classic()
```



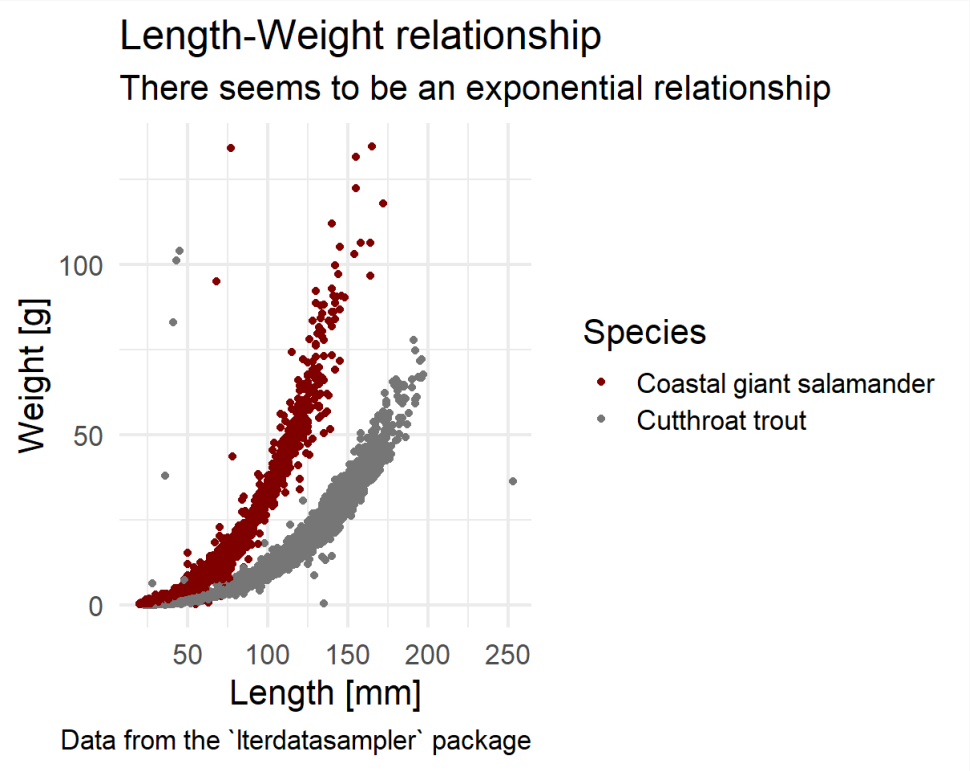

```
1  g +
2    theme_bw()
```



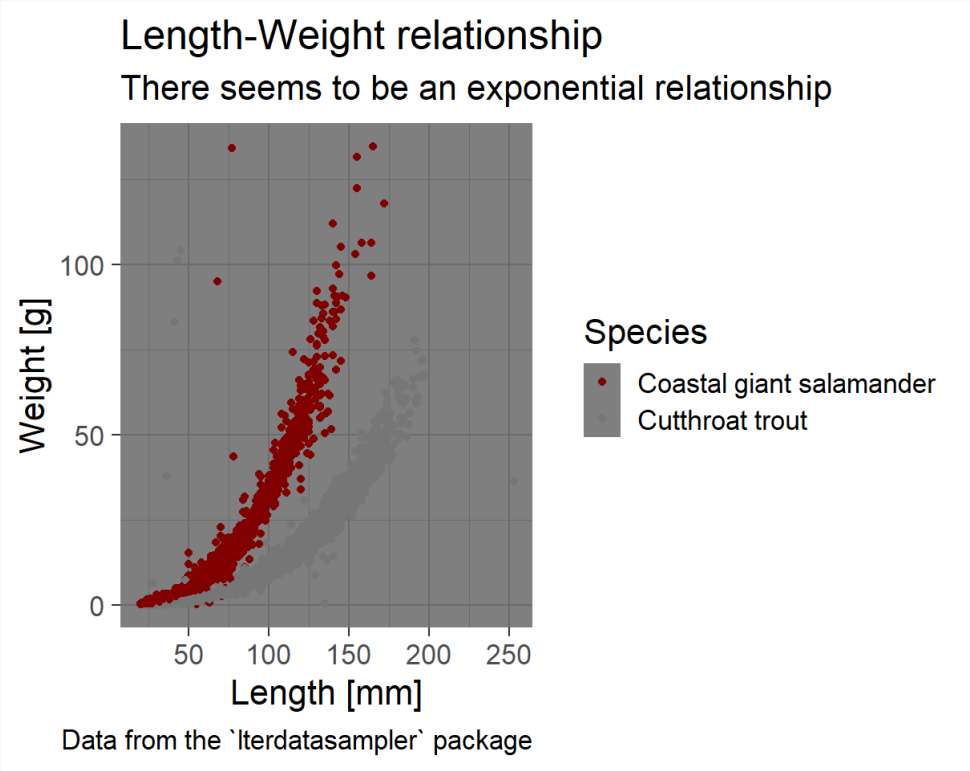
`theme_*`: change appearance

`ggplot2` offers many pre-defined themes that we can apply to change the appearance of a plot.

```
1  g +
2    theme_minimal()
```




```
1  g +
2    theme_dark()
```



`theme()`: customize theme

You can manually change a theme or even create an entire theme yourself. The elements you can control in the theme are:

- titles (plot, axis, legend, ...)
- labels
- background
- borders
- grid lines
- legends

If you want a full list of what you can customize, have a look at

```
1  ?theme
```

- Look here for an overview of the elements that you can change and the corresponding functions

`theme()`: customize theme

To edit a theme, just add another `theme()` layer to your plot.

```
g +
  theme_minimal() +
  theme(
    legend.position = "bottom",
    axis.text = element_text(face = "bold"),
    plot.background = element_rect(
      fill = "lightgrey",
      color = "darkred"
    )
  )
```

The basic functioning of theme elements is:

```
theme(
  element_name = element_function()
)
```

`theme_set()`: set global theme

You can set a global theme that will be applied to all ggplot objects in the current R session.

```
1  # Globally set theme_minimal as the default theme
2  theme_set(theme_minimal())
```

Add this to the beginning of your script.

You can also specify some defaults, e.g. the text size:

```
1  theme_set(theme_minimal(base_size = 16))
```

This is very practical if you want to achieve a consistent look, e.g. for a scientific journal.

ggsave()

A ggplot object can be saved on disk in different formats.

Without specifications:

```
# save plot g in img as my_plot.pdf
ggsave(filename = "img/my_plot.pdf", plot = g)
# save plot g in img as my_plot.png
ggsave(filename = "img/my_plot.png", plot = g)
```

Or with specifications:

```
# save a plot named g in the img directory under the name my_plot.png
# with width 16 cm and height 9 cm
ggsave(filename = "img/my_plot.png",
       plot = g,
       width = 16,
       heigth = 9,
       units = "cm")
```

Have a look at `?ggsave` to see all options.

Now you

Task 2 (30 min)

Make your penguin plots more beautiful

Find the task description here