

Data visualization with ggplot2

Day 2 - Introduction to Data Analysis with R

Selina Baldauf

Freie Universität Berlin - Theoretical Ecology

October 1, 2025

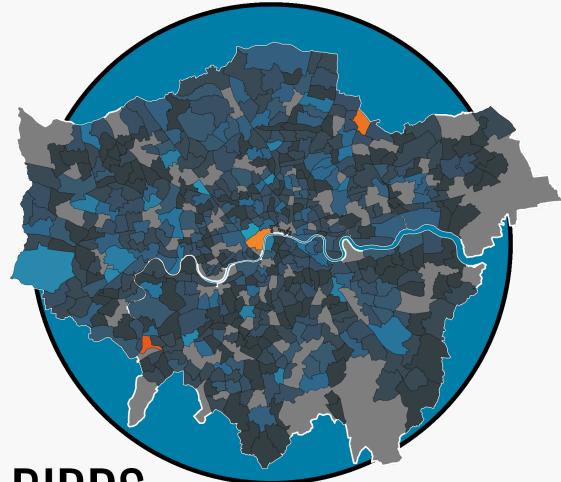
A ggplot showcase

Example plots you can create with ggplot

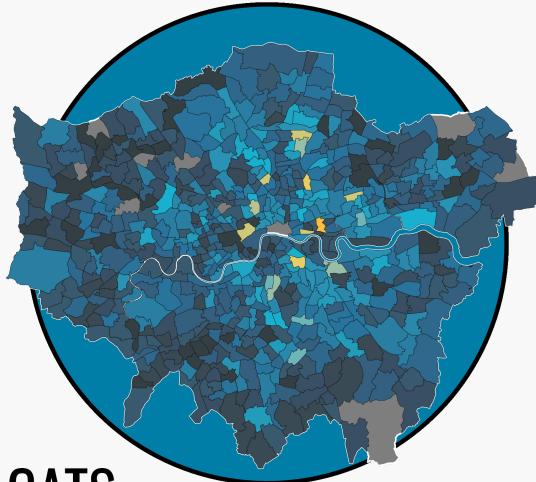
A ggplot showcase

Frequency of Rescues of Birds, Cats and Dogs in London from 2009-2021

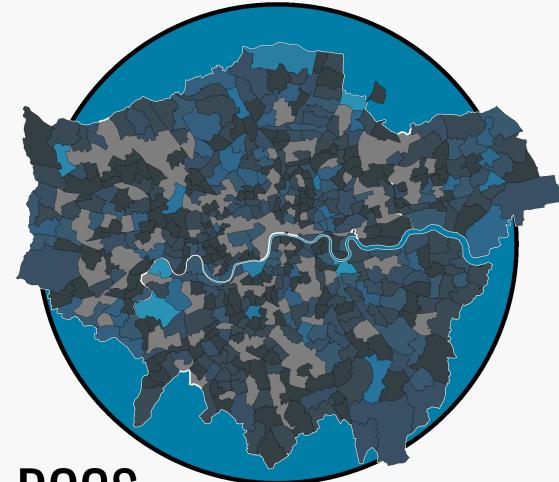
Illustrated below in three choropleth maps are rescues of birds, cats and dogs in London wards. Darker colors indicate lower rescue numbers while brighter colors indicate a greater number of rescues in that ward.



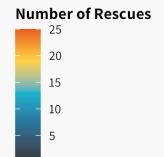
BIRDS



CATS



DOGS



Data: London.gov | Graphic: @jakekaupp

Visualization by [Jake Kaupp](#), code available on [Github](#)

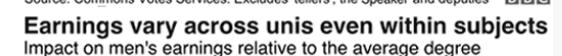
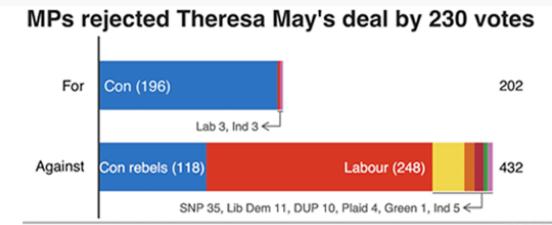
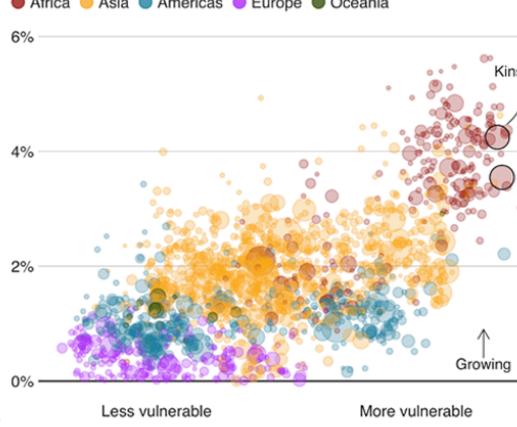
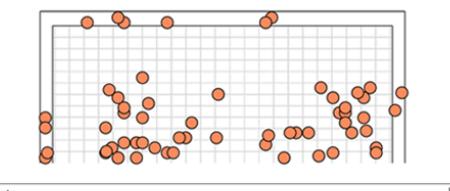
A ggplot showcase



Source: AP, 19:01 ET

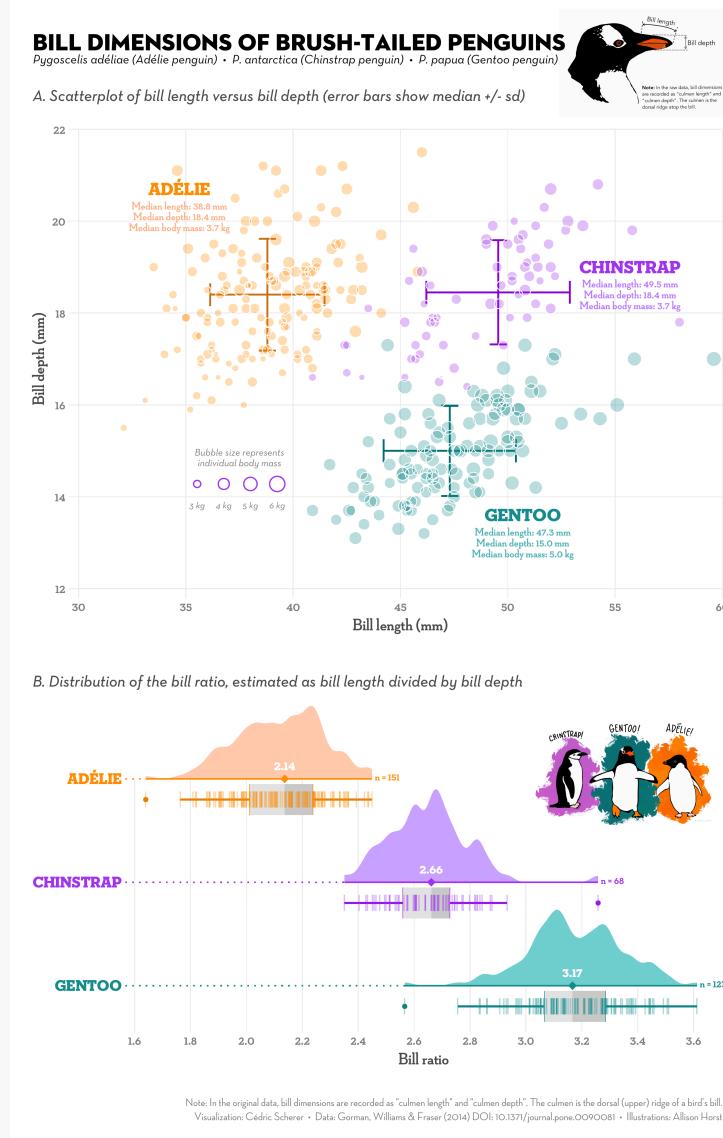


Roberto Baggio's penalty miss in the 1994 final against Brazil



Visualizations produced by the BBC News data team

A ggplot showcase



Visualization by Cédric Scherer, code available on [Github](#)
Selina Baldauf // Data visualization with ggplot2

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, themes, colors, animation, ...
 - See [here](#) for a list of ggplot extensions
- 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]



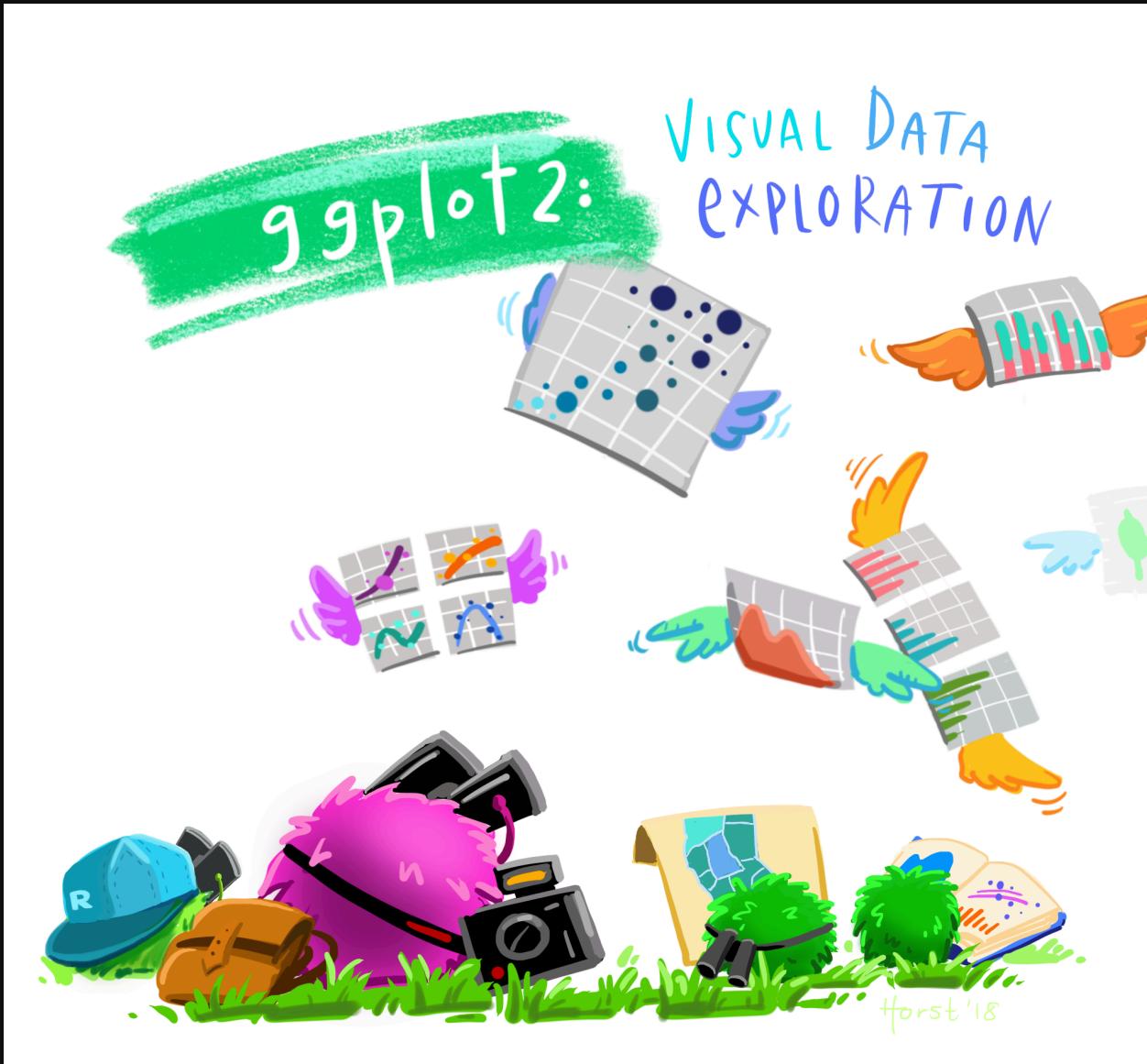
References: Kaylor, M.J. and D.R. Warren. (2017) and
Gregory, S.V. and I. Arismendi. (2020) as provided in the
Selina Baldauf // Data visualization with ggplot2

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

The data

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

```
library(lterdatasampler)
#> Error in library(lterdatasampler): there is no package called 'lterdatasampler'
vertebrates <- and_vertebrates |>
  select(year, section, unittype, species, length_1_mm, weight_g) |>
  filter(species != "Cascade torrent salamander")
#> Error: object 'and_vertebrates' not found
vertebrates
#> Error: object 'vertebrates' not found
```



Artwork by Allison Horst

ggplot(data)

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

```
library(ggplot2)  
# or library(tidyverse)  
  
ggplot(data = vertebrates)
```

#> Error: object 'vertebrates' not found

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

aes(x, y)

The **aesthetics** define how data variables are mapped plot properties.

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

#> Error: object 'vertebrates' not found

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

aes(x, y)

The **aesthetics** define how data variables are mapped plot properties.

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

#> Error: object 'vertebrates' not found

This is the same but shorter:

```
ggplot(  
  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

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

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

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

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

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

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
j <- data.frame(grp = c("A", "B"), fit = 4:5, se = 1:2)

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

j + geom_errorbar()
x, y, 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

from [ggplot cheatsheet](#)

geom_point

```
ggplot(  
  data = vertebrates,  
  aes(  
    x = length_1_mm,  
    y = weight_g  
  )  
) +  
  geom_point()
```

#> Error: object 'vertebrates' not found

- 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

geom_point

```
ggplot() +  
  geom_point(  
    data = vertebrates,  
    aes(  
      x = length_1_mm,  
      y = weight_g  
    )  
  )
```

#> Error: object 'vertebrates' not found

- **data** and **aes** can also be local to a layer:

Here, it does not make a difference in the result.

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:

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

#> Error: object 'vertebrates' not found

- 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:

```
ggplot(  
  data = vertebrates,  
  aes(  
    x = length_1_mm,  
    y = weight_g,  
    size = species  
  )  
) +  
  geom_point()  
#> Error: object 'vertebrates' not found
```

aes(shape): mapping shape to a variable

We can do the same with shape:

```
ggplot(  
  data = vertebrates,  
  aes(  
    x = length_1_mm,  
    y = weight_g,  
    shape = species  
  )  
) +  
  geom_point()
```

#> Error: object 'vertebrates' not found

Combine color, size and shape

We can also combine these aesthetics and map different variables

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

#> Error: object 'vertebrates' not found

- 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 = vertebrates,  
  aes(  
    x = length_1_mm,  
    y = weight_g,  
    color = species  
  )  
) +  
  geom_point()
```

#> Error: object 'vertebrates' not found

- 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 = vertebrates,  
  aes(  
    x = length_1_mm,  
    y = weight_g,  
    color = species  
  )  
) +  
  geom_point() +  
  scale_x_log10() +  
  scale_y_log10()  
#> Error: object 'vertebrates' not found
```

- Scales can be changed for all elements of **aes**:

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 = 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()  
#> Error: object 'vertebrates' not found
```

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

geom_boxplot

Compare groups using a boxplot

```
ggplot(  
  vertebrates,  
  aes(  
    x = species,  
    y = length_1_mm  
  )  
) +  
  geom_boxplot()
```

#> Error: object 'vertebrates' not found

geom_boxplot

Compare groups using a boxplot

```
ggplot(  
  vertebrates,  
  aes(  
    x = species,  
    y = length_1_mm  
  )  
) +  
  geom_boxplot(notch = TRUE)
```

#> Error: object 'vertebrates' not found

- 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

```
ggplot(  
  vertebrates,  
  aes(  
    x = species,  
    y = length_1_mm,  
    color = unittype  
  )  
) +  
  geom_boxplot()
```

#> Error: object 'vertebrates' not found

geom_boxplot

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

```
ggplot(  
  vertebrates,  
  aes(  
    x = species,  
    y = length_1_mm,  
    fill = unittype  
  )  
) +  
  geom_boxplot(notch = TRUE)
```

#> Error: object 'vertebrates' not found

geom_histogram

```
ggplot(  
  vertebrates,  
  aes(  
    x = length_1_mm,  
    fill = section  
  )  
) +  
  geom_histogram()
```

#> Error: object 'vertebrates' not found

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

geom_histogram

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

#> Error: object 'vertebrates' not found

- 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(  
  vertebrates,  
  aes(  
    x = section,  
    y = species,  
    fill = weight_g  
  )  
) +  
  geom_tile()
```

#> Error: object 'vertebrates' not found

- 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 = vertebrates,  
  aes(  
    x = length_1_mm,  
    y = weight_g,  
    color = species  
  )  
) +  
  geom_point() +  
  facet_wrap(~section)
```

#> Error: object 'vertebrates' not found

Small multiples with `facet_grid`

Split your plots along two variables with `facet_grid`

```
ggplot(  
  data = vertebrates,  
  aes(  
    x = length_1_mm,  
    y = weight_g,  
    color = unittype  
  )  
) +  
  geom_point() +  
  facet_grid(section ~ species)
```

#> Error: object 'vertebrates' not found

- `facet_grid(rows ~ columns)`

Now you

Task 1.1 - 1.2 (45 min)

Exploratory data analysis with the penguin data set

Find the task description [here](#)

(Don't do the "Beautify" task)

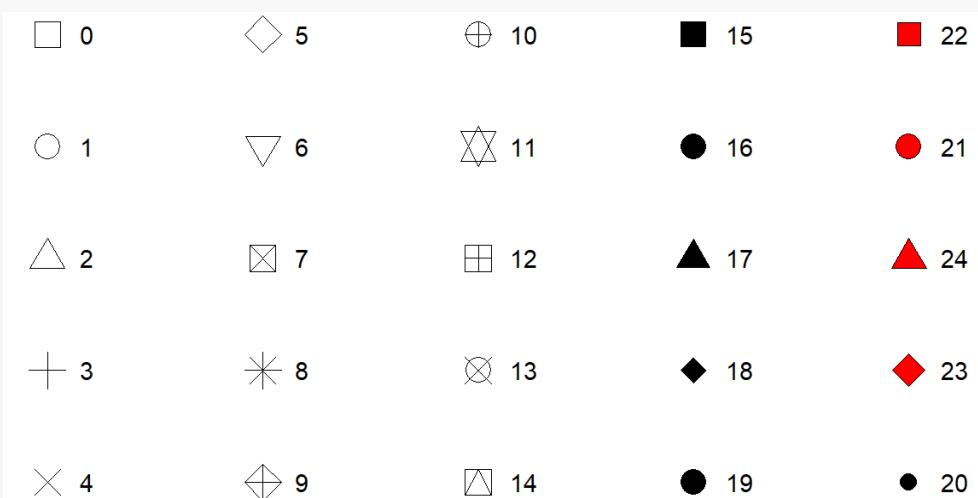


Artwork by Allison Horst

Change appearance of points

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

#> Error: object 'vertebrates' not found



Shape and color codes

Change color scale

We can also save a plot in a variable

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

#> Error: object 'vertebrates' not found
#> Error: object 'g' not found

- 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"  
)  
#> Error: object 'g' not found
```

- 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"  
    )  
  )
```

#> Error: object 'g' not found

- 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.

```
# install.packages("paletteer")
library(paletteer)
g <- g +
  scale_color_paletteer_d(
    palette = "ggsci::default_uchicago"
  )
g
```

```
#> Error in library(paletteer): there is no package
#> called 'paletteer'
#> Error: object 'g' not found
#> Error: object 'g' not found
```

- 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(  
  vertebrates,  
  aes(  
    x = section,  
    y = length_1_mm,  
    color = unittype)) +  
  geom_boxplot() +  
  scale_color_paletteer_d(  
    palette = "ggsci::default_uchicago"  
)  
#> Error: object 'vertebrates' not found
```

```
ggplot(  
  vertebrates,  
  aes(  
    x = section,  
    y = length_1_mm,  
    fill = unittype)) +  
  geom_boxplot() +  
  scale_fill_paletteer_d(  
    palette = "ggsci::default_uchicago"  
)  
#> Error: object 'vertebrates' not found
```

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"
  )
#> Error: object 'g' not found
g
#> Error: object 'g' not found
```

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

theme_*: change appearance

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

```
g +
  theme_classic()
```

```
#> Error: object 'g' not found
```

```
g +
  theme_bw()
```

```
#> Error: object 'g' not found
```

theme_*: change appearance

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

```
g +
  theme_minimal()
```

```
#> Error: object 'g' not found
```

```
g +
  theme_dark()
```

```
#> Error: object 'g' not found
```

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

```
?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"
    )
  )
```

#> Error: object 'g' not found

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.

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

Add this to the beginning of your script.

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

```
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,  
  height = 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](#)