Data visualization with ggplot

Based on R-ecology lesson - Data carpentry

Marco Chiapello, PhD

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Ascomb's quartet

Use the file example "scraping.R" in Resource directory

Plotting systems

- **Base package**
  - Static canvas
  - They can not be modified once they are plotted
- **Grid package**
  - Provide low-level graphic functions to construct complex plots
  - Two fundamentals components:
    - Create graphic outputs
    - Layer and position outputs with veiwports

What is ggplot2

- ggplot2 is a plotting system for R, based on the **grammar of graphics**
- ggplot2 makes **simple to create complex plots** from data in a dataframe
- help creating **publication quality plots** with a **minimal amount of settings** and tweaking
- ggplot graphics are built step by step by **adding new elements**

Plotting with ggplot2

To build a ggplot we need to:

- **bind the plot** to a specific data frame using the data argument

```
library(tidyverse)
surveys_complete <- read.csv("surveys_complete.csv")
ggplot(data = surveys_complete)
```

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library(tidyverse)
surveys_complete <- read.csv("surveys_complete.csv")
ggplot(data = surveys_complete)
```

- define **aesthetics** (aes), by selecting the variables to be plotted

```
ggplot(data = surveys_complete,
       aes(x = weight, y = hindfoot_length))
```

Plotting with ggplot2

- add **geoms** – graphical representation of the data in the plot

```
ggplot(data = surveys_complete,
    aes(x = weight, y = hindfoot_length)) +
  geom_point()
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```

- The + in the ggplot2 package is particularly useful because it allows you to modify existing ggplot objects

Plotting with ggplot2

- Set up plot "templates" and conveniently explore different types of plots

```r
# Create
surveys_plot <- ggplot(data = surveys_complete,
                       aes(x = weight, y = hindfoot_length))

# Draw the plot
surveys_plot + geom_point()
surveys_plot + geom_line()
surveys_plot + geom_count()
surveys_plot + geom_point() + geom_rug()
```

Building your plots iteratively

Building plots with ggplot is typically an **iterative process**

We start by:

- defining the dataset

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Building plots with ggplot is typically an **iterative process**

We start by:

- defining the dataset
- lay the axes
- choose a geom

```
surveys_plot <- ggplot(data = surveys_complete,
                       aes(x = weight, y = hindfoot_length))
surveys_plot + geom_point()
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Building your plots iteratively

We start **modifying this plot** to extract more information from it:

- Add transparency to avoid overplotting

```
surveys_plot + geom_point(alpha = 0.1)
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surveys_plot + geom_point(alpha = 0.1, color = "blue")
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- Color each species in the plot differently

```
surveys_plot + geom_point(alpha = 0.1, aes(color = species_id))
```

Challange

- Plot a scatter plot with different colors for male and female
- Plot a scatter plot with different shapes for male and female
- Plot a scatter plot with different color and shapes for male and female
- Plot a scatter plot with point size 10

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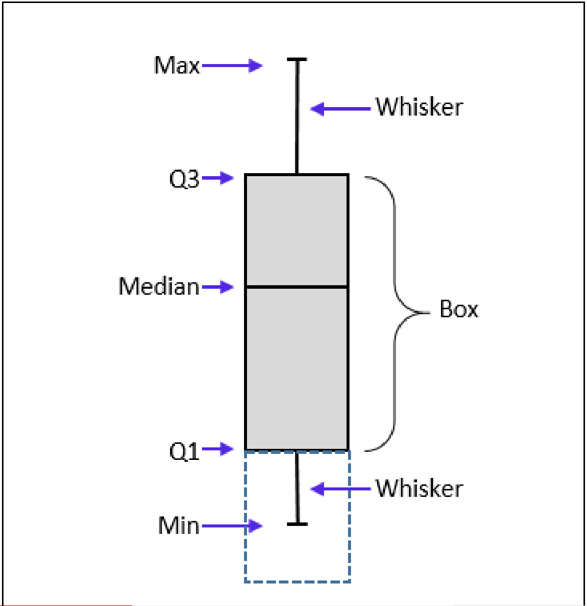
```
surveys_plot + geom_point(aes(color = sex))

surveys_plot + geom_point(aes(shape = sex))

surveys_plot + geom_point(aes(color = sex, shape = sex))

surveys_plot + geom_point(aes(color = sex, shape = sex),
                          size = 10)
```

Boxplot



Boxplot

Visualising the distribution of hindfoot_length **within each species**

```
surveys_plot <- ggplot(data = surveys_complete,
                       aes(x = species_id, y = hindfoot_length))
surveys_plot + geom_boxplot()
```

Boxplot

- By **adding points** to boxplot, we can have a better idea of the number of measurements and of their distribution

```
surveys_plot + geom_boxplot(alpha = 0) +
               geom_jitter(alpha = 0.3, color = "tomato")
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Boxplot

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```

- **Boxplots are useful summaries**, BUT **hide the shape** of the distribution.
- Notice how the boxplot layer is behind the jitter layer?
- What do you need to change in the code to put the boxplot in front of the points such that it's not hidden?

Challenge

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- An alternative to the boxplot is the violin plot, where the shape is drawn.
  - Replace the box plot we produced with a violin plot

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  - Create boxplot for species_id and weight and represent weight on the log10 scale; see scale_y_log10()

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ggplot(data = surveys_complete, aes(x = species_id, y = weight)) +
      geom_boxplot(alpha = 0)
ggplot(data = surveys_complete, aes(x = species_id, y = weight)) +
      geom_boxplot(alpha = 0) + scale_y_log10()
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- Then add color to the datapoints on your boxplot according to the plot from which the sample was taken (plot_id)

```
ggplot(data = surveys_complete, aes(x = species_id, y = weight)) +
      geom_jitter(aes(color = as.factor(plot_id))) +
      geom_boxplot(alpha = 0) +
      scale_y_log10()
```

Plotting time series data

- Let's calculate **number of counts per year** for each species
  - To do that we need to **group data** first and count records within each group

```
yearly_counts <- surveys_complete %>%
                 group_by(year, species_id) %>%
                 tally
```

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```

- Timelapse data can be visualised as a line plot with years on x-axis and counts on y-axis

```
timeseries_plot <- ggplot(data = yearly_counts, aes(x = year,
                                                     y = n))
timeseries_plot + geom_line()
```

Plotting time series data

- Unfortunately this does not work, because we plot data for **all the species together**
  - We need to group the data by species_id

```
timeseries_plot <- ggplot(data = yearly_counts,
                          aes(x = year, y = n, group = species_id))
timeseries_plot + geom_line()
```

Plotting time series data

- We will be able to distinguish species in the plot if we will **add colors**

```
timeseries_plot <- ggplot(data = yearly_counts,
                          aes(x = year, y = n,
                              group = species_id,
                              colour = species_id))
timeseries_plot + geom_line()
```

Challenge

- Create a new data set called month_counts [group by month and species_id]
- Plot time series
- Add points

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```
month_counts <- surveys_complete %>%
                 group_by(month, species_id) %>%
                 tally
timeseries_plot <- ggplot(data = month_counts,
                          aes(x = as.factor(month), y = n,
                              group = species_id,
                              colour = species_id))
timeseries_plot + geom_line()
timeseries_plot + geom_line() + geom_point()
```

Faceting

- ggplot has a special technique called faceting that allows to **split one plot into multiple plots** based on a factor included in the dataset

```
timeseries_plot <- ggplot(data = yearly_counts,
                          aes(x = year, y = n, group = species_id,
                              colour = species_id))
timeseries_plot + geom_line() + facet_wrap(~ species_id)
```

Challenge

- Now we would like to also **split line in each plot by sex** of each individual measured

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```
yearly_sex_counts <- surveys_complete %>%
                     group_by(year, species_id, sex) %>%
                     tally
```

Challenge

- Now we would like to also **split line in each plot by sex** of each individual measured

```
yearly_sex_counts <- surveys_complete %>%
                     group_by(year, species_id, sex) %>%
                     tally
```

```
timeseries_plot <- ggplot(data = yearly_sex_counts,
                         aes(x = year, y = n, color = sex,
                             group = sex))

timeseries_plot + geom_line() + facet_wrap(~ species_id)
```

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- Now we would like to also **split line in each plot by sex** of each individual measured

```
yearly_sex_counts <- surveys_complete %>%
                     group_by(year, species_id, sex) %>%
                     tally
```

```
timeseries_plot <- ggplot(data = yearly_sex_counts,
                          aes(x = year, y = n, color = sex,
                              group = sex))

timeseries_plot + geom_line() + facet_wrap(~ species_id)
```

- Add a double split

```
timeseries_plot + geom_line() + facet_wrap(species_id ~ sex)
```

Customization

- Take a look at the ggplot2 cheat sheet, and think of ways to improve the plot
- Usually plots with white background look more readable when printed. We can set the background to white using the function theme_bw()

```
timeseries_plot + geom_line() +
    theme_bw() +
    facet_wrap(~ species_id)
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Customization

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- Usually plots with white background look more readable when printed. We can set the background to white using the function theme_bw()

```
timeseries_plot + geom_line() +
    theme_bw() +
    facet_wrap(~ species_id)
```

- Remove completely the grid

```
timeseries_plot + geom_line() +
    theme_bw() +
    theme(panel.grid.major.x = element_blank(),
       panel.grid.minor.x = element_blank(),
       panel.grid.major.y = element_blank(),
       panel.grid.minor.y = element_blank()) +
    facet_wrap(~ species_id)
```

Customization

- Let's change names of axes to something more informative

```
timeseries_plot + geom_line() + facet_wrap(~ species_id) +
    labs(title = 'Observed species in time',
         x = 'Year of observation',
         y = 'Number of species') +
    theme_bw()
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- The axes have more informative names, but their readability can be improved

```
timeseries_plot + geom_line() + facet_wrap(~ species_id) +
    labs(title = 'Observed species in time',
        x = 'Year of observation',
        y = 'Number of species') +
    theme_bw() +
    theme(text=element_text(size=16, family="Arial"))
```

- Let's **change the orientation of the labels** and adjust them vertically and horizontally so they don't overlap

```
timeseries_plot + geom_line() + facet_wrap(~ species_id) +
    labs(title = 'Observed species in time',
        x = 'Year of observation',
        y = 'Number of species') +
    theme_bw() +
    theme(axis.text.x = element_text(colour="grey20", size=12,
                                     angle=90, hjust=.5, vjust=.5),
          axis.text.y = element_text(colour="grey20", size=12),
          text=element_text(size=16, family="Arial"))
```

Customization

- If you like the changes you created to the default theme

```
arial_grey_theme <-
        theme(axis.text.x = element_text(colour="grey20",
                            size=12, angle=90, hjust=.5, vjust=.5),
              axis.text.y = element_text(colour="grey20", size=12),
              text=element_text(size=16, family="Arial"))

ggplot(surveys_complete, aes(x = species_id, y = hindfoot_length)) +
    geom_boxplot() +
    arial_grey_theme
```