

# DATA VISUALIZATION WITH GGLOT

BASED ON R-ECOLOGY LESSON - DATA CARPENTRY

Marco Chiapello, PhD

March 29, 2017

## **Ascomb's quartet**

Use the file example “scraping.R” in Resource directory

- **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 GGLOT2

- 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 GGLOT2

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)
```

# 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)
```

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

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

# PLOTTING WITH GGLOT2

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

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

# PLOTTING WITH GGLOT2

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

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

- 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

*# 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

# BUILDING YOUR PLOTS ITERATIVELY

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

We start by:

- defining the dataset
- lay the axes

# BUILDING YOUR PLOTS ITERATIVELY

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()
```

# 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)
```

# 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)
```

- We can also add colors for all the points

```
surveys_plot + geom_point(alpha = 0.1, color = "blue")
```

# 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)
```

- We can also add colors for all the points

```
surveys_plot + geom_point(alpha = 0.1, color = "blue")
```

- Color each species in the plot differently

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

# CHALLENGE

- 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



# CHALLENGE

- 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

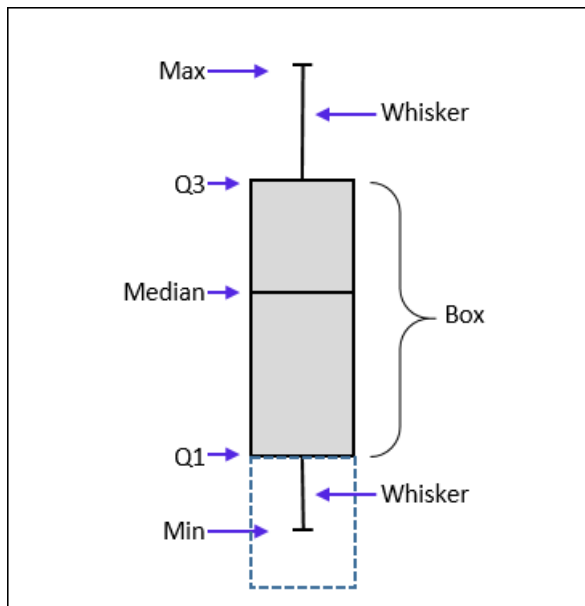
```
surveys_plot + geom_point(aes(color = sex))
```

```
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



## 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")
```

# 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")
```

- **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

- Try to plot before the point and then the boxplot

# CHALLENGE

- Try to plot before the point and then the boxplot

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

# CHALLENGE

- Try to plot before the point and then the boxplot

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

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



# CHALLENGE

- Try to plot before the point and then the boxplot

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

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

```
surveys_plot + geom_violin(alpha = 0)
```

# CHALLENGE

- In many types of data, it is important to consider the scale of the observations
  - ▶ Create boxplot for `species_id` and `weight` and represent `weight` on the `log10` scale; see `scale_y_log10()`

# CHALLENGE

- In many types of data, it is important to consider the scale of the observations
  - ▶ Create boxplot for species\_id and weight and represent weight on the log10 scale; see scale\_y\_log10()

```
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()
```

# CHALLENGE

- In many types of data, it is important to consider the scale of the observations
  - ▶ Create boxplot for species\_id and weight and represent weight on the log10 scale; see scale\_y\_log10()

```
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()
```

- Then add color to the datapoints on your boxplot according to the plot from which the sample was taken (plot\_id)

# CHALLENGE

- In many types of data, it is important to consider the scale of the observations
  - ▶ Create boxplot for species\_id and weight and represent weight on the log10 scale; see scale\_y\_log10()

```
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()
```

- 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
```

# 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
```

- 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

# CHALLENGE

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

```
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()
```

- 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

# 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
```

# 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)
```

# 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)
```

- 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)
```

# 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)
```

- 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()
```

# 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()
```

- 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"))
```

- If you like the changes you created, you can save them as an object to easily apply them

```
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
```

# CHALLENGE

- With all of this information in hand, please **try to improve one of the plots we generated**, creating a beautiful graph of your own

# SAVE PLOT

- After creating your plot, you can save it to a file in your favourite format

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

ggsave("name_of_file.png", my_plot, width=15, height=10)
```



# CHALLENGE

- Use **your own data** or
- **Download the data** from [[https://figshare.com/articles/Ecology\\_experimental\\_design/1244589](https://figshare.com/articles/Ecology_experimental_design/1244589)]
- Play with the data and **plot them as beautiful as you like**