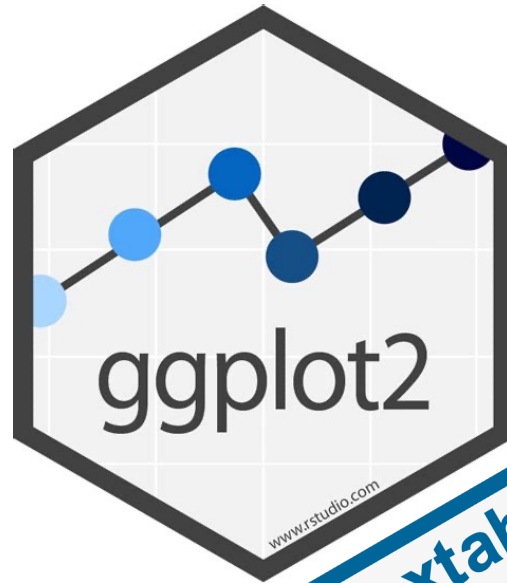
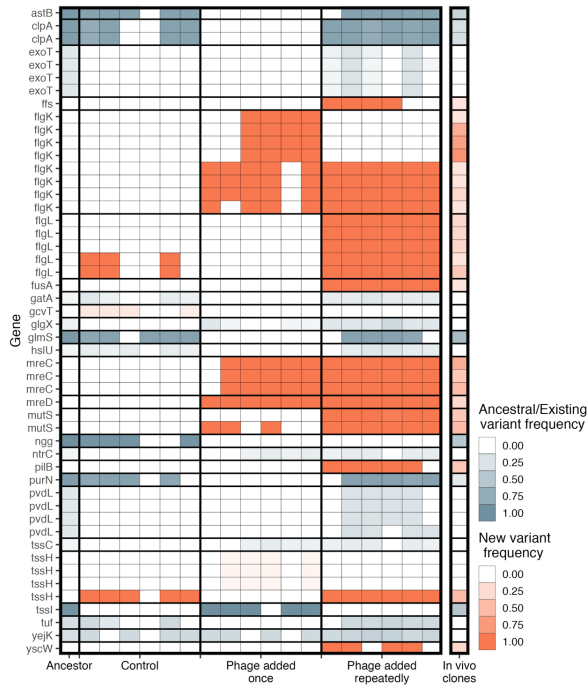


Reproducible publication-ready plots and tables with ggplot2 and flextable



Treatment	Time contrast	Odds-ratio	SE	z-ratio	p-value
Phage 1	1 / 2	0.0866	0.0579	-3.66	0.000747
Phage 1	1 / 3	0.255	0.173	-2.02	0.108
Phage 1	2 / 3	2.94	1.51	2.1	0.0899
Phage 2	1 / 2	0.0000000812	0.0000354	-0.00427	1
Phage 2	1 / 3	0.0000000571	0.0000249	-0.00435	1
Phage 2	2 / 3	0.703	0.432	-0.573	0.835
Phage 1 and 2	1 / 2	0.0648	0.0538	-3.3	0.00282
Phage 1 and 2	1 / 3	0.0187	0.0157	-4.76	0.0000583
Phage 1 and 2	2 / 3	0.289	0.124	-2.9	0.0103



Daniel Padfield

✉ d.padfield@exeter.ac.uk

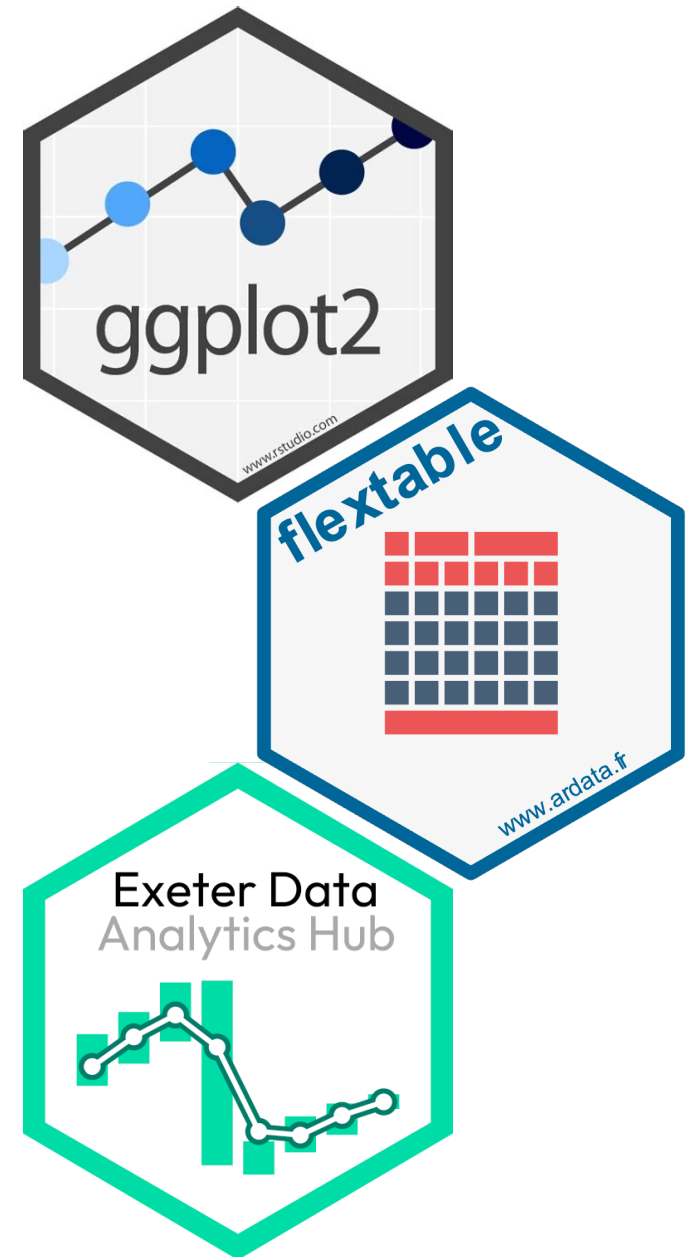
🐙 padpadpadpad



University of Exeter

Housekeeping

- Have brought your laptop and a plot or table you want to make.
- Please interrupt me if you have questions (I may not have all the answers).
- You may know more than me! Please share your knowledge if you have it.
- Want to do something in flextable or ggplot2 and do not know how?
 - Join the ExeDataAnalytics Team on Microsoft Teams and ask in the "Ask for Help" tab.
 - Reproducible examples using reprex get you kudos:
<https://reprex.tidyverse.org/>
- Introductory walkthroughs for both [ggplot2](#) and [flextable](#) are available on our webpage.

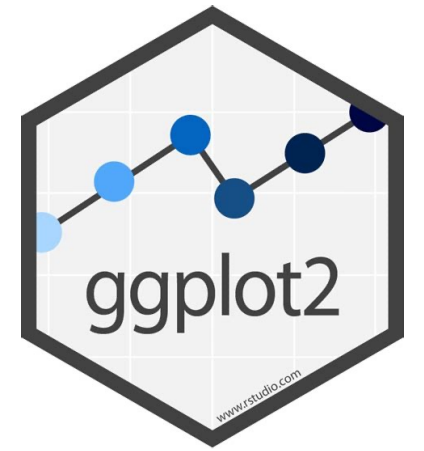


The importance of reproducible plots and tables

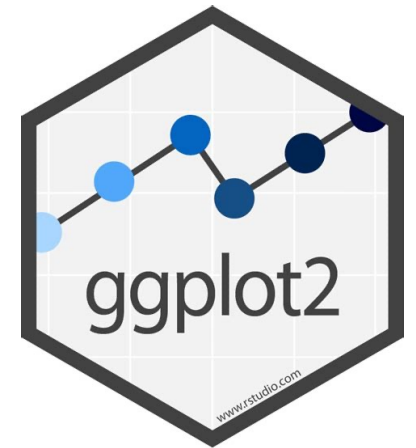
- Fewer errors
- Easier to update
- Easier to re-use
- **Can you think of any more benefits or why it is important?**

A brief introduction to ggplot2

- **ggplot2** is a system for creating graphics based on [The Grammar of Graphics](#).
- Part of the **tidyverse** packages alongside **dplyr**, **tidyr**, **purrr** etc
- One of the most popular R packages (downloaded >119m times)
- Used widely in academia, industry, and journalism.



A brief introduction to ggplot2

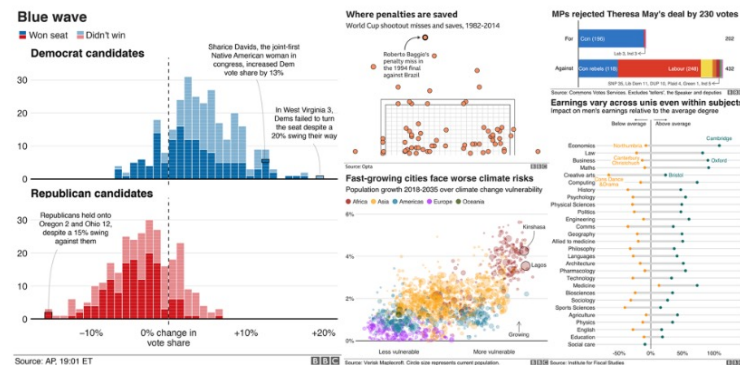


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How to create BBC style graphics

At the BBC data team, we have developed an R package and an R cookbook to make the process of creating publication-ready graphics in our in-house style using R's ggplot2 library a more reproducible process, as well as making it easier for people new to R to create graphics.

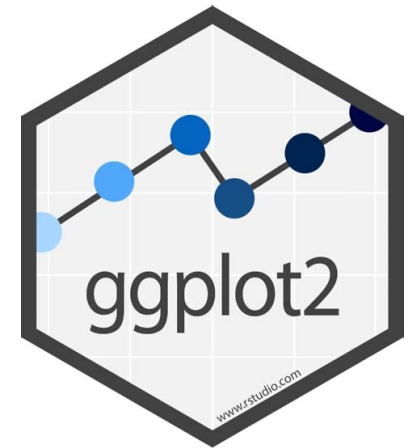
The cookbook below should hopefully help anyone who wants to make graphics like these:



We'll get to how you can put together the various elements of these graphics, but **let's get the admin out of the way first...**

<https://bbc.github.io/rcookbook/>

A brief introduction to ggplot2

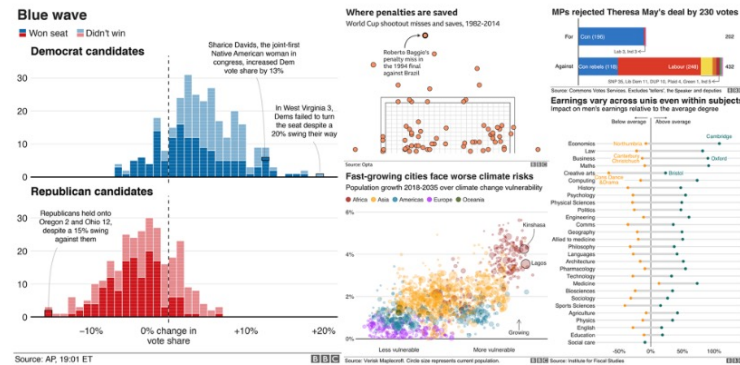


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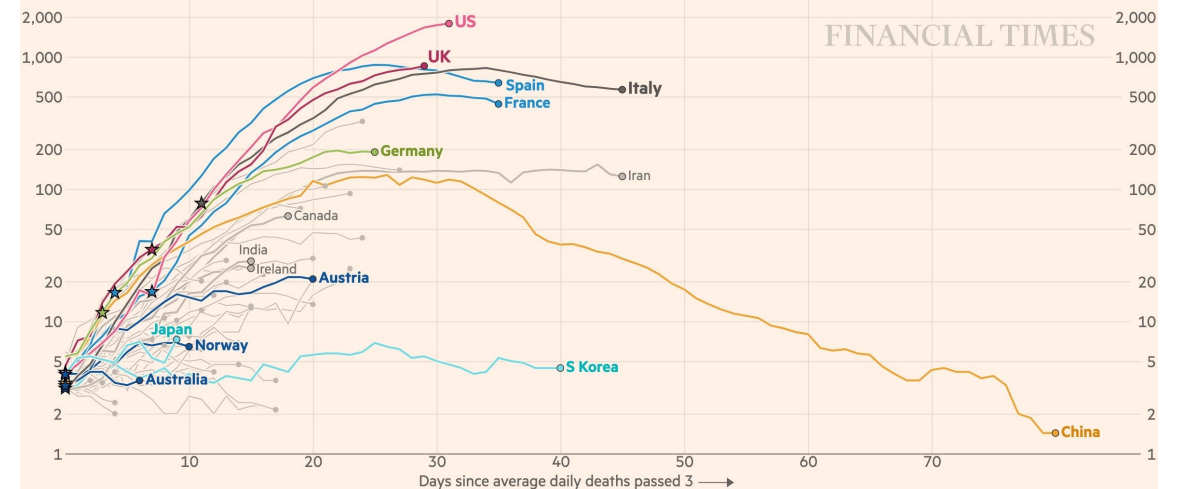


Source: AP, 19:01 ET
We'll get to how you can put together the various elements of these graphics, but let's get the admin out of the way first...

<https://bbc.github.io/rcookbook/>

Italy and Spain's daily death tolls are falling; in the UK and US daily deaths still trend upward

Daily deaths with coronavirus (7-day rolling average), by number of days since 3 daily deaths first recorded
Stars represent national lockdowns ★

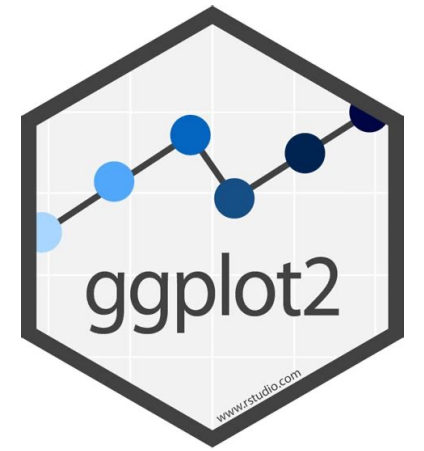


FT graphic: John Burn-Murdoch / @burnmurdoch
Source: FT analysis of European Centre for Disease Prevention and Control; FT research. Data updated April 13, 19:00 GMT
© FT

John Burn Murdoch at the Financial Times

The basics of a ggplot2

Making a plot using **ggplot2** is like writing a recipe.

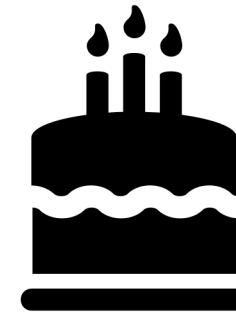
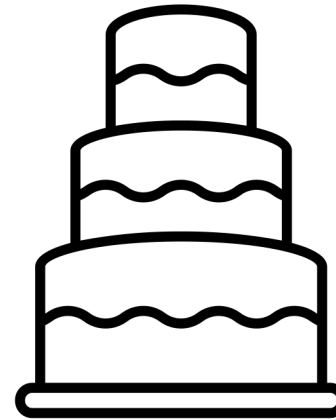
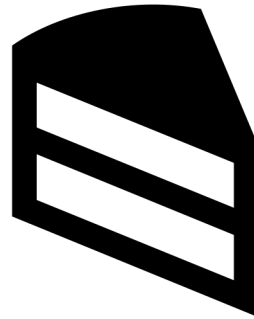


Ingredients

- flour
- eggs
- sugar
- butter
- chocolate

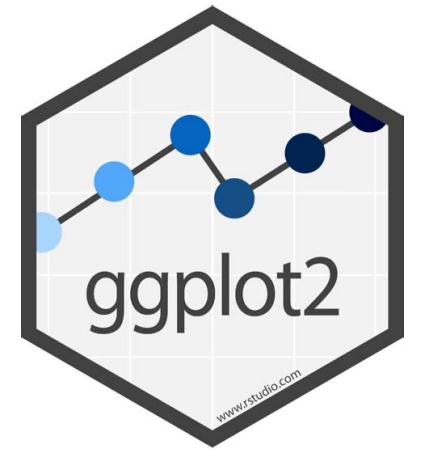
Recipe

1. Mix flour sugar eggs and butter
2. Put chocolate in
3. Bake



The basics of a ggplot2

Making a plot using **ggplot2** is like writing a recipe.

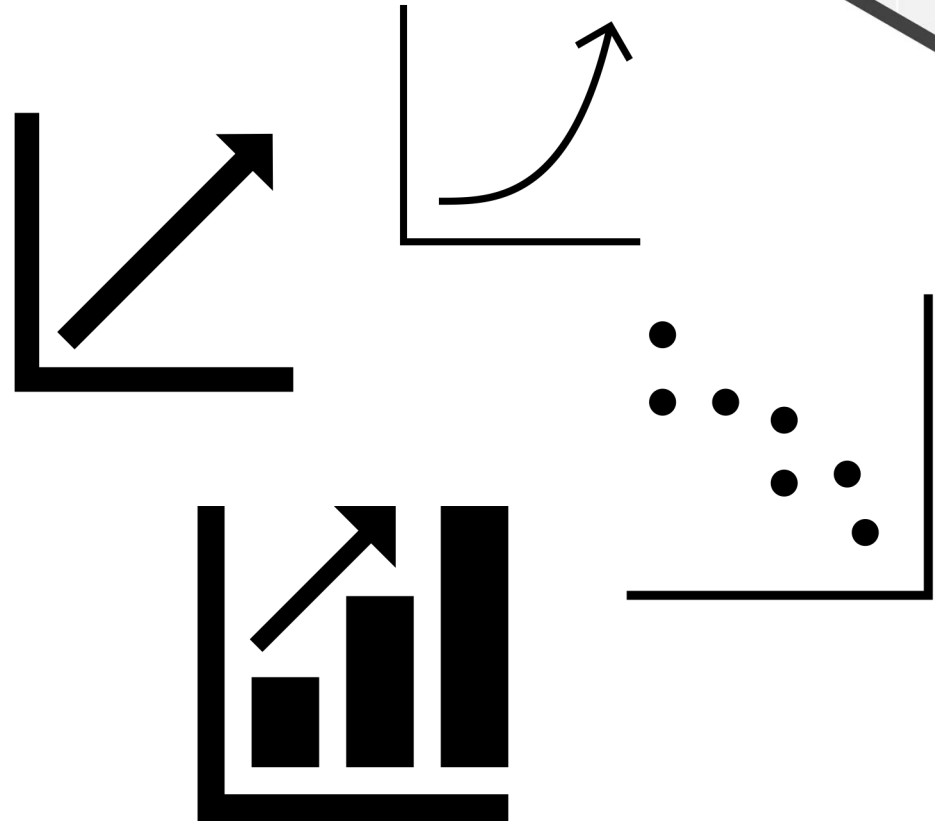


Ingredients

- Empty plot
- Boxplot
- Raw data points
- Labels
- Theme
- Axis limits

Recipe

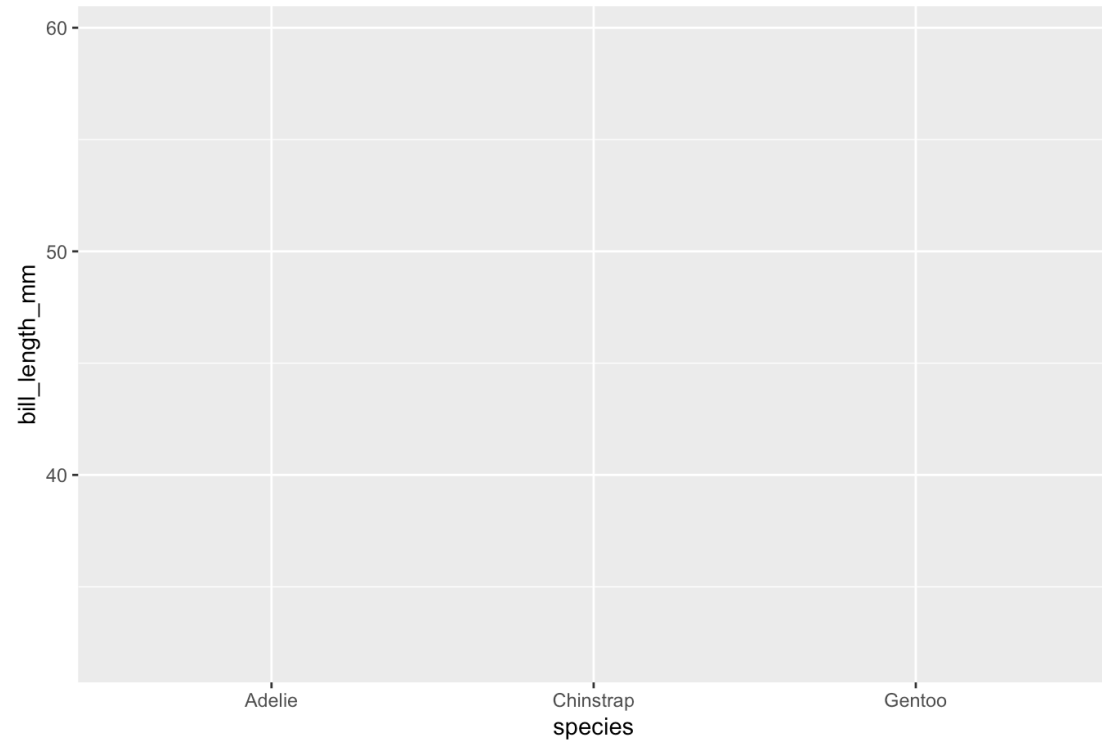
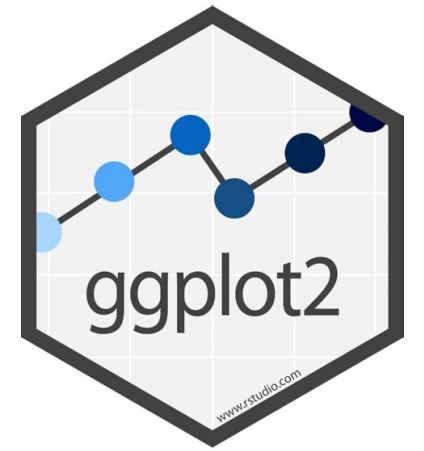
1. Start with an empty plot
2. Place the boxplot on top
3. Sprinkle over raw data points
4. Change the theme
5. Alter the axis limits



The basics of a ggplot2

Making a plot using **ggplot2** is like writing a recipe.

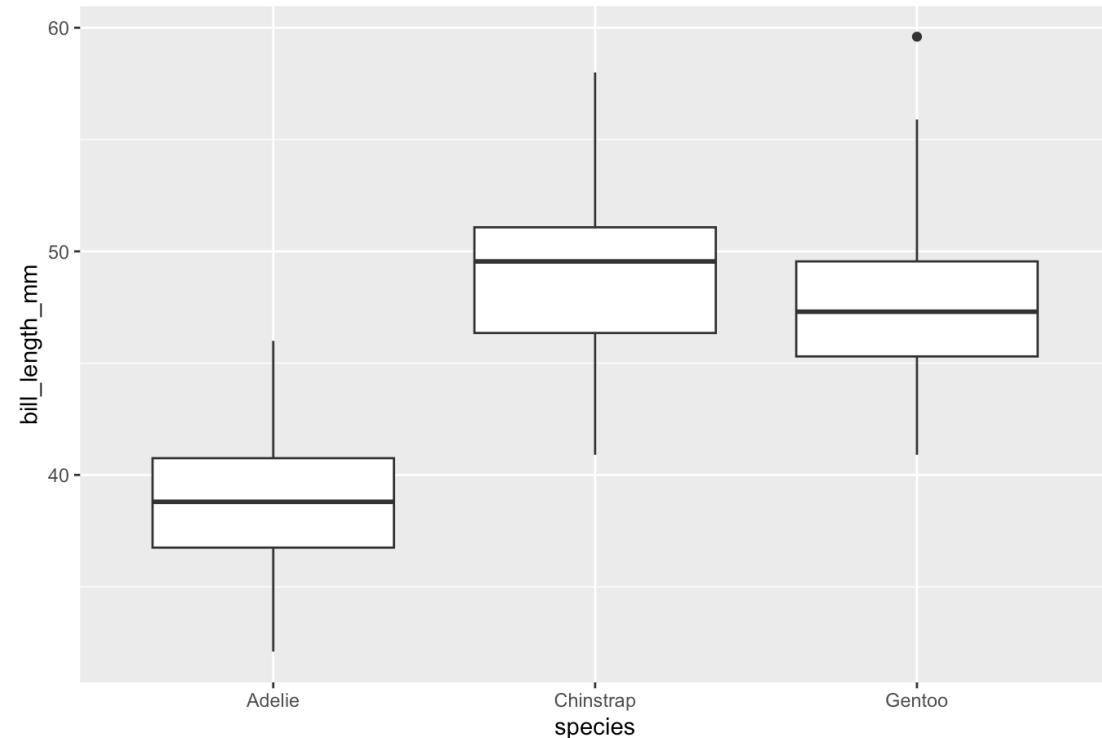
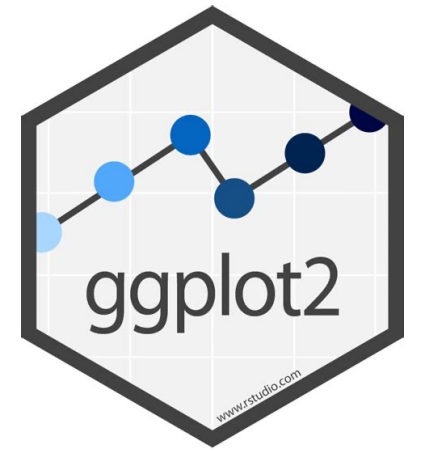
```
ggplot(penguins, aes(x=species, y=bill_length_mm))
```



The basics of a ggplot2

Making a plot using **ggplot2** is like writing a recipe.

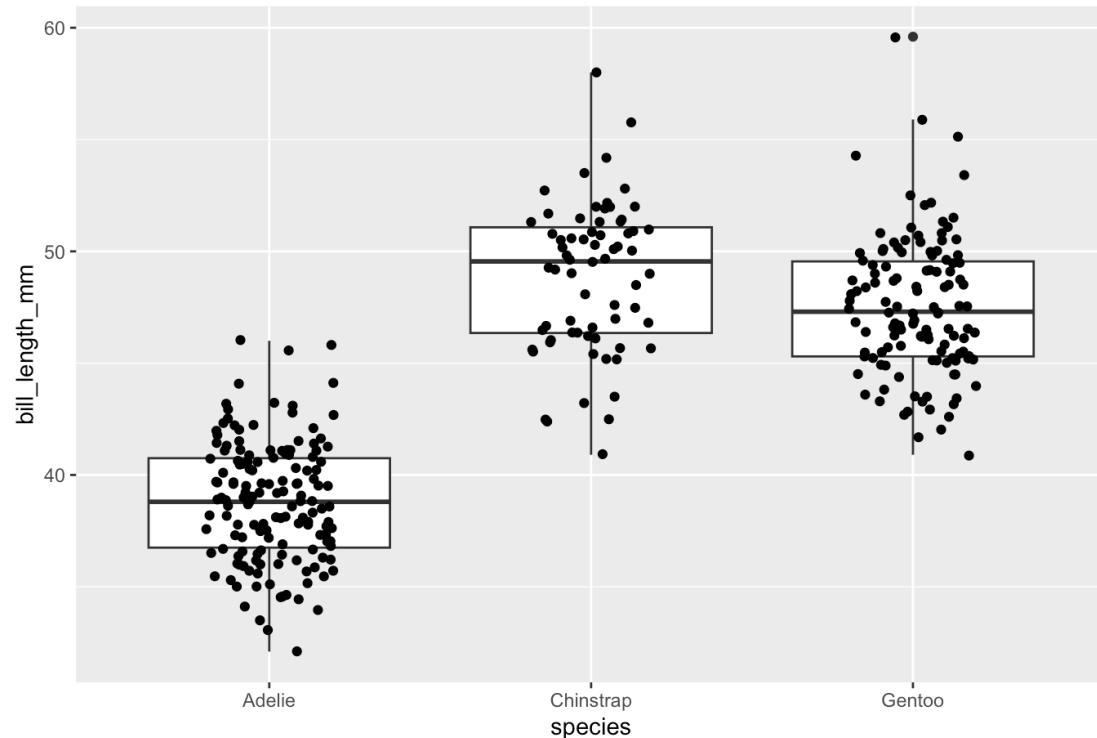
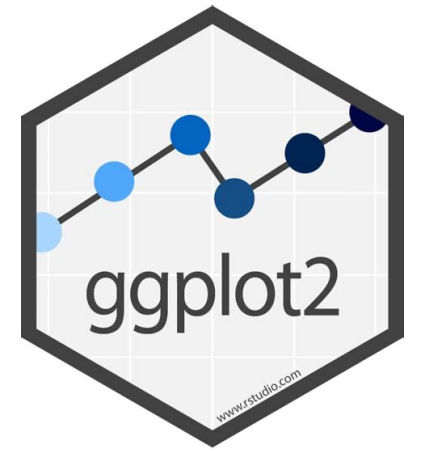
```
ggplot(penguins, aes(x=species, y=bill_length_mm)) +  
  geom_boxplot()
```



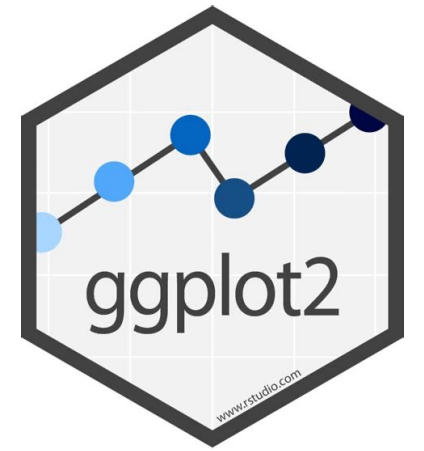
The basics of a ggplot2

Making a plot using **ggplot2** is like writing a recipe.

```
ggplot(penguins, aes(x=species, y=bill_length_mm)) +  
  geom_boxplot() +  
  geom_jitter(width = 0.2)
```

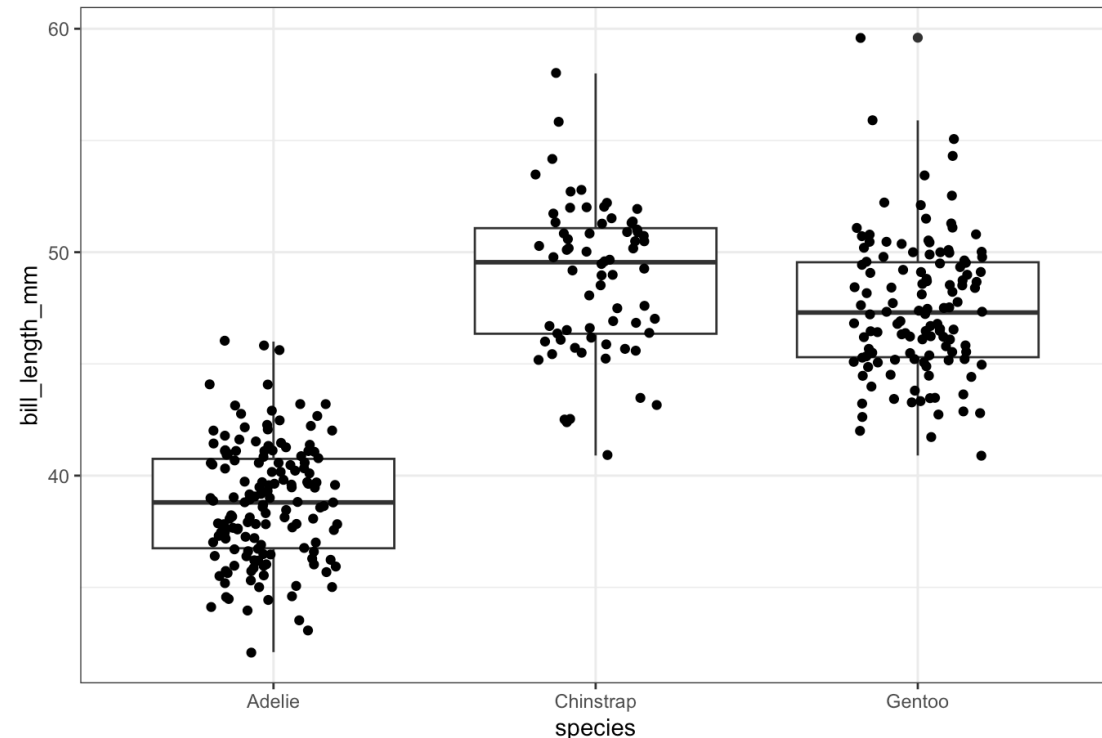


The basics of a ggplot2



Making a plot using **ggplot2** is like writing a recipe.

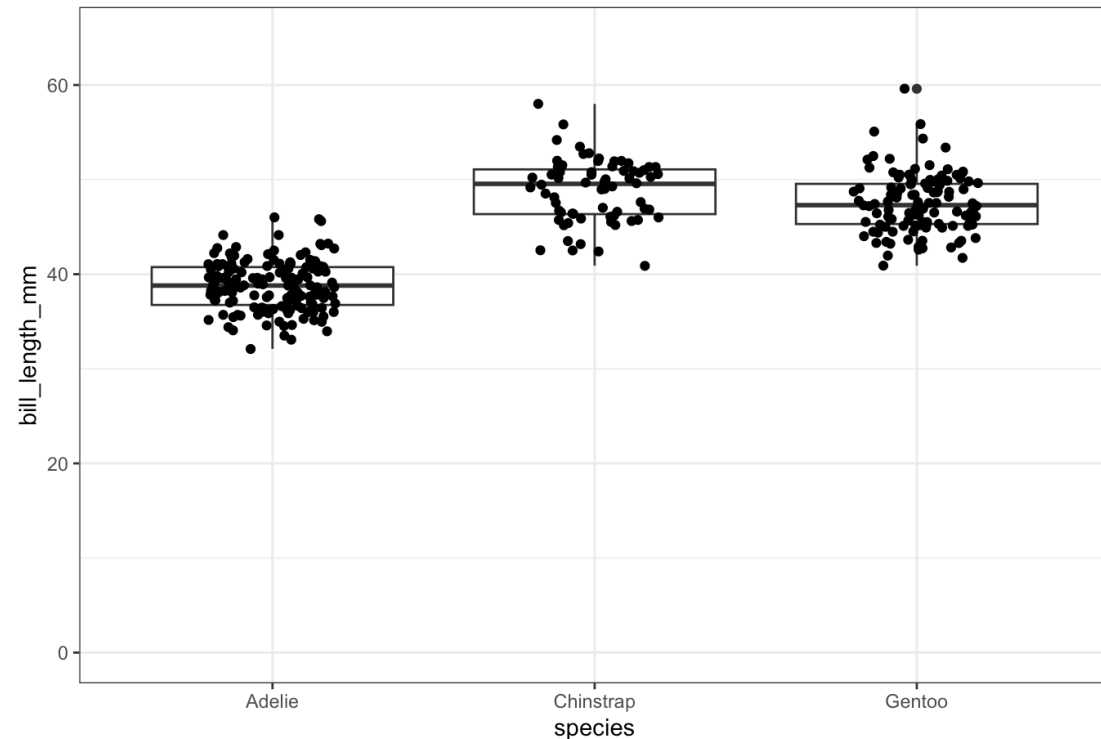
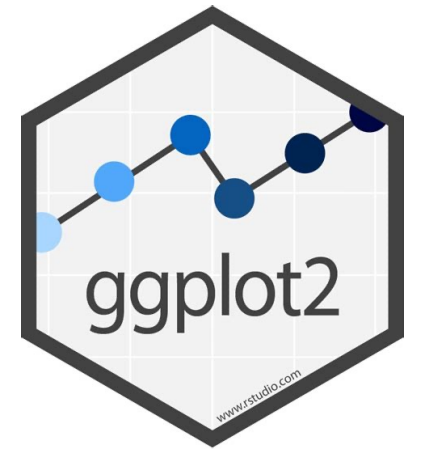
```
ggplot(penguins, aes(x=species, y=bill_length_mm)) +  
  geom_boxplot() +  
  geom_jitter(width = 0.2) +  
  theme_bw()
```



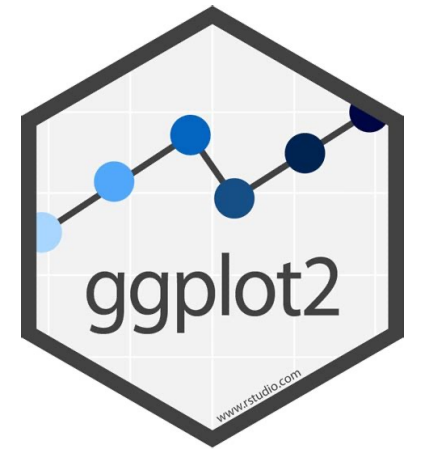
The basics of a ggplot2

Making a plot using **ggplot2** is like writing a recipe.

```
ggplot(penguins, aes(x=species, y=bill_length_mm)) +  
  geom_boxplot() +  
  geom_jitter(width = 0.2) +  
  theme_bw() +  
  ylim(c(0,65))
```



The basics of a ggplot2

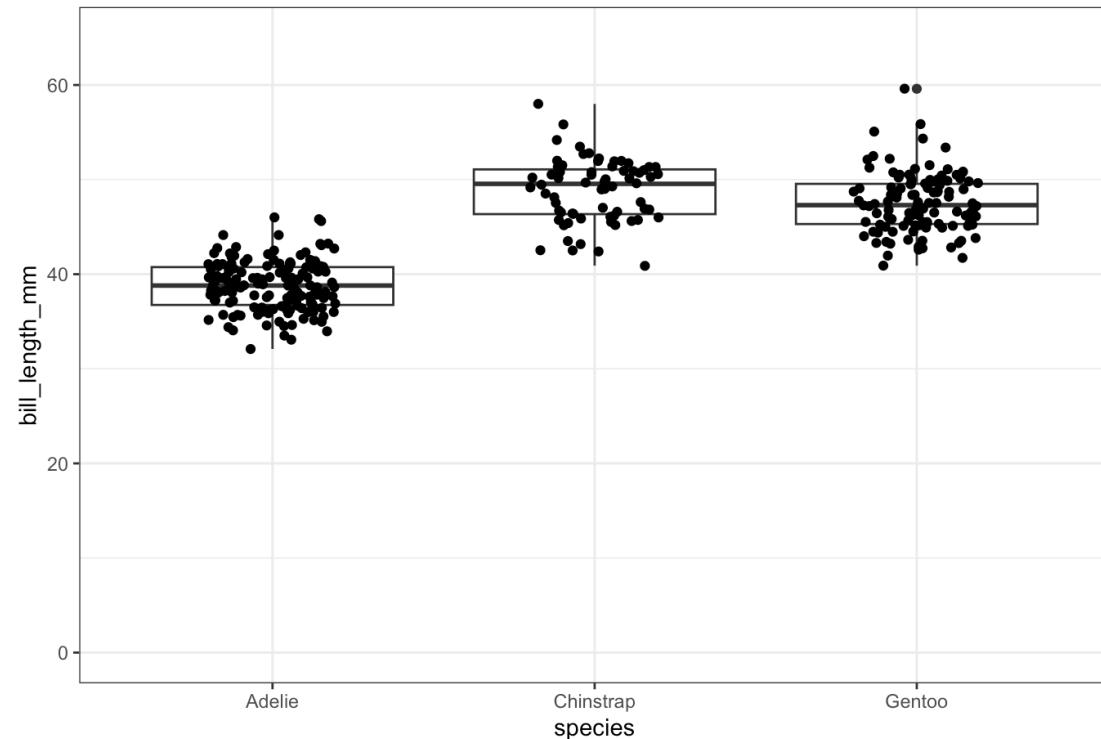


Making a plot using **ggplot2** is like writing a recipe.

```
ggplot(penguins, aes(x=species, y=bill_length_mm)) +  
  geom_boxplot() +  
  geom_jitter(width = 0.2) +  
  theme_bw() +  
  ylim(c(0,65))
```

Use **aes()** when you want something in the plot to be dependent on the data.

Add a new layer using '+' and start a new code line to make it easy to use.



ggplot2 tips and tricks

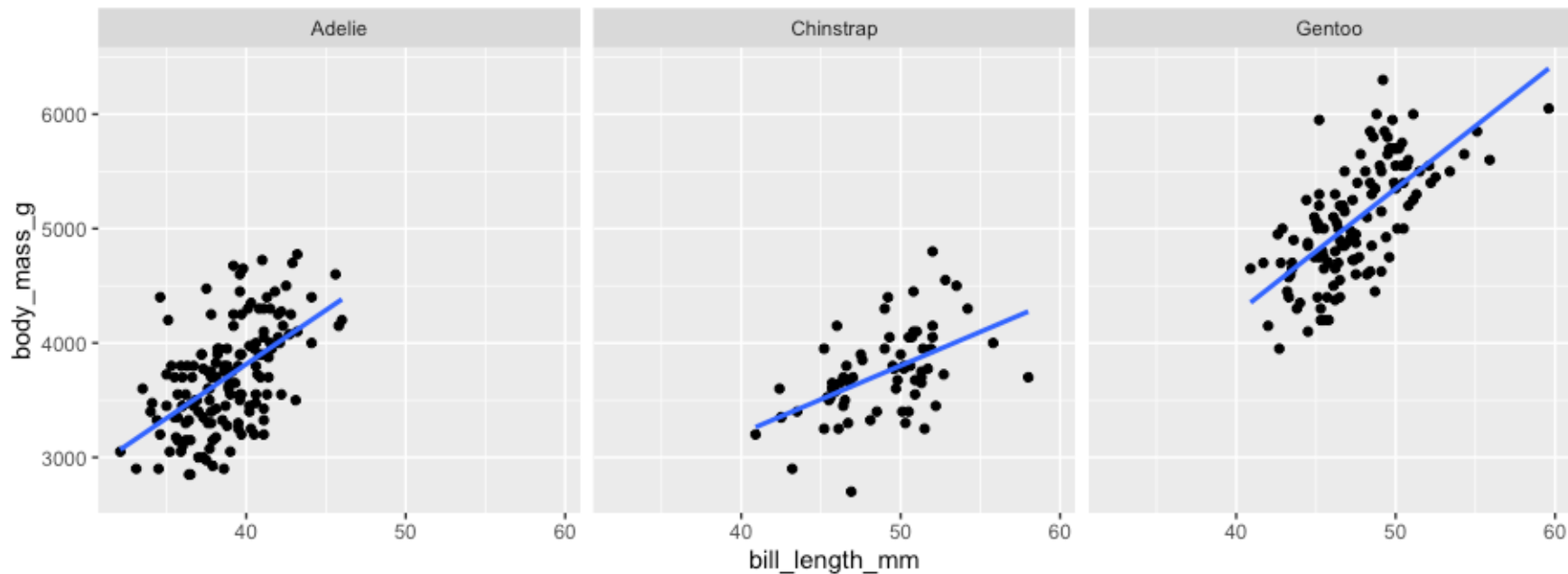
Automatically label facets with letters.

```
ggplot(penguins, aes(bill_length_mm, body_mass_g)) +  
  geom_point() +  
  geom_smooth(method = 'lm', se = FALSE) +  
  facet_wrap(~species)
```

ggplot2 tips and tricks

Automatically label facets with letters.

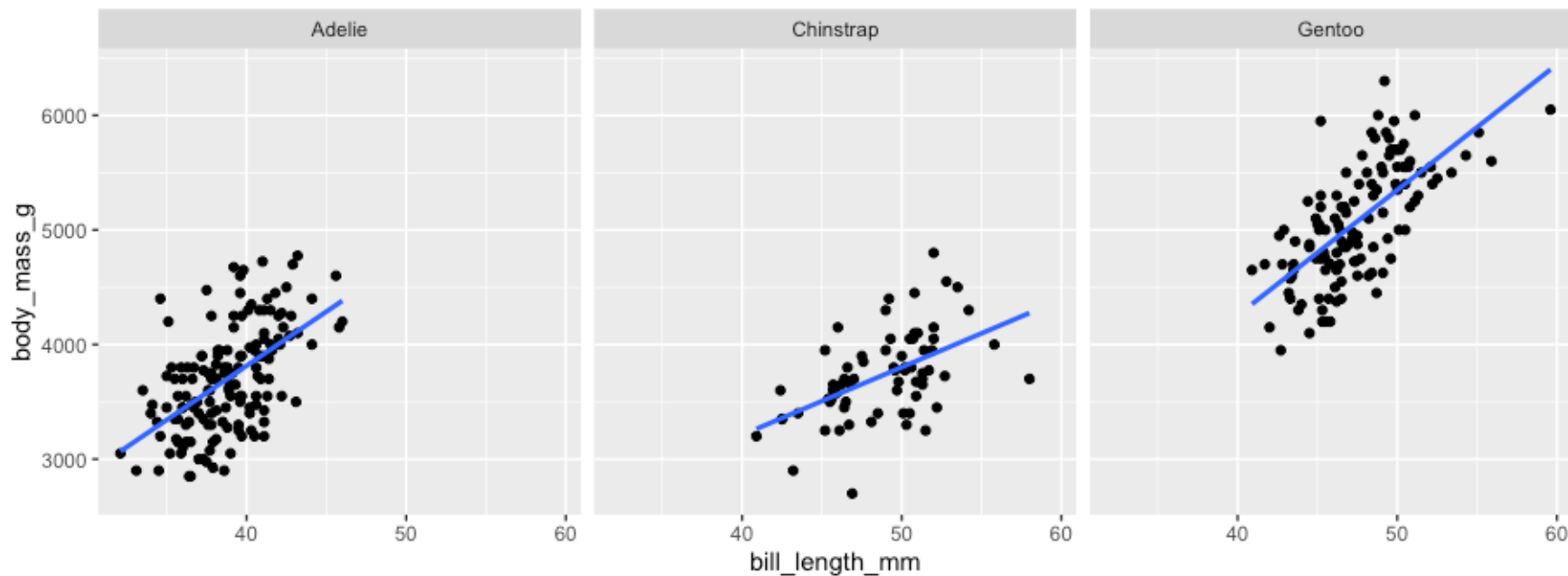
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  geom_smooth(method = 'lm', se = FALSE) +  
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ggplot2 tips and tricks

Automatically label facets with letters.

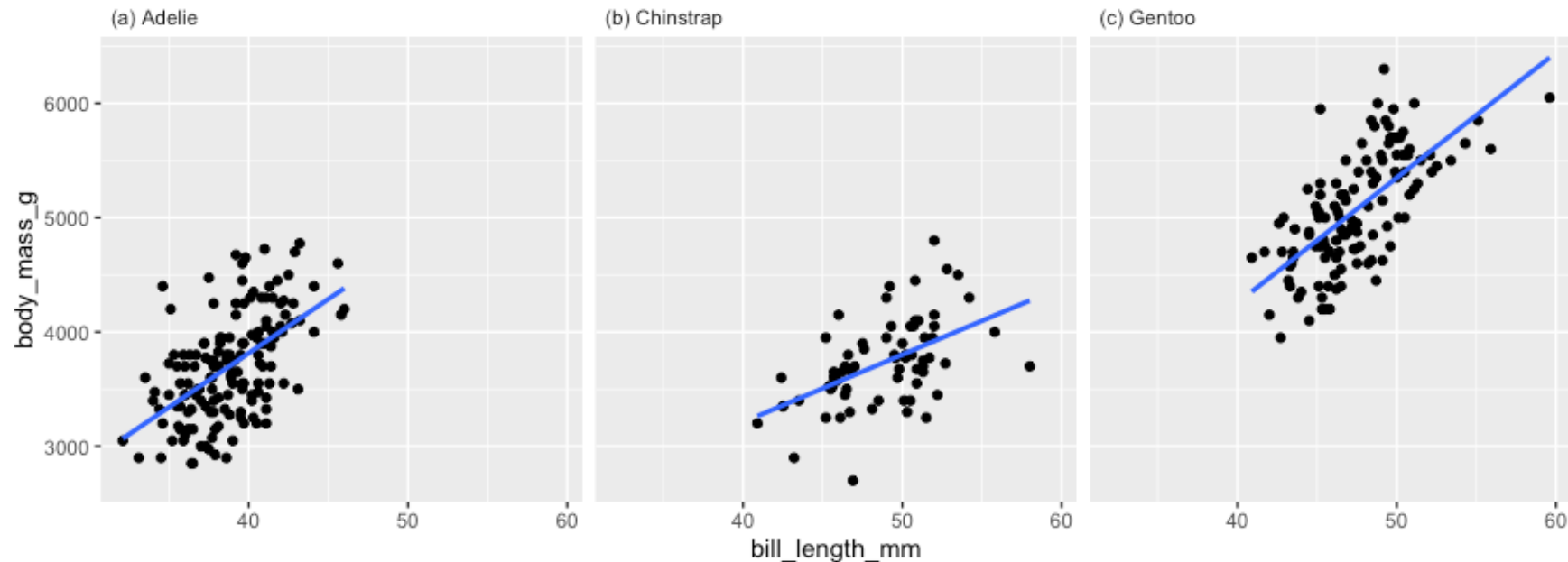
```
ggplot(penguins, aes(bill_length_mm, body_mass_g)) +  
  geom_point() +  
  geom_smooth(method = 'lm', se = FALSE) +  
  facet_wrap(~species, labeller = labeller(species = letter_facets)) +  
  theme(strip.background = element_blank(),  
        strip.text = element_text(hjust = 0))
```



ggplot2 tips and tricks

Automatically label facets with letters.

```
ggplot(penguins, aes(bill_length_mm, body_mass_g)) +  
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```

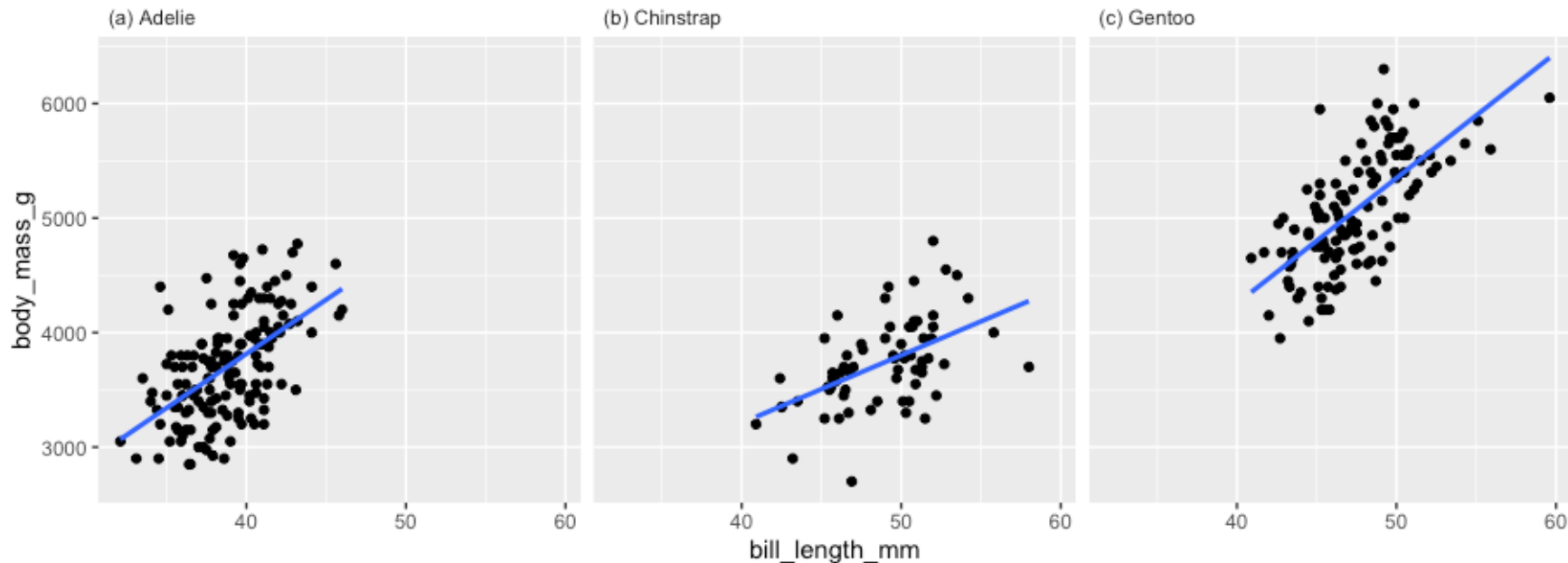


ggplot2 tips and tricks

Automatically label facets with letters.

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ggplot(penguins, aes(bill_length_mm, body_mass_g)) +  
  geom_point() +  
  geom_smooth(method = 'lm', se = FALSE) +  
  facet_wrap(~species, labeller = labeller(species = letter_facets)) +  
  theme(strip.background = element_blank(),  
        strip.text = element_text(hjust = 0))
```

```
# create function to add letter to facet labels  
letter_facets <- function(string){  
  len <- length(string)  
  string = paste("(", letters[1:len], ") ", string, sep = "")  
  return(string)  
}
```



ggplot2 tips and tricks

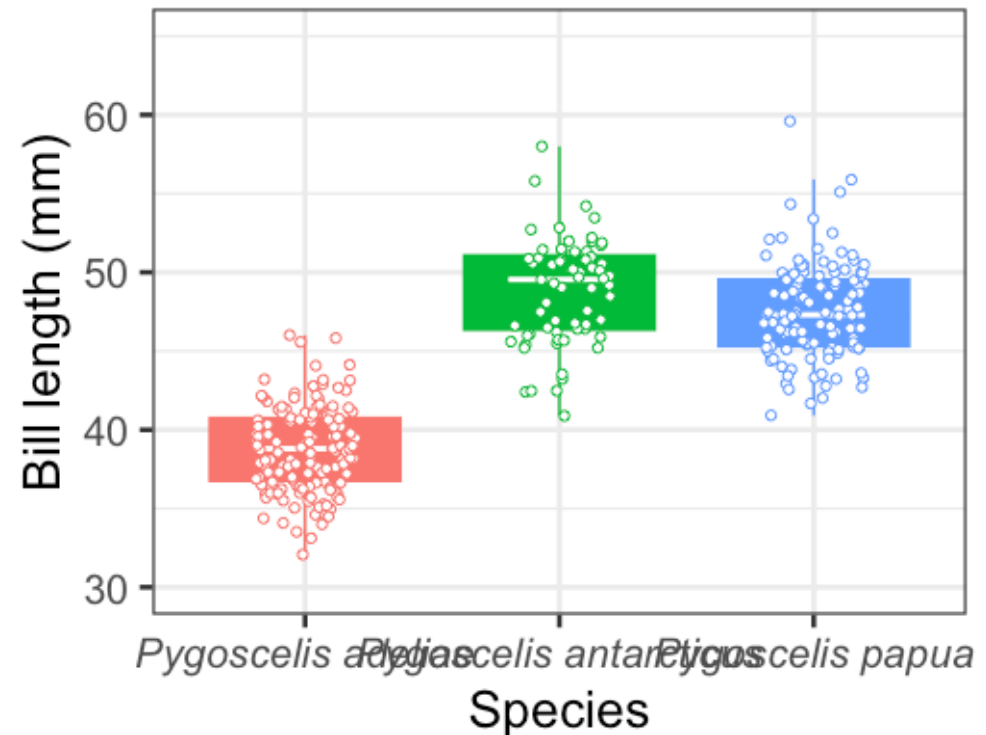
Soft wrap or stagger text labels to stop them overlapping.

```
ggplot(d, aes(latin_name, bill_length_mm, col = species, fill = species)) +  
  geom_boxplot(outlier.shape = NA) +  
  stat_summary(geom = "crossbar", fatten = 2, color = "white", width = 0.4,  
              fun.data = function(x){return(c(y = stats::median(x), ymin = stats::median(x), ymax = stats::median(x)))}) +  
  geom_jitter(width = 0.2, shape = 21, fill = 'white') +  
  theme_bw(base_size = 20) +  
  labs(x = 'Species',  
       y = 'Bill length (mm)') +  
  ylim(c(30,65)) + guides(col = 'none',  
                          fill = 'none') +  
  theme(axis.text.x = element_text(face = "italic"))
```

ggplot2 tips and tricks

Soft wrap or stagger text labels to stop them overlapping.

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ggplot(d, aes(latin_name, bill_length_mm, col = species, fill = species)) +  
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              fun.data = function(x){return(c(y = stats::median(x), ymin = stats::median(x), ymax = stats::median(x)))}) +  
  geom_jitter(width = 0.2, shape = 21, fill = 'white') +  
  theme_bw(base_size = 20) +  
  labs(x = 'Species',  
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  ylim(c(30,65)) + guides(col = 'none',  
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  theme(axis.text.x = element_text(face = "italic"))
```

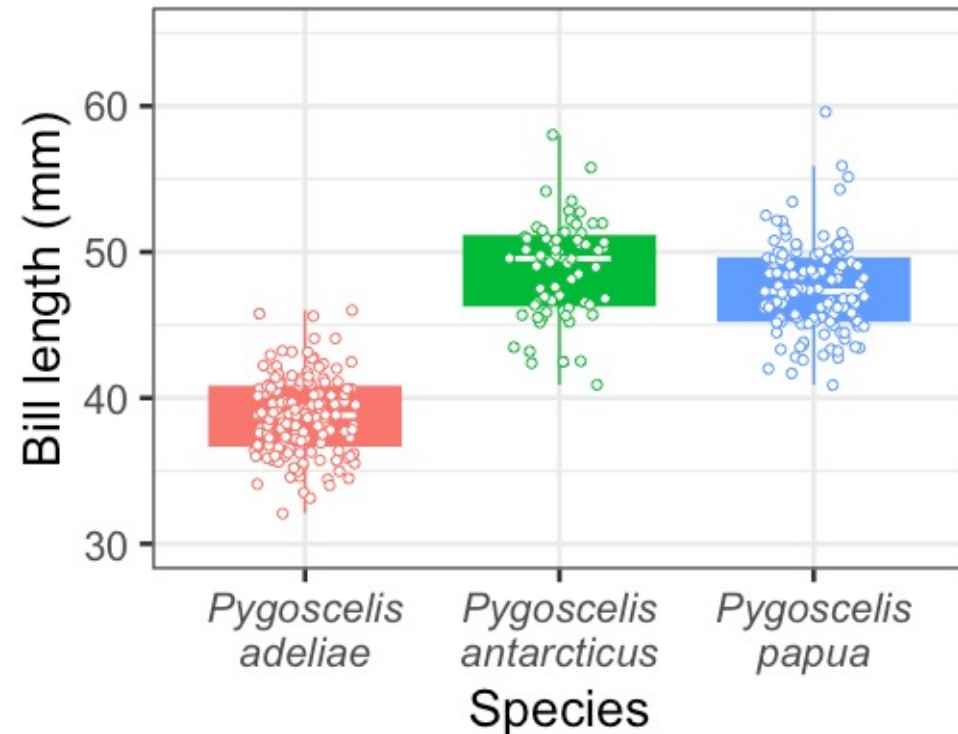


ggplot2 tips and tricks

Soft wrap or stagger text labels to stop them overlapping.

```
ggplot(d, aes(latin_name, bill_length_mm, col = species, fill = species)) +  
  geom_boxplot(outlier.shape = NA) +  
  stat_summary(geom = "crossbar", fatten = 2, color = "white", width = 0.4,  
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  geom_jitter(width = 0.2, shape = 21, fill = 'white') +  
  theme_bw(base_size = 20) +  
  labs(x = 'Species',  
       y = 'Bill length (mm)') +  
  ylim(c(30,65)) + guides(col = 'none',  
                           fill = 'none') +  
  theme(axis.text.x = element_text(face = "italic")) +  
  scale_x_discrete(labels = scales::label_wrap(10))
```

Automatic wrap using `scales::label_wrap()`.

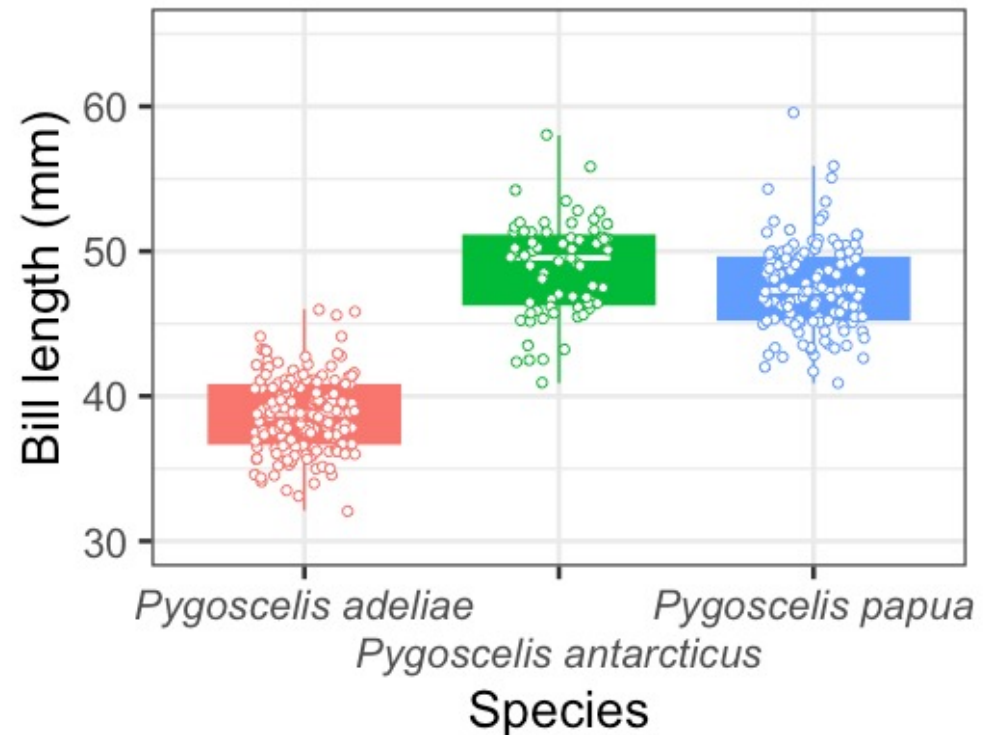


ggplot2 tips and tricks

Soft wrap or stagger text labels to stop them overlapping.

```
ggplot(d, aes(latin_name, bill_length_mm, col = species, fill = species)) +  
  geom_boxplot(outlier.shape = NA) +  
  stat_summary(geom = "crossbar", fatten = 2, color = "white", width = 0.4,  
              fun.data = function(x){return(c(y = stats::median(x), ymin = stats::median(x), ymax = stats::median(x)))}) +  
  geom_jitter(width = 0.2, shape = 21, fill = 'white') +  
  theme_bw(base_size = 20) +  
  labs(x = 'Species',  
       y = 'Bill length (mm)') +  
  ylim(c(30,65)) + guides(col = 'none',  
                          fill = 'none') +  
  theme(axis.text.x = element_text(face = "italic")) +  
  scale_x_discrete(guide = guide_axis(n.dodge = 2))
```

Dodge labels using `guide_axis()`.



ggplot2 tips and tricks

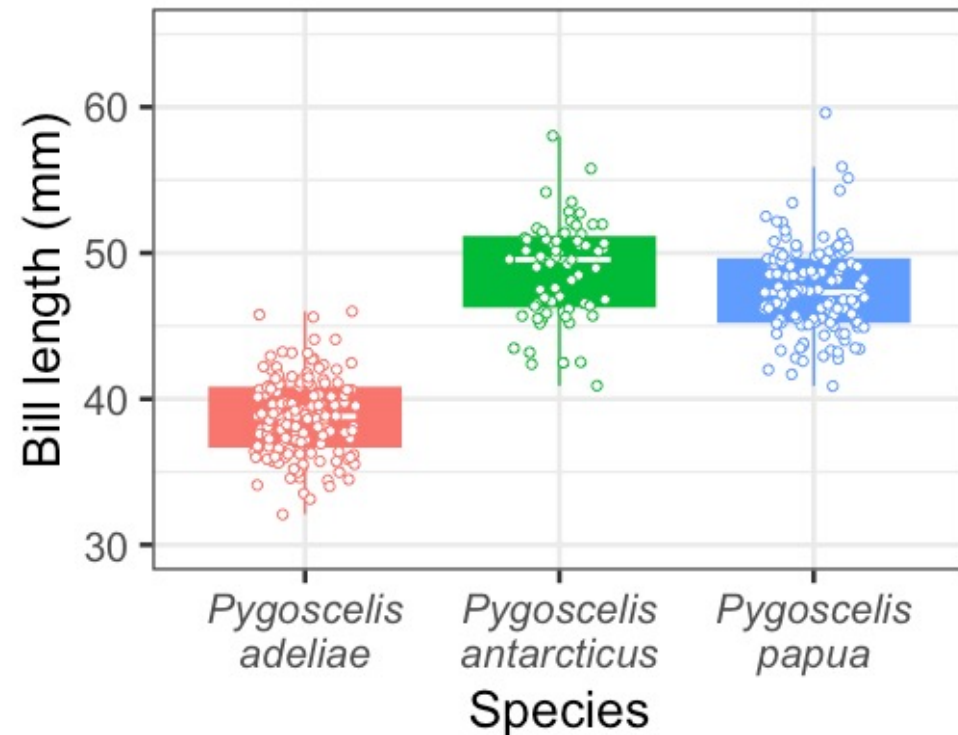
Add a final NULL layer to allow you to comment out layers.

```
ggplot(d, aes(latin_name, bill_length_mm, col = species, fill = species)) +  
  geom_boxplot(outlier.shape = NA) +  
  stat_summary(geom = "crossbar", fatten = 2, color = "white", width = 0.4,  
              fun.data = function(x){return(c(y = stats::median(x), ymin = stats::median(x), ymax = stats::median(x)))}) +  
  geom_jitter(width = 0.2, shape = 21, fill = 'white') +  
  theme_bw(base_size = 20) +  
  labs(x = 'Species',  
       y = 'Bill length (mm)') +  
  ylim(c(30,65)) +  
  guides(col = 'none',  
         fill = 'none') + # turn off legend  
  theme(axis.text.x = element_text(face = "italic")) +  
  scale_x_discrete(labels = scales::label_wrap(10)) +  
  #scale_x_discrete(guide = guide_axis(n.dodge = 2)) +  
  NULL
```


ggplot2 tips and tricks

Add a final NULL layer to allow you to comment out layers.

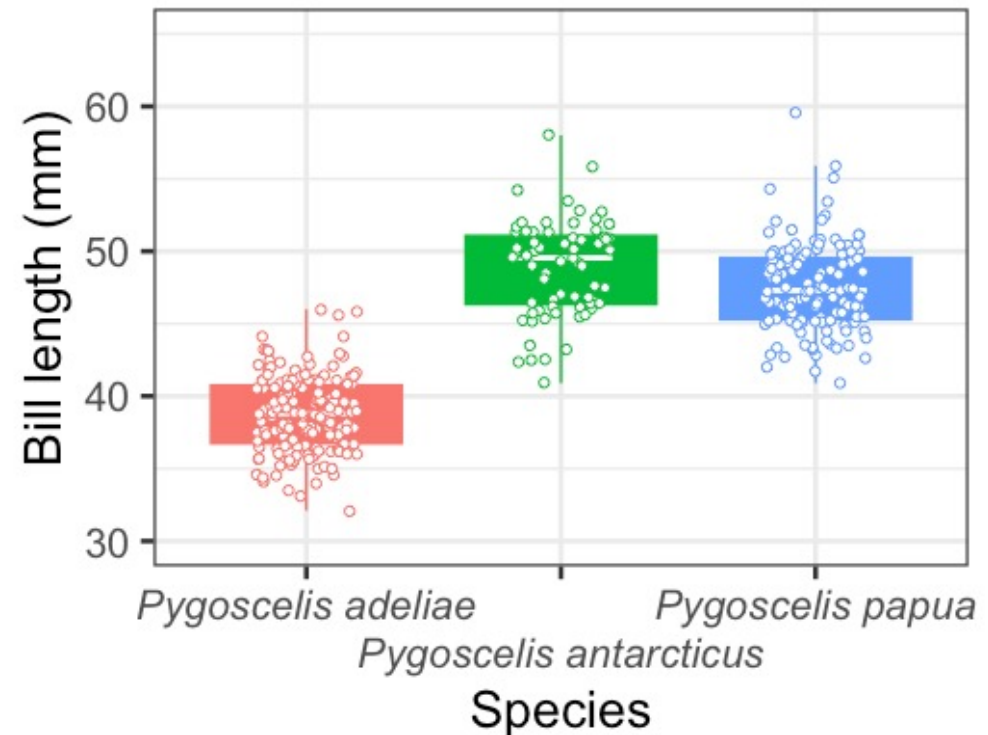
```
ggplot(d, aes(latin_name, bill_length_mm, col = species, fill = species)) +  
  geom_boxplot(outlier.shape = NA) +  
  stat_summary(geom = "crossbar", fatten = 2, color = "white", width = 0.4,  
              fun.data = function(x){return(c(y = stats::median(x), ymin = stats::median(x), ymax = stats::median(x)))}) +  
  geom_jitter(width = 0.2, shape = 21, fill = 'white') +  
  theme_bw(base_size = 20) +  
  labs(x = 'Species',  
       y = 'Bill length (mm)') +  
  ylim(c(30,65)) +  
  guides(col = 'none',  
         fill = 'none') + # turn off legend  
  theme(axis.text.x = element_text(face = "italic")) +  
  scale_x_discrete(labels = scales::label_wrap(10)) +  
  #scale_x_discrete(guide = guide_axis(n.dodge = 2)) +  
  NULL
```



ggplot2 tips and tricks

Add a final NULL layer to allow you to comment out layers.

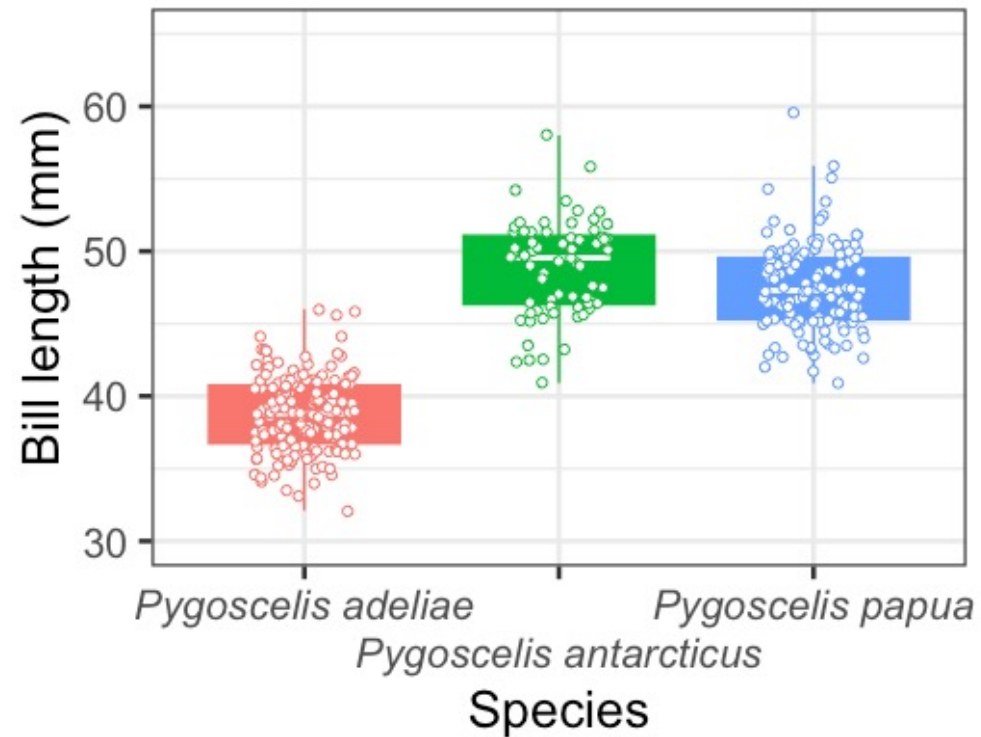
```
ggplot(d, aes(latin_name, bill_length_mm, col = species, fill = species)) +  
  geom_boxplot(outlier.shape = NA) +  
  stat_summary(geom = "crossbar", fatten = 2, color = "white", width = 0.4,  
              fun.data = function(x){return(c(y = stats::median(x), ymin = stats::median(x), ymax = stats::median(x)))}) +  
  geom_jitter(width = 0.2, shape = 21, fill = 'white') +  
  theme_bw(base_size = 20) +  
  labs(x = 'Species',  
       y = 'Bill length (mm)') +  
  ylim(c(30,65)) +  
  guides(col = 'none',  
         fill = 'none') + # turn off legend  
  theme(axis.text.x = element_text(face = "italic")) +  
  #scale_x_discrete(labels = scales::label_wrap(10)) +  
  scale_x_discrete(guide = guide_axis(n.dodge = 2)) +  
  NULL
```



ggplot2 tips and tricks

Save out plot using `ggsave()`.

```
ggsave('plots/penguins.pdf', last_plot(), width = 7, height = 5)  
ggsave('plots/penguins.png', last_plot(), width = 7, height = 5)
```



ggplot2 extensions

ggplot2 extensions

Patchwork for aligning plots.

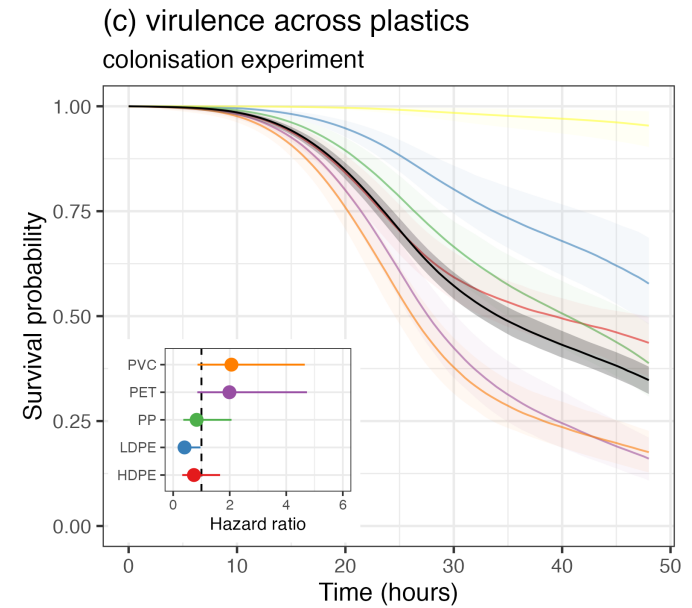
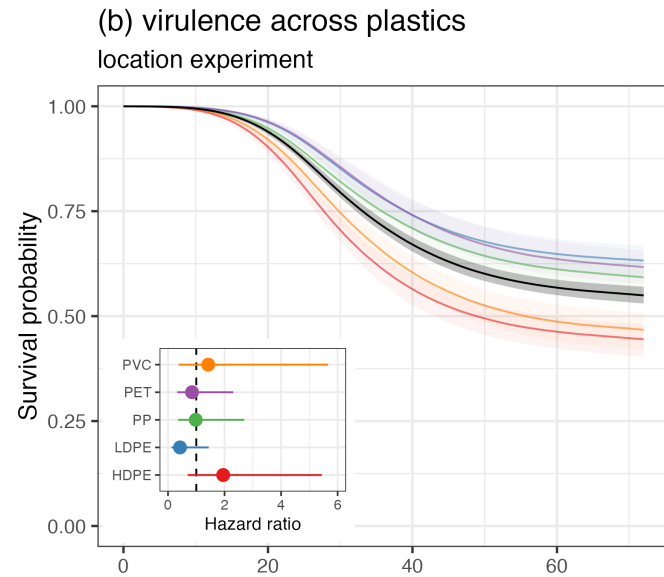
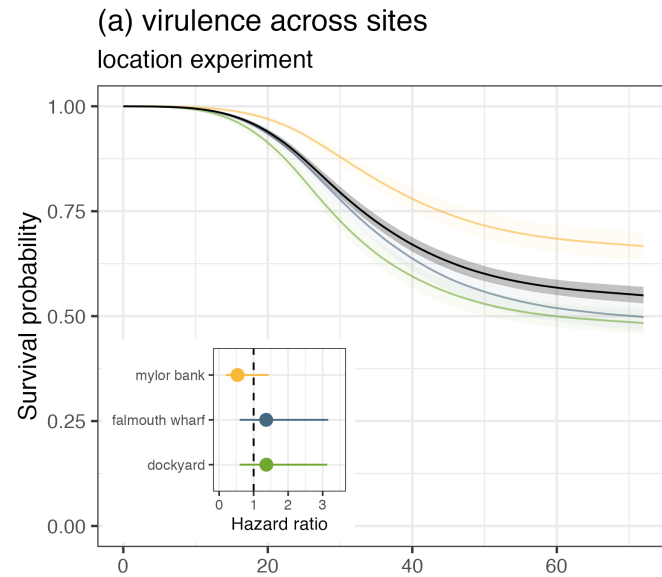
```
plot1 + plot2 + plot_layout(widths = c(0.5,0.5))
```



ggplot2 extensions

Patchwork for aligning plots.

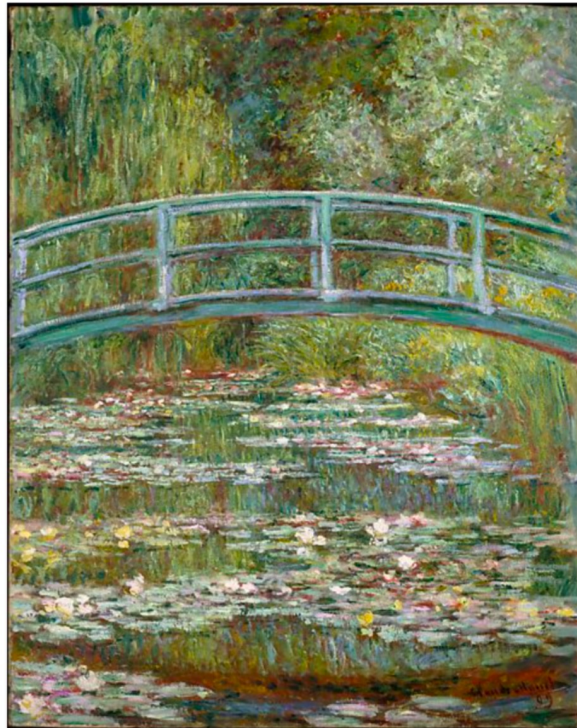
```
plot1 + plot2 + plot_layout(widths = c(0.5,0.5))
```



ggplot2 extensions

MetBrewer for beautiful colour schemes.

Adds to **scale_color_manual()** and **scale_fill_manual()**

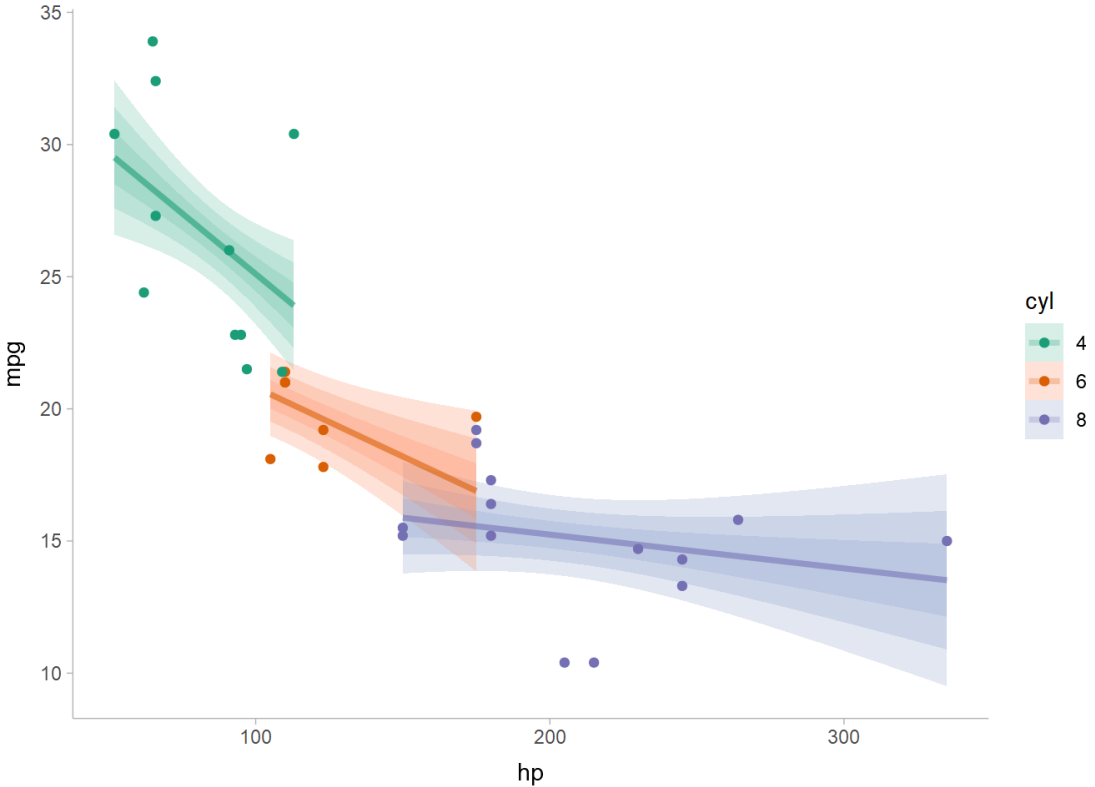
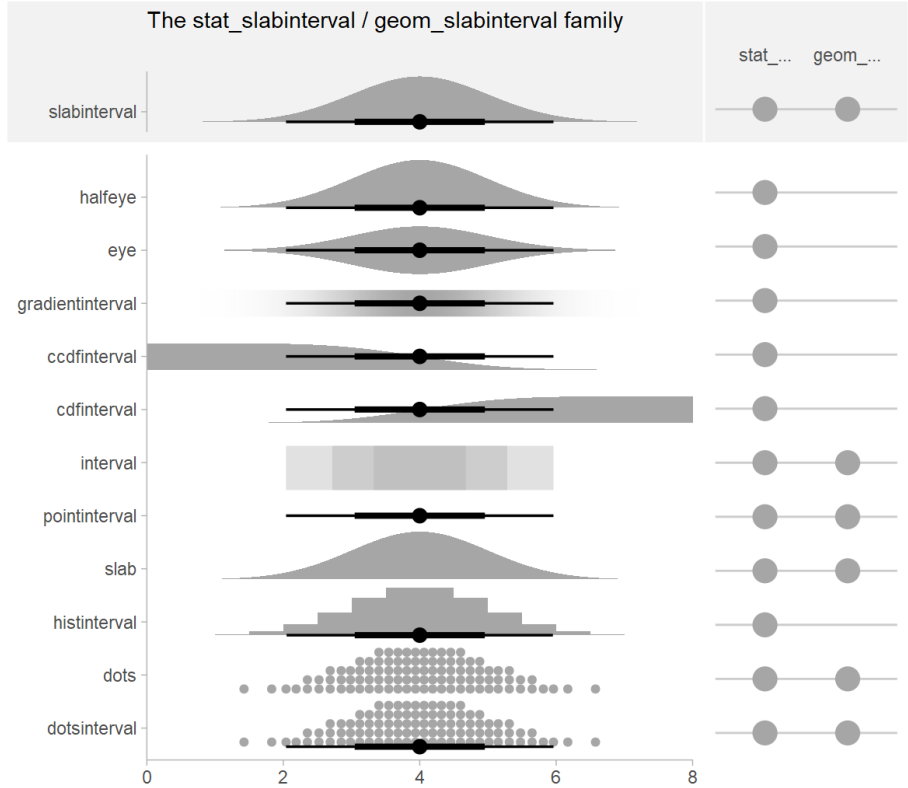


Bridge over a Pond of Water
Lilies, 1899, Claude Monet



ggplot2 extensions

ggdist for visualising distributions and uncertainty.



ggplot2 extensions

ggtree for making phylogenetic trees.

gganimate for making animations.

ggnewscale for adding new (colour) scales.

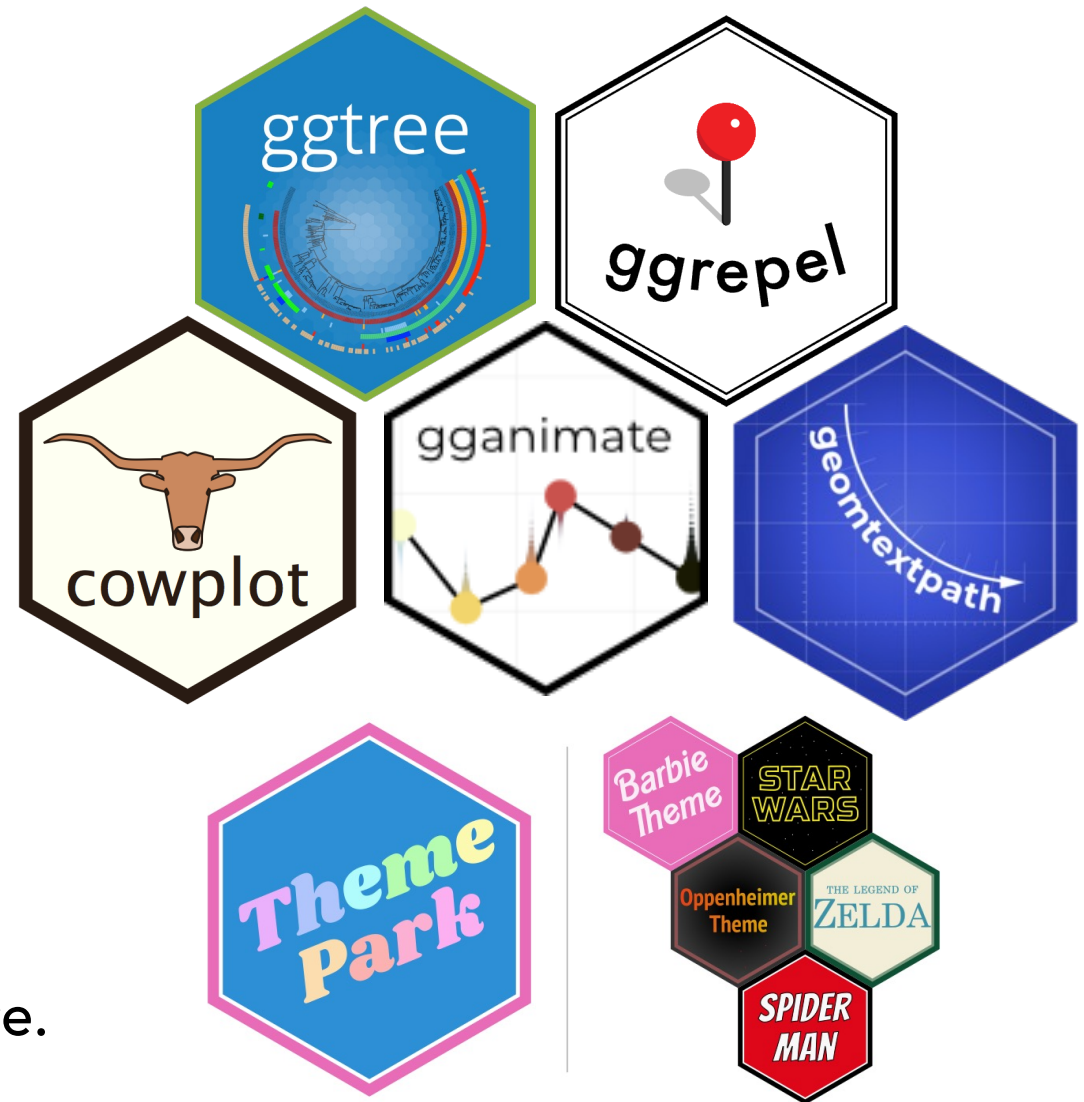
palettetown for Pokemon inspired colour palettes.

cowplot for aligning and labelling plots.

geomtextpath for curved text annotations.

ggrepel for better spaced text annotations.

themepark for themes based around popular culture.



Learn more about ggplot2

- **ggplot2** has a very well documented [website](#).
- There is a whole [book](#) on how to use **ggplot2**.
- We have written a [walkthrough](#) of our favourite tips and tricks.
- I end up on Cedric Scherer's [blog post](#) a lot.
- StackOverflow, ChatGPT, #TidyTuesday all good places to get help and inspiration.

A brief introduction to flextable

- **flextable** makes it easy to create table for reporting and publications.
- Can embed tables into Rmarkdown, pdf, Word, pdfs. I like saving mine as images.
- Downloaded 1.5 million times!



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contrast      estimate    SE  df t.ratio p.value
Adelie - Chinstrap    -32.4 67.5 339  -0.480  0.8807
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P value adjustment: tukey method for comparing a family of 3 estimates



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Chinstrap - Gentoo	-1,342.93	69.86	339.00	-19.22	<0.0001

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isolate	AMR gene	isolate	AMR gene
1	multidrug efflux RND transporter permease subunit SdeB class C beta-lactamase	14	multidrug efflux RND transporter permease subunit SdeY multidrug efflux RND transporter permease subunit SdeB class C beta-lactamase SRT-3
2	multidrug efflux RND transporter permease subunit SdeY multidrug efflux RND transporter permease subunit SdeB class C beta-lactamase SRT-3 tetracycline efflux MFS transporter Tet(41) multidrug efflux MFS transporter SmlY aminoglycoside 6'-N-acetyltransferase	15	class A beta-lactamase BlaP
3	class A beta-lactamase BlaP	16	multidrug efflux RND transporter permease subunit SdeB multidrug efflux RND transporter permease subunit SdeY multidrug efflux RND transporter permease subunit OqxB phosphoethanolamine-lipid A transferase MCR-10.1 multidrug efflux MFS transporter SmlY tetracycline efflux MFS transporter Tet(41) class C beta-lactamase SRT-3 class A extended-spectrum beta-lactamase OXY-6-2 cephalosporin-hydrolyzing class C beta-lactamase MIR-12 aminoglycoside 6'-N-acetyltransferase
4	multidrug efflux MFS transporter SmlY tetracycline efflux MFS transporter Tet(41) class C beta-lactamase SRT-3 multidrug efflux RND transporter permease subunit SdeB multidrug efflux RND transporter permease subunit SdeY aminoglycoside 6'-N-acetyltransferase	17	multidrug efflux MFS transporter SmlY tetracycline efflux MFS transporter Tet(41) class C beta-lactamase SRT-3 multidrug efflux RND transporter permease subunit SdeB multidrug efflux RND transporter permease subunit SdeY aminoglycoside 6'-N-acetyltransferase class A beta-lactamase FONA-6
5	multidrug efflux RND transporter permease subunit SdeB class C beta-lactamase	18	multidrug efflux MFS transporter SmlY tetracycline efflux MFS transporter Tet(41) class C beta-lactamase SRT-3 multidrug efflux RND transporter permease subunit SdeB multidrug efflux RND transporter permease subunit SdeY aminoglycoside 6'-N-acetyltransferase
6	class A beta-lactamase BlaP	19	class C beta-lactamase multidrug efflux RND transporter permease subunit SdeB
7	cephalosporin-hydrolyzing class C beta-lactamase MIR-16 multidrug efflux RND transporter permease subunit OqxB9 fosfomycin resistance glutathione transferase FosA	20	class C beta-lactamase multidrug efflux RND transporter permease subunit SdeB
8	class A beta-lactamase BlaP		
9	cephalosporin-hydrolyzing class C beta-lactamase MIR-16 multidrug efflux RND transporter permease subunit OqxB9 fosfomycin resistance glutathione transferase FosA		
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11	class A beta-lactamase FONA-4		
12	trimethoprim-resistant dihydrofolate reductase DfrE ABC-F type ribosomal protection protein Lsa(A)		
13	multidrug efflux MFS transporter SmlY tetracycline efflux MFS transporter Tet(41) class C beta-lactamase SRT-3 multidrug efflux RND transporter permease subunit SdeB multidrug efflux RND transporter permease subunit SdeY aminoglycoside 6'-N-acetyltransferase		

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contrast	estimate	SE	df	t.ratio	p.value
Adelie - Chinstrap	-32.42598	67.51168	339	-0.4803018	0.88
Adelie - Gentoo	-1,375.35401	56.14797	339	-24.4951686	<0.0001
Chinstrap - Gentoo	-1,342.92802	69.85693	339	-19.2239776	<0.0001

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  colformat_double(j = c(2:6), digits = 2) %>%
  align(align = 'center', part = 'header') %>%
  align(align = 'left', part = 'body') %>%
  font(fontname = 'Times', part = 'all')
```

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  font(fontname = 'Times', part = 'all') %>%
  bold(~p.value == "<0.0001", j = "p.value")
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  align(align = 'center', part = 'header') %>%
  align(align = 'left', part = 'body') %>%
  font(fontname = 'Times', part = 'all') %>%
  bold(~p.value == "<0.0001", j = "p.value") %>%
  fontsize(size = 12, part = 'all')
```

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  align(align = 'center', part = 'header') %>%
  align(align = 'left', part = 'body') %>%
  font(fontname = 'Times', part = 'all') %>%
  bold(~p.value == "<0.0001", j = "p.value") %>%
  fontsize(size = 12, part = 'all') %>%
  autofit()
```

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Adelie - Chinstrap   -32.4 67.5 339  -0.480 0.8807
Adelie - Gentoo    -1375.4 56.1 339 -24.495 <.0001
Chinstrap - Gentoo -1342.9 69.9 339 -19.224 <.0001
```

P value adjustment: tukey method for comparing a family of 3 estimates



Uses the pipe operator '`%>%`' to start a new layer

```
contrasts$contrasts %>%
  data.frame() %>%
  mutate(p.value = ifelse(p.value < 0.0001, "<0.0001", as.character(round(p.value, 2)))) %>%
  flextable() %>%
  set_header_labels(contrast = 'Contrast',
                    emmean = 'Estimate',
                    SE = 's.e.',
                    df = 'd.f.',
                    t.ratio = "t-ratio",
                    p.value = "p value") %>%
  italic(j = c(3:6), part = 'header') %>%
  colformat_double(j = c(2:6), digits = 2) %>%
  align(align = 'center', part = 'header') %>%
  align(align = 'left', part = 'body') %>%
  font(fontname = 'Times', part = 'all') %>%
  bold(~p.value == "<0.0001", j = "p.value") %>%
  fontsize(size = 12, part = 'all') %>%
  autofit()
```

Contrast	estimate	s.e.	d.f.	t-ratio	p value
Adelie - Chinstrap	-32.43	67.51	339.00	-0.48	0.88
Adelie - Gentoo	-1,375.35	56.15	339.00	-24.50	<0.0001
Chinstrap - Gentoo	-1,342.93	69.86	339.00	-19.22	<0.0001

Save out table using `save_as_image()`

Learn more about flextable

- **flextable** has a very well documented [website](#).
- There is a whole online [book](#) on how to use **flextable**.
- We have written a [walkthrough](#) of our favourite tips and tricks.
- Post on the Teams Channel and we can learn **together!**
- Look up other people's code on GitHub.



Time to have some fun!



ggplot2

1. Beautify a plot you have already started.
2. Make your first **ggplot** using **palmerpenguins** and change some of the defaults colours/shapes/themes
3. Change the font used in a **ggplot2**
4. Align multiple plots using **patchwork** or **cowplot**
5. Make an animation using **gganimate**

flextable

1. Make a table you need to make
2. Make your first **flextable** using **palmerpenguins** and try rename some column names and round numbers to two decimal places
3. Merge some cells vertically that contain the same value
4. Make some cells bold

Share it with us on the Teams Channel!