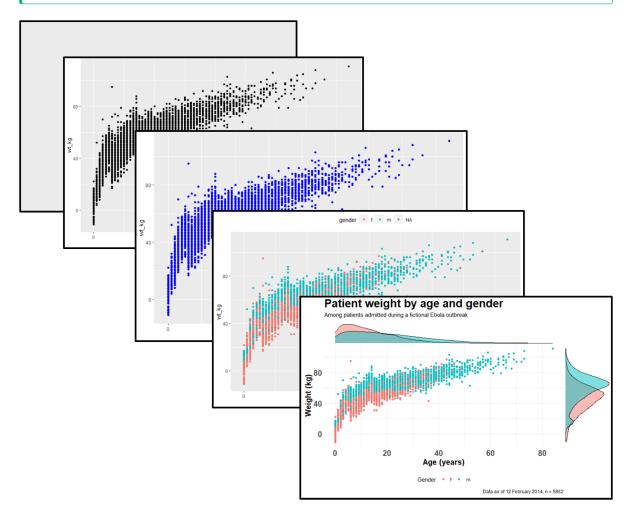
# Themes and Specialized Plots

# Extended Materials

You can find the original, extended version of these materials from chapters 30 and 31.



ggplot2 is the most popular data visualisation R package. Its ggplot() function is at the core of this package, and this whole approach is colloquially known as "ggplot" with the resulting figures sometimes affectionately called "ggplots". The "gg" in these names reflects the "grammar of graphics" used to construct the figures. ggplot2 benefits from a wide variety of supplementary R packages that further enhance its functionality.

The data visualization with ggplot cheatsheet from the RStudio website is a great reference to have on-hand when creating pltos. If you want inspiration for ways to creatively visualise your data, we suggest reviewing websites like the R graph gallery and Data-to-viz.

::: {.callout-note appearance="minimal" collapse="true"} ## Data Preparation

## Data import and cleaning

We'll import and clean the data identically to the previous chapter.

```
linelist <- rio::import("data/case_linelists/linelist_cleaned.rds")</pre>
# make display version of columns with more friendly names
linelist <- linelist %>%
 mutate(
                                                      # m to Male
# f to Female,
    gender_disp = case_when(gender == "m" ~ "Male",
                            gender == "f" ~ "Female",
                            is.na(gender) ~ "Unknown"), # NA to Unknown
    outcome_disp = replace_na(outcome, "Unknown")
                                                         # replace NA outcome with "unkn
 )
symptoms_data <- linelist %>%
  select(c(case_id, fever, chills, cough, aches, vomit))
symptoms_data_long <- symptoms_data %>%  # begin with "mini" linelist called symptoms_da
 pivot_longer(
                                           # pivot all columns except case id (all the sym
    cols = -case_id,
                                           # assign name for new column that holds the sym
    names_to = "symptom_name",
    values_to = "symptom_is_present") %% # assign name for new column that holds the val
 mutate(symptom_is_present = replace_na(symptom_is_present, "unknown")) # convert NA to "
```

### **Themes**

One of the best parts of **ggplot2** is the amount of control you have over the plot - you can define anything! As mentioned above, the design of the plot that is *not* related to the data shapes/geometries are adjusted within the **theme()** function. For example, the plot background color, presence/absence of gridlines, and the font/size/color/alignment of text (titles, subtitles, captions, axis text...). These adjustments can be done in one of two ways:

• Add a *complete theme* theme\_() function to make sweeping adjustments - these include theme\_classic(), theme\_minimal(), theme\_dark(), theme\_light() theme\_grey(),

theme\_bw() among others

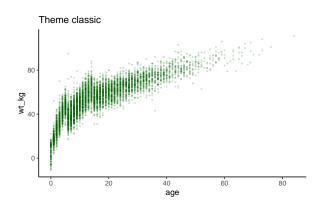
• Adjust each tiny aspect of the plot individually within theme()

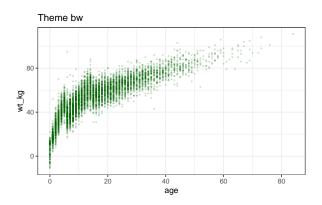
### Complete themes

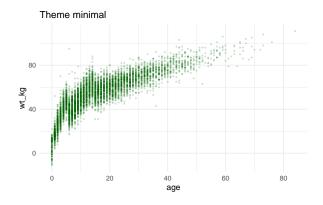
As they are quite straight-forward, we will demonstrate the complete theme functions below and will not describe them further here. Note that any micro-adjustments with theme() should be made *after* use of a complete theme.

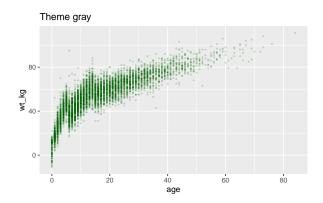
Write them with empty parentheses.

```
ggplot(data = linelist, mapping = aes(x = age, y = wt_kg))+
 geom_point(color = "darkgreen", size = 0.5, alpha = 0.2)+
 labs(title = "Theme classic")+
 theme classic()
ggplot(data = linelist, mapping = aes(x = age, y = wt_kg))+
 geom_point(color = "darkgreen", size = 0.5, alpha = 0.2)+
 labs(title = "Theme bw")+
 theme_bw()
ggplot(data = linelist, mapping = aes(x = age, y = wt_kg))+
 geom_point(color = "darkgreen", size = 0.5, alpha = 0.2)+
 labs(title = "Theme minimal")+
 theme_minimal()
ggplot(data = linelist, mapping = aes(x = age, y = wt_kg))+
 geom_point(color = "darkgreen", size = 0.5, alpha = 0.2)+
 labs(title = "Theme gray")+
 theme_gray()
```









### Modify theme

The theme() function can take a large number of arguments, each of which edits a very specific aspect of the plot. There is no way we could cover all of the arguments, but we will describe the general pattern for them and show you how to find the argument name that you need. The basic syntax is this:

- 1. Within theme() write the argument name for the plot element you want to edit, like
  plot.title =
- 2. Provide an element\_() function to the argument
- Most often, use element\_text(), but others include element\_rect() for canvas background colors, or element\_blank() to remove plot elements
- 4. Within the element\_() function, write argument assignments to make the fine adjustments you desire

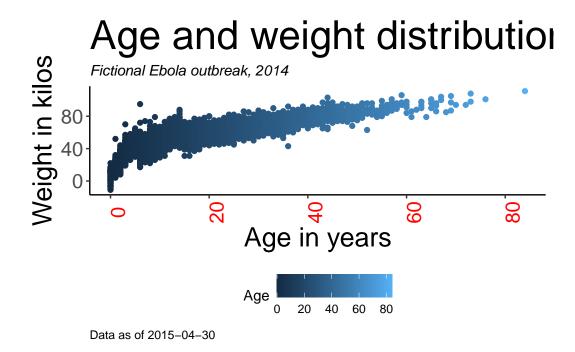
So, that description was quite abstract, so here are some examples.

The below plot looks quite silly, but it serves to show you a variety of the ways you can adjust your plot.

- We begin with the plot age\_by\_wt defined just above and add theme\_classic()
- For finer adjustments we add theme() and include one argument for each plot element to adjust

It can be nice to organize the arguments in logical sections. To describe just some of those used below:

- legend.position = is unique in that it accepts simple values like "bottom", "top", "left", and "right". But generally, text-related arguments require that you place the details within element\_text().
- Title size with element\_text(size = 30)
- The caption horizontal alignment with element\_text(hjust = 0) (from right to left)
- The subtitle is italicized with element\_text(face = "italic")



Here are some especially common theme() arguments. You will recognize some patterns, such as appending .x or .y to apply the change only to one axis.

theme() argument	What it adjusts
<pre>plot.title = element_text()</pre>	The title
<pre>plot.subtitle = element_text()</pre>	The subtitle
<pre>plot.caption = element_text()</pre>	The caption (family, face, color, size, angle, vjust, hjust)
<pre>axis.title = element_text()</pre>	Axis titles (both x and y) (size, face, angle, color)
<pre>axis.title.x = element_text()</pre>	Axis title x-axis only (use .y for y-axis only)
<pre>axis.text = element_text()</pre>	Axis text (both x and y)
<pre>axis.text.x = element_text()</pre>	Axis text x-axis only (use .y for y-axis only)
<pre>axis.ticks = element_blank()</pre>	Remove axis ticks
<pre>axis.line = element_line()</pre>	Axis lines (colour, size, linetype: solid
_	dashed dotted etc)
<pre>strip.text = element_text()</pre>	Facet strip text (colour, face, size, angle)
<pre>strip.background = element_rect()</pre>	facet strip (fill, colour, size)

But there are so many theme arguments! How could I remember them all? Do not worry - it is impossible to remember them all. Luckily there are a few tools to help you:

The **tidyverse** documentation on modifying theme, which has a complete list.



Tip

Run theme\_get() from ggplot2 to print a list of all 90+ theme() arguments to the console.



Tip

If you ever want to remove an element of a plot, you can also do it through theme(). Just pass element\_blank() to an argument to have it disappear completely. For legends, set legend.position = "none".

## Scales for color, fill, axes, etc.

In **ggplot2**, when aesthetics of plotted data (e.g. size, color, shape, fill, plot axis) are mapped to columns in the data, the exact display can be adjusted with the corresponding "scale" command. In this section we explain some common scale adjustments.

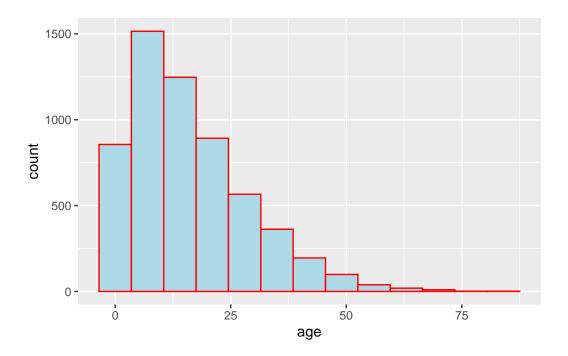
#### Color schemes

One thing that can initially be difficult to understand with **ggplot2** is control of color schemes. Note that this section discusses the color of plot objects (geoms/shapes) such as points, bars, lines, tiles, etc.

To control "color" of plot objects you will be adjusting either the color = aesthetic (the exterior color) or the fill = aesthetic (the interior color). One exception to this pattern is geom\_point(), where you really only get to control color =, which controls the color of the point (interior and exterior).

When setting colour or fill you can use colour names recognized by R like "red" (see complete list or enter ?colors), or a specific hex colour such as "#ff0505".

```
# histogram -
ggplot(data = linelist, mapping = aes(x = age))+
                                                        # set data and axes
 geom histogram(
                               # display histogram
   binwidth = 7,
                                 # width of bins
    color = "red",
                                 # bin line color
    fill = "lightblue")
                                 # bin interior color (fill)
```



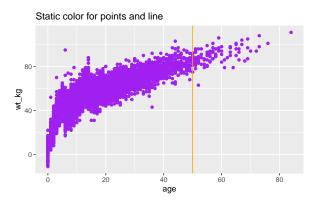
Aesthetics such as fill = and color = can be defined either *outside* of a mapping = aes() statement or *inside* of one. If *outside* the aes(), the assigned value should be static (e.g. color = "blue") and will apply for *all* data plotted by the geom. If *inside*, the aesthetic should be mapped to a column, like color = hospital, and the expression will vary by the value for that row in the data. A few examples:

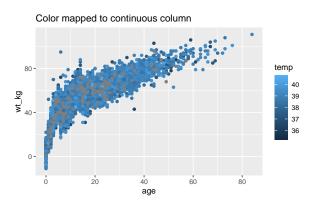
```
# Static color for points and for line
ggplot(data = linelist, mapping = aes(x = age, y = wt_kg))+
geom_point(color = "purple")+
geom_vline(xintercept = 50, color = "orange")+
labs(title = "Static color for points and line")

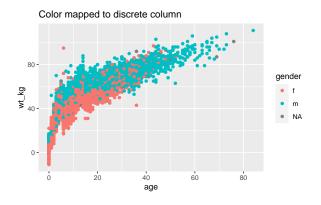
# Color mapped to continuous column
ggplot(data = linelist, mapping = aes(x = age, y = wt_kg))+
geom_point(mapping = aes(color = temp))+
labs(title = "Color mapped to continuous column")

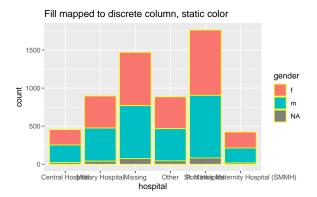
# Color mapped to discrete column
ggplot(data = linelist, mapping = aes(x = age, y = wt_kg))+
geom_point(mapping = aes(color = gender))+
labs(title = "Color mapped to discrete column")
```

```
# bar plot, fill to discrete column, color to static value
ggplot(data = linelist, mapping = aes(x = hospital))+
geom_bar(mapping = aes(fill = gender), color = "yellow")+
labs(title = "Fill mapped to discrete column, static color")
```









#### **Scales**

Once you map a column to a plot aesthetic (e.g. x = y = fill = color = w), your plot will gain a scale/legend. See above how the scale can be continuous, discrete, date, etc. values depending on the class of the assigned column. If you have multiple aesthetics mapped to columns, your plot will have multiple scales.

You can control the scales with the appropriate scales\_() function. The scale functions of ggplot() have 3 parts that are written like this: scale\_AESTHETIC\_METHOD().

- 1) The first part, scale\_(), is fixed.
- 2) The second part, the AESTHETIC, should be the aesthetic that you want to adjust the scale for (\_fill\_, \_shape\_, \_color\_, \_size\_, \_alpha\_...) the options here also include \_x\_ and \_y\_.
- 3) The third part, the METHOD, will be either \_discrete(), continuous(), \_date(), \_gradient(), or \_manual() depending on the class of the column and how you want to control it. There are others, but these are the most-often used.

Be sure that you use the correct function for the scale! Otherwise your scale command will not appear to change anything. If you have multiple scales, you may use multiple scale functions to adjust them! For example:

### Scale arguments

Each kind of scale has its own arguments, though there is some overlap. Query the function like ?scale\_color\_discrete in the R console to see the function argument documentation.

For continuous scales, use breaks = to provide a sequence of values with seq() (take to =, from =, and by = as shown in the example below. Set expand = c(0,0) to eliminate padding space around the axes (this can be used on any \_x\_ or \_y\_ scale.

For discrete scales, you can adjust the order of level appearance with breaks =, and how the values display with the labels = argument. Provide a character vector to each of those (see example below). You can also drop NA easily by setting na.translate = FALSE.

#### Manual adjustments

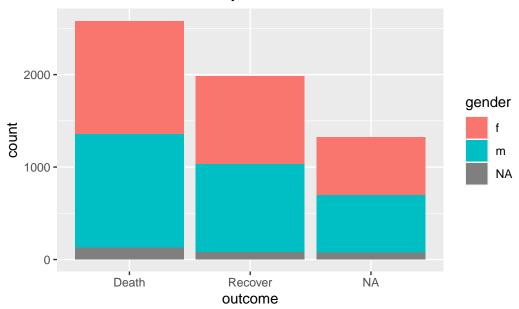
One of the most useful tricks is using "manual" scaling functions to explicitly assign colors as you desire. These are functions with the syntax scale\_xxx\_manual() (e.g. scale\_colour\_manual() or scale\_fill\_manual()). Each of the below arguments are demonstrated in the code example below.

- Assign colors to data values with the values = argument
- Specify a color for NA with na.value =
- Change how the values are written in the legend with the labels = argument
- Change the legend title with name =

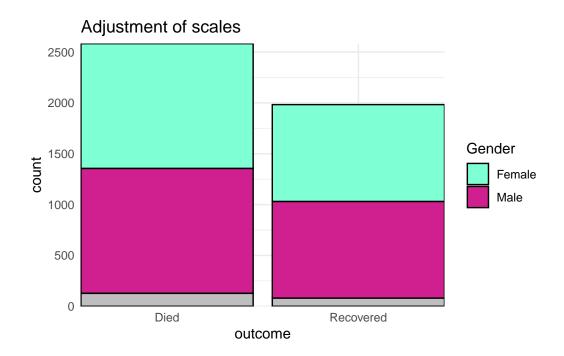
Below, we create a bar plot and show how it appears by default, and then with three scales adjusted - the continuous y-axis scale, the discrete x-axis scale, and manual adjustment of the fill (interior bar color).

```
# BASELINE - no scale adjustment
ggplot(data = linelist)+
  geom_bar(mapping = aes(x = outcome, fill = gender))+
  labs(title = "Baseline - no scale adjustments")
```

# Baseline - no scale adjustments



```
# SCALES ADJUSTED
ggplot(data = linelist)+
 geom_bar(mapping = aes(x = outcome, fill = gender), color = "black")+
 theme_minimal()+
                                     # simplify background
 scale_y_continuous(
                                     # continuous scale for y-axis (counts)
   expand = c(0,0),
                                     # no padding
   breaks = seq(from = 0,
                 to = 3000,
                 by = 500))+
 scale_x_discrete(
                                      # discrete scale for x-axis (gender)
   expand = c(0,0),
                                      # no padding
                                      # show all factor levels (even if not in data)
   drop = FALSE,
   na.translate = FALSE,
                                      # remove NA outcomes from plot
   labels = c("Died", "Recovered"))+ # Change display of values
                                      # Manually specify fill (bar interior color)
 scale_fill_manual(
   values = c("m" = "violetred",
                                      # reference values in data to assign colors
```



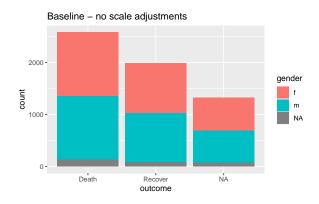
### Continuous axes scales

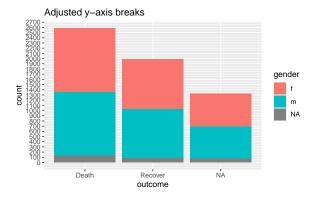
When data are mapping to the plot axes, these too can be adjusted with scales commands. A common example is adjusting the display of an axis (e.g. y-axis) that is mapped to a column with continuous data.

We may want to adjust the breaks or display of the values in the ggplot using scale\_y\_continuous(). As noted above, use the argument breaks = to provide a sequence of values that will serve as "breaks" along the scale. These are the values at which numbers will display. To this argument, you can provide a c() vector containing the desired break values, or you can provide a regular sequence of numbers using the base R function seq(). This seq() function accepts to =, from =, and by =.

```
# BASELINE - no scale adjustment
ggplot(data = linelist)+
  geom_bar(mapping = aes(x = outcome, fill = gender))+
  labs(title = "Baseline - no scale adjustments")

#
ggplot(data = linelist)+
  geom_bar(mapping = aes(x = outcome, fill = gender))+
  scale_y_continuous(
   breaks = seq(
     from = 0,
     to = 3000,
     by = 100)
)+
labs(title = "Adjusted y-axis breaks")
```





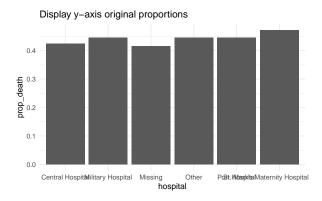
# \* Display percents

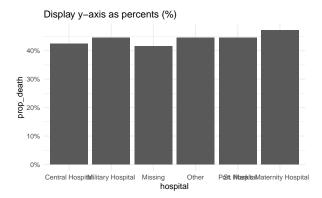
If your original data values are proportions, you can easily display them as percents with "%" by providing labels = scales::percent in your scales command, as shown below.

While an alternative would be to convert the values to character and add a "%" character to the end, this approach will cause complications because your data will no longer be continuous numeric values.

```
# Original y-axis proportions
###################################
linelist %>%
                                              # start with linelist
 group_by(hospital) %>%
                                              # group data by hospital
 summarise(
                                             # create summary columns
                                               # total number of rows in group
   n = n()
   deaths = sum(outcome == "Death", na.rm=T),
                                              # number of deaths in group
   prop_death = deaths/n) %>%
                                               # proportion deaths in group
                                             # begin plotting
 ggplot(
   mapping = aes(
     x = hospital,
     y = prop_death))+
 geom_col()+
 theme_minimal()+
 labs(title = "Display y-axis original proportions")
# Display y-axis proportions as percents
linelist %>%
 group_by(hospital) %>%
 summarise(
   n = n(),
   deaths = sum(outcome == "Death", na.rm=T),
   prop_death = deaths/n) %>%
  ggplot(
   mapping = aes(
     x = hospital,
     y = prop_death))+
 geom_col()+
 theme minimal()+
 labs(title = "Display y-axis as percents (%)")+
 scale_y_continuous(
   labels = scales::percent
                                              # display proportions as percents
```







## \* Log scale

To transform a continuous axis to log scale, add trans = "log2" to the scale command. For purposes of example, we create a data frame of regions with their respective preparedness\_index and cumulative cases values.

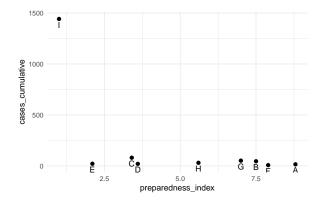
```
plot_data <- data.frame(
    region = c("A", "B", "C", "D", "E", "F", "G", "H", "I"),
    preparedness_index = c(8.8, 7.5, 3.4, 3.6, 2.1, 7.9, 7.0, 5.6, 1.0),
    cases_cumulative = c(15, 45, 80, 20, 21, 7, 51, 30, 1442)
)
plot_data</pre>
```

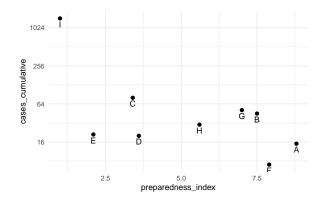
region preparedness\_index cases\_cumulative

1	Α	8.8	15
2	В	7.5	45
3	C	3.4	80
4	D	3.6	20
5	E	2.1	21
6	F	7.9	7
7	G	7.0	51
8	Н	5.6	30
9	I	1.0	1442

The cumulative cases for region "I" are dramatically greater than all the other regions. In circumstances like this, you may elect to display the y-axis using a log scale so the reader can see differences between the regions with fewer cumulative cases.

```
# Original y-axis
preparedness_plot <- ggplot(data = plot_data,</pre>
       mapping = aes(
         x = preparedness_index,
         y = cases_cumulative))+
  geom_point(size = 2)+
                                    # points for each region
  geom_text(
    mapping = aes(label = region),
    vjust = 1.5)+
                                    # add text labels
  theme_minimal()
preparedness_plot
                                    # print original plot
# print with y-axis transformed
preparedness_plot+
                                      # begin with plot saved above
  scale_y_continuous(trans = "log2") # add transformation for y-axis
```





#### **Gradient scales**

Fill gradient scales can involve additional nuance. The defaults are usually quite pleasing, but you may want to adjust the values, cutoffs, etc.

To demonstrate how to adjust a continuous color scale, we'll use a data set that contains the ages of cases and of sources in a contact tracing case.

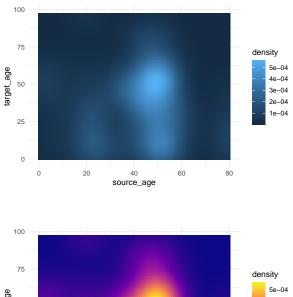
```
case_source_relationships <- rio::import("data/godata/relationships_clean.rds") %>%
   select(source_age, target_age)
```

Below, we produce a "raster" heat tile density plot. Note how the fill scale is continuous.

```
trans_matrix <- ggplot(
    data = case_source_relationships,
    mapping = aes(x = source_age, y = target_age))+
    stat_density2d(
    geom = "raster",
    mapping = aes(fill = after_stat(density)),
    contour = FALSE)+
    theme_minimal()</pre>
```

Now we show some variations on the fill scale:

```
trans_matrix
trans_matrix + scale_fill_viridis_c(option = "plasma")
```

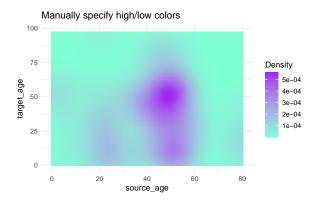


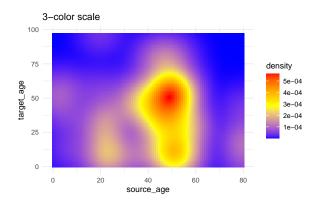
Now we show some examples of actually adjusting the break points of the scale:

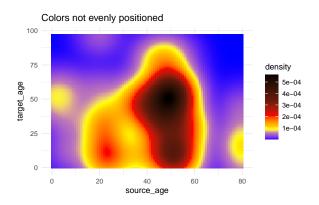
- scale\_fill\_gradient() accepts two colors (high/low)
- scale\_fill\_gradientn() accepts a vector of any length of colors to values = (intermediate values will be interpolated)
- Use scales::rescale() to adjust how colors are positioned along the gradient; it rescales your vector of positions to be between 0 and 1.

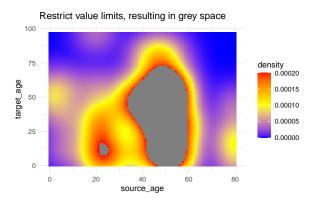
```
trans_matrix +
  scale_fill_gradient(  # 2-sided gradient scale
  low = "aquamarine",  # low value
  high = "purple",  # high value
  na.value = "grey",  # value for NA
  name = "Density")+  # Legend title
  labs(title = "Manually specify high/low colors")
```

```
# 3+ colors to scale
trans_matrix +
 scale_fill_gradientn( # 3-color scale (low/mid/high)
    colors = c("blue", "yellow", "red") # provide colors in vector
 labs(title = "3-color scale")
# Use of rescale() to adjust placement of colors along scale
trans_matrix +
  scale_fill_gradientn(
                          # provide any number of colors
    colors = c("blue", "yellow", "red", "black"),
    values = scales::rescale(c(0, 0.05, 0.07, 0.10, 0.15, 0.20, 0.3, 0.5)) # positions for
    )+
 labs(title = "Colors not evenly positioned")
# use of limits to cut-off values that get fill color
trans_matrix +
  scale_fill_gradientn(
    colors = c("blue", "yellow", "red"),
    limits = c(0, 0.0002))+
 labs(title = "Restrict value limits, resulting in grey space")
```









# **Palettes**

# \* Colorbrewer and Viridis

More generally, if you want predefined palettes, you can use the scale\_xxx\_brewer or scale\_xxx\_viridis\_y functions.

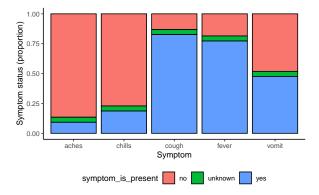
The 'brewer' functions can draw from colorbrewer.org palettes.

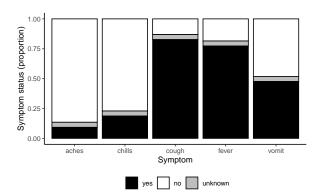
The 'viridis' functions draw from viridis (colourblind friendly!) palettes, which "provide colour maps that are perceptually uniform in both colour and black-and-white. They are also designed to be perceived by viewers with common forms of colour blindness." (read more here and here). Define if the palette is discrete, continuous, or binned by specifying this at the end of the function (e.g. discrete is scale\_xxx\_viridis\_d).

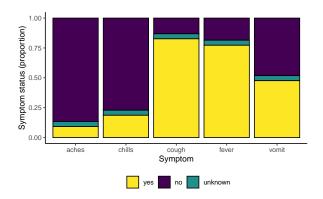
It is advised that you test your plot in this color blindness simulator. If you have a red/green color scheme, try a "hot-cold" (red-blue) scheme instead as described here

Here is an example of using various color schemes.

```
# begin with linelist
symp_plot <- linelist %>%
 select(c(case id, fever, chills, cough, aches, vomit)) %>%
                                                                  # select columns
 pivot_longer(
                                                                  # pivot longer
    cols = -case_id,
    names_to = "symptom_name",
    values_to = "symptom_is_present") %>%
                                                                  # replace missing values
    symptom_is_present = replace_na(symptom_is_present, "unknown")) %>%
 ggplot(
                                                                  # begin ggplot!
    mapping = aes(x = symptom_name, fill = symptom_is_present))+
  geom bar(position = "fill", col = "black") +
 theme_classic() +
 theme(legend.position = "bottom")+
 labs(
   x = "Symptom",
    y = "Symptom status (proportion)"
 )
symp_plot # print with default colors
#####################################
# print with manually-specified colors
symp_plot +
 scale_fill_manual(
    values = c("yes" = "black",
                                        # explicitly define colours
               "no" = "white".
               "unknown" = "grey"),
    breaks = c("yes", "no", "unknown"), # order the factors correctly
   name = ""
                                        # set legend to no title
```



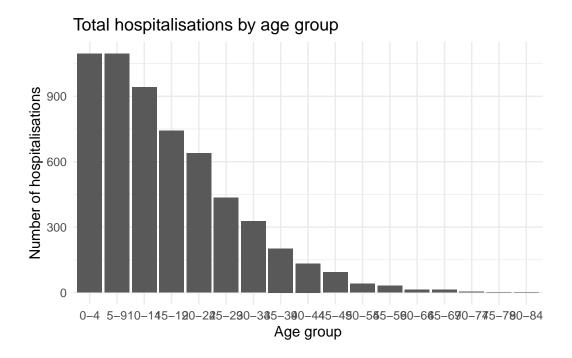




### Change order of discrete variables

Changing the order that discrete variables appear in is often difficult to understand for people who are new to ggplot2 graphs. It's easy to understand how to do this however once you understand how ggplot2 handles discrete variables under the hood. Generally speaking, if a discrete variable is used, it is automatically converted to a factor type - which orders factors by alphabetical order by default. To handle this, you simply have to reorder the factor levels to reflect the order you would like them to appear in the chart. For more detailed information on how to reorder factor objects, see the factor section of the guide.

We can look at a common example using age groups - by default the 5-9 age group will be placed in the middle of the age groups (given alphanumeric order), but we can move it behind the 0-4 age group of the chart by releveling the factors.



# Advanced ggplot (optional)

These are a collection of less common plot types, ggplot2 extensions, and advanced examples of some of the things you can do visualizing data in R.

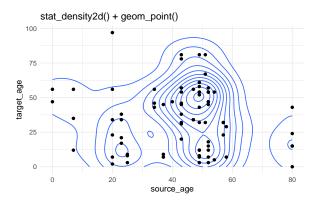
#### **Contour lines**

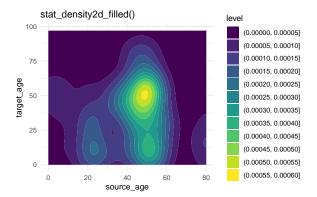
Contour plots are helpful when you have many points that might cover each other ("overplotting"). The case-source data used above are again plotted, but more simply using stat\_density2d() and stat\_density2d\_filled() to produce discrete contour levels - like a topographical map. Read more about the statistics here.

```
case_source_relationships %>%
  ggplot(aes(x = source_age, y = target_age))+
  stat_density2d()+
  geom_point()+
  theme_minimal()+
  labs(title = "stat_density2d() + geom_point()")

case_source_relationships %>%
```

```
ggplot(aes(x = source_age, y = target_age))+
stat_density2d_filled()+
theme_minimal()+
labs(title = "stat_density2d_filled()")
```





## Marginal distributions

To show the distributions on the edges of a <code>geom\_point()</code> scatterplot, you can use the <code>ggExtra</code> package and its function <code>ggMarginal()</code>. Save your original ggplot as an object, then pass it to <code>ggMarginal()</code> as shown below. Here are the key arguments:

- You must specify the type = as either "histogram", "density" "boxplot", "violin", or "densigram".
- By default, marginal plots will appear for both axes. You can set margins = to "x" or "y" if you only want one.

- Other optional arguments include fill = (bar color), color = (line color), size = (plot size relative to margin size, so larger number makes the marginal plot smaller).
- You can provide other axis-specific arguments to xparams = and yparams =. For example, to have different histogram bin sizes, as shown below.

You can have the marginal plots reflect groups (columns that have been assigned to color = in your ggplot() mapped aesthetics). If this is the case, set the ggMarginal() argument groupColour = or groupFill = to TRUE, as shown below.

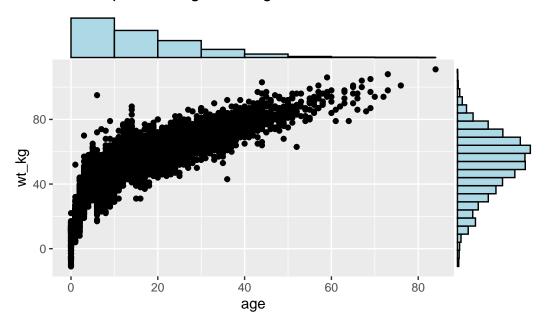
Read more at this vignette, in the R Graph Gallery or the function R documentation ?ggMarginal.

```
# Install/load ggExtra
pacman::p_load(ggExtra)

# Basic scatter plot of weight and age
scatter_plot <- ggplot(data = linelist)+
  geom_point(mapping = aes(y = wt_kg, x = age)) +
  labs(title = "Scatter plot of weight and age")</pre>
```

To add marginal histograms use type = "histogram". You can optionally set groupFill = TRUE to get stacked histograms.

# Scatter plot of weight and age

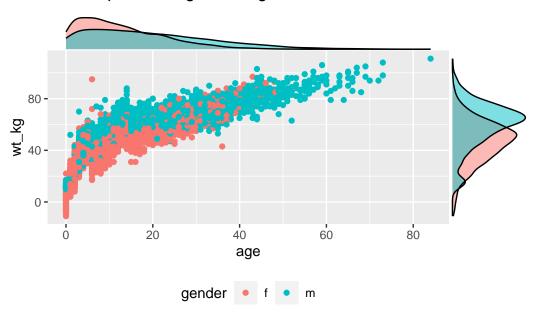


Marginal density plot with grouped/colored values:

```
# Scatter plot, colored by outcome
# Outcome column is assigned as color in ggplot. groupFill in ggMarginal set to TRUE
scatter_plot_color <- ggplot(data = linelist %>% drop_na(gender))+
    geom_point(mapping = aes(y = wt_kg, x = age, color = gender)) +
    labs(title = "Scatter plot of weight and age")+
    theme(legend.position = "bottom")

ggMarginal(scatter_plot_color, type = "density", groupFill = TRUE)
```

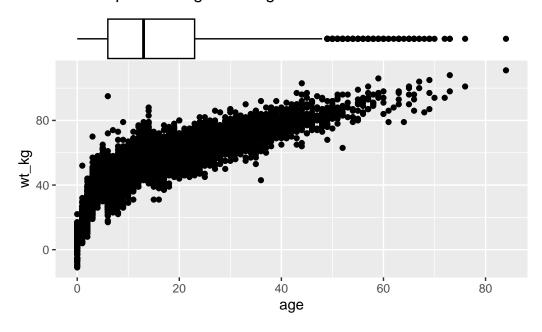
# Scatter plot of weight and age



Set the size = arguemnt to adjust the relative size of the marginal plot. Smaller number makes a larger marginal plot. You also set color =. Below are is a marginal boxplot, with demonstration of the margins = argument so it appears on only one axis:

```
# with boxplot
ggMarginal(
   scatter_plot,
   margins = "x",  # only show x-axis marginal plot
   type = "boxplot")
```

# Scatter plot of weight and age



#### **Smart Labeling**

In **ggplot2**, it is also possible to add text to plots. However, this comes with the notable limitation where text labels often clash with data points in a plot, making them look messy or hard to read. There is no ideal way to deal with this in the base package, but there is a **ggplot2** add-on, known as **ggrepel** that makes dealing with this very simple!

The ggrepel package provides two new functions, geom\_label\_repel() and geom\_text\_repel(), which replace geom\_label() and geom\_text(). Simply use these functions instead of the base functions to produce neat labels. Within the function, map the aesthetics aes() as always, but include the argument label = to which you provide a column name containing the values you want to display (e.g. patient id, or name, etc.). You can make more complex labels by combining columns and newlines (\n) within str\_glue() as shown below.

#### A few tips:

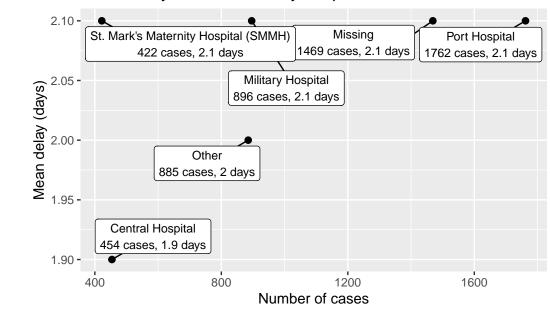
- Use min.segment.length = 0 to always draw line segments, or min.segment.length = Inf to never draw them
- Use size = outside of aes() to set text size

- Use force = to change the degree of repulsion between labels and their respective points (default is 1)
- Include fill = within aes() to have label colored by value
  - A letter "a" may appear in the legend add guides(fill = guide\_legend(override.aes
    = aes(color = NA)))+ to remove it

See this is very in-depth tutorial for more.

```
pacman::p_load(ggrepel)
linelist %>%
                                                            # start with linelist
  group_by(hospital) %>%
                                                            # group by hospital
  summarise(
                                                            # create new dataset with summa
                                                              # number of cases per hospita
    n_{cases} = n(),
    delay_mean = round(mean(days_onset_hosp, na.rm=T),1),
                                                              # mean delay per hospital
  ) %>%
  ggplot(mapping = aes(x = n_cases, y = delay_mean))+
                                                            # send data frame to ggplot
  geom_point(size = 2)+
                                                            # add points
  geom_label_repel(
                                                            # add point labels
    mapping = aes(
      label = stringr::str_glue(
        "{hospital}\n{n cases} cases, {delay mean} days") # how label displays
      ),
    size = 3,
                                                            # text size in labels
    min.segment.length = 0)+
                                                            # show all line segments
                                                            # add axes labels
    title = "Mean delay to admission, by hospital",
    x = "Number of cases",
    y = "Mean delay (days)")
```

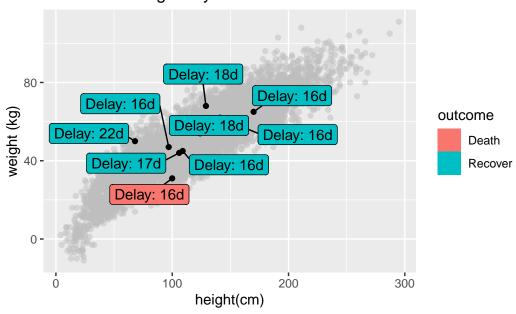
# Mean delay to admission, by hospital



You can label only a subset of the data points - by using standard ggplot() syntax to provide different data = for each geom layer of the plot. Below, All cases are plotted, but only a few are labeled.

```
ggplot()+
 # All points in grey
 geom_point(
    data = linelist,
                                                        # all data provided to this layer
    mapping = aes(x = ht_cm, y = wt_kg),
    color = "grey",
    alpha = 0.5)+
                                                                # grey and semi-transparent
 # Few points in black
 geom_point(
    data = linelist %>% filter(days_onset_hosp > 15), # filtered data provided to this la
    mapping = aes(x = ht_cm, y = wt_kg),
    alpha = 1) +
                                                                # default black and not tra
 # point labels for few points
 geom_label_repel(
    data = linelist %>% filter(days_onset_hosp > 15), # filter the data for the labels
   mapping = aes(
```

# Cases with long delay to admission



## Highlighting

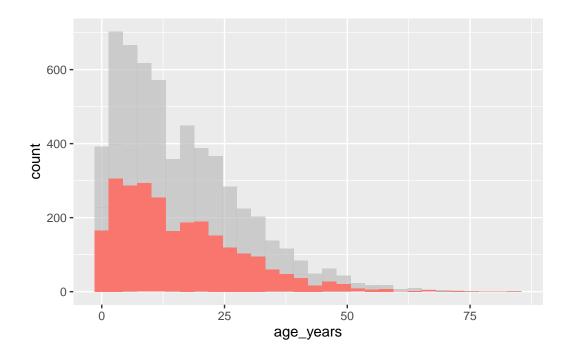
Highlighting specific elements in a chart is a useful way to draw attention to a specific instance of a variable while also providing information on the dispersion of the full dataset. While this is not easily done in base **ggplot2**, there is an external package that can help to do this known as **gghighlight**. This is easy to use within the ggplot syntax.

The **gghighlight** package uses the **gghighlight()** function to achieve this effect. To use this function, supply a logical statement to the function - this can have quite flexible outcomes, but here we'll show an example of the age distribution of cases in our linelist, highlighting them by outcome.

```
# load gghighlight
library(gghighlight)

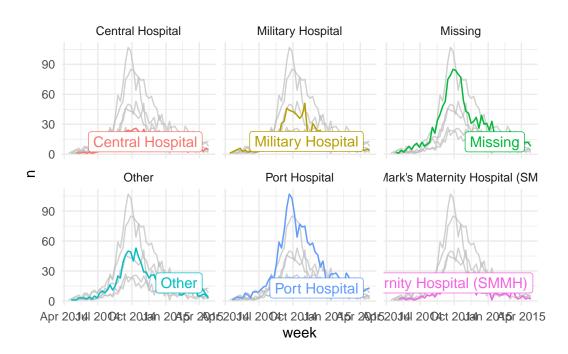
# replace NA values with unknown in the outcome variable
linelist <- linelist %>%
    mutate(outcome = replace_na(outcome, "Unknown"))

# produce a histogram of all cases by age
ggplot(
    data = linelist,
    mapping = aes(x = age_years, fill = outcome)) +
    geom_histogram() +
    gghighlight::gghighlight(outcome == "Death")  # highlight instances where the patient
```



This also works well with faceting functions - it allows the user to produce facet plots with the background data highlighted that doesn't apply to the facet! Below we count cases by week and plot the epidemic curves by hospital (color = and facet\_wrap() set to hospital

column).



### Plotting multiple datasets

Note that properly aligning axes to plot from multiple datasets in the same plot can be difficult. Consider one of the following strategies:

- Merge the data prior to plotting, and convert to "long" format with a column reflecting the dataset
- Use **cowplot** or a similar package to combine two plots (see below)

#### Combine plots

Two packages that are very useful for combining plots are **cowplot** and **patchwork**. In this page we will mostly focus on **cowplot**, with occassional use of **patchwork**.

Here is the online introduction to cowplot. You can read the more extensive documentation for each function online here. We will cover a few of the most common use cases and functions below.

The **cowplot** package works in tandem with **ggplot2** - essentially, you use it to arrange and combine ggplots and their legends into compound figures. It can also accept **base** R graphics.

```
pacman::p_load(
  tidyverse,  # data manipulation and visualisation
  cowplot,  # combine plots
  patchwork  # combine plots
)
```

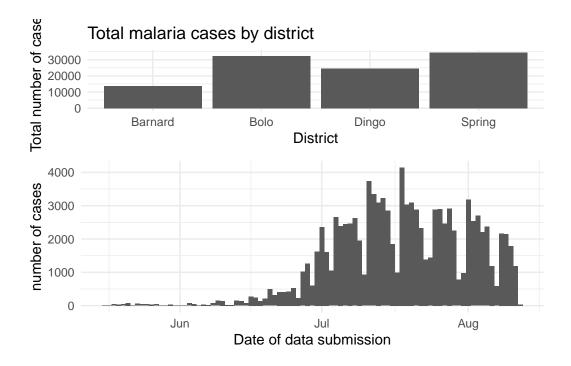
While faceting is a convenient approach to plotting, sometimes its not possible to get the results you want from its relatively restrictive approach. Here, you may choose to combine plots by sticking them together into a larger plot. There are three well known packages that are great for this - **cowplot**, **gridExtra**, and **patchwork**. However, these packages largely do the same things, so we'll focus on **cowplot** for this section.

# \* plot\_grid()

The **cowplot** package has a fairly wide range of functions, but the easiest use of it can be achieved through the use of plot\_grid(). This is effectively a way to arrange predefined plots in a grid formation. We can work through another example with the malaria dataset - here we can plot the total cases by district, and also show the epidemic curve over time.

```
malaria_data <- rio::import("data/malaria_facility_count_data.rds")

# bar chart of total cases by district
p1 <- ggplot(malaria_data, aes(x = District, y = malaria_tot)) +
    geom_bar(stat = "identity") +
    labs(
        x = "District",
        y = "Total number of cases",
        title = "Total malaria cases by district"
    ) +
    theme_minimal()</pre>
```



## \* Combine legends

If your plots have the same legend, combining them is relatively straight-forward. Simple use the **cowplot** approach above to combine the plots, but remove the legend from one of them (de-duplicate).

If your plots have different legends, you must use an alternative approach:

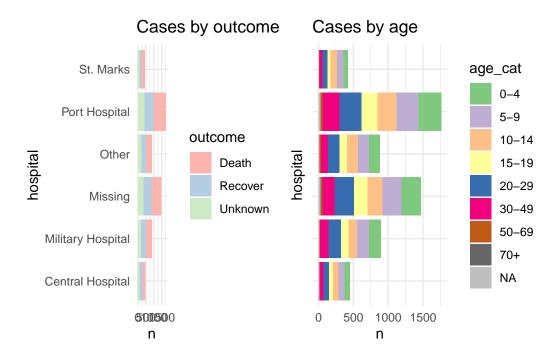
- 1) Create and save your plots without legends using theme(legend.position = "none")
- 2) Extract the legends from each plot using get\_legend() as shown below but extract legends from the plots modified to actually show the legend
- 3) Combine the legends into a legends panel
- 4) Combine the plots and legends panel

For demonstration we show the two plots separately, and then arranged in a grid with their own legends showing (ugly and inefficient use of space):

```
p1 <- linelist %>%
 mutate(hospital = recode(hospital, "St. Mark's Maternity Hospital (SMMH)" = "St. Marks")
  count(hospital, outcome) %>%
  ggplot()+
  geom_col(mapping = aes(x = hospital, y = n, fill = outcome))+
  scale_fill_brewer(type = "qual", palette = 4, na.value = "grey")+
  coord_flip()+
  theme_minimal()+
  labs(title = "Cases by outcome")
p2 <- linelist %>%
 mutate(hospital = recode(hospital, "St. Mark's Maternity Hospital (SMMH)" = "St. Marks")
  count(hospital, age_cat) %>%
  ggplot()+
  geom_col(mapping = aes(x = hospital, y = n, fill = age_cat))+
  scale_fill_brewer(type = "qual", palette = 1, na.value = "grey")+
  coord_flip()+
  theme_minimal()+
  theme(axis.text.y = element_blank())+
  labs(title = "Cases by age")
```

Here is how the two plots look when combined using plot\_grid() without combining their legends:

```
cowplot::plot_grid(p1, p2, rel_widths = c(0.3))
```

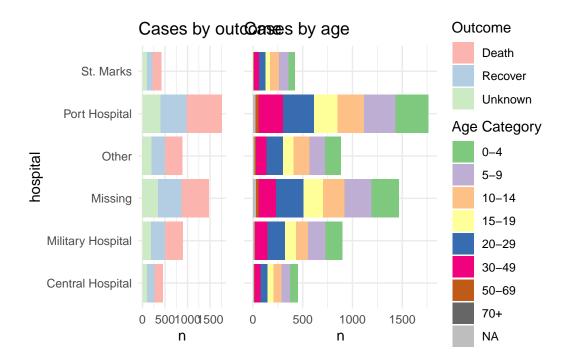


And now we show how to combine the legends. Essentially what we do is to define each plot without its legend (theme(legend.position = "none"), and then we define each plot's legend separately, using the get\_legend() function from cowplot. When we extract the legend from the saved plot, we need to add + the legend back in, including specifying the placement ("right") and smaller adjustments for alignment of the legends and their titles. Then, we combine the legends together vertically, and then combine the two plots with the newly-combined legends. Voila!

```
# Define plot 1 without legend
p1 <- linelist %>%
  mutate(hospital = recode(hospital, "St. Mark's Maternity Hospital (SMMH)" = "St. Marks")
  count(hospital, outcome) %>%
  ggplot()+
  geom_col(mapping = aes(x = hospital, y = n, fill = outcome))+
  scale_fill_brewer(type = "qual", palette = 4, na.value = "grey")+
  coord_flip()+
  theme_minimal()+
  theme(legend.position = "none")+
  labs(title = "Cases by outcome")

# Define plot 2 without legend
```

```
p2 <- linelist %>%
  mutate(hospital = recode(hospital, "St. Mark's Maternity Hospital (SMMH)" = "St. Marks")
  count(hospital, age_cat) %>%
  ggplot()+
  geom\ col(mapping = aes(x = hospital, y = n, fill = age\_cat))+
  scale_fill_brewer(type = "qual", palette = 1, na.value = "grey")+
  coord_flip()+
  theme_minimal()+
  theme(
    legend.position = "none",
    axis.text.y = element_blank(),
    axis.title.y = element_blank()
  )+
  labs(title = "Cases by age")
# extract legend from p1 (from p1 + legend)
leg_p1 <- cowplot::get_legend(p1 +</pre>
                                 theme(legend.position = "right",
                                                                         # extract vertical
                                       legend.justification = c(0,0.5)) + # so legends alignment
                                 labs(fill = "Outcome"))
                                                                          # title of legend
# extract legend from p2 (from p2 + legend)
leg_p2 <- cowplot::get_legend(p2 +</pre>
                                 theme(legend.position = "right",
                                                                     # extract vertica
                                       legend.justification = c(0,0.5))+ # so legends alignment
                                 labs(fill = "Age Category"))
                                                                         # title of legend
# create a blank plot for legend alignment
#blank_p <- patchwork::plot_spacer() + theme_void()</pre>
# create legends panel, can be one on top of the other (or use spacer commented above)
legends <- cowplot::plot_grid(leg_p1, leg_p2, nrow = 2, rel_heights = c(.3, .7))</pre>
# combine two plots and the combined legends panel
combined <- cowplot::plot_grid(p1, p2, legends, ncol = 3, rel_widths = c(.4, .4, .2))
combined # print
```



This solution was learned from this post with a minor fix to align legends from this post.

TIP: Fun note - the "cow" in cowplot comes from the creator's name - Claus O. Wilke.

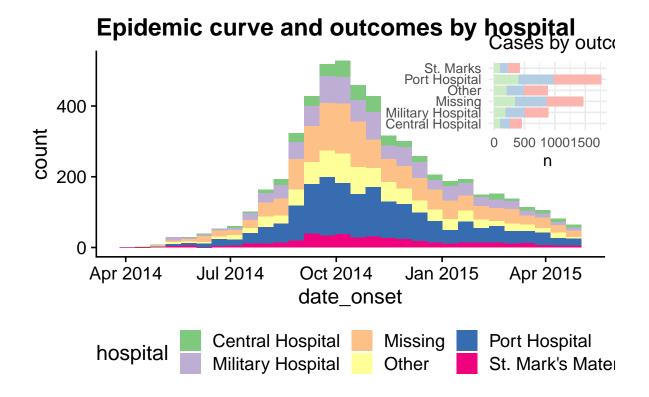
## \* Inset plots

You can inset one plot in another using **cowplot**. Here are things to be aware of:

- Define the main plot with theme\_half\_open() from cowplot; it may be best to have the legend either on top or bottom
- Define the inset plot. Best is to have a plot where you do not need a legend. You can remove plot theme elements with element\_blank() as shown below.
- Combine them by applying ggdraw() to the main plot, then adding draw\_plot() on the inset plot and specifying the coordinates (x and y of lower left corner), height and width as proportion of the whole main plot.

```
# Define main plot
main_plot <- ggplot(data = linelist)+
  geom_histogram(aes(x = date_onset, fill = hospital))+
  scale_fill_brewer(type = "qual", palette = 1, na.value = "grey")+
  theme_half_open()+</pre>
```

```
theme(legend.position = "bottom")+
 labs(title = "Epidemic curve and outcomes by hospital")
# Define inset plot
inset_plot <- linelist %>%
 mutate(hospital = recode(hospital, "St. Mark's Maternity Hospital (SMMH)" = "St. Marks")
 count(hospital, outcome) %>%
 ggplot()+
   geom_col(mapping = aes(x = hospital, y = n, fill = outcome))+
   scale_fill_brewer(type = "qual", palette = 4, na.value = "grey")+
    coord_flip()+
   theme_minimal()+
    theme(legend.position = "none",
          axis.title.y = element_blank())+
   labs(title = "Cases by outcome")
# Combine main with inset
cowplot::ggdraw(main_plot)+
     draw_plot(inset_plot,
              x = .6, y = .55, \#x = .07, y = .65,
              width = .4, height = .4)
```



This technique is explained more in these two vignettes:

Wilke lab draw\_plot() documentation