seaborn_tutorial

February 6, 2025

1 Introduction to Seaborn

Seaborn is a Python visualisation library built on matplotlib. It provides a high-level interface for drawing attractive and informative statistical graphics. This tutorial will guide you through some of the fundamental plotting functions used in exploratory data analysis.

For more information you can check out the Seaborn documentation: https://seaborn.pydata.org/index.html

You will need to make sure that Seaborn is installed before importing. Here we follow the convention of importing Seaborn as sns.

[1]:
```
import seaborn as sns
```

1.1 Load the dataset

First we need to load a dataset. For this tutorial, we will use Seaborn to load one of the datasets that it makes available for testing and practice. You can see the full set of Seaborn datasets here: https://github.com/mwaskom/seaborn-data

Here we'll go with the penguins dataset.

[2]:
```
penguins_df = sns.load_dataset("penguins")
```

This gives us a regular Pandas DataFrame.

[3]:
```
penguins_df.sample(10)
```

[3]:

	species	island	bill_length_mm	bill_depth_mm	flipper_length_mm	\
323	Gentoo	Biscoe	49.1	15.0	228.0	
316	Gentoo	Biscoe	49.4	15.8	216.0	
9	Adelie	Torgersen	42.0	20.2	190.0	
166	Chinstrap	Dream	45.9	17.1	190.0	
343	Gentoo	Biscoe	49.9	16.1	213.0	
37	Adelie	Dream	42.2	18.5	180.0	
145	Adelie	Dream	39.0	18.7	185.0	
60	Adelie	Biscoe	35.7	16.9	185.0	
57	Adelie	Biscoe	40.6	18.8	193.0	
204	Chinstrap	Dream	45.7	17.3	193.0	

```
     body_mass_g     sex
323       5500.0    Male
316       4925.0    Male
9         4250.0     NaN
166       3575.0  Female
343       5400.0    Male
37        3550.0  Female
145       3650.0    Male
60        3150.0  Female
57        3800.0    Male
204       3600.0  Female
```

[4]:
```
penguins_df.describe().T
```

[4]:
```
                   count         mean         std     min       25%      50%  \
bill_length_mm     342.0    43.921930    5.459584    32.1    39.225    44.45
bill_depth_mm      342.0    17.151170    1.974793    13.1    15.600    17.30
flipper_length_mm  342.0   200.915205   14.061714   172.0   190.000   197.00
body_mass_g        342.0  4201.754386  801.954536  2700.0  3550.000  4050.00

                     75%     max
bill_length_mm      48.5    59.6
bill_depth_mm       18.7    21.5
flipper_length_mm  213.0   231.0
body_mass_g        4750.0  6300.0
```

[5]:
```
penguins_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 344 entries, 0 to 343
Data columns (total 7 columns):
 #   Column             Non-Null Count  Dtype
---  ------             --------------  -----
 0   species            344 non-null    object
 1   island             344 non-null    object
 2   bill_length_mm     342 non-null    float64
 3   bill_depth_mm      342 non-null    float64
 4   flipper_length_mm  342 non-null    float64
 5   body_mass_g        342 non-null    float64
 6   sex                333 non-null    object
dtypes: float64(4), object(3)
memory usage: 18.9+ KB
```

1.2 Visualise our data

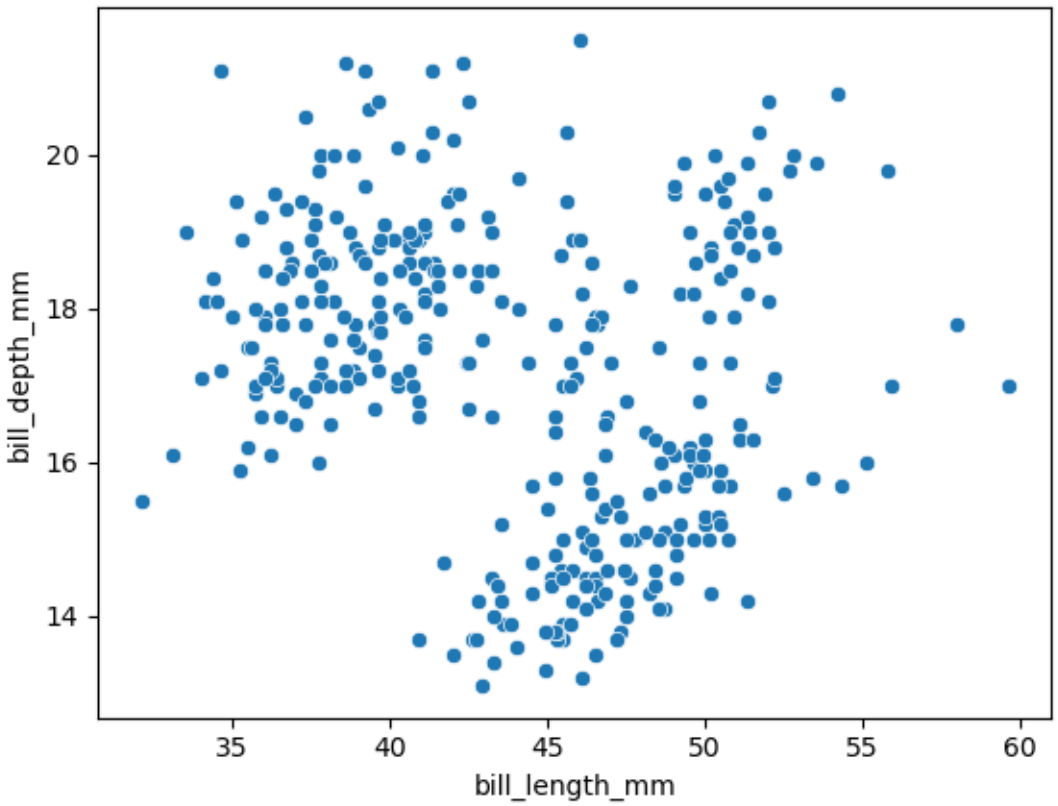
1.2.1 Scatter plots

With a scatter plot, we can plot 2D points. In the example below we plot bill length against bill depth.

For more info on how to customise a scatterplot see: https://seaborn.pydata.org/generated/seaborn.scatterplot.htm

[6]:
```
sns.scatterplot(data=penguins_df,
                x="bill_length_mm",
                y="bill_depth_mm")
```

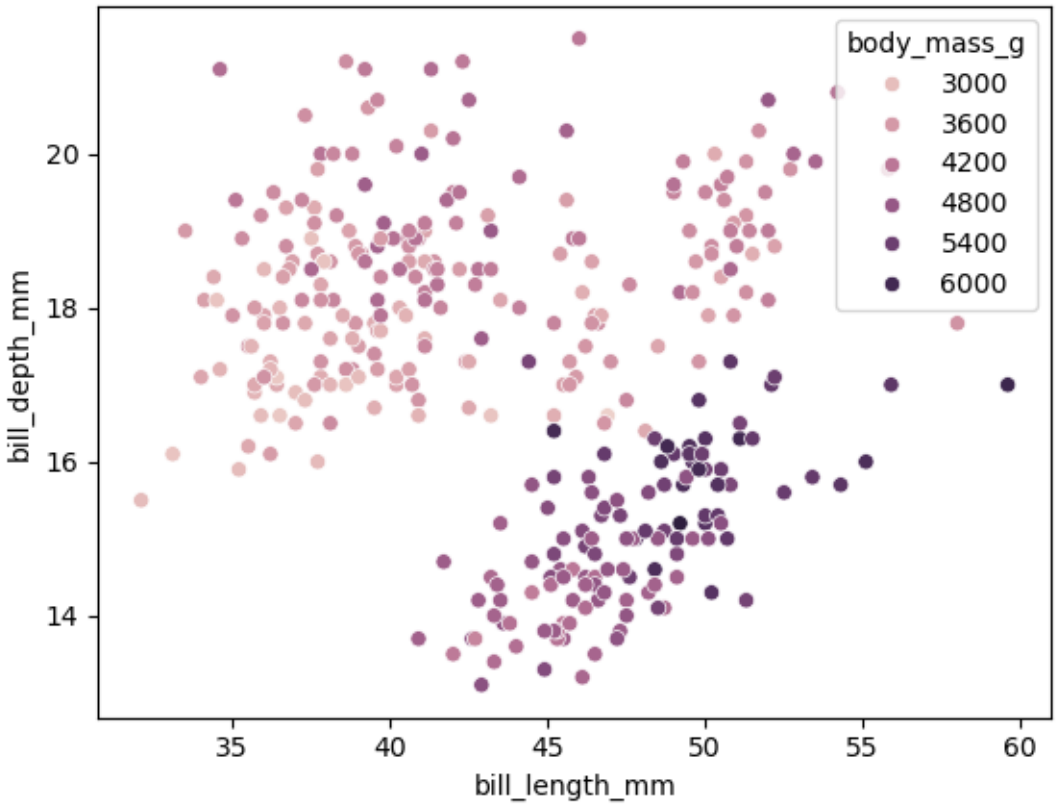
[6]: <Axes: xlabel='bill_length_mm', ylabel='bill_depth_mm'>



Using the hue argument, we can represent a third numeric or categorical variable. Here we use hue to show the body mass.

[7]:
```
sns.scatterplot(data=penguins_df,
                x="bill_length_mm",
                y="bill_depth_mm",
                hue="body_mass_g")
```

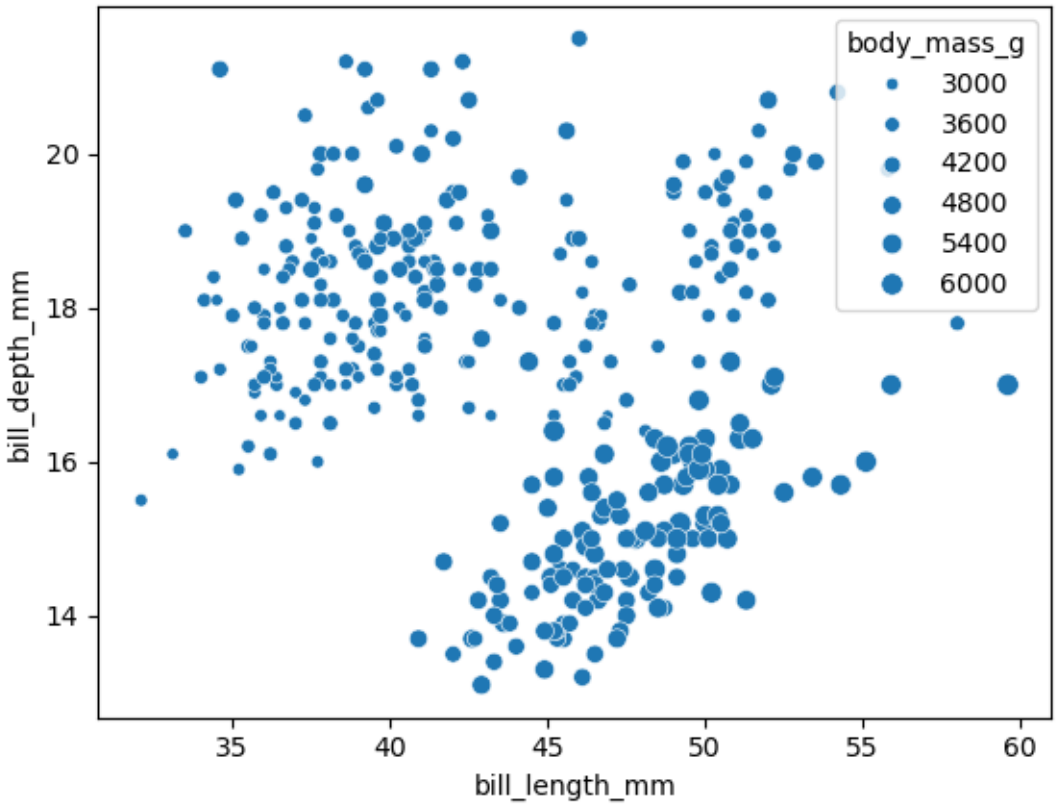
[7]: <Axes: xlabel='bill_length_mm', ylabel='bill_depth_mm'>



We can also use the size argument to represent another variable. Here we represent body mass with different sized points rather than different coloured points.

[8]:
```
sns.scatterplot(data=penguins_df,
                x="bill_length_mm",
                y="bill_depth_mm",
                size="body_mass_g")
```

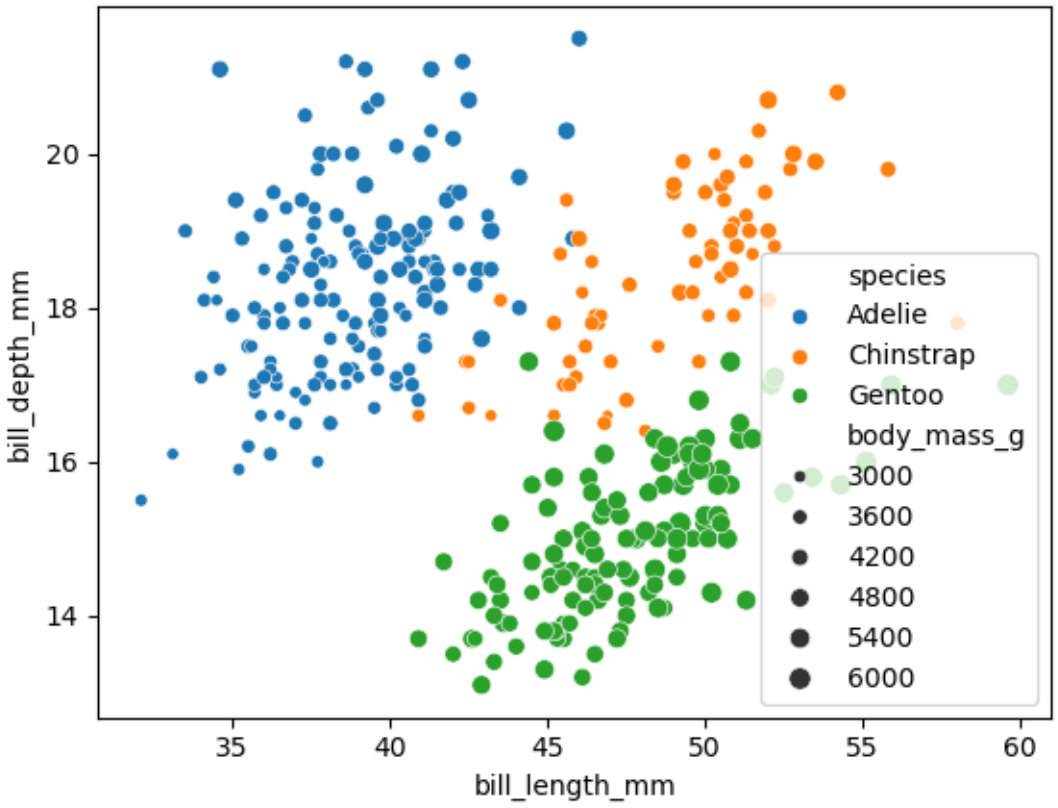
[8]:
```
<Axes: xlabel='bill_length_mm', ylabel='bill_depth_mm'>
```



We can use both hue and size. In the example below we show four different variables.

[9]:
```
sns.scatterplot(data=penguins_df,
                x="bill_length_mm",
                y="bill_depth_mm",
                hue="species",
                size="body_mass_g")
```

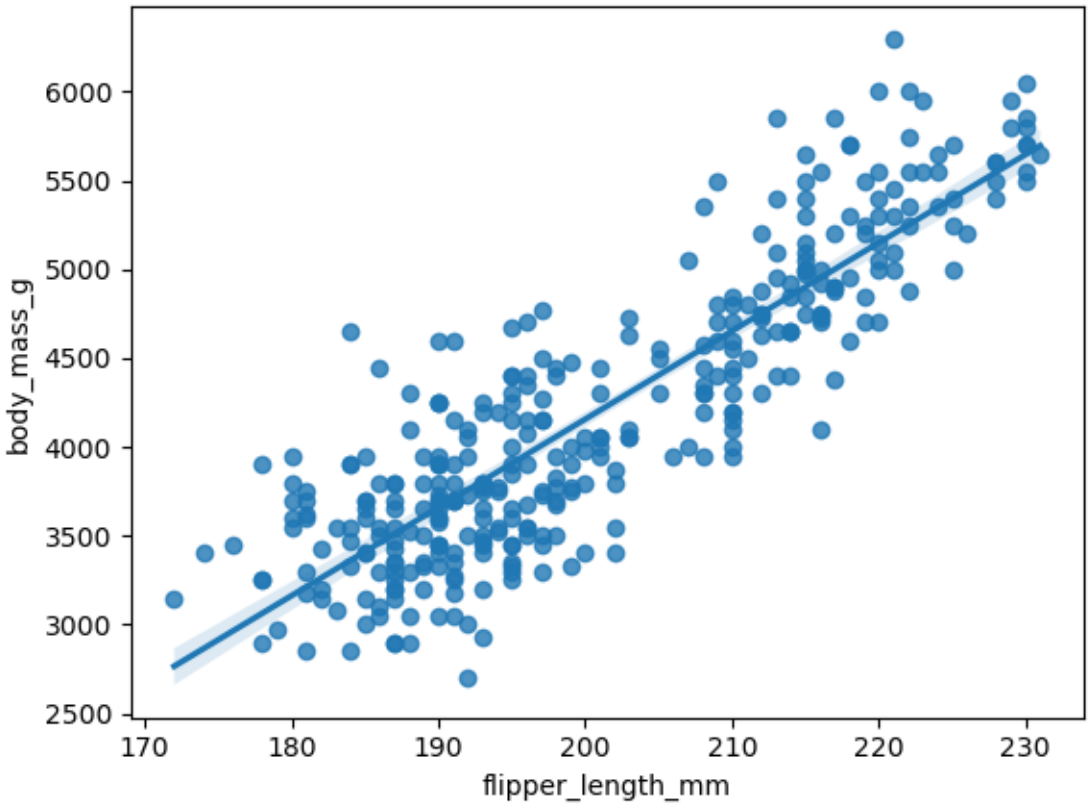
[9]:
```
<Axes: xlabel='bill_length_mm', ylabel='bill_depth_mm'>
```



Adding a regression line Here we switch to regplot in order to show a regression line. See the following for more information on regplot: https://seaborn.pydata.org/generated/seaborn.regplot.html

[10]:
```
sns.regplot(data=penguins_df,
            x="flipper_length_mm",
            y="body_mass_g")
```

[10]:
```
<Axes: xlabel='flipper_length_mm', ylabel='body_mass_g'>
```



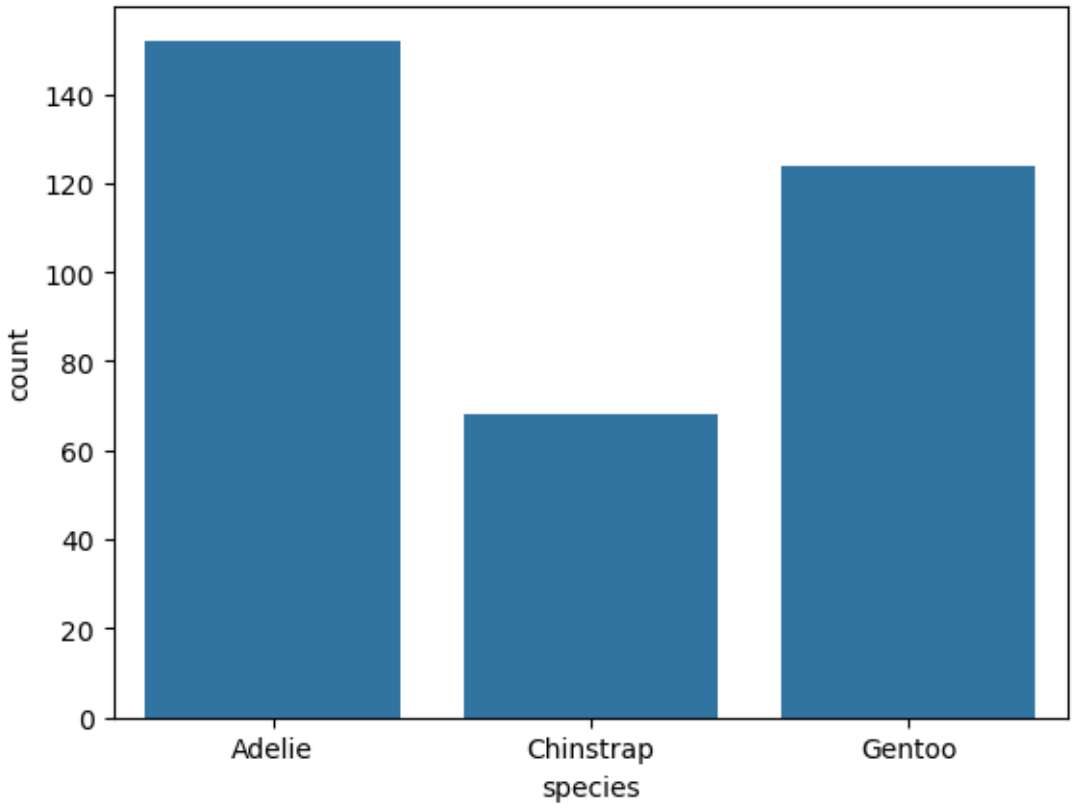
1.2.2 Count plots

Count plots "show the counts of observations in each categorical bin using bars" - https://seaborn.pydata.org/generated/seaborn.countplot.html.

Here we show the counts of penguins of different species.

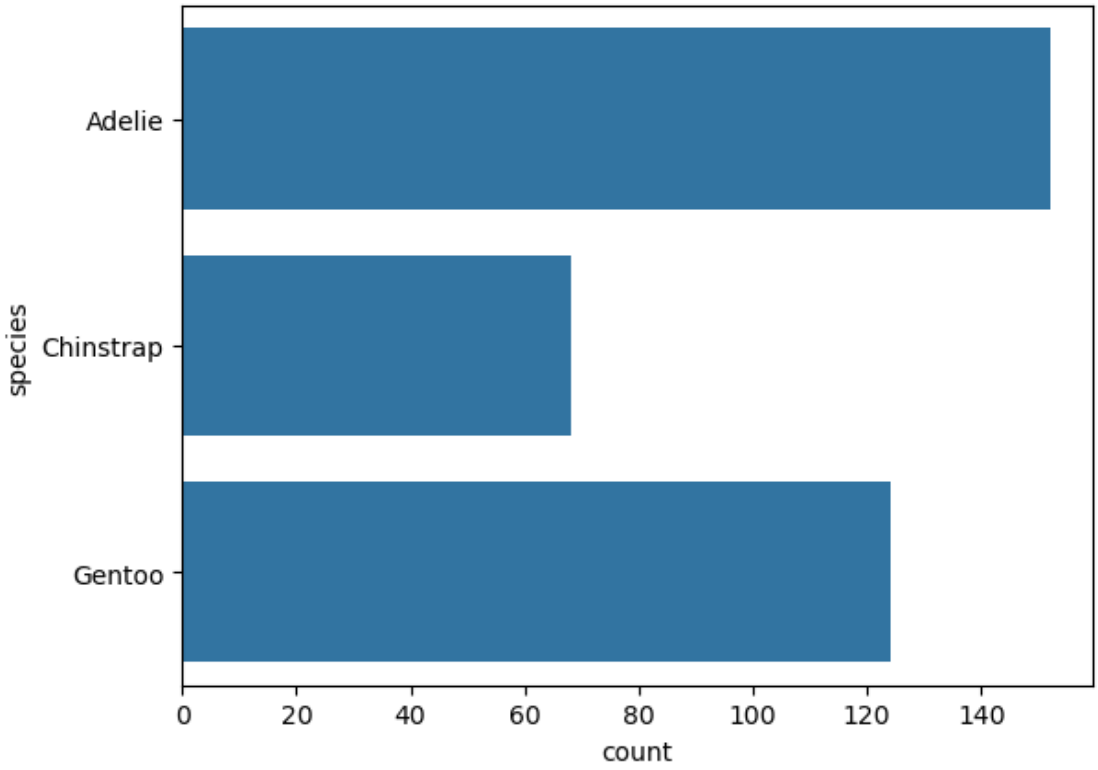
[11]:
```
sns.countplot(data=penguins_df,
              x="species")
```

[11]:
```
<Axes: xlabel='species', ylabel='count'>
```



[12]:
```
sns.countplot(data=penguins_df,
              y="species")
```

[12]:
```
<Axes: xlabel='count', ylabel='species'>
```



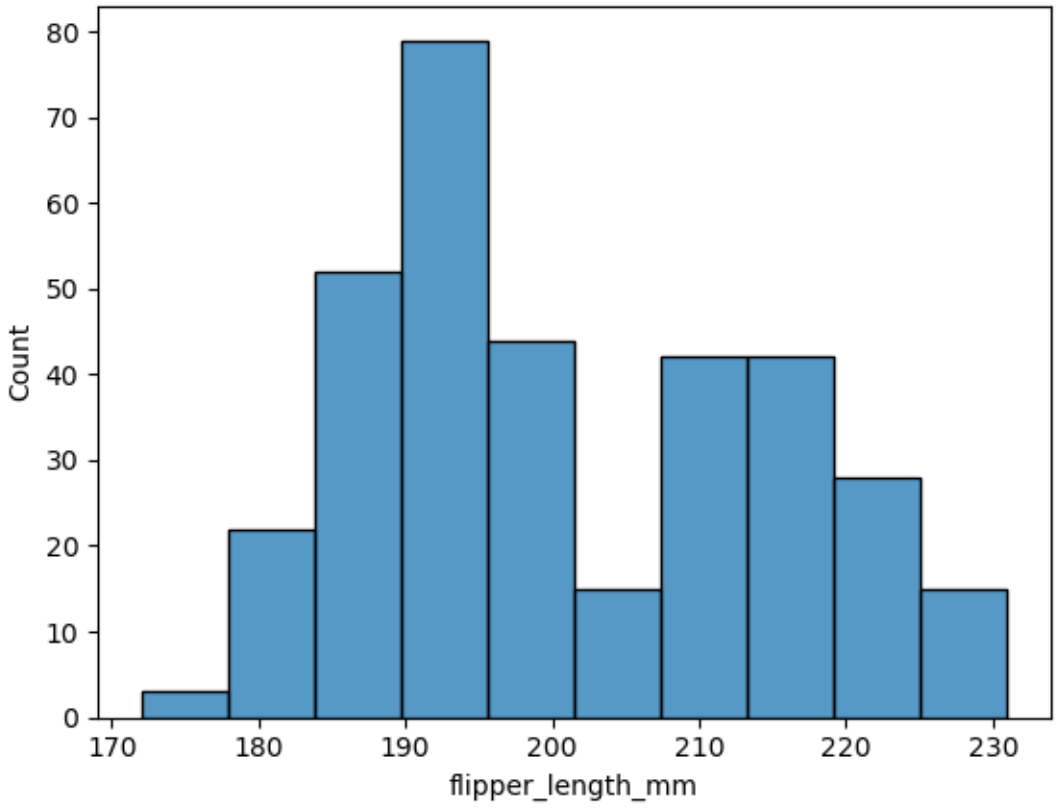
1.2.3 Histograms

"A histogram is a classic visualization tool that represents the distribution of one or more variables by counting the number of observations that fall within discrete bins." - https://seaborn.pydata.org/generated/seaborn.histplot.html

Here we use histplot to show the distribution of the flipper_length_mm values.

[13]:
```
sns.histplot(data=penguins_df,
             x="flipper_length_mm")
```

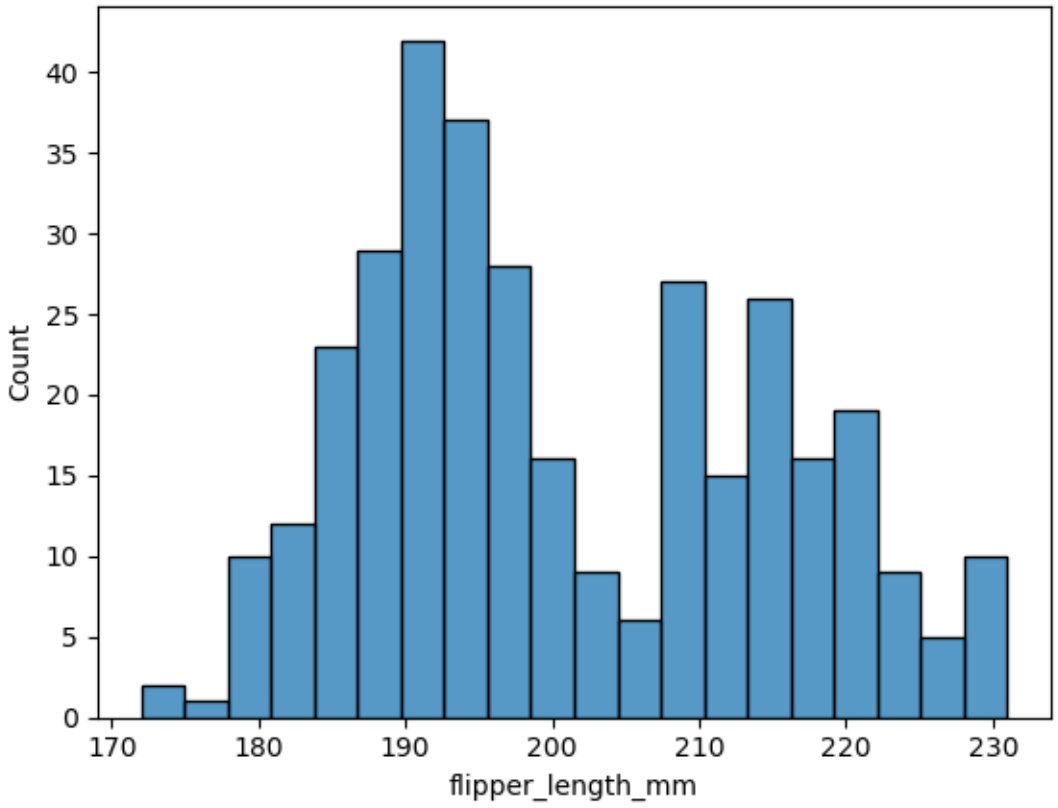
[13]:
```
<Axes: xlabel='flipper_length_mm', ylabel='Count'>
```



There are many different ways to customise and configure the histogram as documented in the link above. For example, here we change the number of bins to 20.

[14]:
```
sns.histplot(data=penguins_df,
             x="flipper_length_mm",
             bins=20)
```

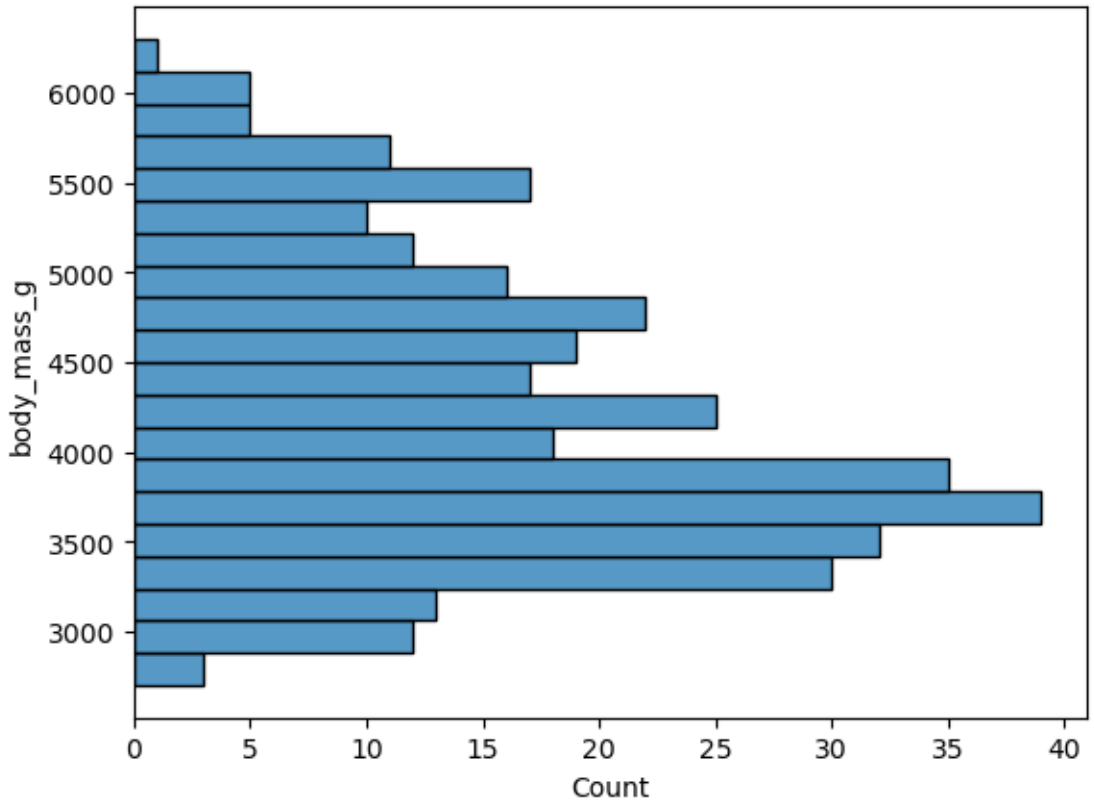
[14]:
```
<Axes: xlabel='flipper_length_mm', ylabel='Count'>
```



And here we show a horizontal histogram by setting y rather x. In this case we're showing the distribution of body mass.

[15]:
```
sns.histplot(data=penguins_df,
             y="body_mass_g",
             bins=20)
```

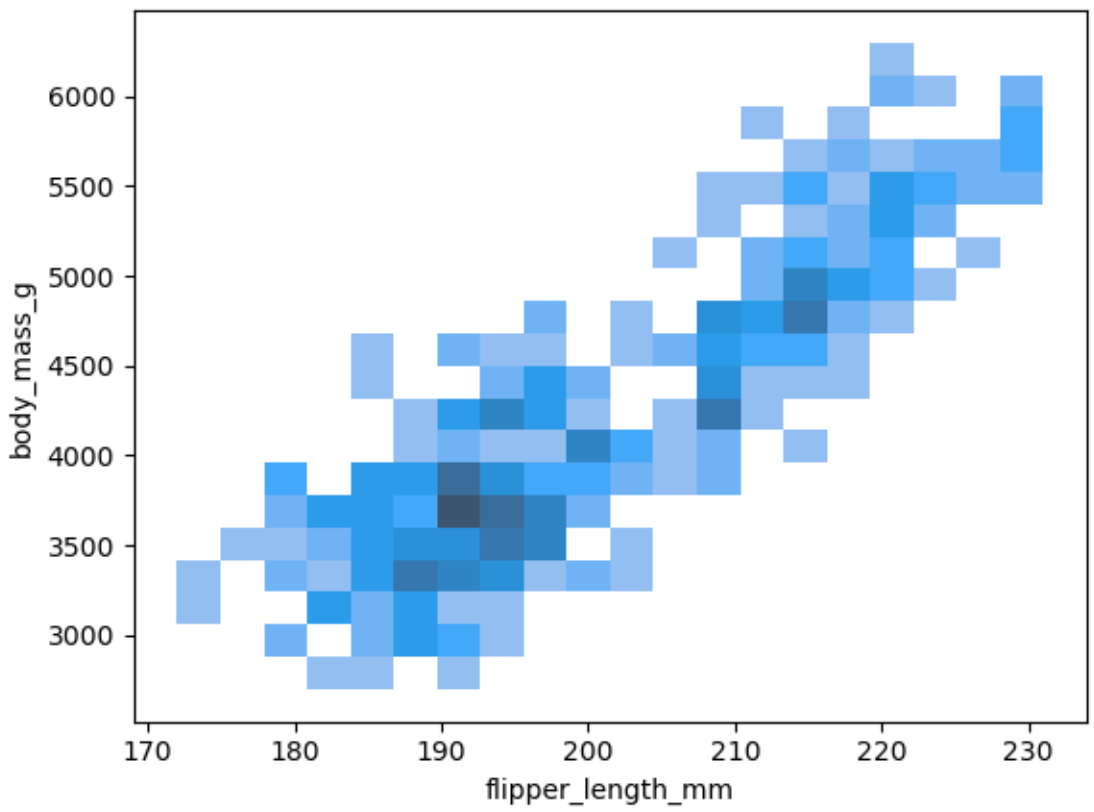
[15]:
```
<Axes: xlabel='Count', ylabel='body_mass_g'>
```



We can also create a bivariate histogram, where the data is grouped into 2D bins, by setting both x and y.

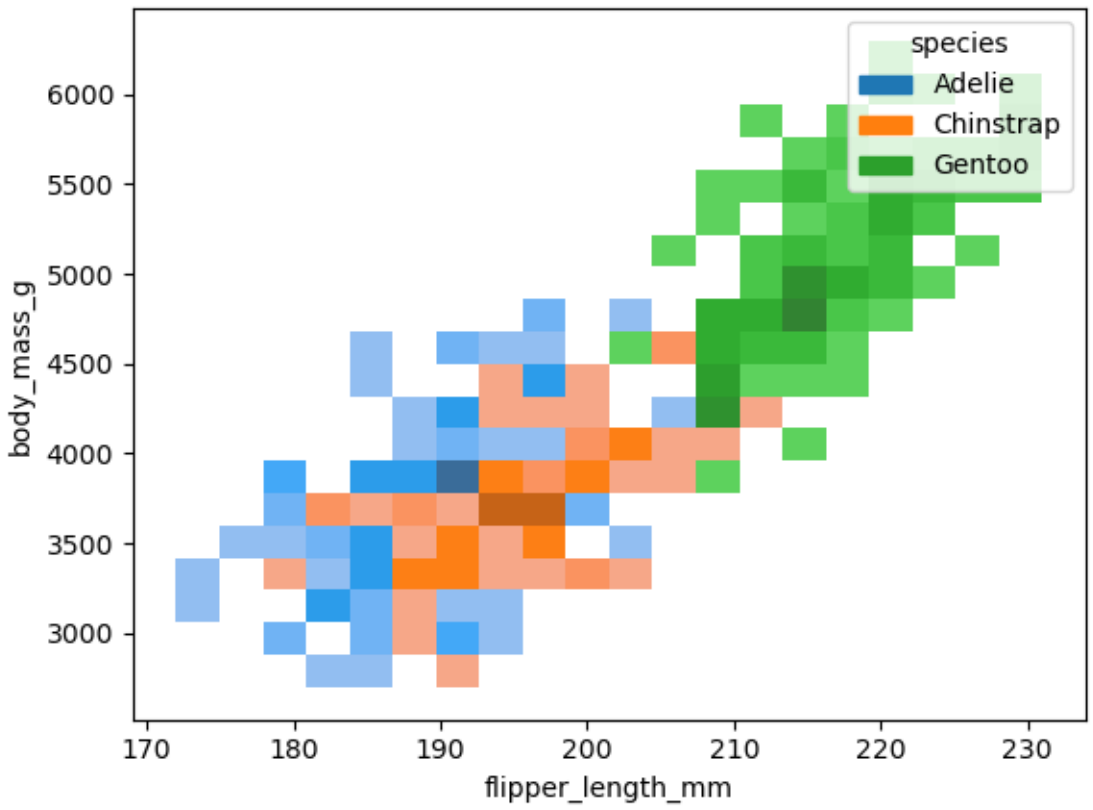
[16]:
```
sns.histplot(data=penguins_df,
             x="flipper_length_mm",
             y="body_mass_g",
             bins=20)
```

[16]:
```
<Axes: xlabel='flipper_length_mm', ylabel='body_mass_g'>
```



[17]:
```
sns.histplot(data=penguins_df,
             x="flipper_length_mm",
             y="body_mass_g",
             hue="species",
             bins=20)
```

[17]: <Axes: xlabel='flipper_length_mm', ylabel='body_mass_g'>



1.2.4 Joint plots

Joint plots allow us to draw a plot of two variables with bivariate and univariate graphs.

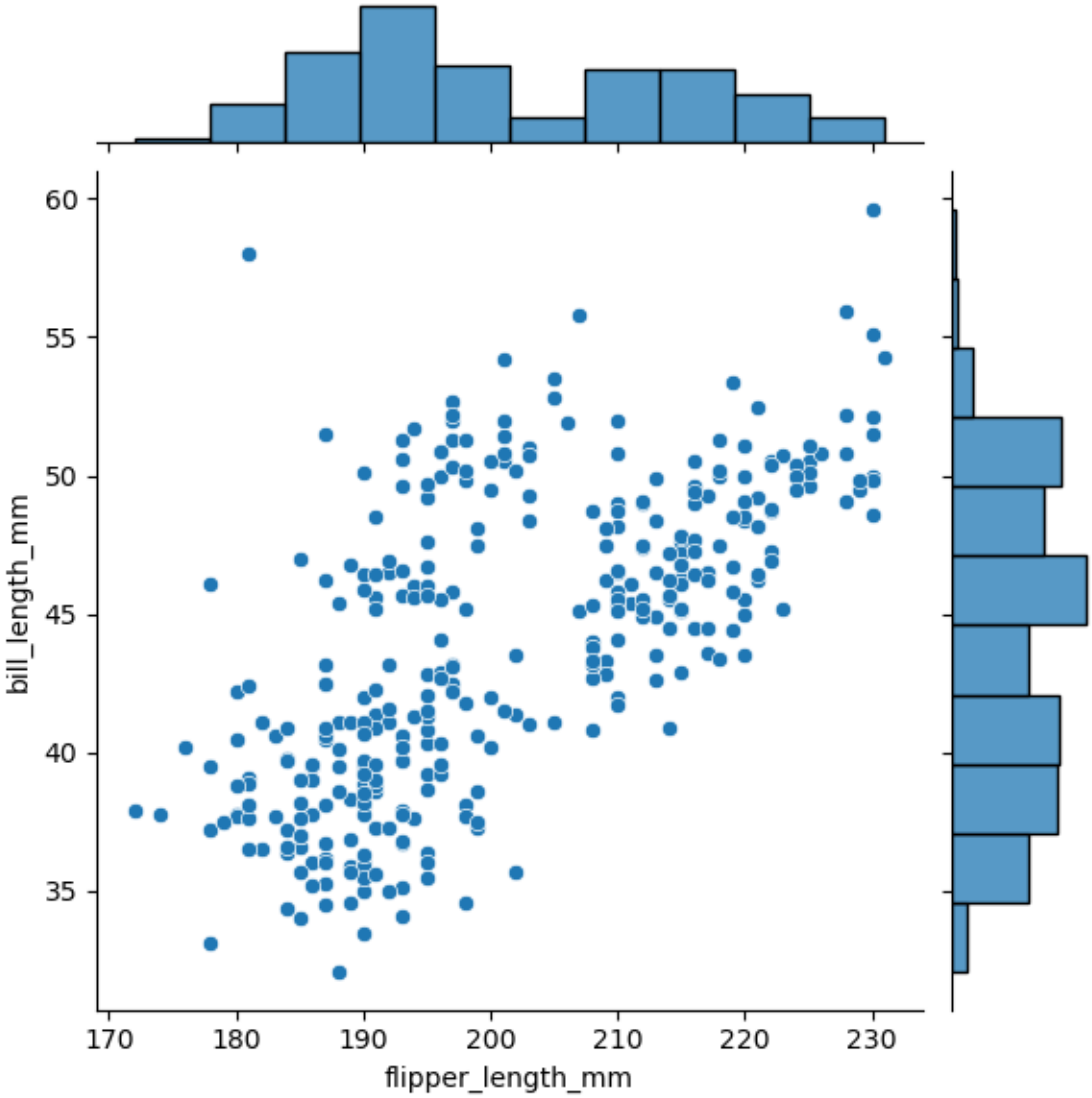
There are many other options for jointplot that will give different visualisations of the data, see https://seaborn.pydata.org/generated/seaborn.jointplot.html

See also JointGrid: https://seaborn.pydata.org/generated/seaborn.JointGrid.html#seaborn.JointGrid

Here we plot flipper length against bill length. Notice that we get a scatter plot and two histograms.

[18]:
```
sns.jointplot(data=penguins_df,
              x="flipper_length_mm",
              y="bill_length_mm")
```

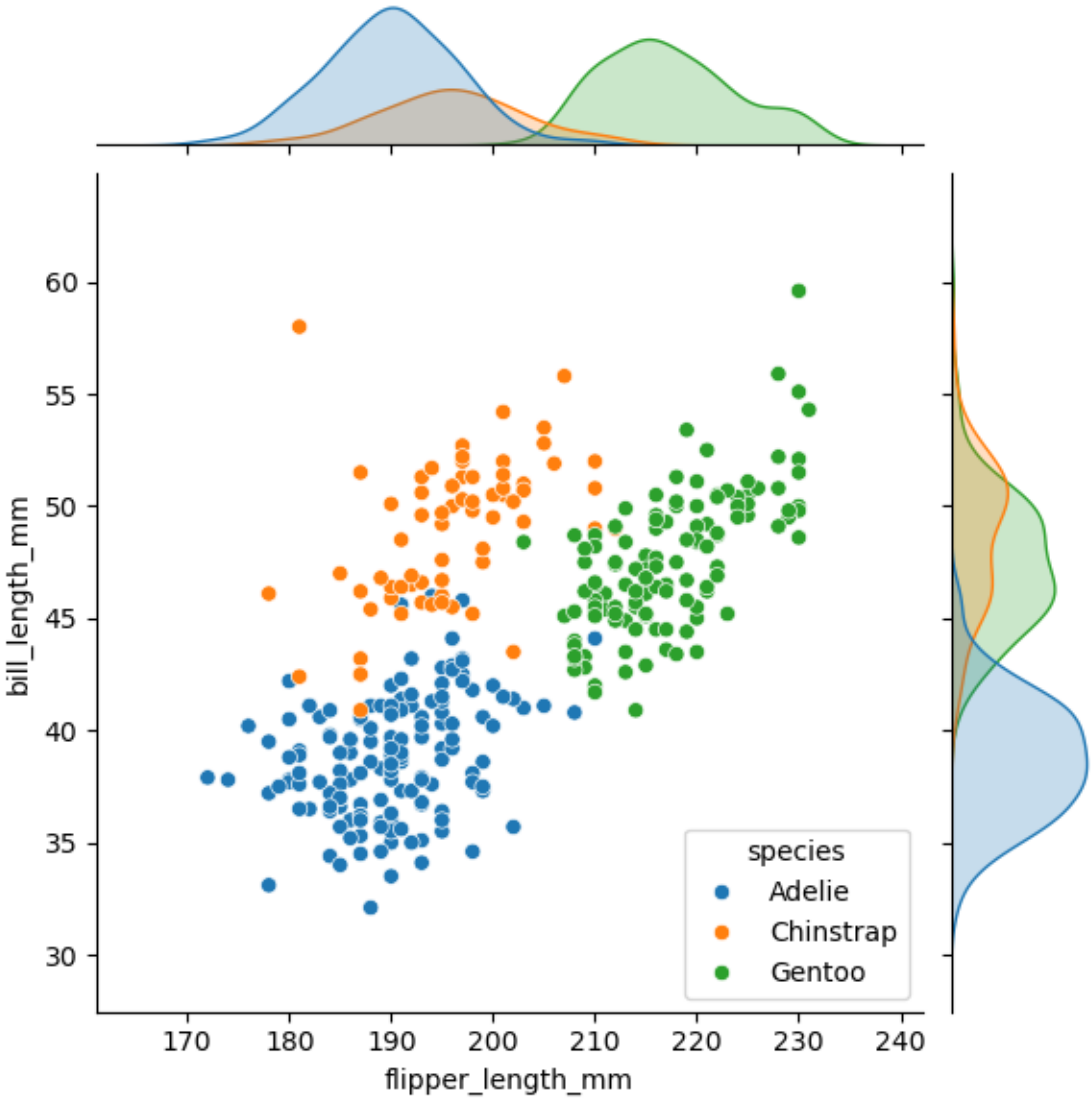
[18]:
```
<seaborn.axisgrid.JointGrid at 0x24dce6a1dc0>
```



We can again use the hue argument to represent a third variable, either categorical or numeric, with colour. Here we show the penguin species.

[19]:
```
sns.jointplot(data=penguins_df,
              x="flipper_length_mm",
              y="bill_length_mm",
              hue="species")
```

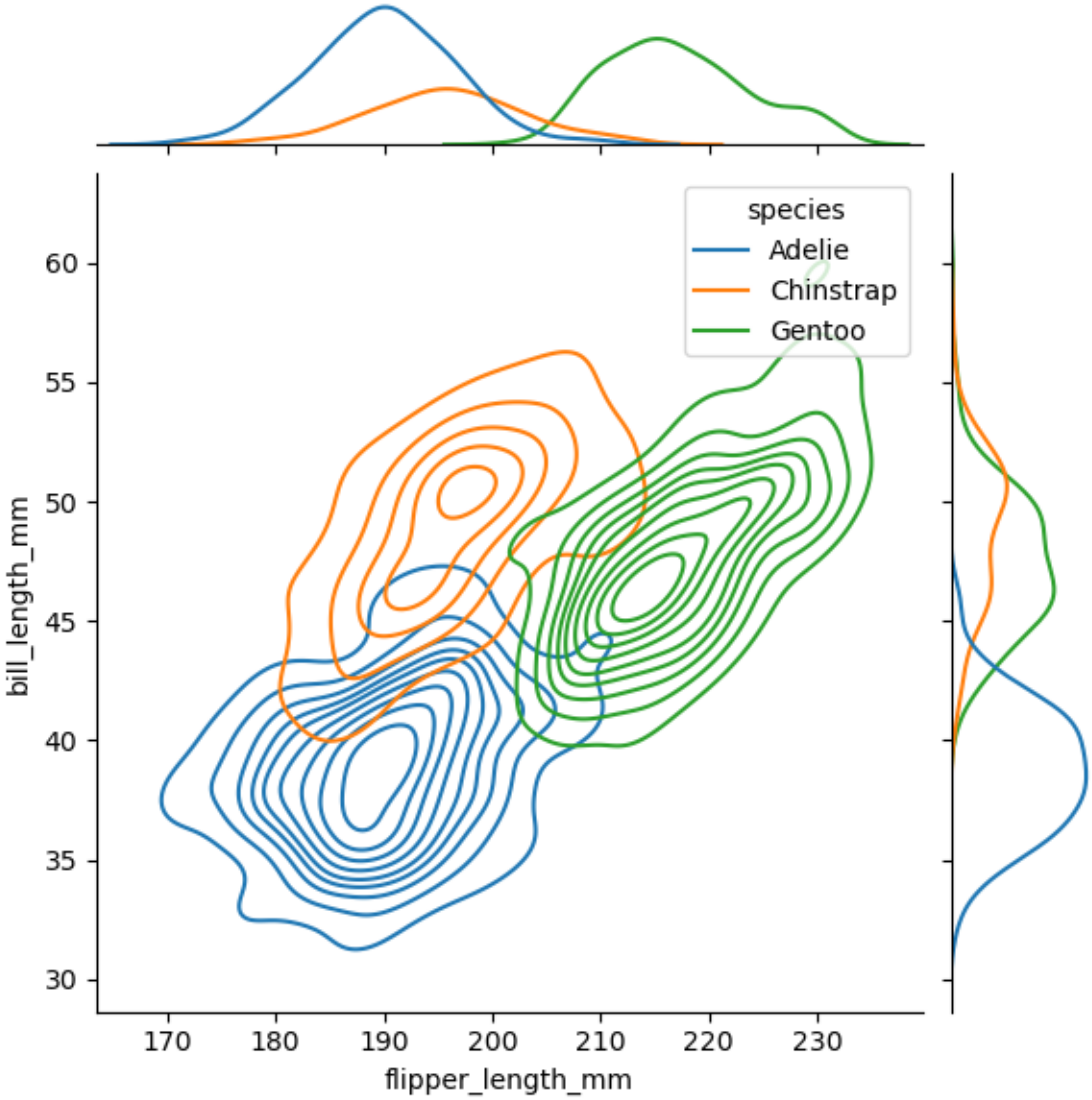
[19]: <seaborn.axisgrid.JointGrid at 0x24dcfa9e030>



There are various kinds of jointplot. Here we set kind="kde" (kernal density estimate) to show density contours.

[20]:
```
sns.jointplot(data=penguins_df,
              x="flipper_length_mm",
              y="bill_length_mm",
              hue="species",
              kind="kde")
```

[20]: <seaborn.axisgrid.JointGrid at 0x24dcfb10e60>

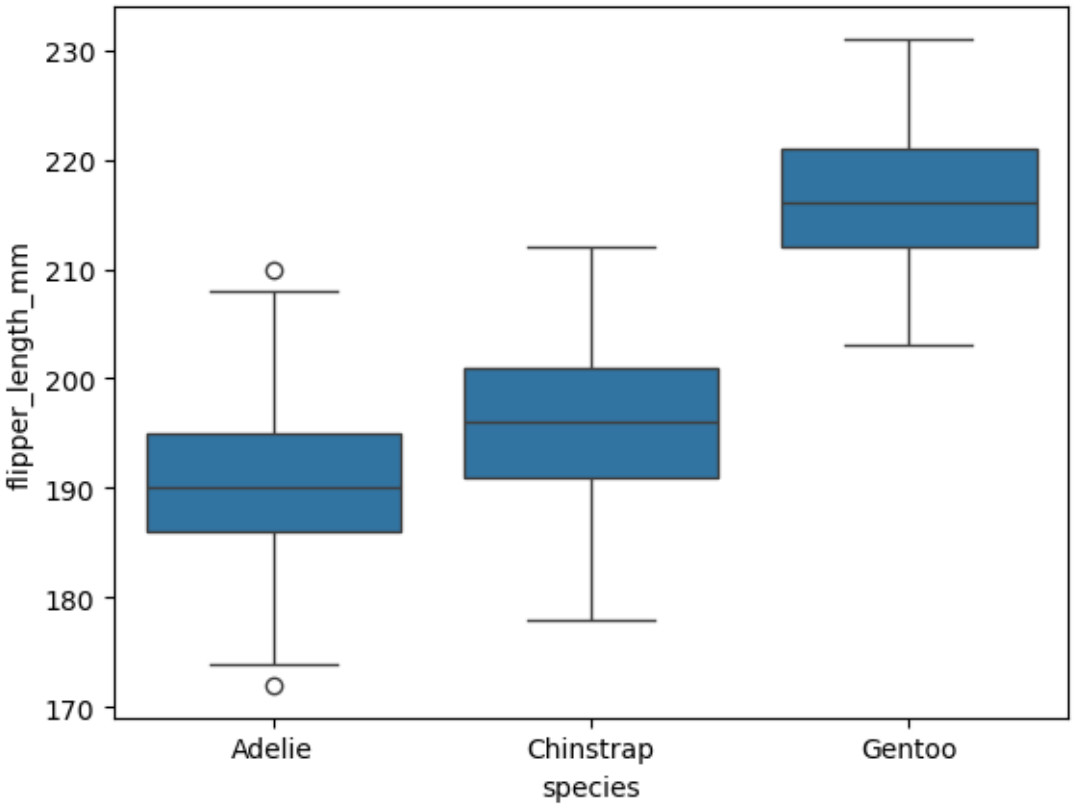


1.2.5 Boxplots

A box plot (or box-and-whisker plot) shows the distribution of quantitative data in a way that facilitates comparisons between variables or across levels of a categorical variable. The box shows the quartiles of the dataset while the whiskers extend to show the rest of the distribution, except for points that are determined to be "outliers" using a method that is a function of the inter-quartile range. - https://seaborn.pydata.org/generated/seaborn.boxplot.html#seaborn.boxplot

[21]:
```
sns.boxplot(data=penguins_df,
            x="species",
            y="flipper_length_mm")
```

[21]:
```
<Axes: xlabel='species', ylabel='flipper_length_mm'>
```



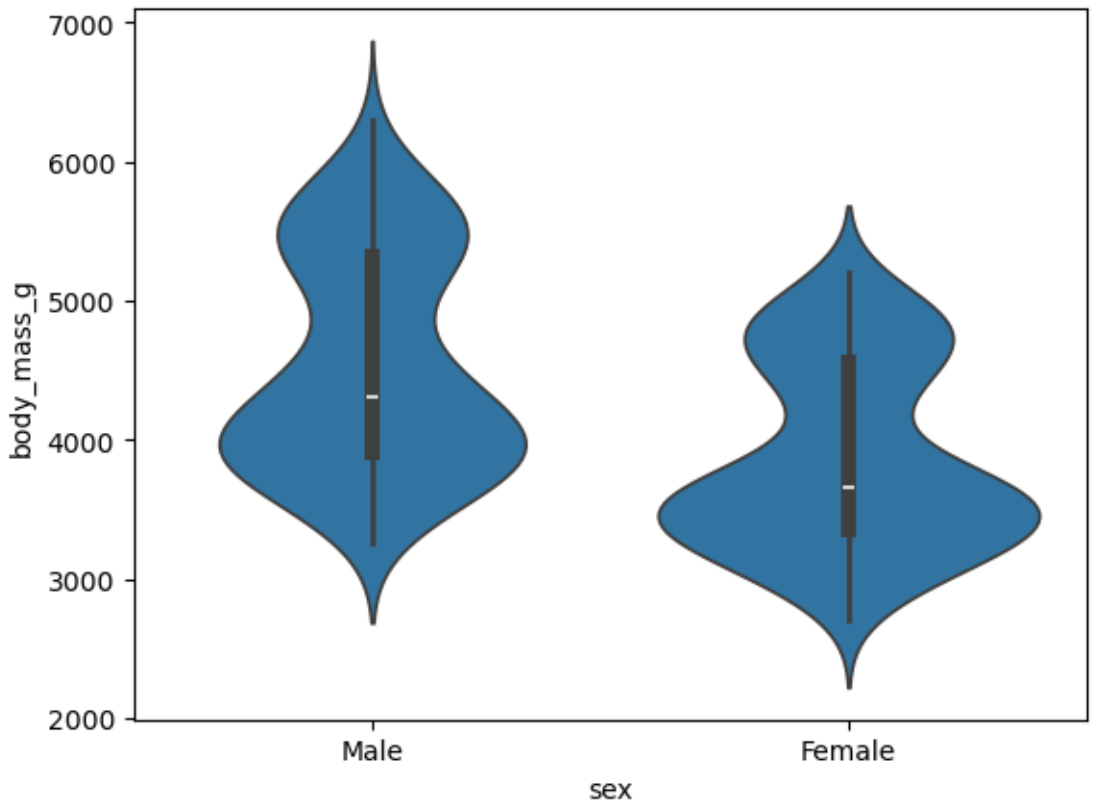
1.2.6 Violin plots

"A violin plot plays a similar role as a box-and-whisker plot. It shows the distribution of data points after grouping by one (or more) variables. Unlike a box plot, each violin is drawn using a kernel density estimate of the underlying distribution." - https://seaborn.pydata.org/generated/seaborn.violinplot.html

In this example we show the body mass grouped by sex.

[22]:
```
sns.violinplot(data=penguins_df,
               x="sex",
               y="body_mass_g")
```

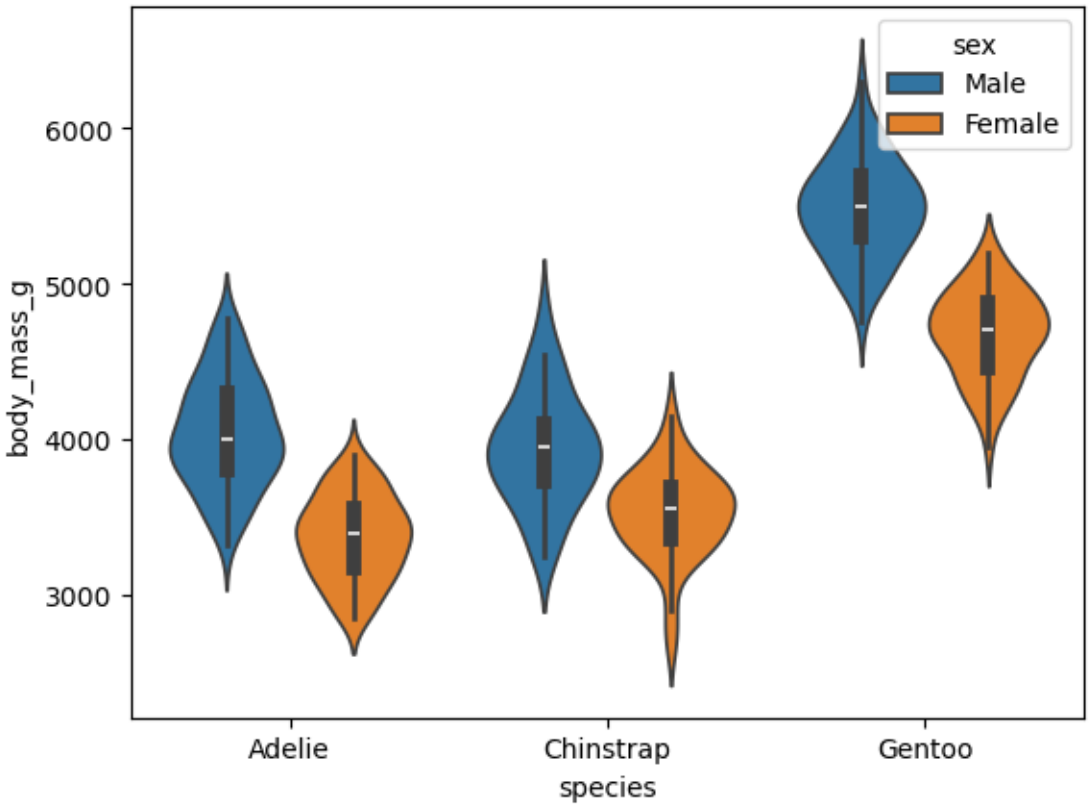
[22]:
```
<Axes: xlabel='sex', ylabel='body_mass_g'>
```



Here we show the distributions of body mass broken down by species and sex.

[23]:
```
sns.violinplot(data=penguins_df,
               x="species",
               y="body_mass_g",
               hue='sex')
```

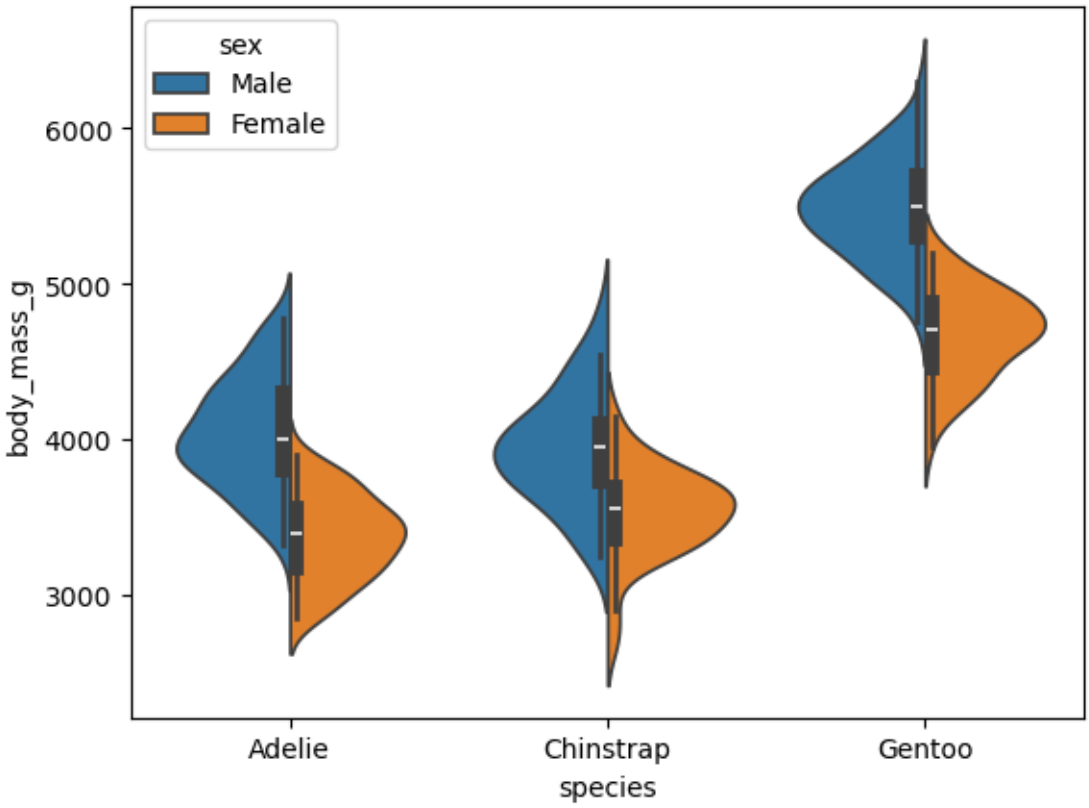
[23]:
```
<Axes: xlabel='species', ylabel='body_mass_g'>
```



This next example is the same as the one above, except that we've set split=True.

[24]:
```
sns.violinplot(data=penguins_df,
               x="species",
               y="body_mass_g",
               hue='sex',
               split=True
               )
```

[24]:
```
<Axes: xlabel='species', ylabel='body_mass_g'>
```



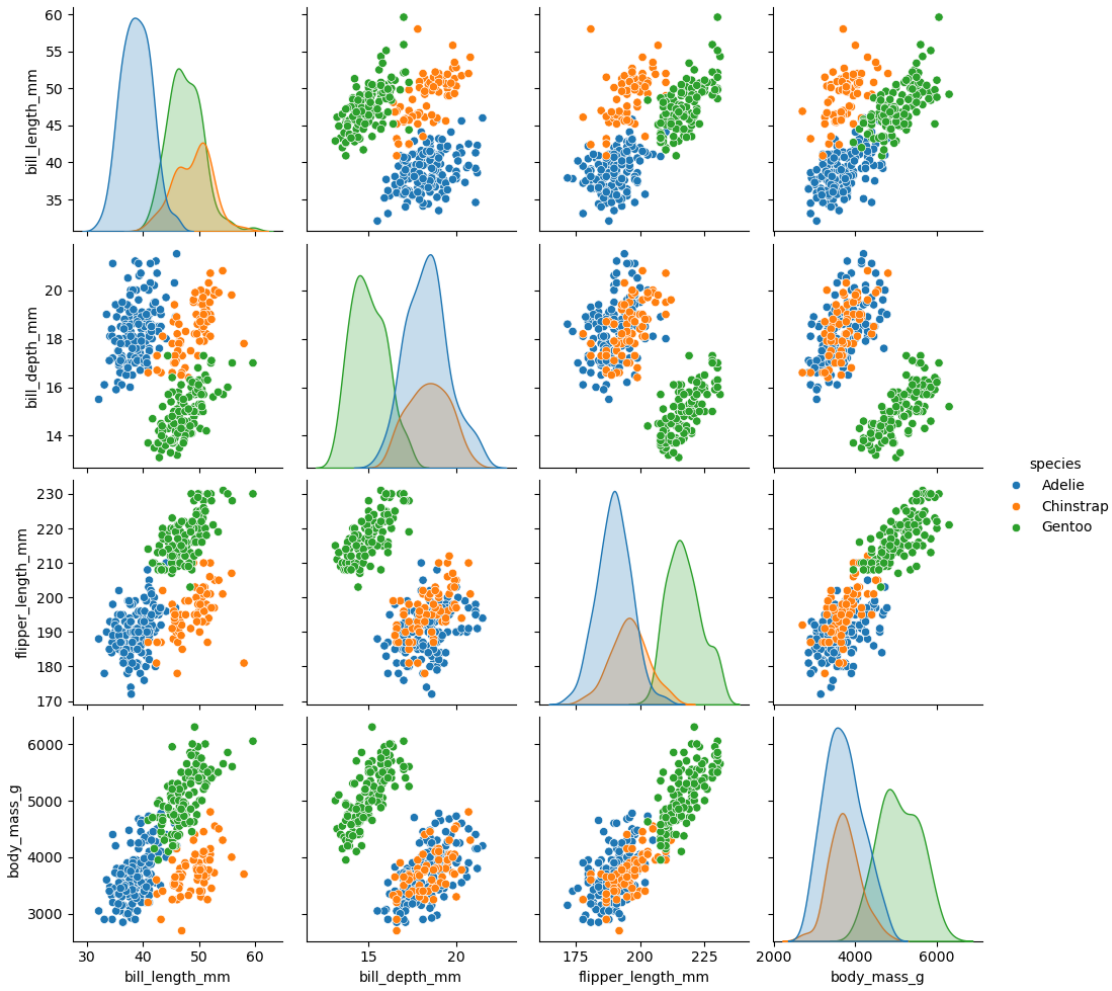
1.2.7 Pair plots

Pair plots allow us to get a great overview our data. In this example we see scatter plots for every pair of numeric variables, along the distributions of each numeric variable. We're also using hue to highlight species.

For more info on customising pairplots see https://seaborn.pydata.org/generated/seaborn.pairplot.html

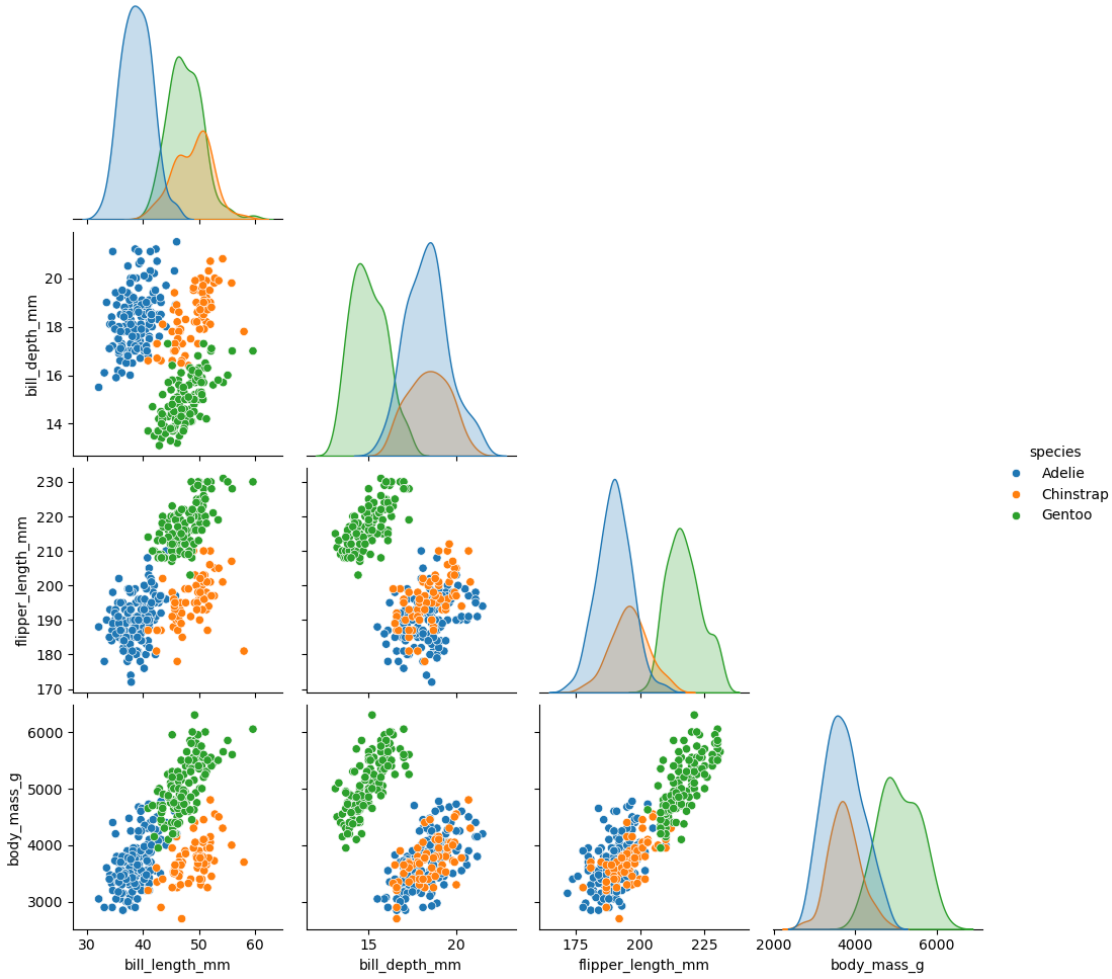
[25]:
```
sns.pairplot(data=penguins_df,
             hue="species")
```

[25]:
```
<seaborn.axisgrid.PairGrid at 0x24dd0539df0>
```



[26]:
```
sns.pairplot(data=penguins_df,
             hue="species",
             corner=True)
```

[26]: <seaborn.axisgrid.PairGrid at 0x24dd1c798b0>



1.2.8 Heatmaps

We can use a heatmap to visualise a grid of numeric values. In this example we will visualise the linear correlations between the numeric variables.

First we will need to work out the correlations. We can do this using Pandas with a little help from NumPy.

[27]:
```
import numpy as np

# Select only numeric columns for correlation
numeric_columns = penguins_df.select_dtypes(include=[np.number])

numeric_columns
```

[27]:

	bill_length_mm	bill_depth_mm	flipper_length_mm	body_mass_g
0	39.1	18.7	181.0	3750.0

```
1              39.5           17.4              186.0       3800.0
2              40.3           18.0              195.0       3250.0
3               NaN            NaN                NaN          NaN
4              36.7           19.3              193.0       3450.0
..              …              …                 …           …
339             NaN            NaN                NaN          NaN
340            46.8           14.3              215.0       4850.0
341            50.4           15.7              222.0       5750.0
342            45.2           14.8              212.0       5200.0
343            49.9           16.1              213.0       5400.0

[344 rows x 4 columns]
```

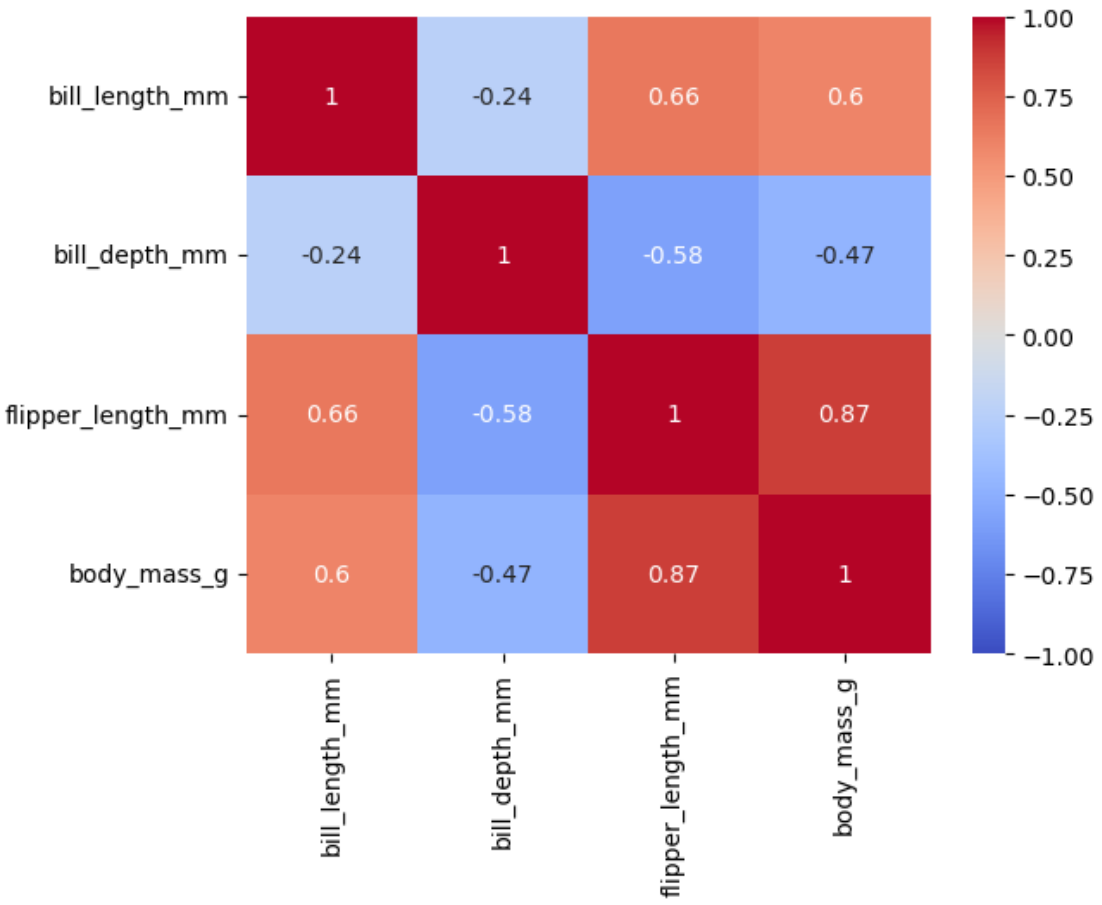
[28]:
```
# Compute the correlation matrix using the corr DataFrame method
correlations = numeric_columns.corr()

correlations
```

[28]:
```
                   bill_length_mm  bill_depth_mm  flipper_length_mm  \
bill_length_mm           1.000000      -0.235053           0.656181
bill_depth_mm           -0.235053       1.000000          -0.583851
flipper_length_mm        0.656181      -0.583851           1.000000
body_mass_g              0.595110      -0.471916           0.871202

                   body_mass_g
bill_length_mm        0.595110
bill_depth_mm        -0.471916
flipper_length_mm     0.871202
body_mass_g           1.000000
```

We can now use a heatmap to make the larger positive and negative correlations easier to spot.

[29]:
```
sns.heatmap(data=correlations,
            annot=True,
            cmap="coolwarm",
            # We can set the limits of the colour scale with vmin and vmax
            vmin=-1,
            vmax=1,
            )
```

[29]:
```
<Axes: >
```



For more on heatmaps see https://seaborn.pydata.org/generated/seaborn.heatmap.html

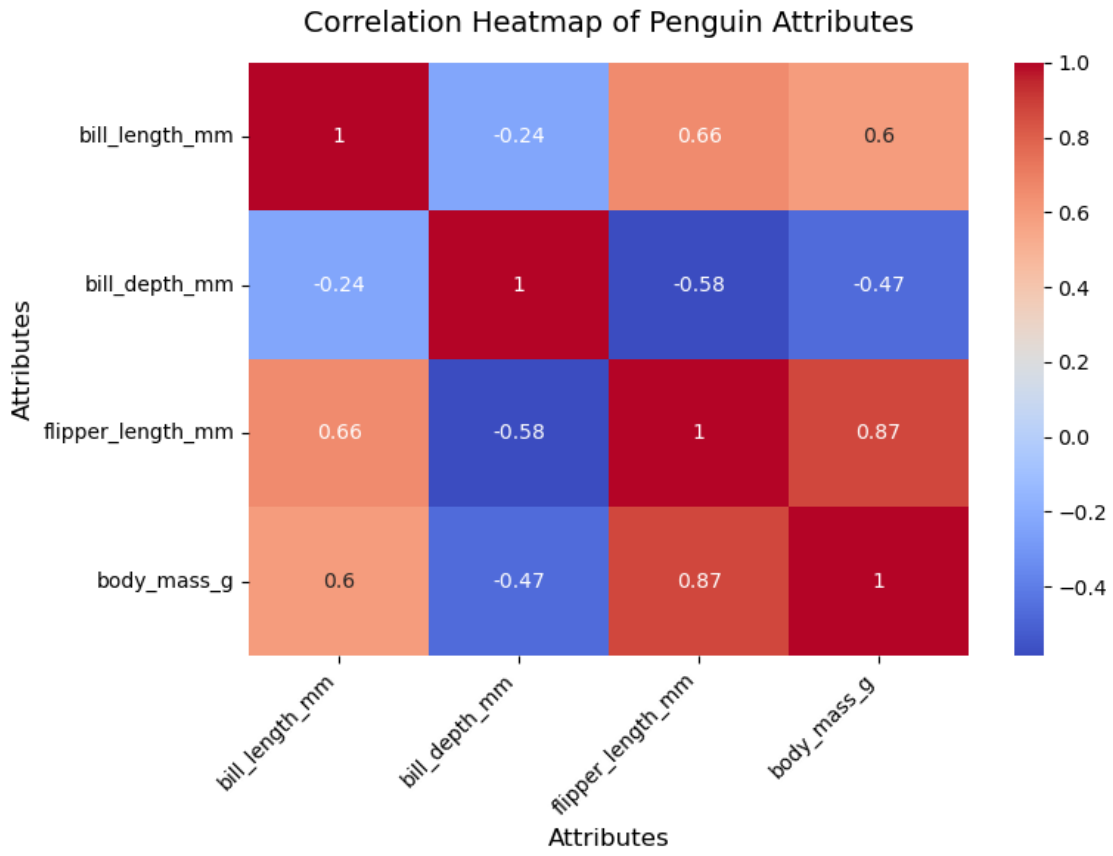
1.3 Using Matplotlib alongside Seaborn

Seaborn is a high-level interface to Matplotlib. This means that we can use both of them together. Seaborn allows us to create a wide range of visualisations quickly and easily. Matplotlib gives us detailed control over our visualisations when we need it.

[30]:
```
import matplotlib.pyplot as plt
```

[31]:
```
# Create heatmap
plt.figure(figsize=(8, 6))
sns.heatmap(data=correlations,
            annot=True,
            cmap="coolwarm",
#            fmt=".3f",
            )

# Add a title and labels
```

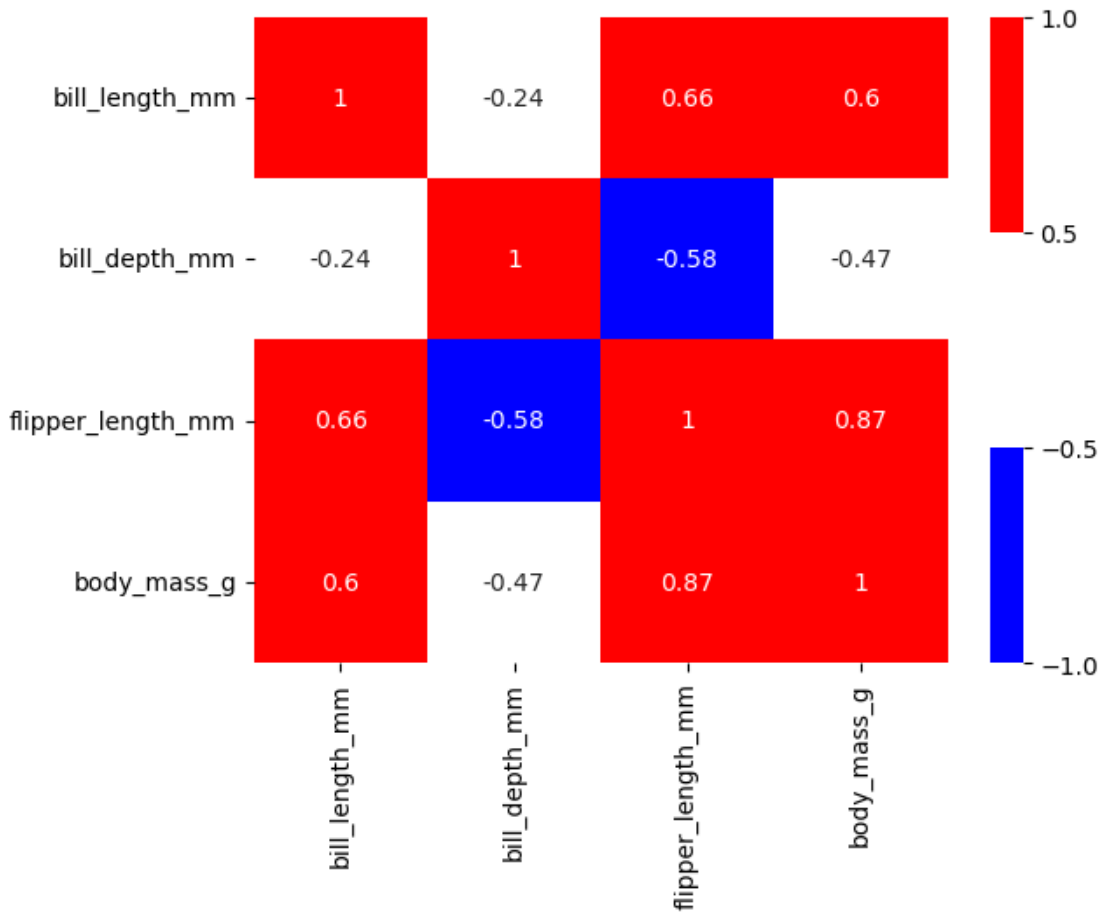
```
plt.title("Correlation Heatmap of Penguin Attributes", fontsize=14, pad=15)
plt.xlabel("Attributes", fontsize=12)
plt.ylabel("Attributes", fontsize=12)

# Rotate x-axis labels for better readability
plt.xticks(rotation=45, ha="right")

# Show the heatmap
plt.tight_layout()
plt.show()
```



In this example we use Matplotlib to customise the colours so that only correlations above 0.5 or below -0.5 are highlighted.

[32]:
```
import matplotlib.colors as mcolors

# Define a three-colour map
cmap = mcolors.ListedColormap(["blue", "white", "red"])

# Boundaries for each colour interval
```

```
bounds = [-1, -0.5, 0.5, 1]

# Associate each range in 'bounds' with one colour in the cmap
norm = mcolors.BoundaryNorm(bounds, len(cmap.colors))

# Plot the heatmap with the custom map and norm
sns.heatmap(
    correlations,
    annot=True,
    cmap=cmap,
    norm=norm,
)
plt.show()
```



Using matplotlib to move the legend. Seaborn's plotting functions return a Matplotlib Axes object which we can store and use to make further changes. In this case we move the position of the legend so that it doesn't obscure the data.

[33]:
```
ax = sns.scatterplot(
    data=penguins_df,
    x="bill_length_mm",
    y="bill_depth_mm",
    hue="species",
    size="body_mass_g"
)
ax.legend(bbox_to_anchor=(1.02, 1), borderaxespad=0)
plt.show()
```