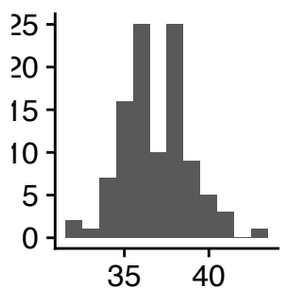
Data visualizations can be generalized as consisting of three parts

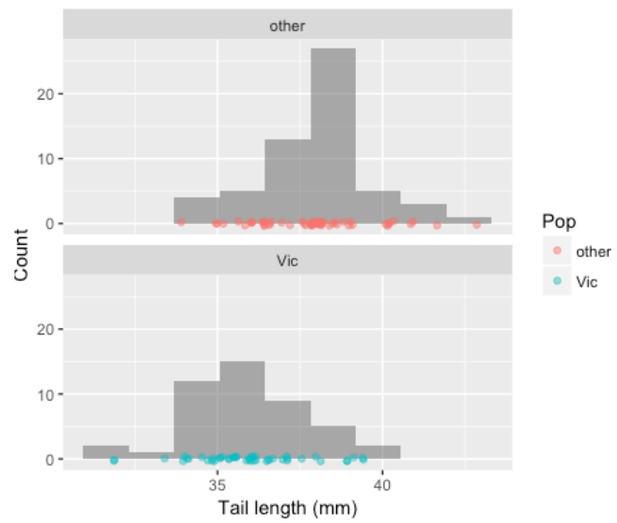
Data + **Geometric Mapping** + **Aesthetic Properties of the Geometric Mapping**

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

+



+

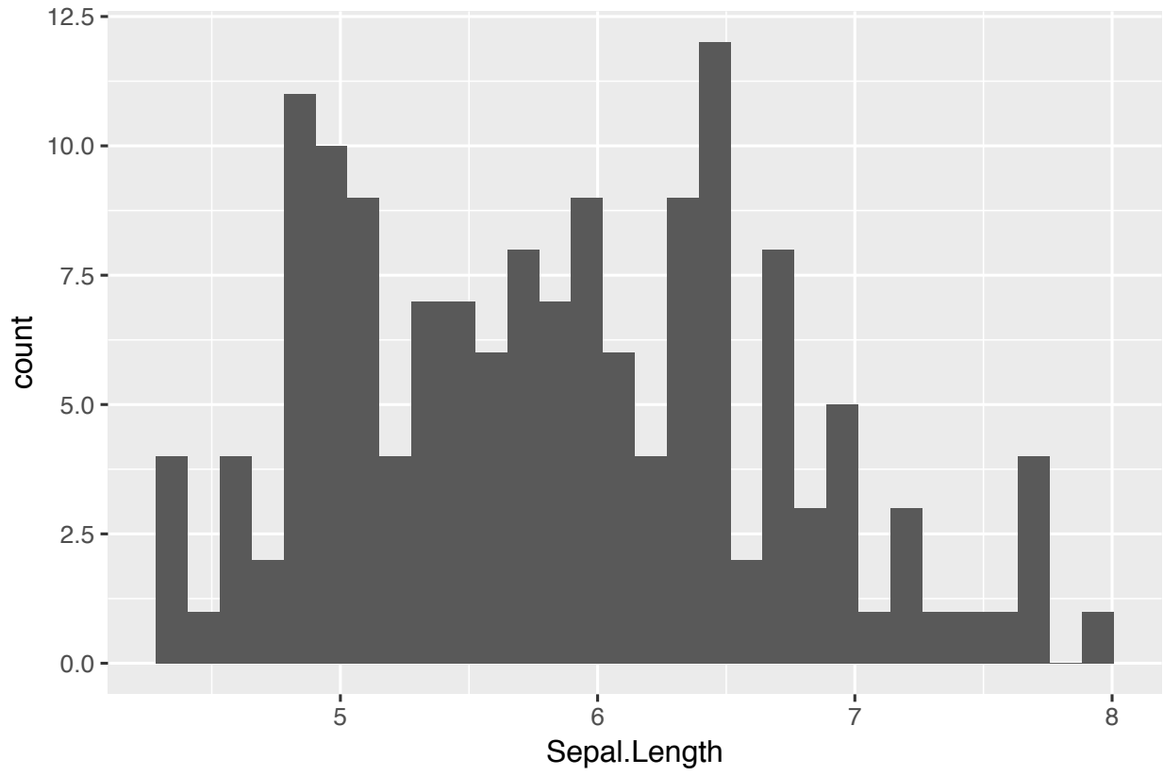



```
ggplot(data = <DATA>) + <GEOM_FUNCTION>(mapping = aes(<MAPPINGS>))
```

Example 1: Creating a histogram

Data + **Geometric Mapping** + **Aesthetic Properties of the Geometric Mapping**

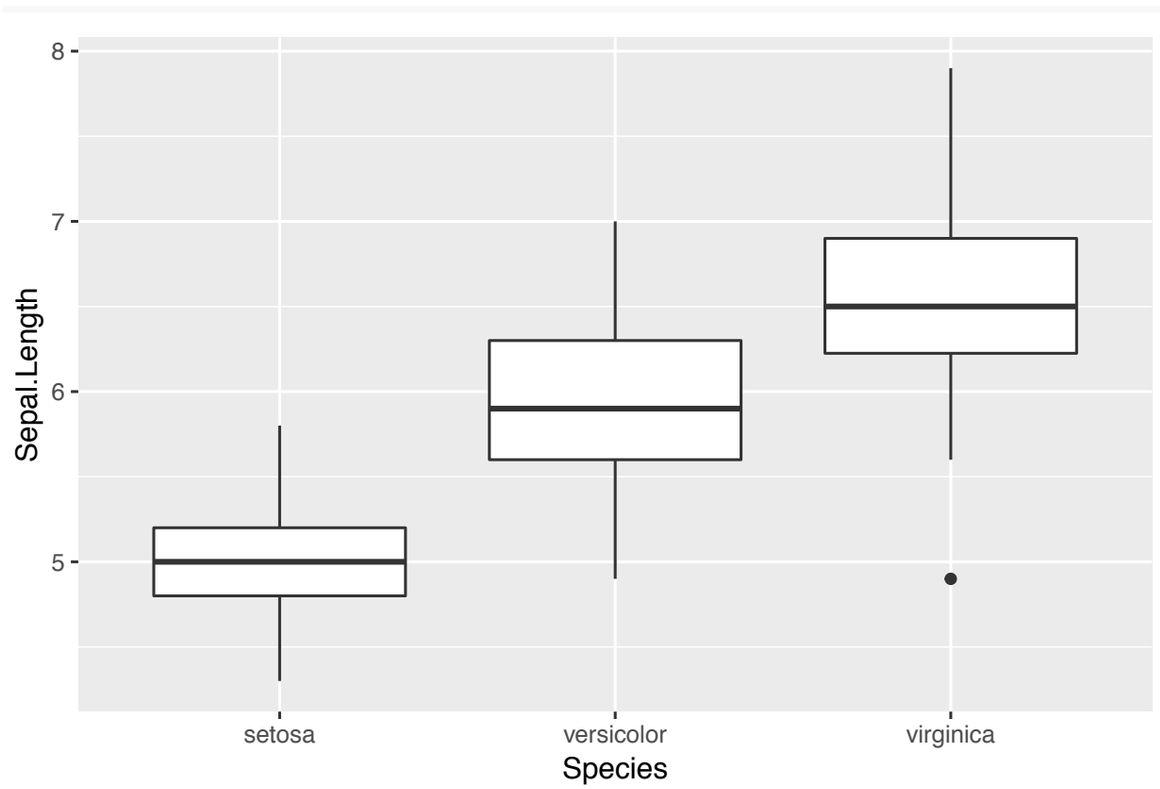
```
ggplot(data = iris) + geom_histogram(mapping = aes(x = Sepal.Length))
```



Example 2: Creating a Boxplot

Data + **Geometric Mapping** + **Aesthetic Properties of the Geometric Mapping**

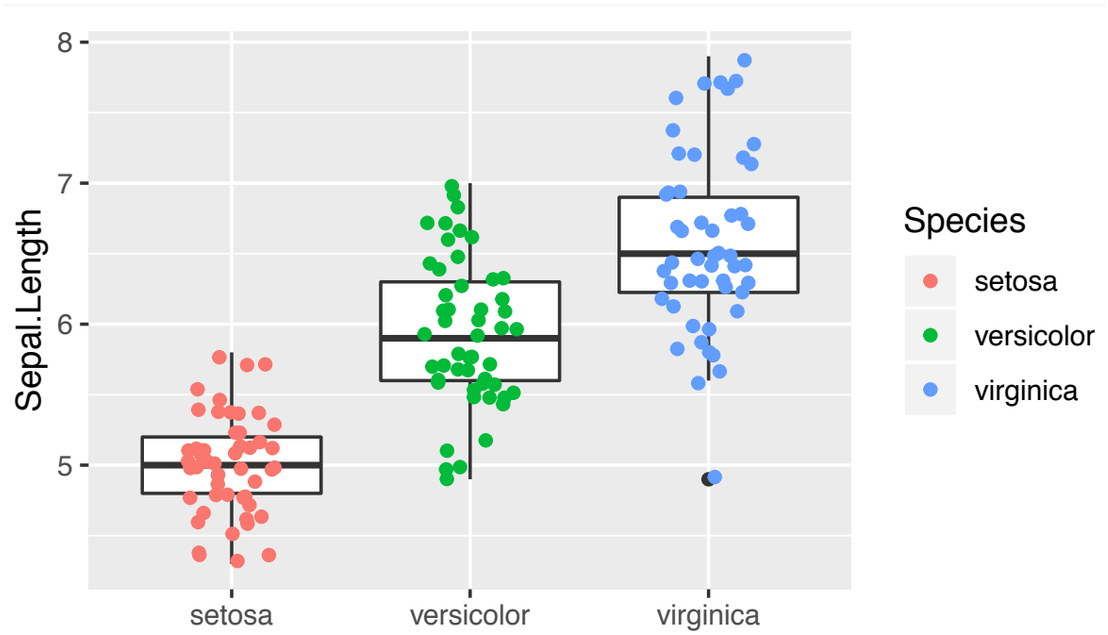
```
ggplot(data = iris) + geom_boxplot(mapping = aes(x = Species,
                                                 y = Sepal.Length))
```



Example 3: Combining Geometric Representations

Data + **Geometric Mapping** + **Aesthetic Properties of the Geometric Mapping**

```
ggplot(data = iris) + geom_boxplot(mapping = aes(x = Species,
                                                 y = Sepal.Length)) +
                      geom_jitter(mapping = aes(x = Species,
                                                y = Sepal.Length,
                                                color = Species),
                                  width = 0.2)
```



Shared aesthetics properties can be specified in `ggplot()` or in an independent `aes()` call

```
ggplot(data = iris, aes(x = Species, y = Sepal.Length)) +
  geom_boxplot() +
  geom_jitter(mapping = aes(color = Species),
              width = 0.2)
```

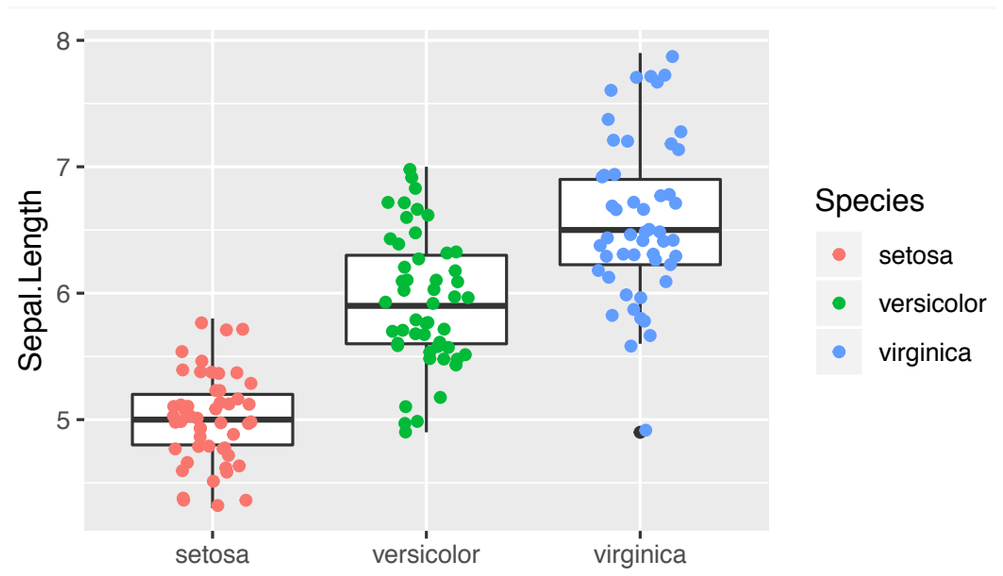
or

```
ggplot(data = iris) +
  aes(x = Species, y = Sepal.Length) +
  geom_boxplot() +
  geom_jitter(mapping = aes(color = Species),
              width = 0.2)
```

Default aesthetic properties

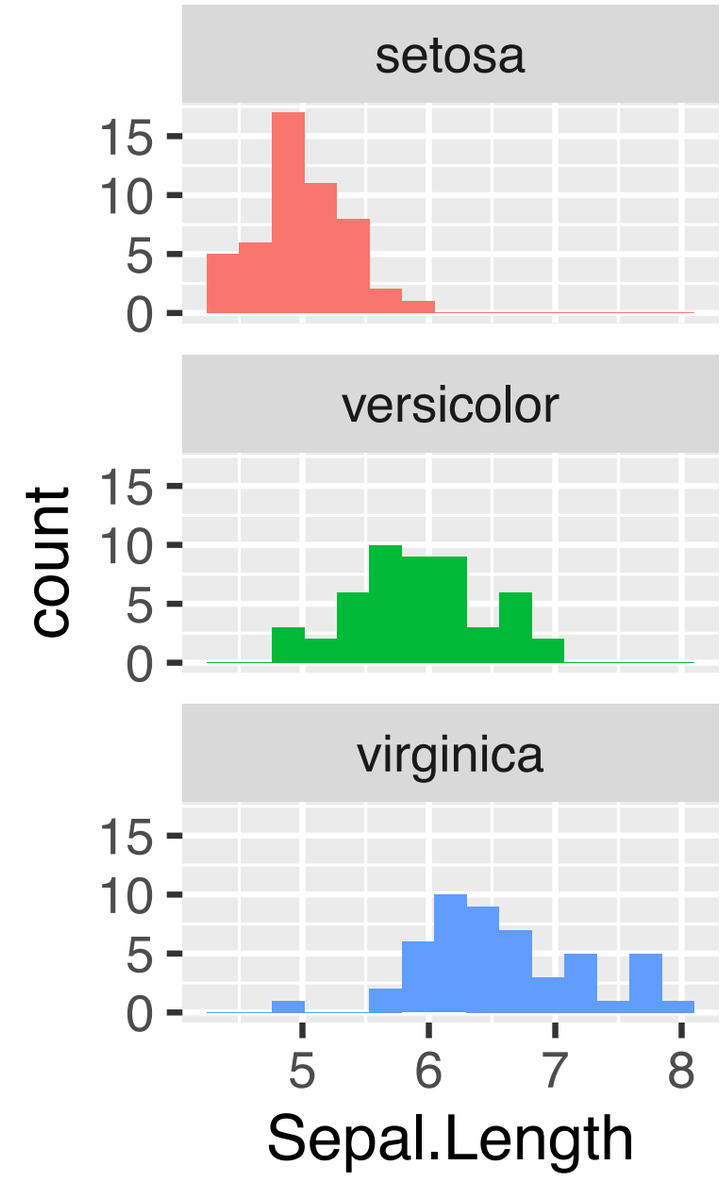
Subsequent geoms inherit the default aesthetics but can specify additional ones

If you don't want to inherit the default aesthetics can specify with argument `inherit.aes = FALSE`



Faceting creates subplots based on conditioning of one or more variables

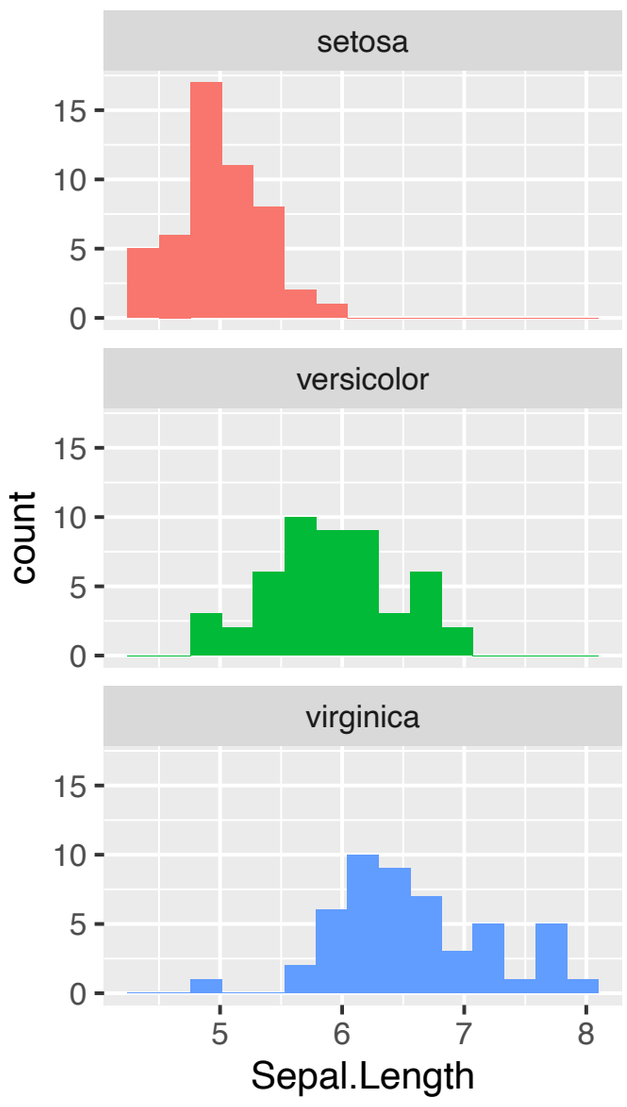
```
ggplot(iris) +
  aes(x = Sepal.Length, fill = Species) +
  geom_histogram(bins = 15) +
  facet_wrap(~Species, ncol = 1)
```



Themes change look-and-feel across the plot

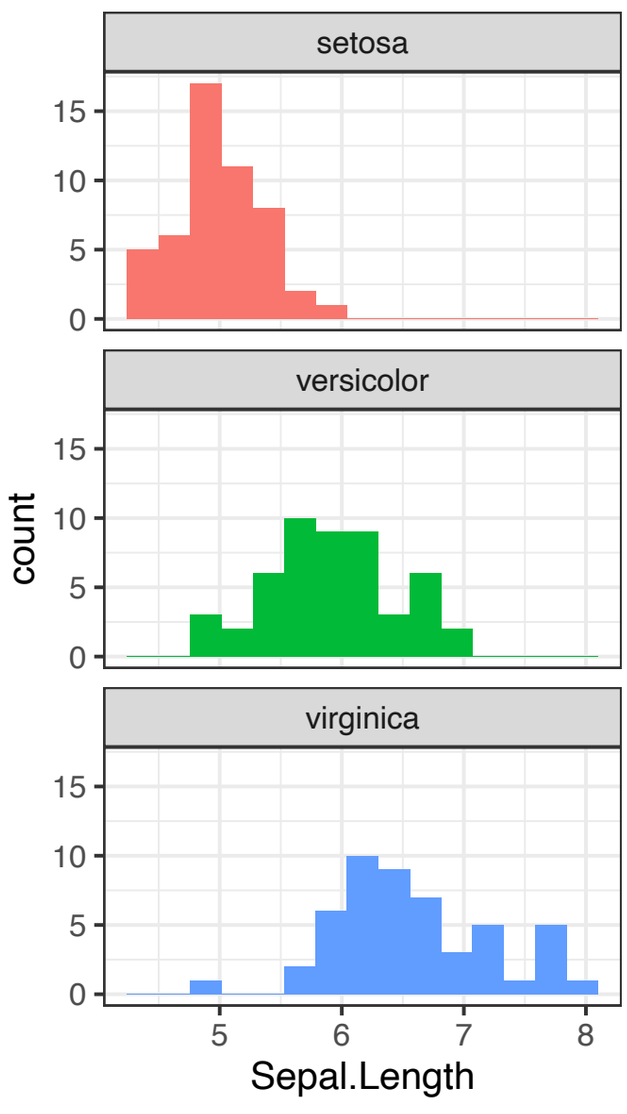
default theme

```
ggplot(data = iris, aes(x = Sepal.Length, fill=Species)) +
  geom_histogram(bins=15) + facet_wrap(~Species,ncol=1) +
  theme(aspect.ratio = 0.5, legend.position = "none")
```



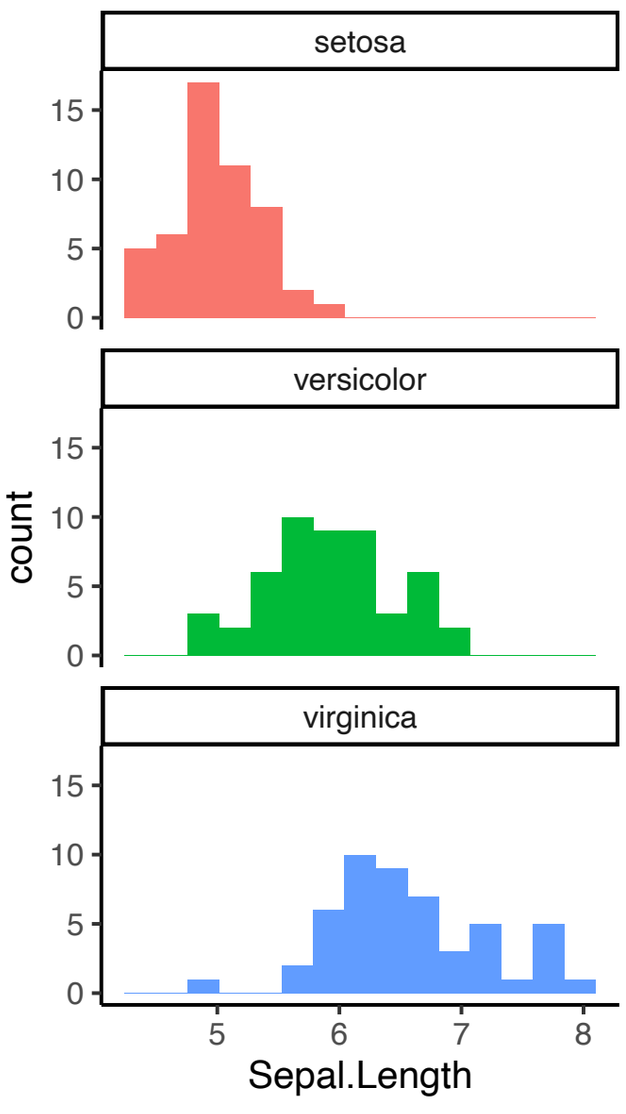
+theme_bw()

```
ggplot(data = iris, aes(x = Sepal.Length, fill=Species)) +
  geom_histogram(bins=15) + facet_wrap(~Species,ncol=1) +
  theme_bw() + theme(aspect.ratio = 0.5, legend.position = "none")
```



+theme_classic()

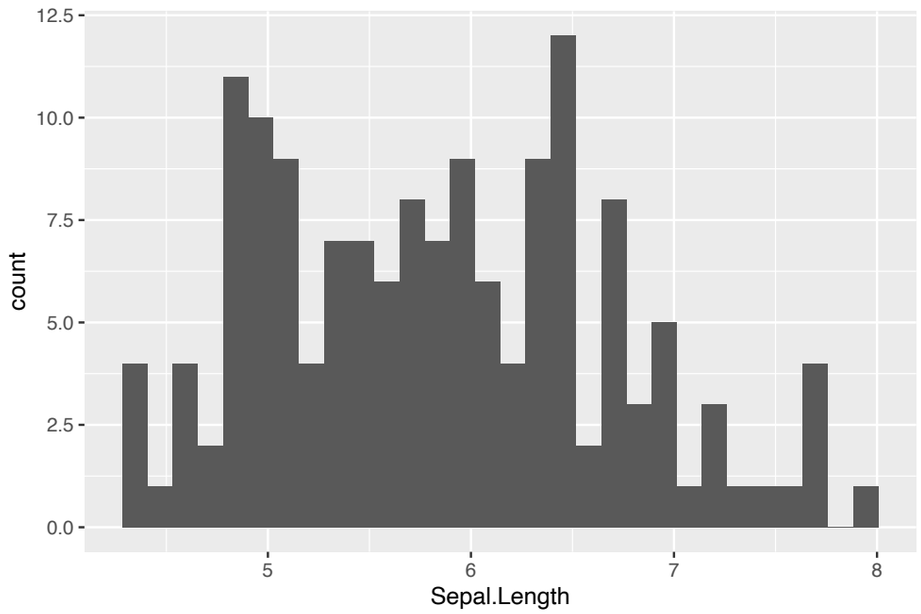
```
ggplot(data = iris, aes(x = Sepal.Length, fill=Species)) +
  geom_histogram(bins=15) + facet_wrap(~Species,ncol=1) +
  theme_classic() + theme(aspect.ratio = 0.5, legend.position = "none")
```



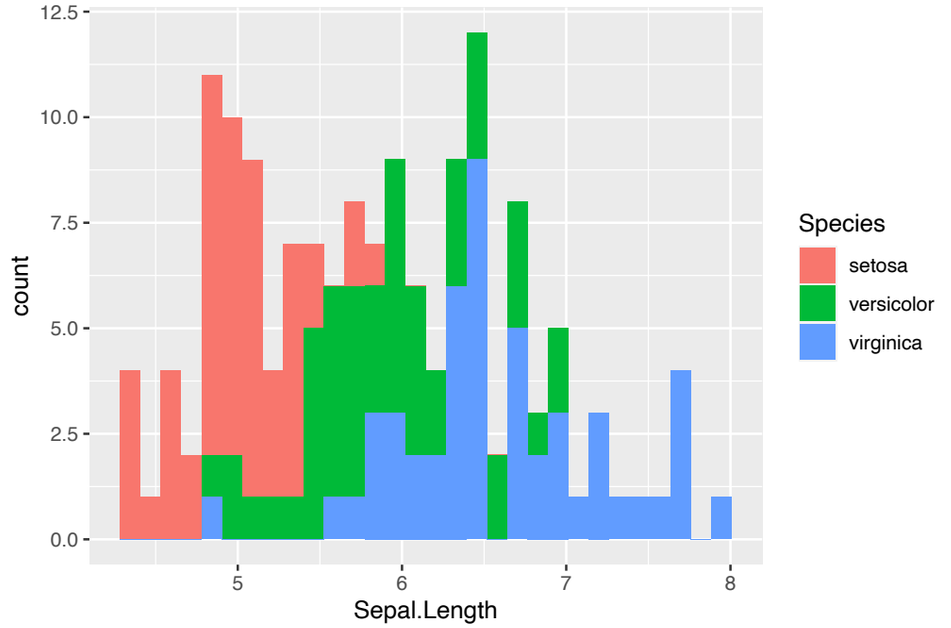
"Geom" tour: Histograms

geom_histogram()

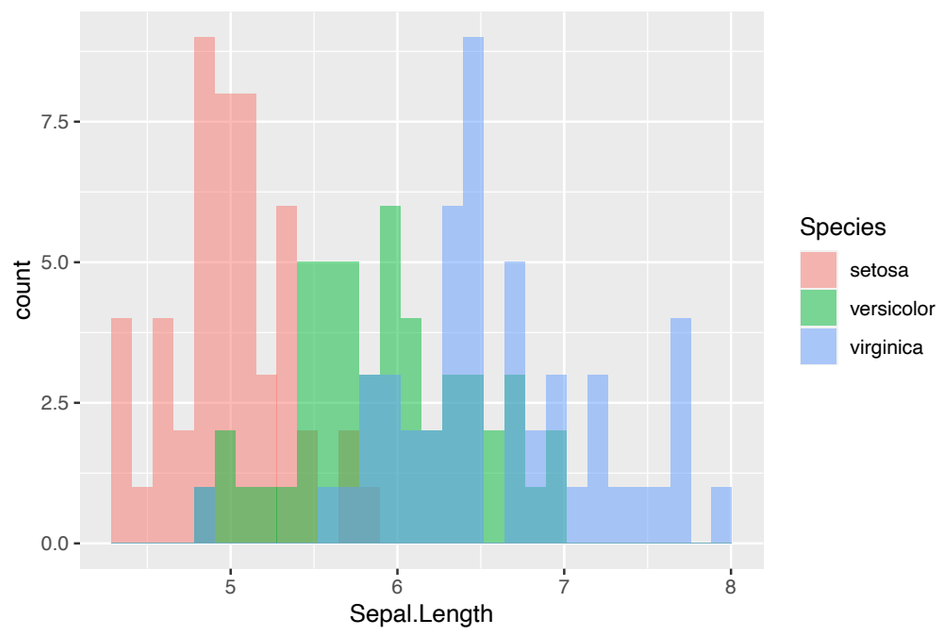
```
ggplot(iris) +
  aes(x = Sepal.Length) +
  geom_histogram()
```




```
ggplot(iris) +
  aes(x = Sepal.Length, fill = Species) +
  geom_histogram()
```



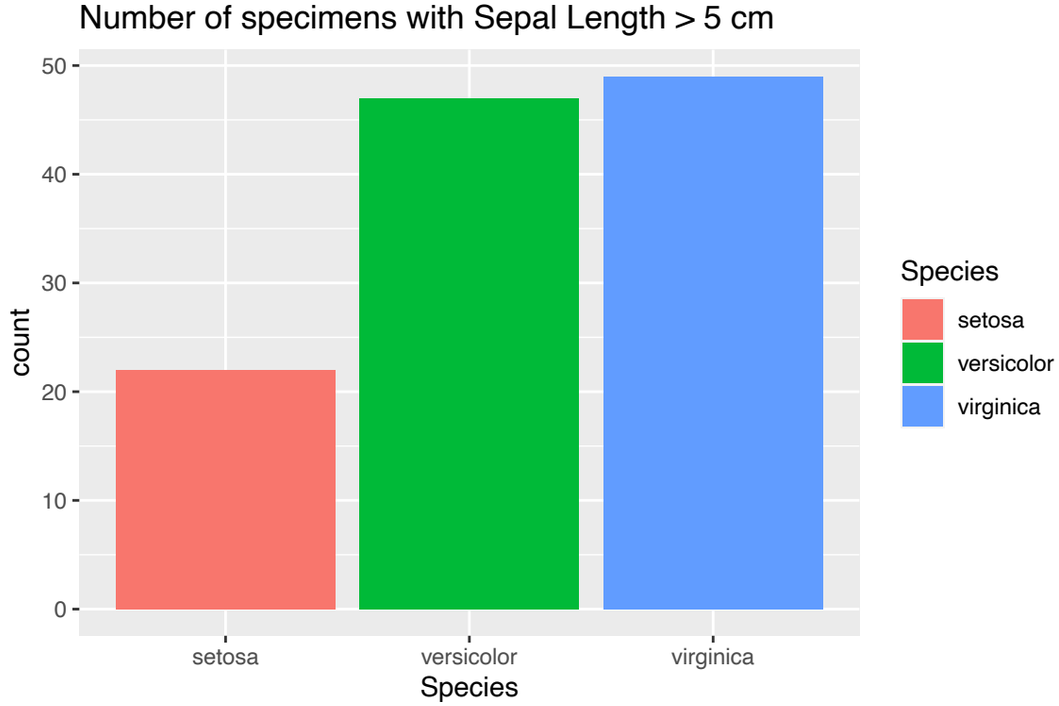

```
ggplot(iris) +
  aes(x = Sepal.Length, fill = Species) +
  geom_histogram(position = "identity", alpha=0.5)
```



"Geom" tour: Bar charts

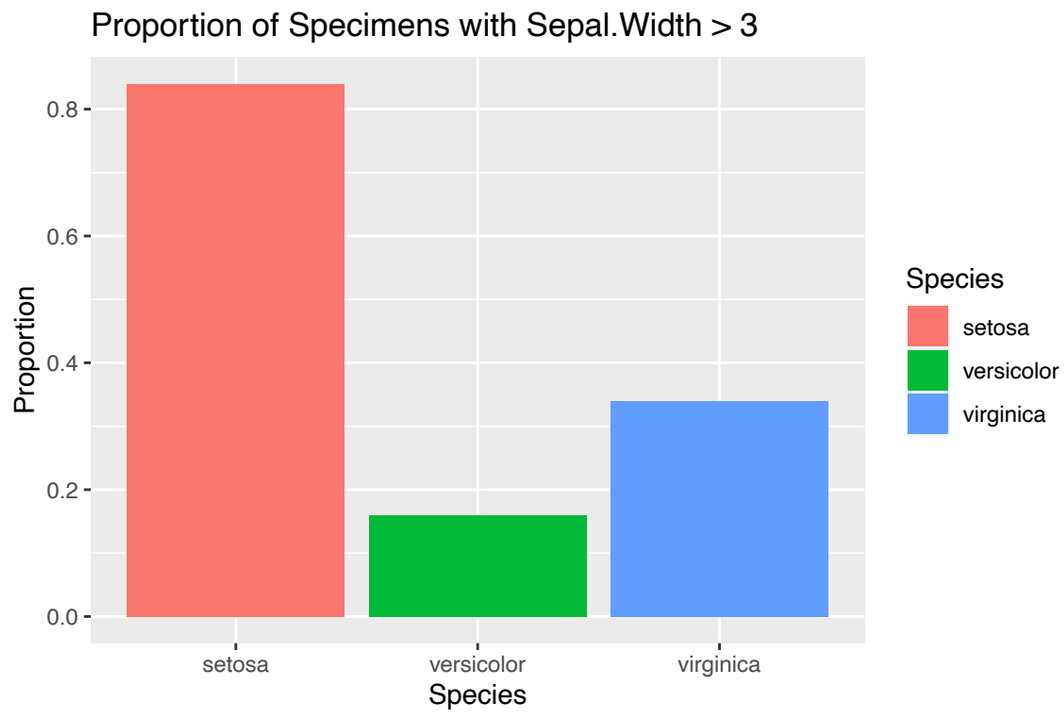
geom_bar()

```
iris |>
  filter(Sepal.Length > 5) |>
  ggplot(aes(x = Species, fill = Species)) +
  geom_bar() +
  labs(title = "Number of specimens with Sepal Length > 5 cm")
```



geom_col()

```
iris |>
  group_by(Species) |>
  summarize(prop_Sepal.Width_gt3 = sum(Sepal.Width > 3)/n()) |>
  ggplot(aes(x = Species, fill = Species,
             y = prop_Sepal.Width_gt3)) +
  geom_col() +
  labs(y = "Proportion",
       title = "Proportion of Specimens with Sepal.Width > 3")
```

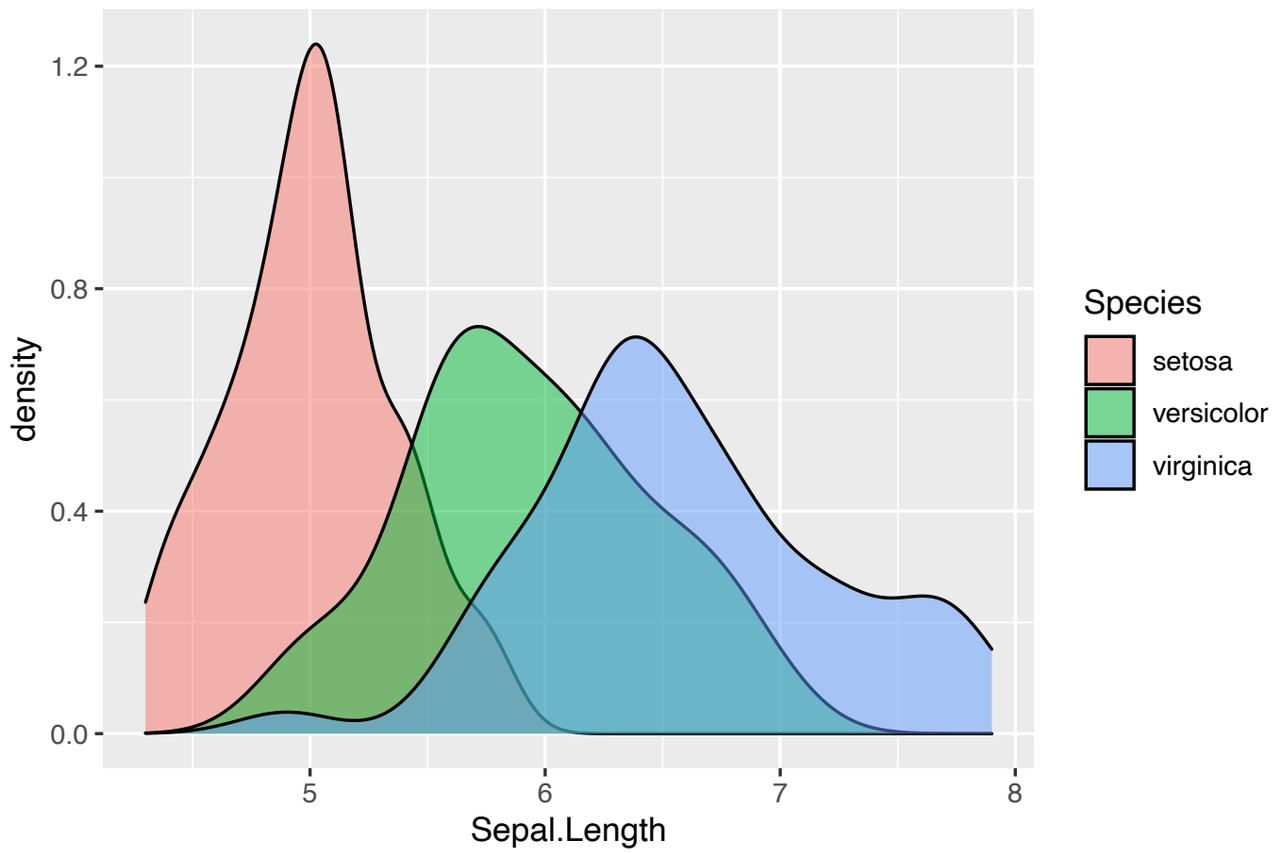


Use `geom_col()` when you've pre-computed the values you want to depict

"Geom" tour: Density and violin plots

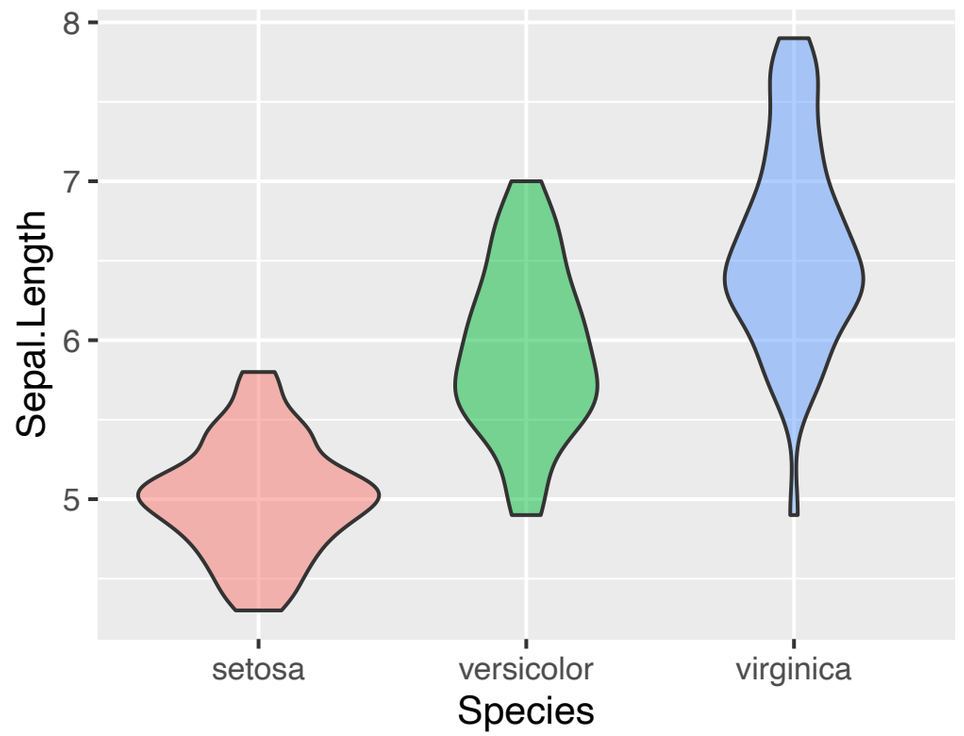
geom_density()

```
ggplot(data = iris, aes(x = Sepal.Length, fill=Species)) +
  geom_density(alpha=0.5)
```



geom_violin()

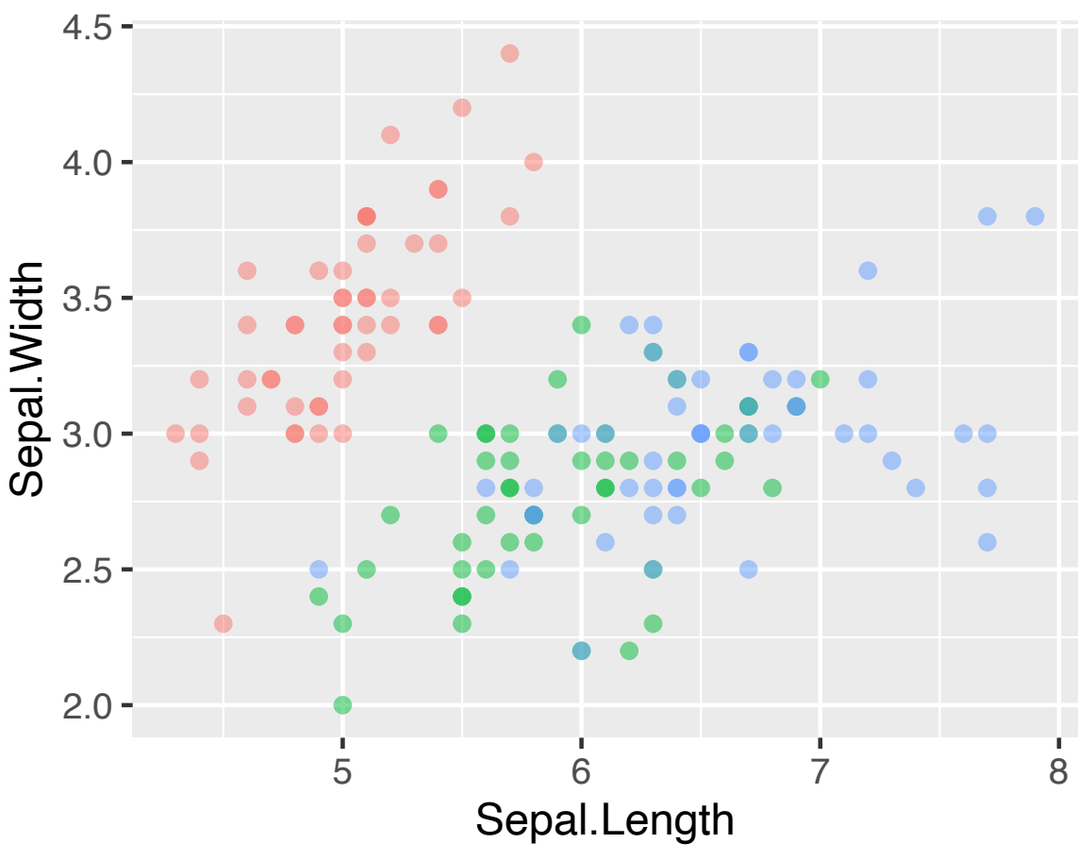
```
ggplot(data = iris, aes(x = Species,
                        y = Sepal.Length,
                        fill=Species)) +
  geom_violin(alpha=0.5)
```



"Geom" tour: Scatter and 2d density

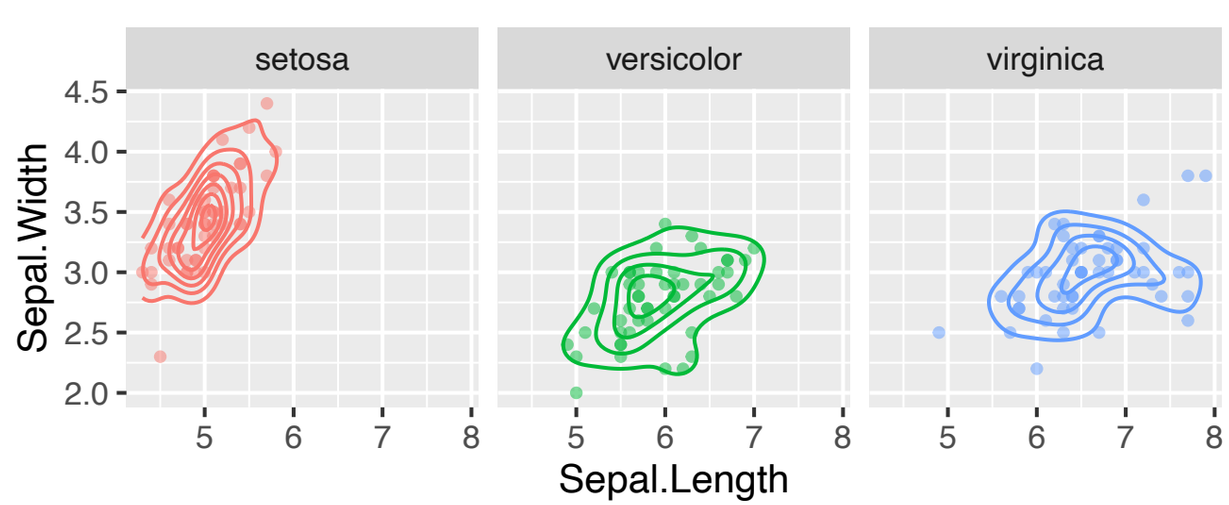
geom_point()

```
ggplot(data = iris, aes(x = Sepal.Length,
                        y = Sepal.Width,
                        color=Species)) +
  geom_point(alpha=0.5)
```



geom_density_2d()

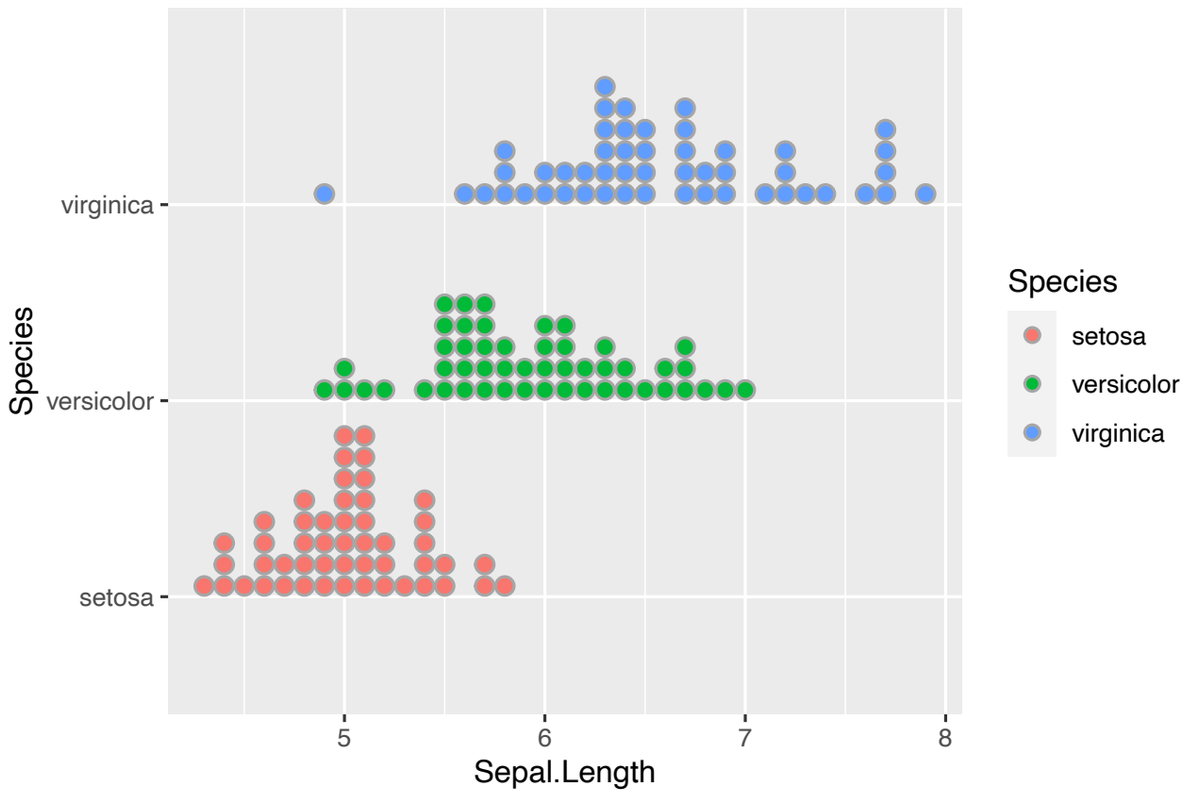
```
ggplot(data = iris, aes(x = Sepal.Length,
                        y = Sepal.Width,
                        color=Species)) +
  geom_density_2d() +
  geom_point(alpha=0.5,size=1) +
  facet_wrap(~Species)
```



ggplot2 extension: `ggdist` for comparing distributions

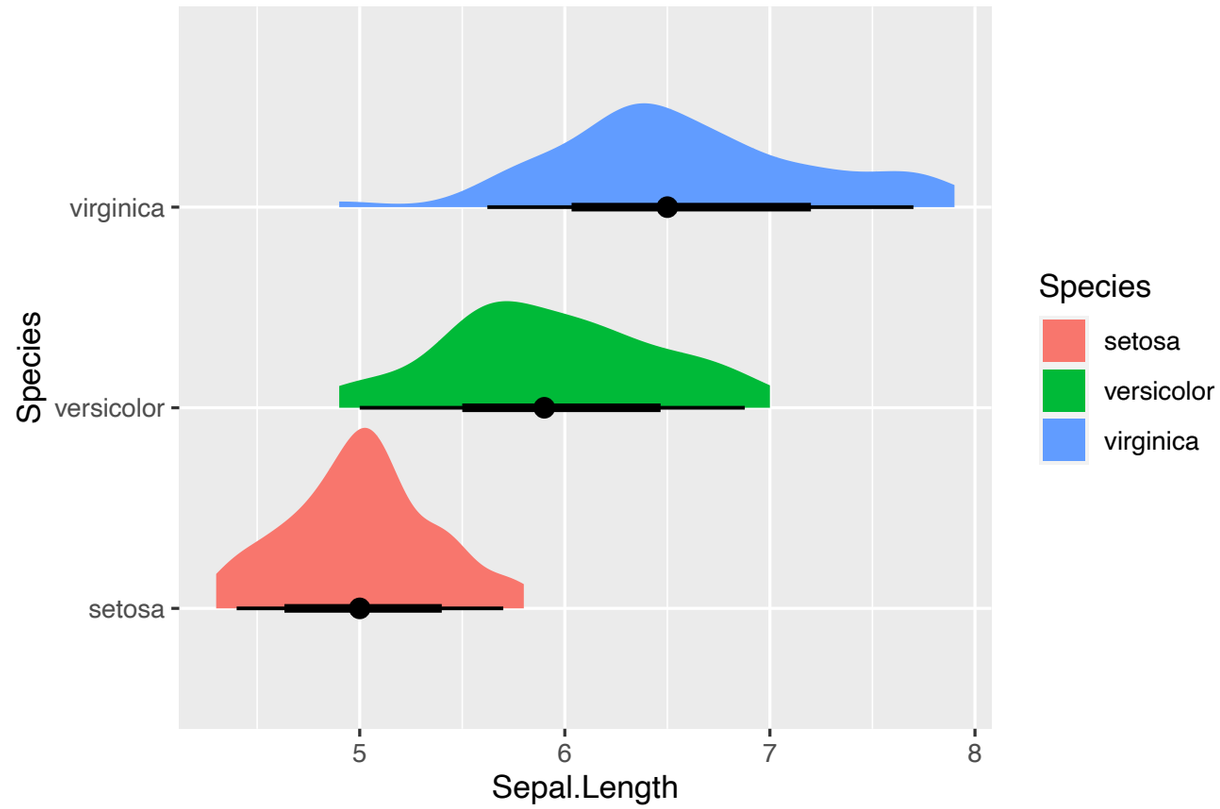
`geom_dots()`

```
library(ggdist)

ggplot(iris, aes(x = Sepal.Length,
                 y = Species,
                 fill=Species)) +
  geom_dots()
```



`stat_slabinterval()`

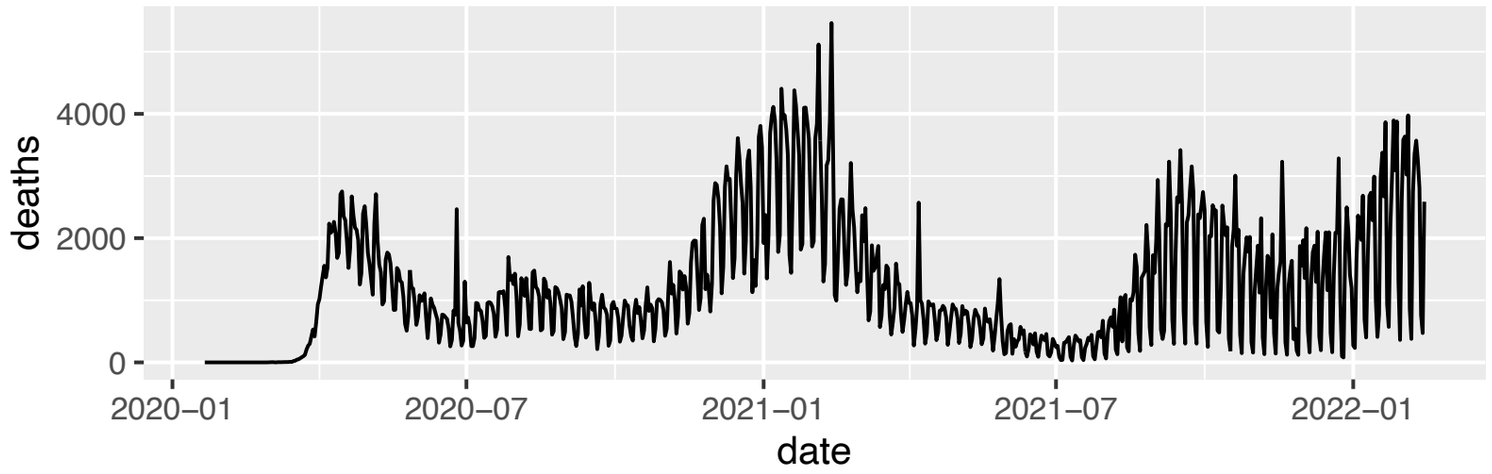
```
ggplot(iris, aes(x = Sepal.Length,
                 y = Species,
                 fill=Species)) +
  stat_slabinterval()
```



"Geom" tour: Line and Area plots

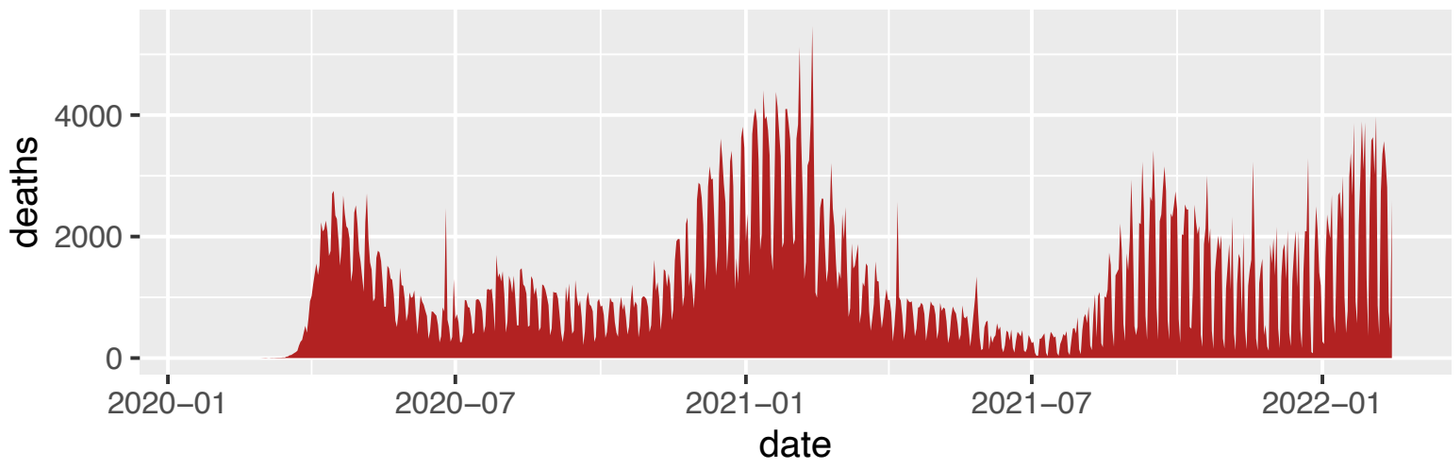
geom_line()

```
ggplot(data = covid, aes(x = date, y = deaths)) +
  geom_line()
```



geom_area()

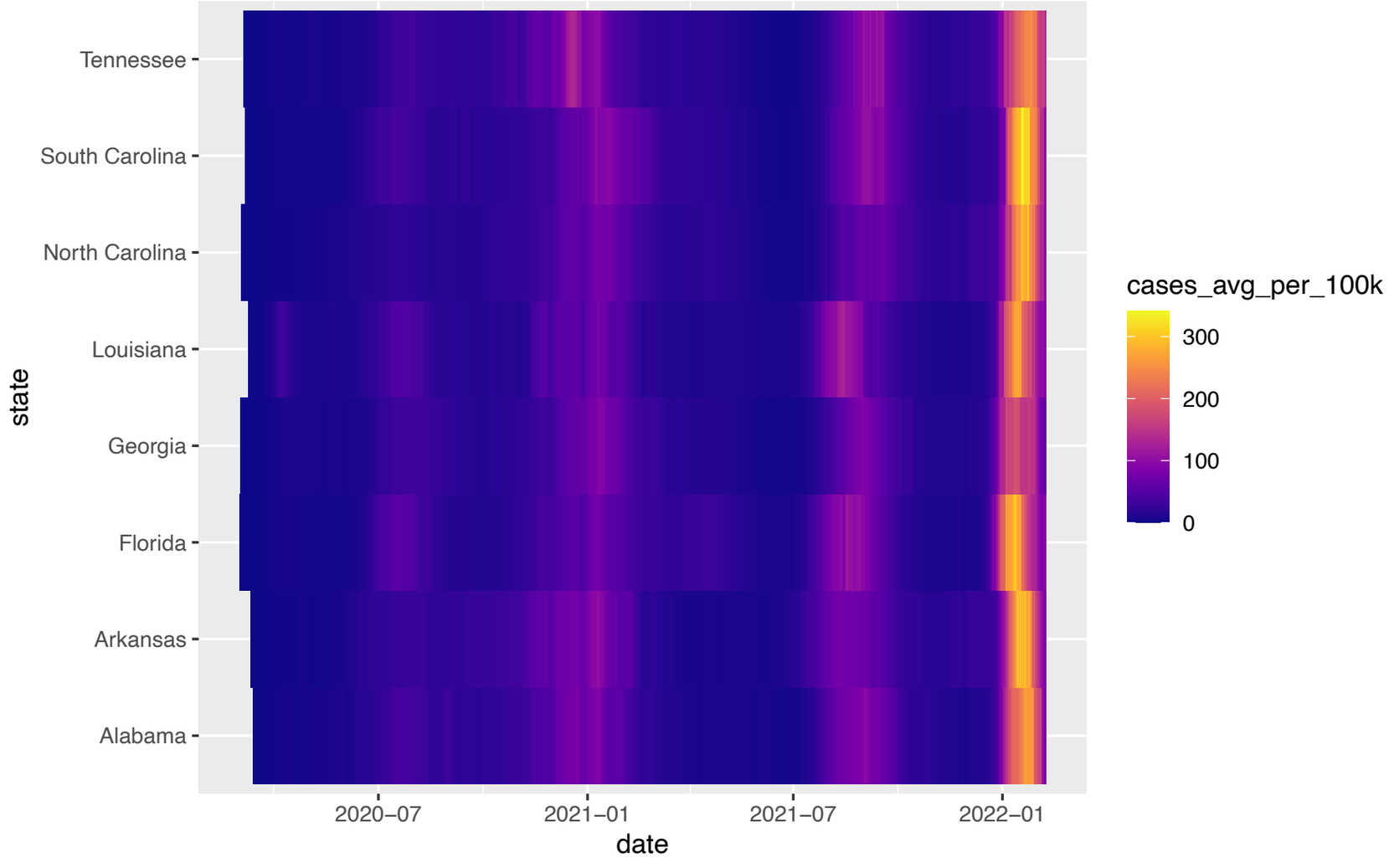
```
ggplot(data = covid, aes(x = date, y = deaths)) +
  geom_area(fill="firebrick")
```



"Geom" tour: Heat maps

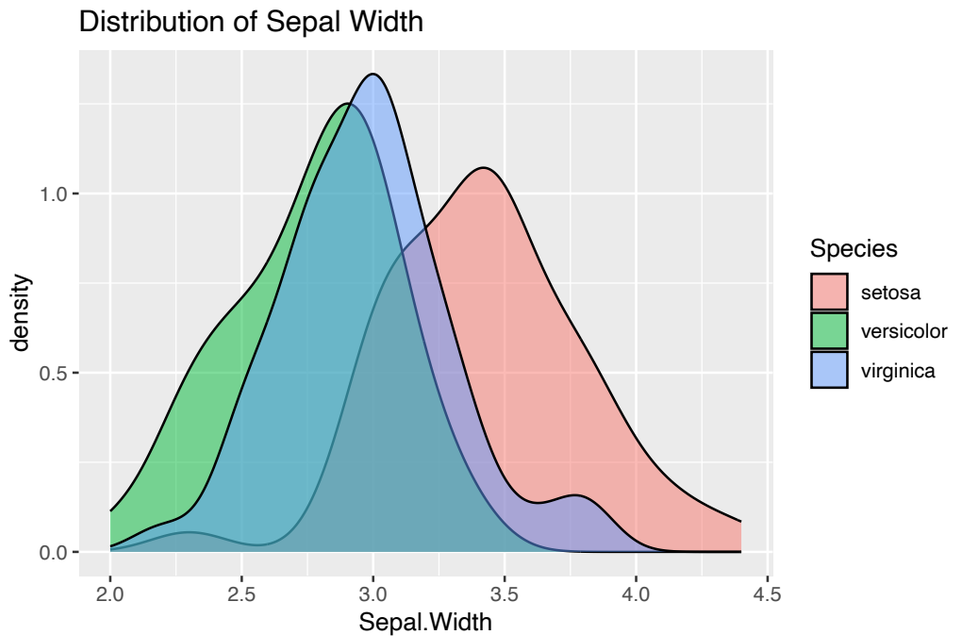
geom_tile() or geom_raster()

```
SE_states <- c("North Carolina","South Carolina",
               "Arkansas","Georgia","Tennessee",
               "Louisiana","Alabama","Florida")

us_states %>%
  filter(state %in% SE_states) %>%
  arrange(state) %>%
  ggplot(aes(x=date, y=state, fill=cases_avg_per_100k)) +
    geom_tile() +
    scale_fill_viridis(option = "C")
```



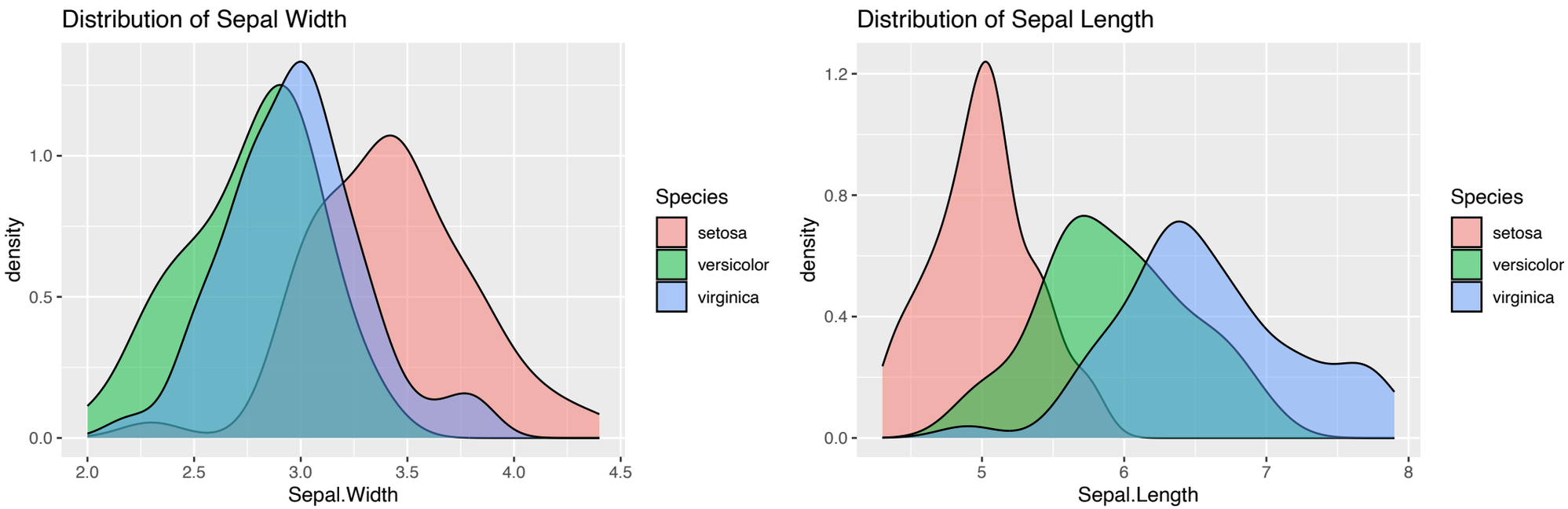
Assigning plots to variables

```
plot_Sepal.Length <-
  ggplot(data = iris, aes(x = Sepal.Length, fill=Species)) +
  geom_density(alpha=0.5) +
  labs(title = "Distribution of Sepal Length")

plot_Sepal.Width <-
  ggplot(data = iris, aes(x = Sepal.Width, fill=Species)) +
  geom_density(alpha=0.5) +
  labs(title = "Distribution of Sepal Width")

plot_Sepal.Ratio <-
  ggplot(data = iris, aes(x = Sepal.Width/Sepal.Length, fill=Species)) +
  geom_density(alpha=0.5) +
  labs(x = "Sepal Ratio (Width / Length)",
       title = "Distribution of Sepal Ratios")

# Note that a plot is not constructed until
# we evaluate one of the variables holding a plot
plot_Sepal.Width
```



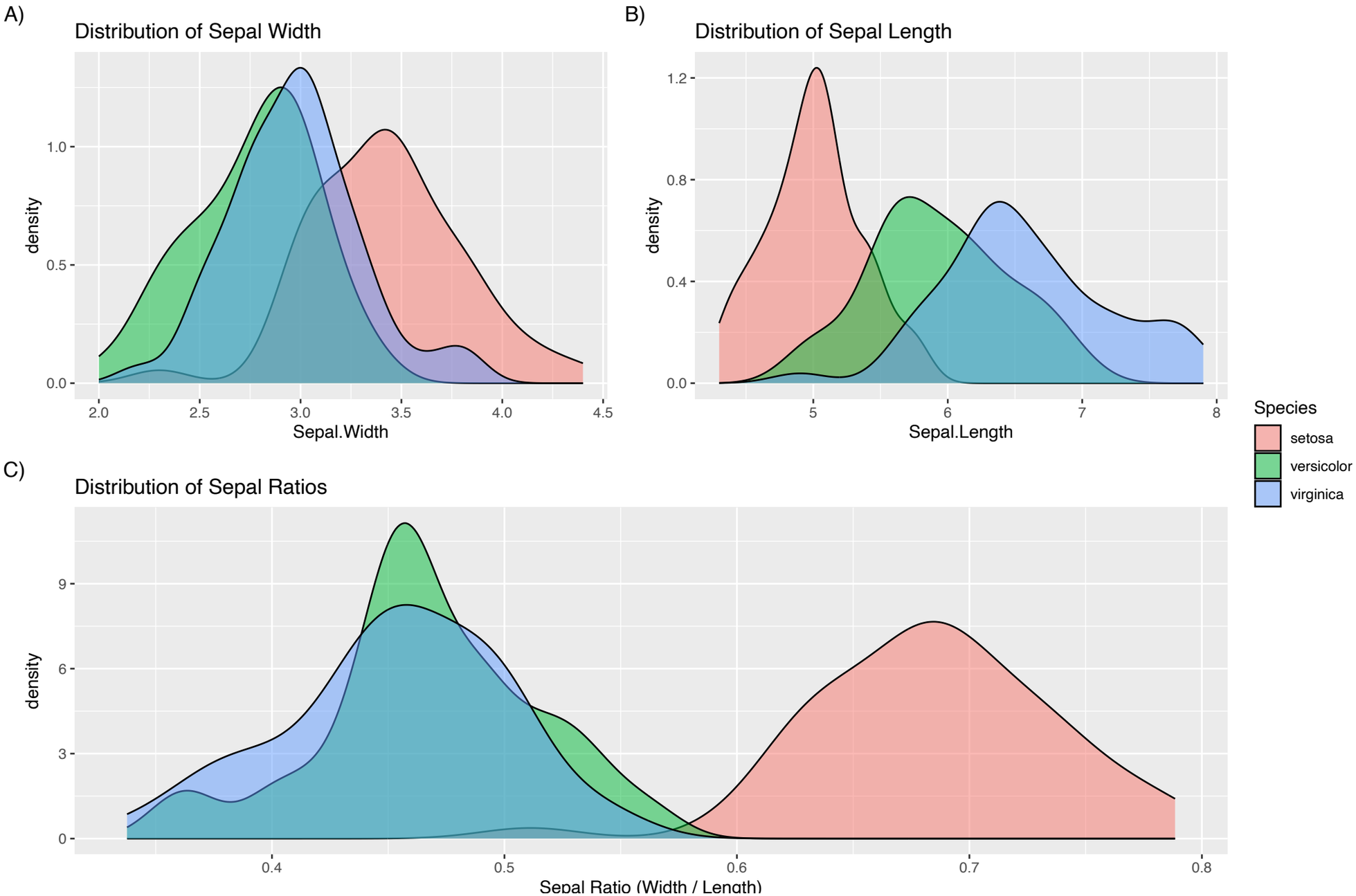
Multi-plot layouts with the `patchwork` library

```
library(patchwork)

# Plots can be laid out side by side using the + operator
plot_Sepal.Width + plot_Sepal.Length
```



Even more complex layouts with patchwork

```
(plot_Sepal.Width | plot_Sepal.Length) / plot_Sepal.Ratio +
  plot_layout(guides = "collect") +
  plot_annotation(tag_levels = 'A', tag_suffix = ")")
```



ggtext allows for simple HTML and markdown formatting of text and labels

```
library(ggtext)

# a named vector provides an explicit map
# between names as given in the data frame
# and the labels we want printed
species_names = c("setosa" = "<i>I. setosa</i>",
                  "versicolor" = "<i>I. versicolor</i>",
                  "virginica" = "<i>I. virginica</i>")

ggplot(iris, aes(x = Sepal.Length, fill=Species)) +
  geom_density(alpha=0.5) +
  labs(title = "Distribution of Sepal Length in three *Iris* species",
       x = "Sepal Length", y = "Density") +
  scale_fill_discrete(labels = species_names) +
  theme(plot.title = element_markdown(),
        legend.text = element_markdown())
```