

# Basic ggplots in R

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## R tutorial 1: Using ggplot to create basic plots

Here, we will use the popular **iris** dataset, collected by Edgar Anderson in 1936, to illustrate how ggplot can be used to create elegant and attractive graphics. It contains sepal and petal measurements for 50 individuals from three *Iris* species; namely *I. setosa*, *I. versicolor*, and *I. virginica*.

Check the R dataset package for other interesting data sets to tinker with.

### Some notes on syntax:

- **package\_name::** specifies the package name, where the two colons access all the functions associated with that package
- Hashes (#) denote comments, that are not read by R. Use these to annotate your code
- In ggplot, the plus sign (+) means that you are adding additional “layers” to your plot
- An equal sign (=) is synonymous with the arrow (->). You can use either to assign names to objects
- Dollar signs (\$) are like keys that access features of an object, such as columns or lists
- Use a question mark (?) to access the help file for a particular package (e.g. **?ggplot**)

### Let's get started!

```
if (!require("pacman"))
  install.packages("pacman")
pacman::p_load(datasets, xlsx, janitor, ggplot2, Rmisc, dplyr, ggpubr)

# access the embedded dataset
iris_data = datasets::iris
iris_data = janitor::clean_names(iris_data)

# for practice, write this data to the project folder as a .csv file
write.csv(iris_data, file = "data/iris_data.csv", quote = FALSE, row.names = FALSE)
# now read it back in
iris_data_readin = read.csv("data/iris_data.csv")

# now as an Excel file
xlsx::write.xlsx(iris_data, file = "data/iris_data.xlsx",
  sheetName = "iris_data", row.names = FALSE)
iris_data_readin_xlsx = xlsx::read.xlsx(file = "data/iris_data.xlsx", sheetIndex = 1)

# make iris species a factor/grouping variable
iris_data$species = as.factor(iris_data$species)
levels(iris_data$species)
```

```
## [1] "setosa"      "versicolor" "virginica"
```

```
# summarySE function gets summary statistics for a chosen variable across groups
petal_summary = Rmisc::summarySE(data = iris_data, measurevar = "petal_length",
                                  groupvars = "species")
```

There are a number of ways in R to refer to a particular column in a data set. Have a look at the code below, where we can access the **sepal\_width** column in five different ways:

```
# using the dollar operator - I find this the most intuitive
iris_data$sepal_width

# this says "access the values in all the rows in column 2"
iris_data[, 2]

# a few other approaches to do exactly the same thing
iris_data[[2]]
iris_data[["sepal_width"]]
iris_data[, "sepal_width"]

# using the dplyr package:

# select
dplyr::select(iris_data, sepal_width)

# pull
iris_data %>%
  dplyr::pull(sepal_width)
```

Perhaps you would like to access the petal lengths for rows 1 to 5 only. Here's how you can do this:

```
iris_data[1:5, 3]
```

```
## [1] 1.4 1.4 1.3 1.5 1.4
```

```
# or using dplyr
iris_data %>%
  dplyr::slice(1:5) %>% # Select rows 1 to 5
  dplyr::pull(3) # pull out the third column only
```

```
## [1] 1.4 1.4 1.3 1.5 1.4
```

```
# Have a look at a summary of a particular subset of your data.
# Here we'll look at sepal lengths:
summary(iris_data$sepal_length)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    4.300   5.100   5.800   5.843   6.400   7.900
```

```
# Take a quick glance at the structure of the dataset:
str(iris_data)
```

```
## 'data.frame': 150 obs. of 5 variables:
## $ sepal_length: num 5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
## $ sepal_width : num 3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
## $ petal_length: num 1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
## $ petal_width : num 0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
## $ species : Factor w/ 3 levels "setosa","versicolor",...: 1 1 1 1 1 1 1 1 1 1 ...
```

```
# Check the data type:
class(iris_data)
```

```
## [1] "data.frame"
```

```
# Have a precursory glance at the first few rows:
head(iris_data)
```

```
## 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
```

```
# use the glimpse function in the dplyr package:
dplyr::glimpse(iris_data)
```

```
## Rows: 150
## Columns: 5
## $ sepal_length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9, 5.4, 4.~
## $ sepal_width <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1, 3.7, 3.~
## $ petal_length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5, 1.5, 1.~
## $ petal_width <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1, 0.2, 0.~
## $ species <fct> setosa, setosa, setosa, setosa, setosa, setosa, setosa, setosa, s~
```

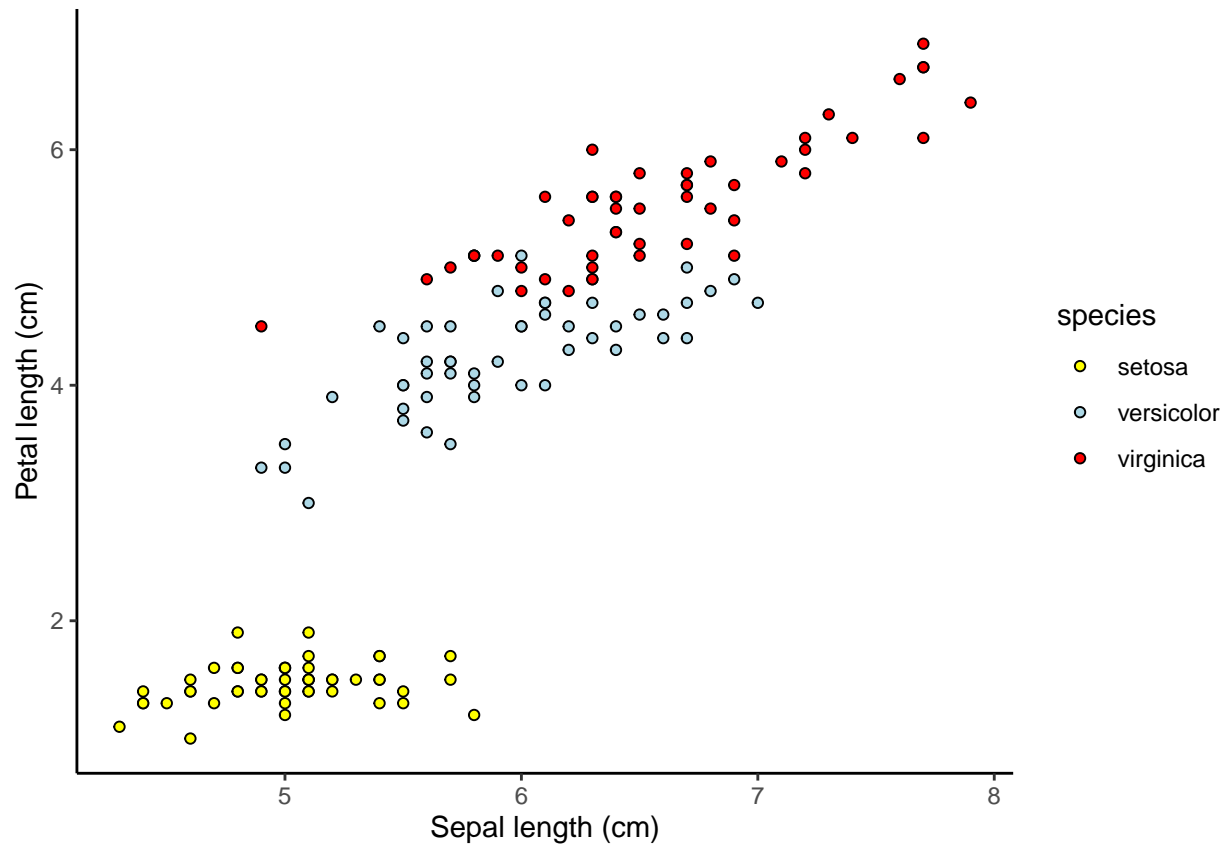
Note that there are always two spaces for values in the square brackets. The first value refers to the row number, and the second is the column number. A comma always separates these values. If there is no value before or after the comma, R assumes that you want all the available values. E.g. `iris_data[,]` means “get the values across all rows and columns”. Read the documentation for the `dplyr` package, as there are so many cool functions to make your life easier!

## ggplot

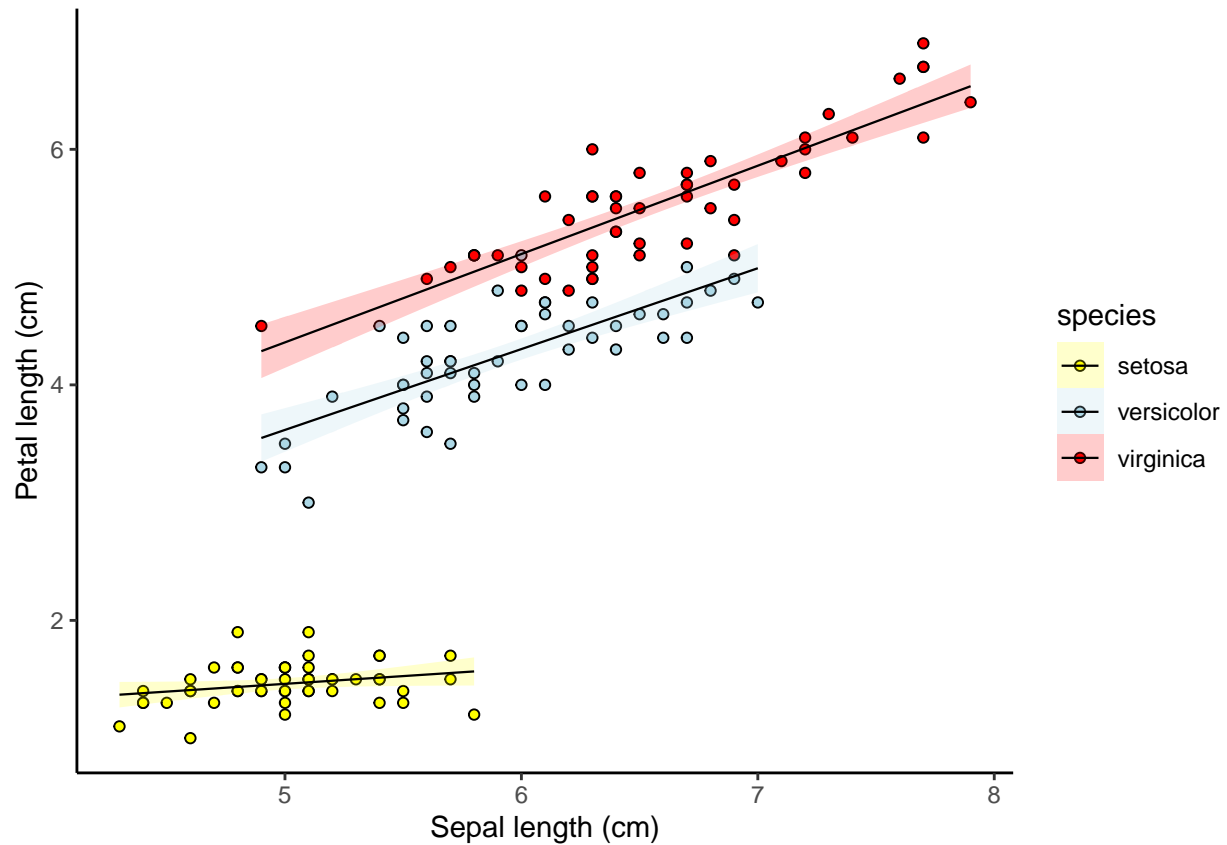
### Using `geom_point()`

`geom_point()` generates dot plots, like this:

```
ggplot2::ggplot(data = iris_data, aes(x=sepal_length, y=petal_length,
                                       fill=species)) +
  geom_point(shape = 21) +
  scale_fill_manual(values = c("yellow", "lightblue", "red")) +
  xlab("Sepal length (cm)") +
  ylab("Petal length (cm)") +
  theme_classic()
```

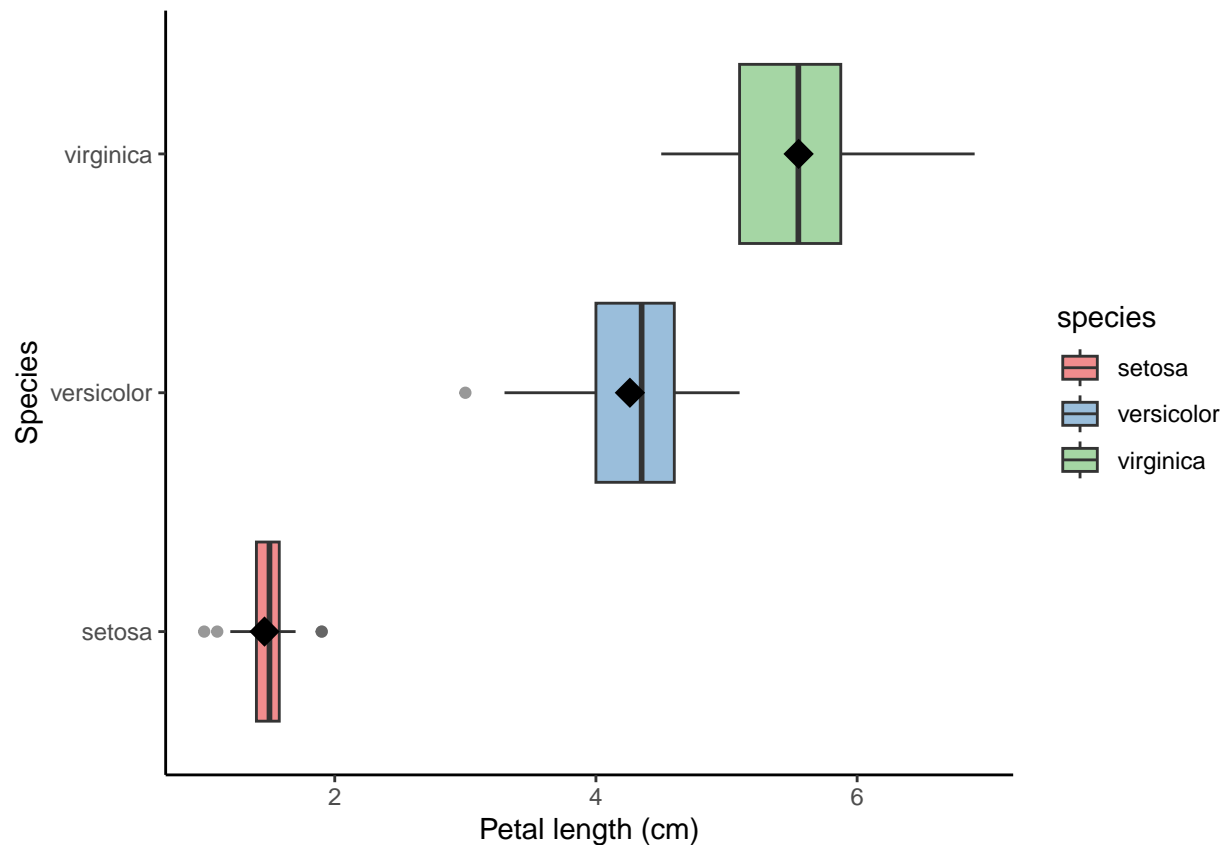


```
# Let's add trendlines
ggplot2::ggplot(data = iris_data, aes(x=sepal_length, y=petal_length,
                                       fill=species)) +
  geom_point(shape = 21) +
  scale_fill_manual(values = c("yellow", "lightblue", "red")) +
  xlab("Sepal length (cm)") +
  ylab("Petal length (cm)") +
  theme_classic() +
  stat_smooth(method = "lm", formula = y~x, geom = "smooth",
             alpha = 0.2, color = "black", linewidth = 0.4, se = TRUE)
```



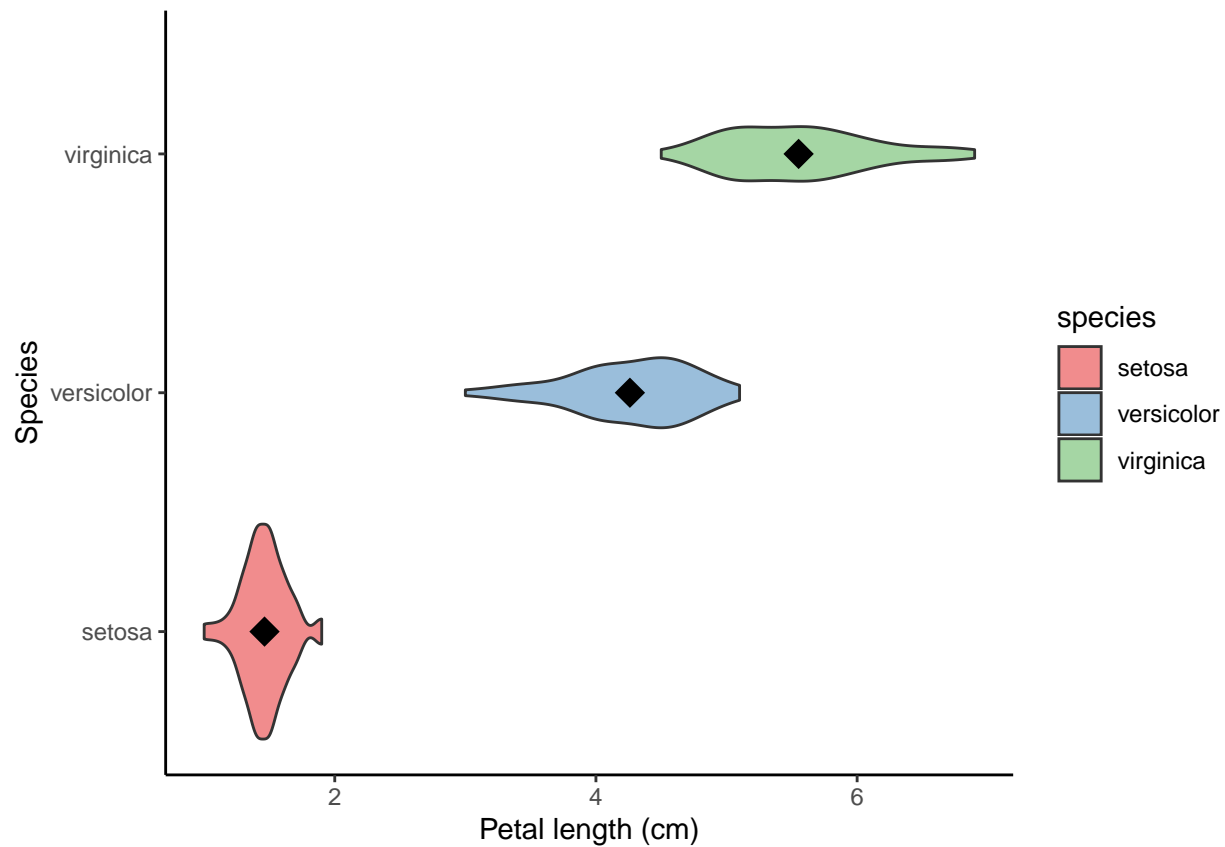
Perhaps we want to create box plots for the three species, showing an overall summary. Below, we can use `stat_summary()` to add points for the mean values for each species. We can either set the colours ourselves for each species using `scale_fill_manual()`, or we can use default colour palettes in R, using `scale_fill_brewer()`:

```
ggplot2::ggplot(data = iris_data, aes(x = species, y=petal_length,
                                      fill=species)) +
  geom_boxplot(alpha = 0.5) +
  scale_fill_brewer(palette="Set1") +
  # scale_fill_manual(values = c("yellow", "lightblue", "red")) +
  stat_summary(fun = mean, geom = "point", shape = 18, size = 5, fill="black") +
  theme(legend.position="none") +
  xlab("Species") +
  ylab("Petal length (cm)") +
  theme_classic() +
  coord_flip()
```



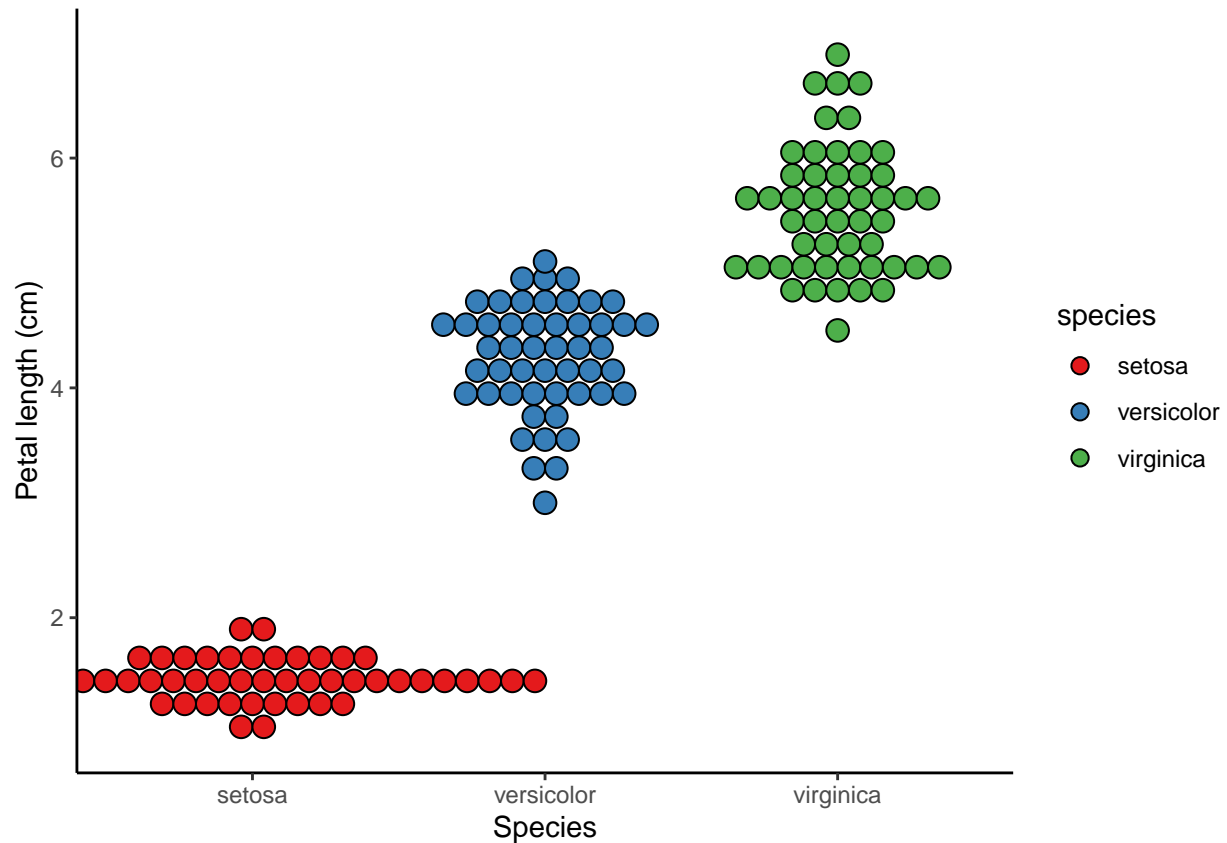
Explore the different **geom** options in the ggplot package - there are quite a few! Perhaps we want to change our boxplots above into violin or dot plots. This is easy, as we can use the same code as above, but just change `geom_box()` into `geom_violin()`:

```
ggplot2::ggplot(data = iris_data, aes(x = species, y=petal_length,
                                     fill=species)) +
  geom_violin(alpha = 0.5) +
  scale_fill_brewer(palette="Set1") +
  # scale_fill_manual(values = c("yellow", "lightblue", "red")) +
  stat_summary(fun = mean, geom = "point", shape = 18, size = 5, fill="black") +
  theme(legend.position="none") +
  xlab("Species") +
  ylab("Petal length (cm)") +
  theme_classic() +
  coord_flip()
```



Or dots:

```
ggplot2::ggplot(data = iris_data, aes(x = species, y=petal_length,
                                     fill=species)) +
  geom_dotplot(binaxis = "y", stackdir = "center") +
  scale_fill_brewer(palette="Set1") +
  # scale_fill_manual(values = c("yellow", "lightblue", "red")) +
  theme(legend.position="none") +
  xlab("Species") +
  ylab("Petal length (cm)") +
  theme_classic()
```



Here, we create a subset for each *Iris* species, using the `filter()` function in the **dplyr** package:

```
setosa = dplyr::filter(iris_data, species=="setosa")
versicolor = dplyr::filter(iris_data, species=="versicolor")
virginica = dplyr::filter(iris_data, species=="virginica")
```

Now we can run a quick correlation test to see if there is a significant correlation between sepal and petal length in *I. versicolor*:

```
cor.test(versicolor$sepal_length, versicolor$petal_length, method = "pearson")
```

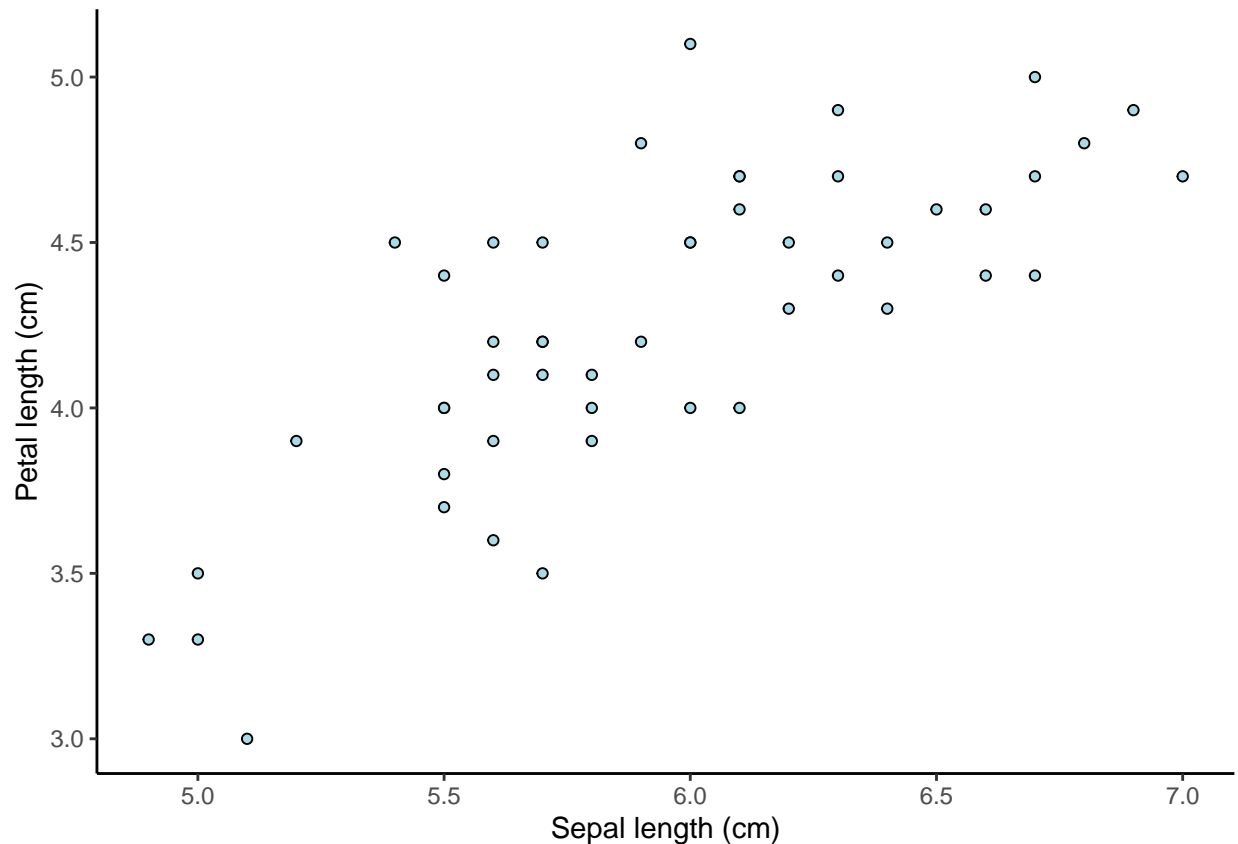
```
##
## Pearson's product-moment correlation
##
## data: versicolor$sepal_length and versicolor$petal_length
## t = 7.9538, df = 48, p-value = 2.586e-10
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.6020680 0.8532995
## sample estimates:
##      cor
## 0.754049
```

Here we see a significant correlation ( $p < 0.05$ ), with a correlation coefficient of  $r = 0.75$ . Typically, a value greater than 0.7 is considered to be strong.



Let's plot only *I. versicolor*, using `dplyr::filter()`:

```
ggplot2::ggplot(data = versicolor,
  aes(x=sepal_length, y=petal_length)) +
  geom_point(shape = 21, fill = "lightblue") +
  xlab("Sepal length (cm)") +
  ylab("Petal length (cm)") +
  theme_classic()
```



Let's run a quick linear model, where we check whether there is a relationship between petal and sepal length:

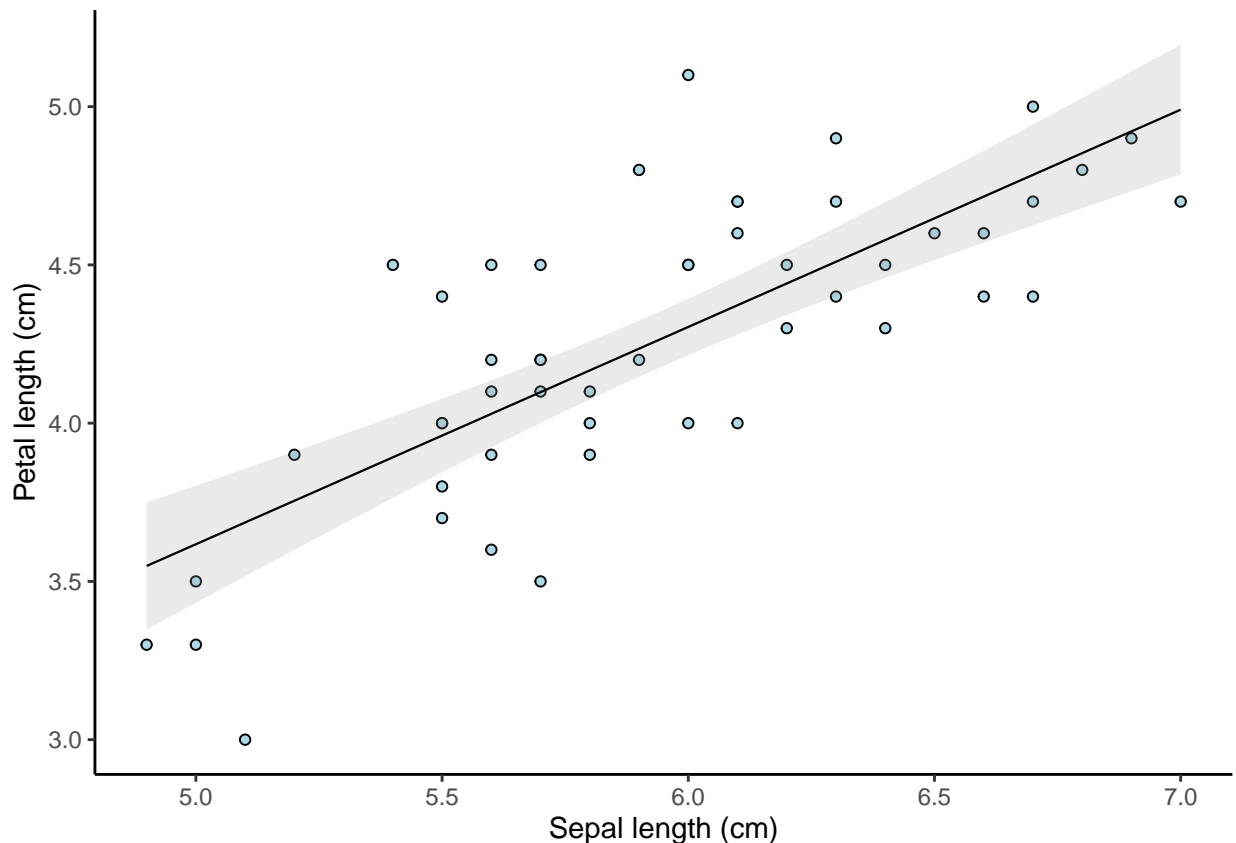
```
versicolor_lm = lm(data = versicolor, petal_length~sepal_length)
summary(versicolor_lm)
```

```
##
## Call:
## lm(formula = petal_length ~ sepal_length, data = versicolor)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.68611 -0.22827 -0.04123  0.19458  0.79607
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
##
```

```
## (Intercept)  0.18512    0.51421    0.360    0.72
## sepal_length 0.68647    0.08631    7.954 2.59e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3118 on 48 degrees of freedom
## Multiple R-squared:  0.5686, Adjusted R-squared:  0.5596
## F-statistic: 63.26 on 1 and 48 DF,  p-value: 2.586e-10
```

If we plot the trend line for this linear regression, the intercept = 0.19, and the gradient = 0.69. The  $R^2$  value is 0.56 ( $p < 0.05$ ). Let's add this line to our dot plot, with a confidence interval band:

```
ggplot2::ggplot(data = versicolor,
                aes(x=sepal_length, y=petal_length)) +
  geom_point(shape = 21, fill = "lightblue") +
  xlab("Sepal length (cm)") +
  ylab("Petal length (cm)") +
  theme_classic() +
  stat_smooth(method = "lm", formula = y~x, geom = "smooth",
             alpha = 0.2, color = "black", linewidth = 0.4, se = TRUE)
```



```
# set se = FALSE to remove the confidence interval band
```

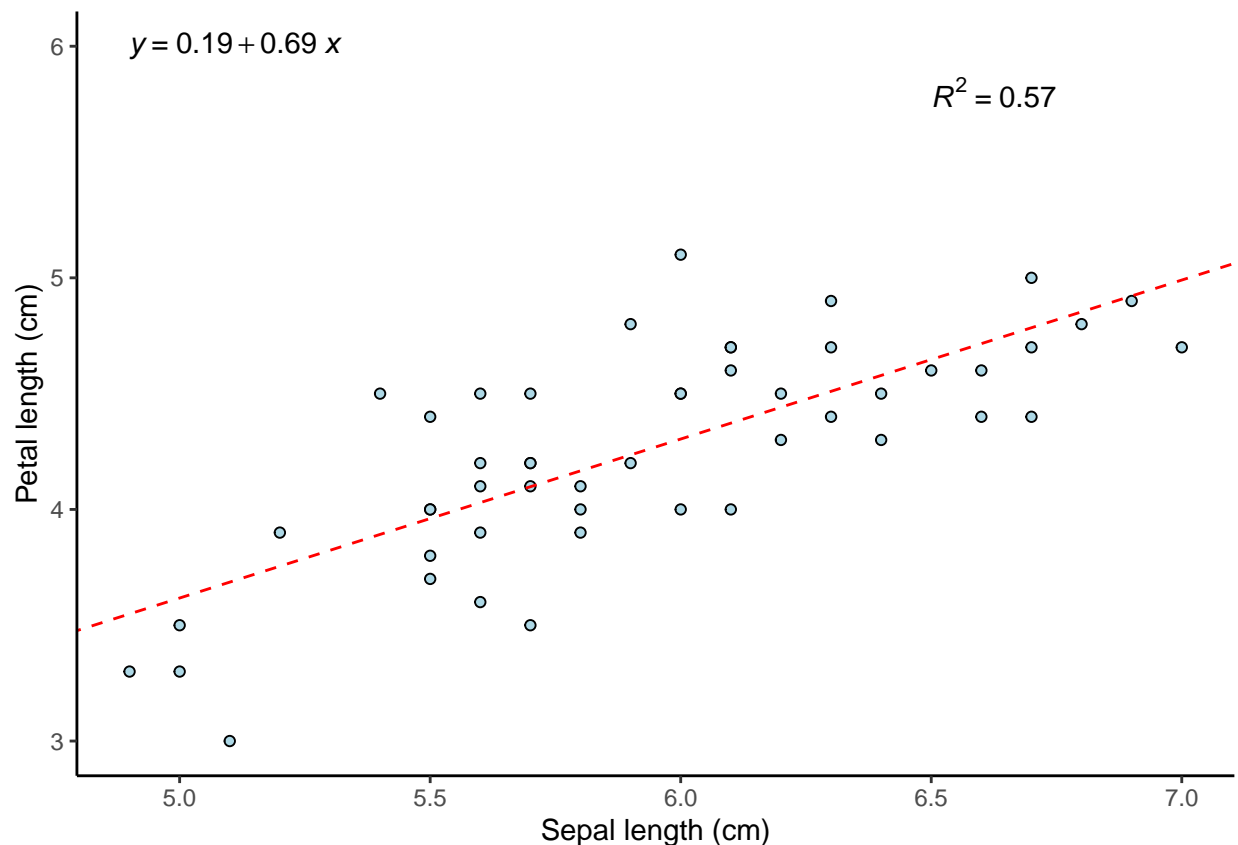
We can also add this line using the `geom_abline()` function:

```

coeff = coefficients(versicolor_lm)
intercept = coeff[1]
gradient = coeff[2]

ggplot2::ggplot(data = versicolor,
                aes(x=sepal_length, y=petal_length)) +
  geom_point(shape = 21, fill = "lightblue") +
  # add the abline
  geom_abline(intercept = intercept, slope = gradient, linewidth = 0.5,
              color = "red", linetype = "dashed") +
  xlab("Sepal length (cm)") +
  ylab("Petal length (cm)") +
  theme_classic() +
  # the stat_regline_equation() function in the ggpubr package
  # adds the equation as text to the plot
  ggpubr::stat_regline_equation(label.y = 6, aes(label = after_stat(c(eq.label)))) +
  # the stat_regline_equation() function in the ggpubr package adds the
  # R-squared value as text to the plot
  ggpubr::stat_regline_equation(label.y = 5.8, label.x = 6.5,
                                aes(label = after_stat(c(rr.label)))) )

```



Add `facet_wrap()` to separate the plots by species:

```

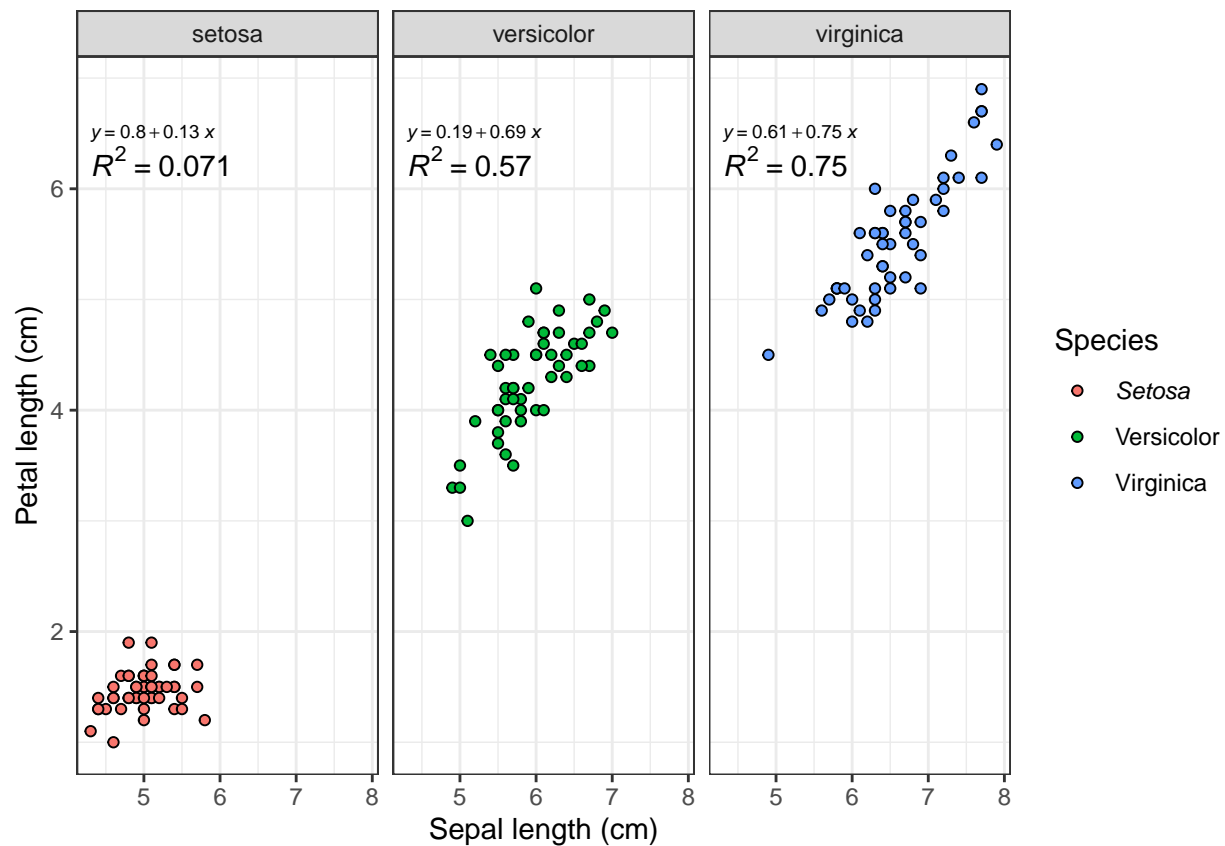
ggplot2::ggplot(data = iris_data, aes(x=sepal_length, y=petal_length, fill=species)) +
  geom_point(shape = 21) +
  scale_fill_manual(values = c("yellow", "lightblue", "red")) +

```

```

xlab("Sepal length (cm)") +
ylab("Petal length (cm)") +
theme_bw() +
facet_wrap(~species) +
guides(fill=guide_legend(title="Species")) +
scale_fill_discrete(labels=c(expression(italic('Setosa')), 'Versicolor', "Virginica")) +
ggpubr::stat_regline_equation(label.y = 6.5, size = 2.5,
                             aes(label = after_stat(c(eq.label)))) ) +
ggpubr::stat_regline_equation(label.y = 6.25,
                             aes(label = after_stat(c(rr.label)))) )

```



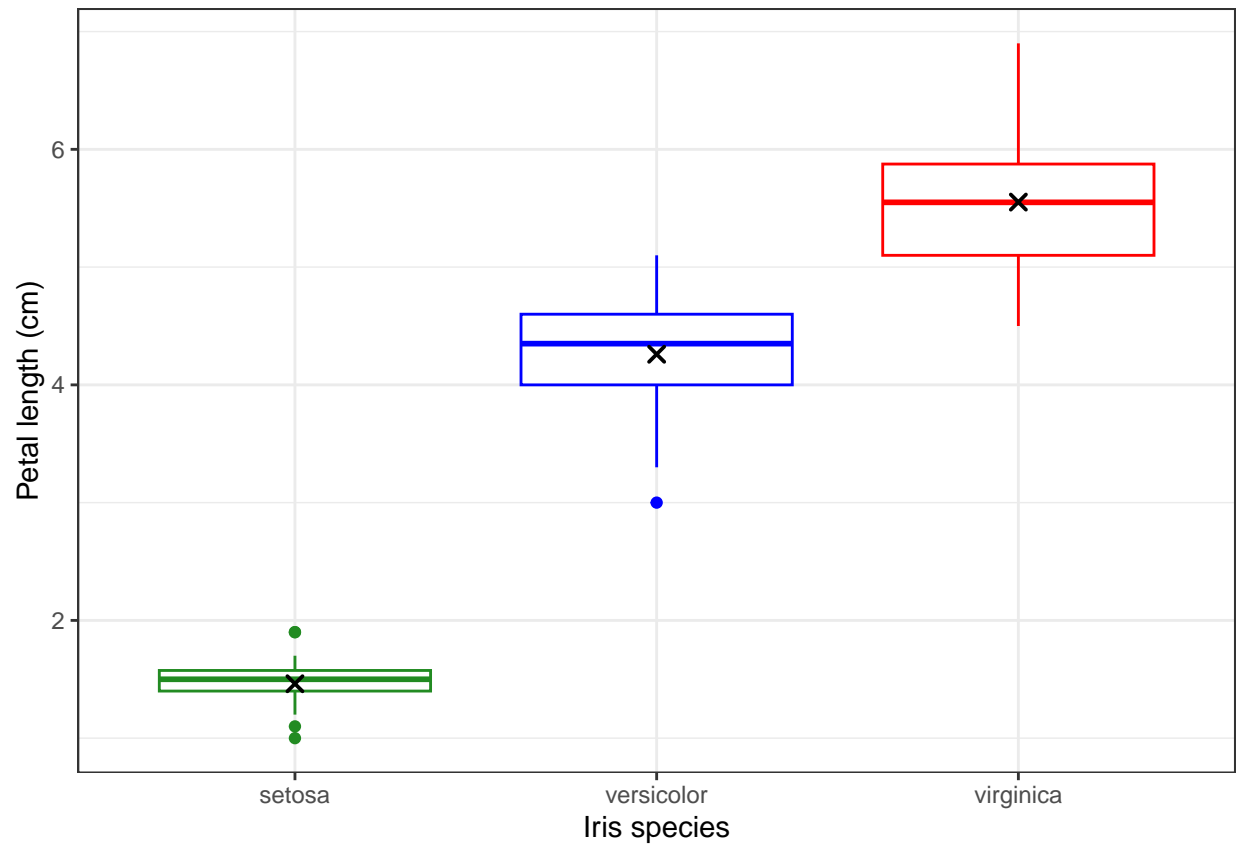
### Using geom\_boxplot()

The `geom_boxplot()` function creates box-and-whisker summary plots for your data:

```

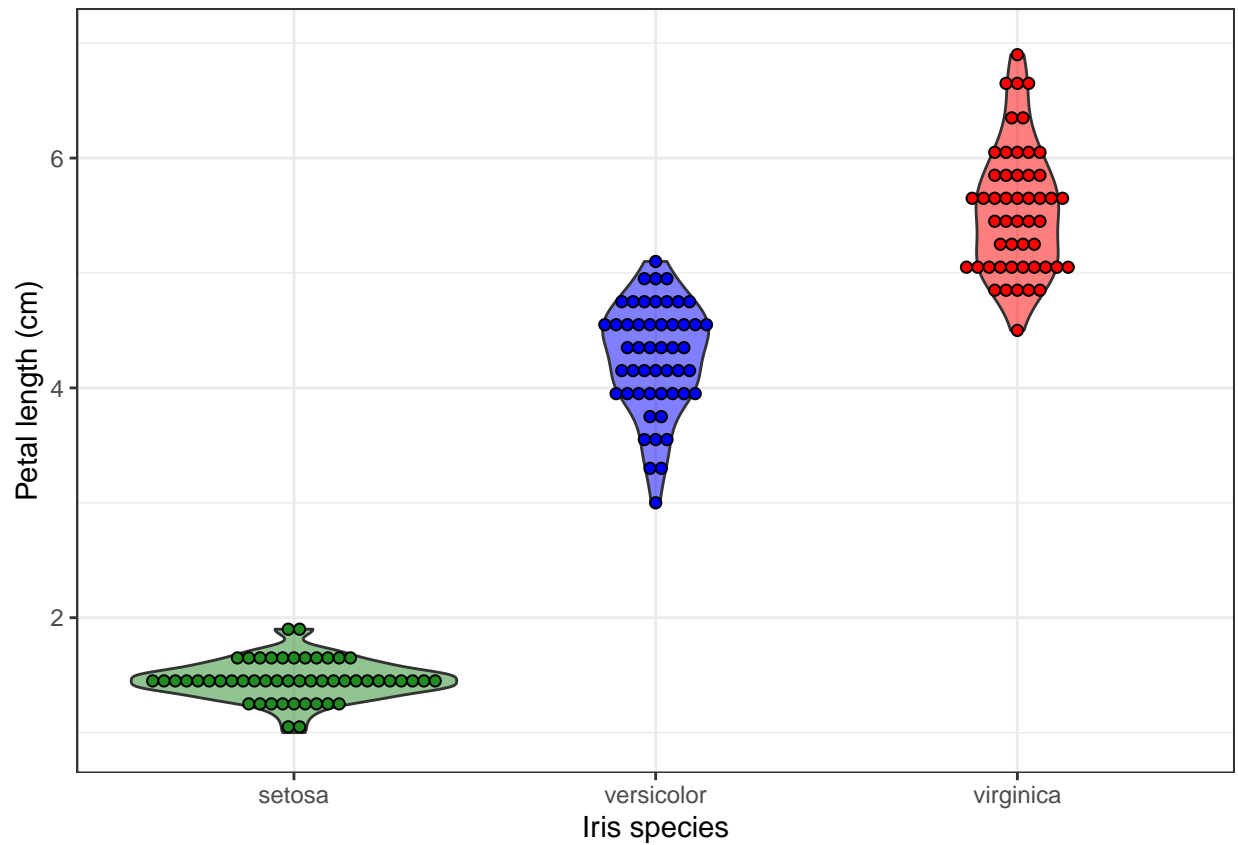
ggplot2::ggplot(data = iris_data, aes(x=species, y=petal_length, color=species)) +
  geom_boxplot() +
  scale_color_manual(values = c("forestgreen", "blue", "red")) +
  xlab("Iris species") +
  ylab("Petal length (cm)") +
  theme_bw() +
  theme(legend.position="none") +
  # add points to denote means
  stat_summary(fun = "mean", colour = "black", shape = 4)

```



Using `geom_violin()`

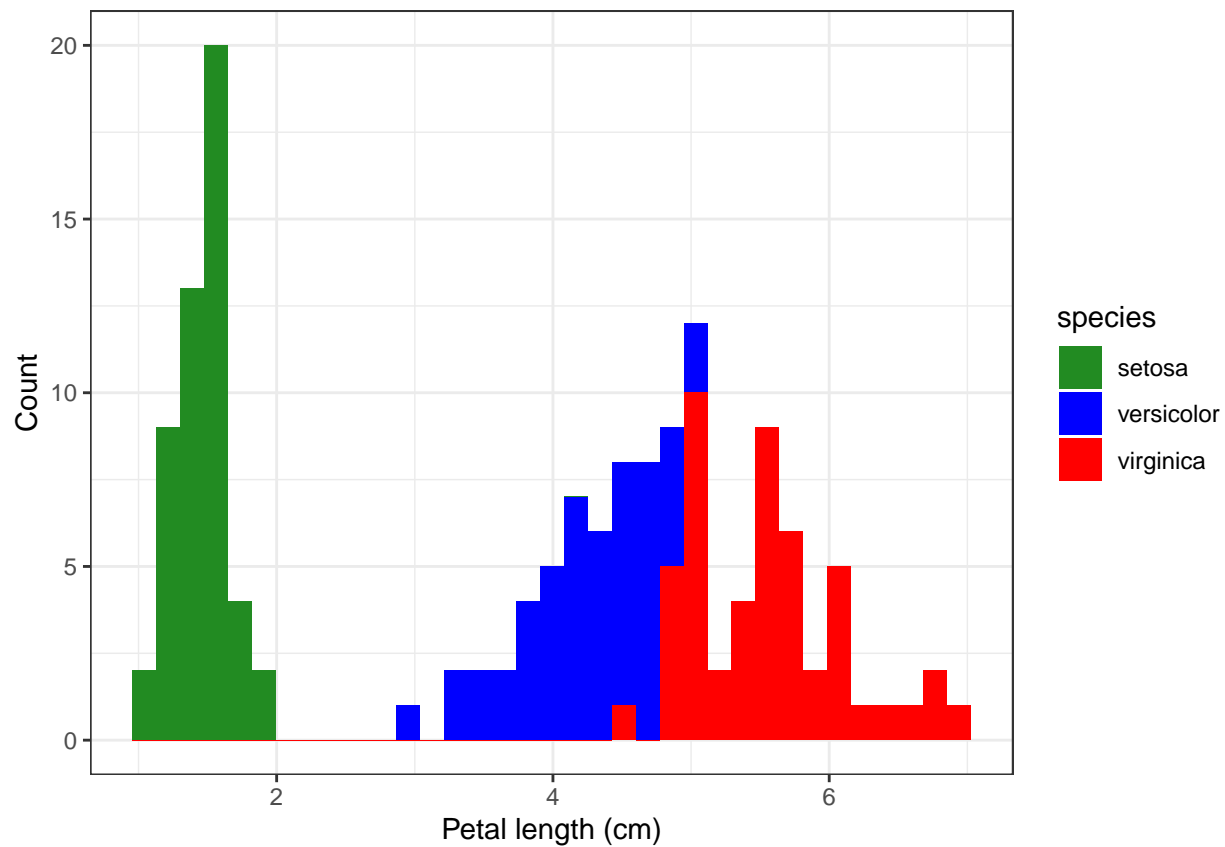
```
ggplot2::ggplot(data = iris_data, aes(x=species, y=petal_length, fill=species)) +
  geom_violin(alpha=0.5) +
  geom_dotplot(binaxis= "y",
               stackdir = "center",
               dotsize = 0.5) +
  scale_fill_manual(values = c("forestgreen", "blue", "red")) +
  xlab("Iris species") +
  ylab("Petal length (cm)") +
  theme_bw() +
  theme(legend.position="none")
```



Using `geom_histogram()`

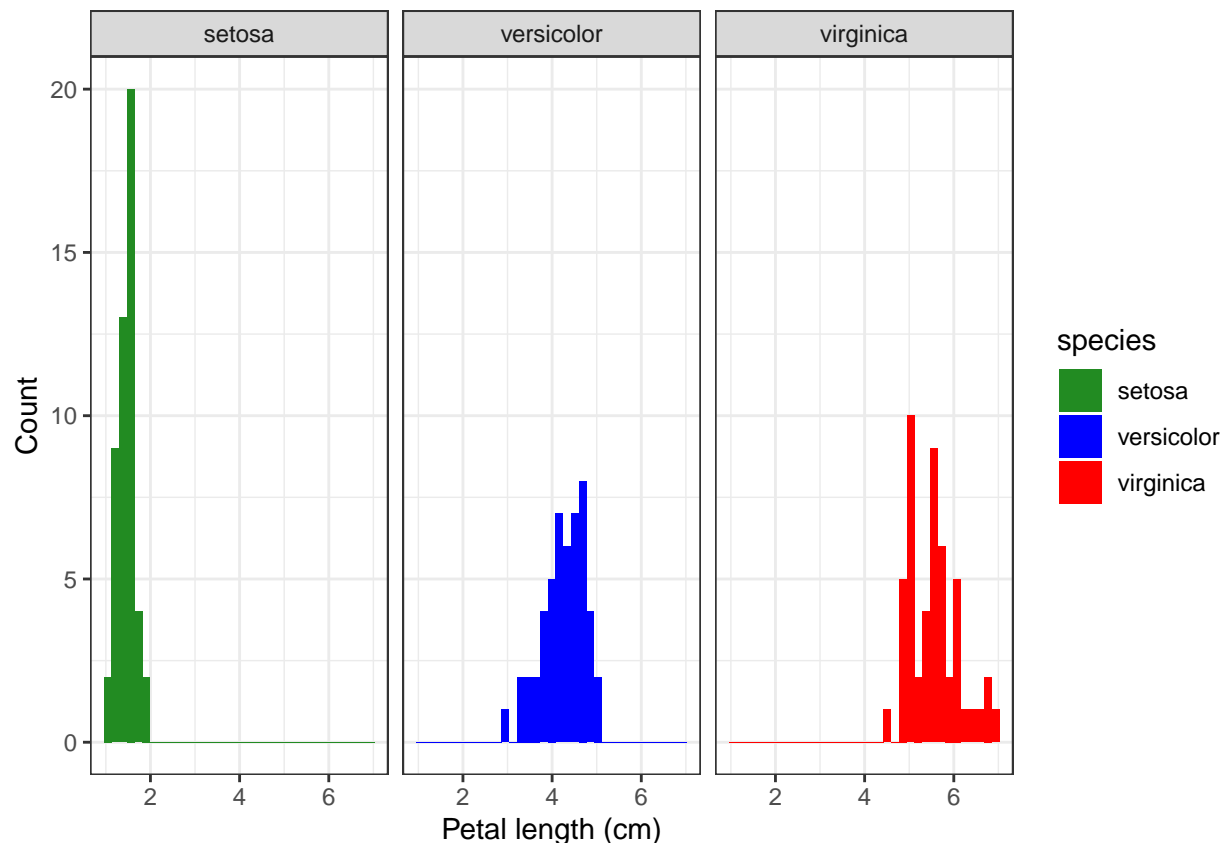
Use `geom_histogram` to generate histogram plots. Set an appropriate bin value:

```
ggplot2::ggplot(data = iris_data, aes(x=petal_length, fill=species)) +
  geom_histogram(bins = 35) +
  scale_fill_manual(values = c("forestgreen", "blue", "red")) +
  xlab("Petal length (cm)") +
  ylab("Count") +
  theme_bw()
```



Use `facet_wrap()` here:

```
ggplot2::ggplot(data = iris_data, aes(x=petal_length, fill=species)) +  
  geom_histogram(bins = 35) +  
  scale_fill_manual(values = c("forestgreen", "blue", "red")) +  
  xlab("Petal length (cm)") +  
  ylab("Count") +  
  theme_bw() +  
  facet_wrap(~species)
```



## Saving your plots as .PNG, .JPG, .PDF, or .SVG

To save a plot, first assign it a name. We will call the last plot we made `petal_length_hist`:

```
petal_length_hist = ggplot2::ggplot(data = iris_data,
                                     aes(x=petal_length, fill=species)) +
  geom_histogram(bins = 35) +
  scale_fill_manual(values = c("forestgreen", "blue", "red")) +
  xlab("Petal length (cm)") +
  ylab("Count") +
  theme_bw() +
  facet_wrap(~species)
```

Now we can use the `ggsave()` function to save it in any format we like. Play around with the dimensions to get an ideal size:

```
# save as PNG
ggplot2::ggsave("outputs/petal_length.png", plot = petal_length_hist,
                dpi = 350, width = 8, height = 4)

# save as PDF
ggplot2::ggsave("outputs/petal_length.pdf", plot = petal_length_hist,
                dpi = 350, width = 8, height = 4)

# save as JPG
ggplot2::ggsave("outputs/petal_length.jpg", plot = petal_length_hist,
                dpi = 350, width = 8, height = 4)
```