YaRrr! The Pirate's Guide to R

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```
## Warning: package 'dplyr' was built under R version 3.4.1
```

```
## Warning: package 'circlize' was built under R version 3.4.1
```

Sammy Davis Jr. was one of the greatest American performers of all time. If you don't know him already, Sammy was an American entertainer who lived from 1925 to 1990. The range of his talents was just incredible. He could sing, dance, act, and play multiple instruments with ease. So how is R like Sammy Davis Jr? Like Sammy Davis Jr., R is incredibly good at doing many different things. R does data analysis like Sammy dances, and creates plot like Sammy sings. If Sammy and R did just one of these things, they'd be great. The fact that they can do both is pretty amazing.

When you evaluate plotting functions in R, R can build the plot in different locations. The default location for plots is in a temporary plotting window within your R programming environment. In RStudio, plots will show up in the Plot window (typically on the bottom right hand window pane). In Base R, plots will show up in a Quartz window.

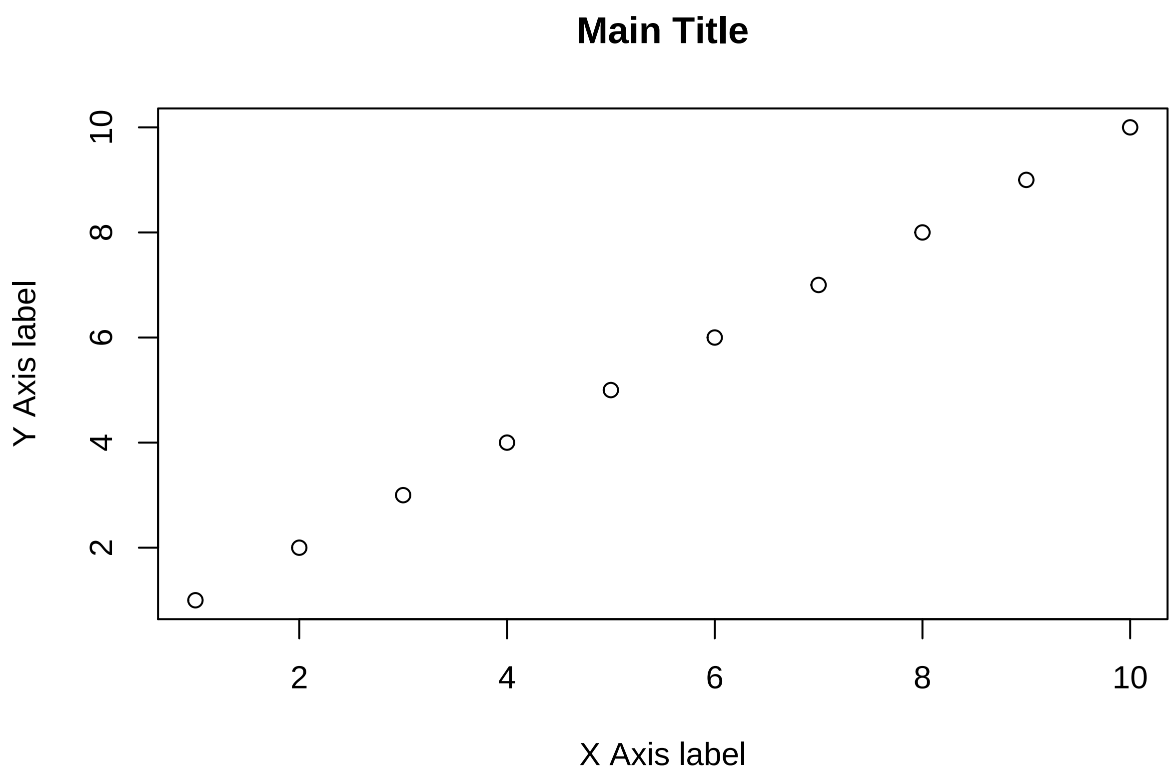
You can think of these plotting locations as canvases. You only have one canvas active at any given time, and any plotting command you run will put more plotting elements on your active canvas. Certain high–level plotting functions like `plot()` and `hist()` create brand new canvases, while other low–level plotting functions like `points()` and `segments()` place elements on top of existing canvases.

Don't worry if that's confusing for now – we'll go over all the details soon.

Let's start by looking at a basic scatterplot in R using the `plot()` function. When you execute the following code, you should see a plot open in a new window:

```r
# A basic scatterplot
plot(x = 1:10,
     y = 1:10,
     xlab = "X Axis label",
     ylab = "Y Axis label",
     main = "Main Title")
```

Figure 11.1: The great Sammy Davis Jr. Do yourself a favor and spend an evening watching videos of him performing on YouTube. Image used entirely without permission.



Let's take a look at the result. We see an x–axis, a y–axis, 10 data points, an x–axis label, a y–axis label, and a main plot title. Some of these items, like the labels and data points, were entered as arguments to the function. For example, the main arguments x and y are vectors indicating the x and y coordinates of the (in this case, 10) data points. The arguments `xlab`, `ylab`, and `main` set the labels to the plot. However, there were many elements that I did not specify – from the x and y axis limits, to the color of the plotting points. As you'll discover later, you can change all of these elements (and many, many more) by specifying additional arguments to the `plot()` function. However, because I did not specify them, R used **default** values – values that R uses unless you tell it to use something else.

For the rest of this chapter, we'll go over the main plotting functions, along with the most common arguments you can use to customize the look of your plot.

11.1 Colors

Most plotting functions have a color argument (usually `col`) that allows you to specify the color of whatever your plotting. There are many ways to specify colors in R, let's start with the easiest ways.

11.1.1 Colors by name

The easiest way to specify a color is to enter its name as a string. For example `col = "red"` is R's default version of the color red. Of course, all the basic colors are there, but R also has tons of quirky colors like `"snow"`, `"papayawhip"` and `"lawngreen"`. Figure 11.2 shows 100 randomly selected named colors.

To see all 657 color names in R, run the code `colors()`. Or to see an interactive demo of colors, run `demo("colors")`.

Figure 11.2: 100 random named colors (out of all 657) in R.

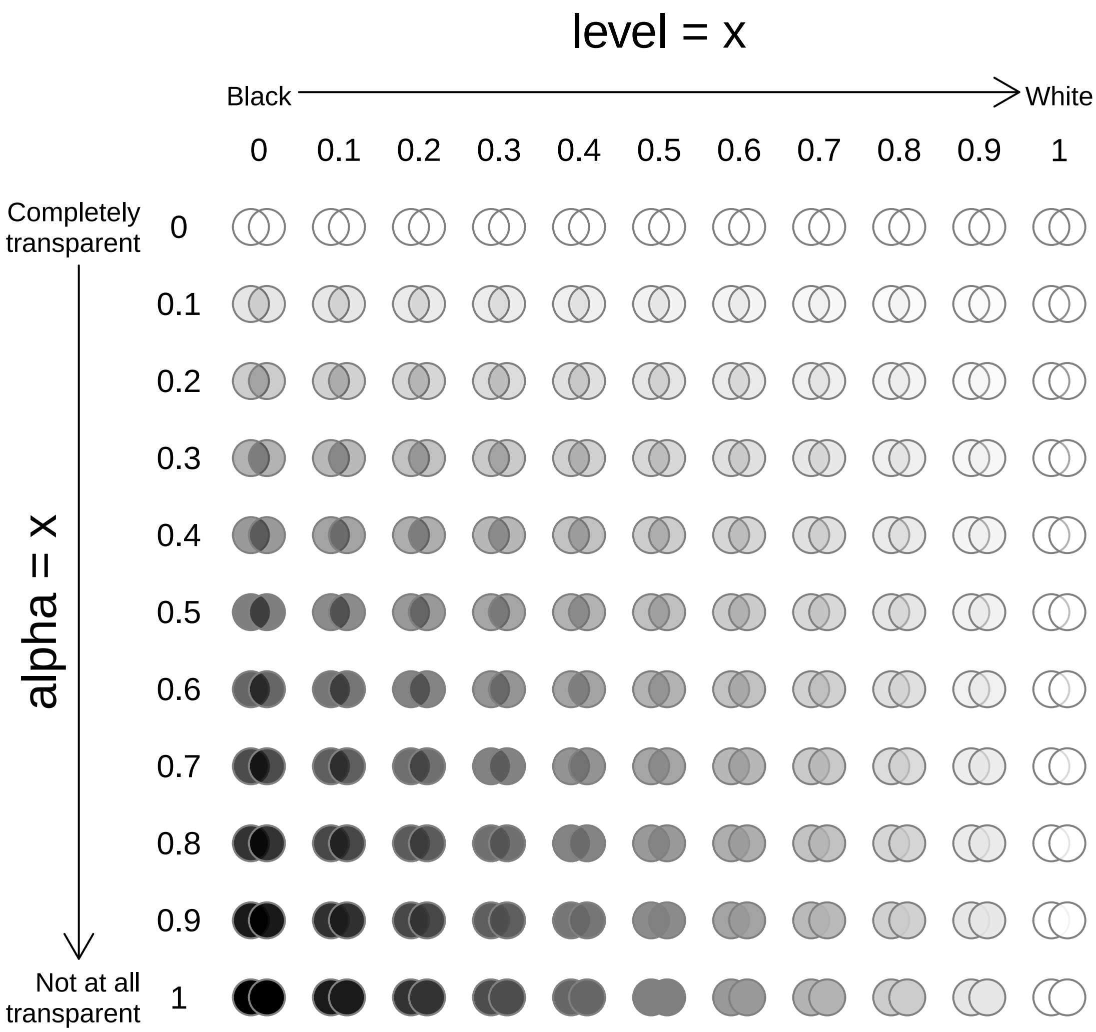


Figure 11.3: Examples of gray(level, alpha)

11.1.2 gray()

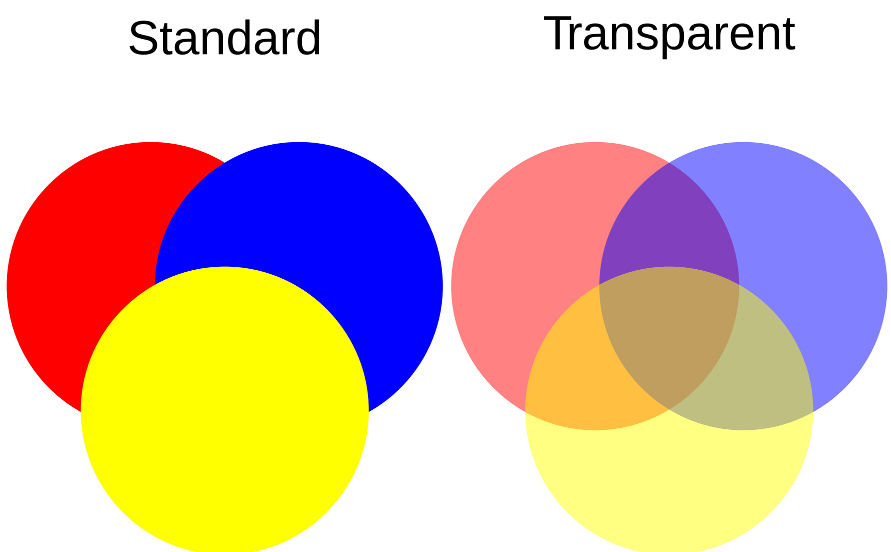
Table 11.1: `gray()` function arguments

Argument	Description
`level`	Lightness: `level = 1` = totally white, `level = 0` = totally black
`alpha`	Transparency: `alpha = 0` = totally transparent, `alpha = 1` = not transparent at all.

If you're into erotic romance and BDSM, then you might be interested in Shades of Gray. If so, the function `gray(x)` is your answer. The `gray()` function takes two arguments, `level` and `alpha`, and returns a shade of gray. For example, `gray(level = 1)` will return white. The second `alpha` argument specifies how transparent to make the color on a scale from 0 (completely transparent), to 1 (not transparent at all). The default value for alpha is 1 (not transparent at all). See Figure 11.3 for examples.

11.1.3 `yarrr::transparent()`

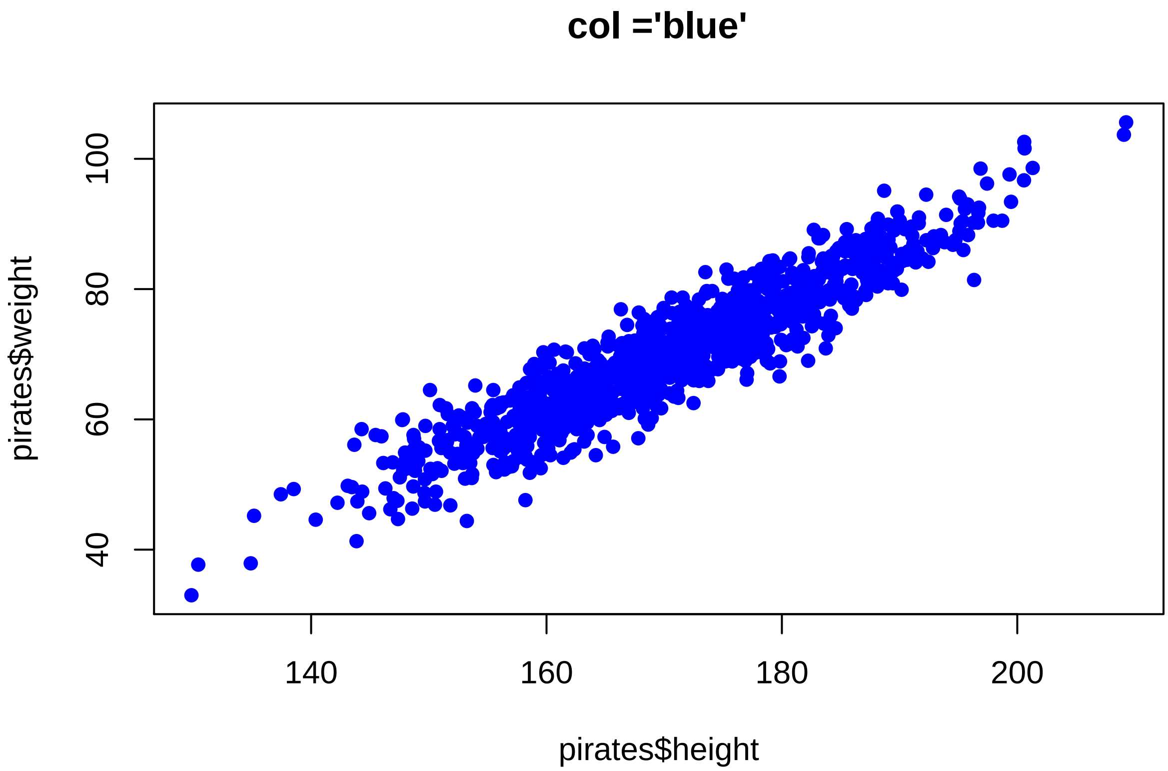
I don't know about you, but I almost always find transparent colors to be more appealing than solid colors. Not only do they help you see when multiple points are overlapping, but they're just much nicer to look at. Just look at the overlapping circles in the plot below.



Unfortunately, as far as I know, base-R does not make it easy to make transparent colors. Thankfully, there is a function in the `yarrr` package called `transparent` that makes it very easy to make any color transparent. To use it, just enter the original color as the main argument `orig.col`, then enter how transparent you want to make it (from 0 to 1) as the second argument `trans.val`.

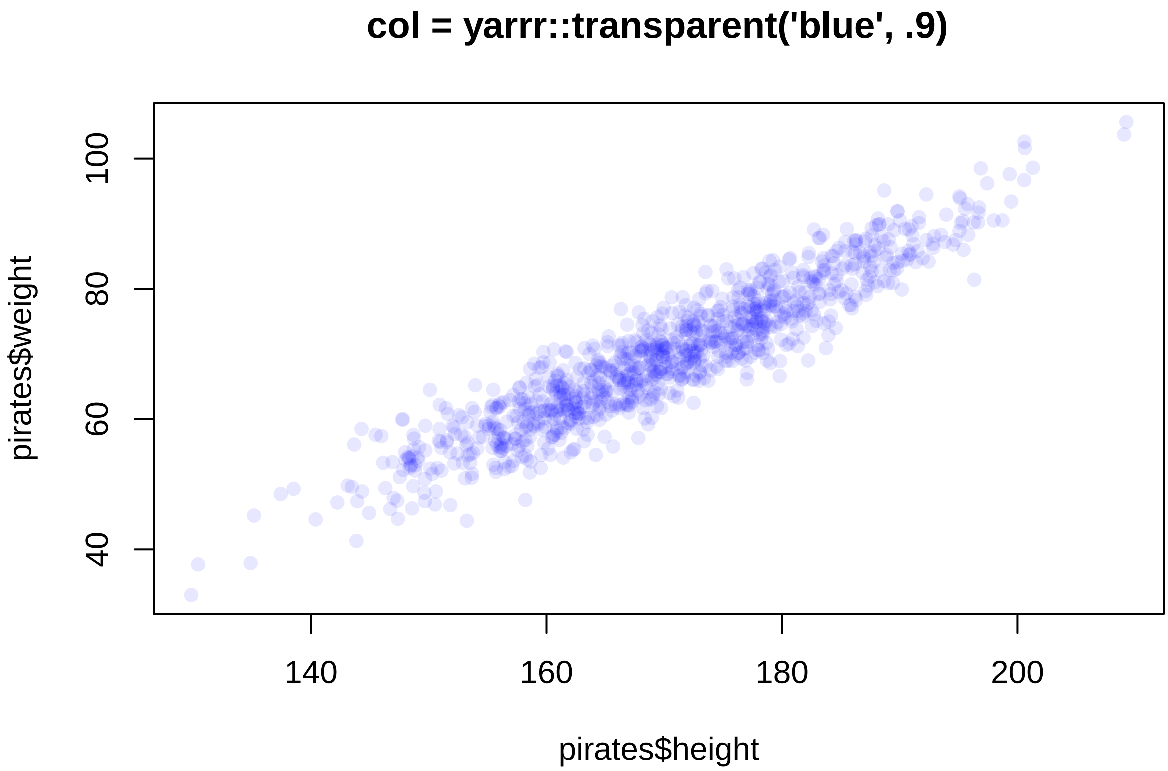
Here is a basic scatterplot with standard (non-transparent) colors:

```
# Plot with Standard Colors
plot(x = pirates$height,
     y = pirates$weight,
     col = "blue",
     pch = 16,
     main = "col ='blue'")
```



Now here's the same plot using the `transparent()` function in the `yarrr` package:

```
# Plot with transparent colors using the transparent() function in the yarrr package
plot(x = pirates$height,
     y = pirates$weight,
     col = yarrr::transparent("blue", trans.val = .9),
     pch = 16,
     main = "col = yarrr::transparent('blue', .9)")
```



Later on in the book, we'll cover more advanced ways to come up with colors using color palettes (using the RColorBrewer package or the `piratepal()` function in the yarrr package) and functions that generate shades of colors based on numeric data (like the `colorRamp2()` function in the `circlize` package).

11.2 Plotting arguments

Most plotting functions have *tons* of optional arguments (also called parameters) that you can use to customize virtually everything in a plot. To see all of them, look at the help menu for `par` by executing `?par`. However, the good news is that you don't need to specify all possible parameters you create a plot. Instead, there are only a few critical arguments that you must specify - usually one or two vectors of data. For any optional arguments that you do not specify, R will use either a default value, or choose a value that makes sense based on the data you specify.

In the following examples, I will to cover the main plotting parameters for each plotting type. However, the best way to learn what you can, and can't, do with plots, is to try to create them yourself!

I think the best way to learn how to create plots is to see some examples. Let's start with the main high-level plotting functions.

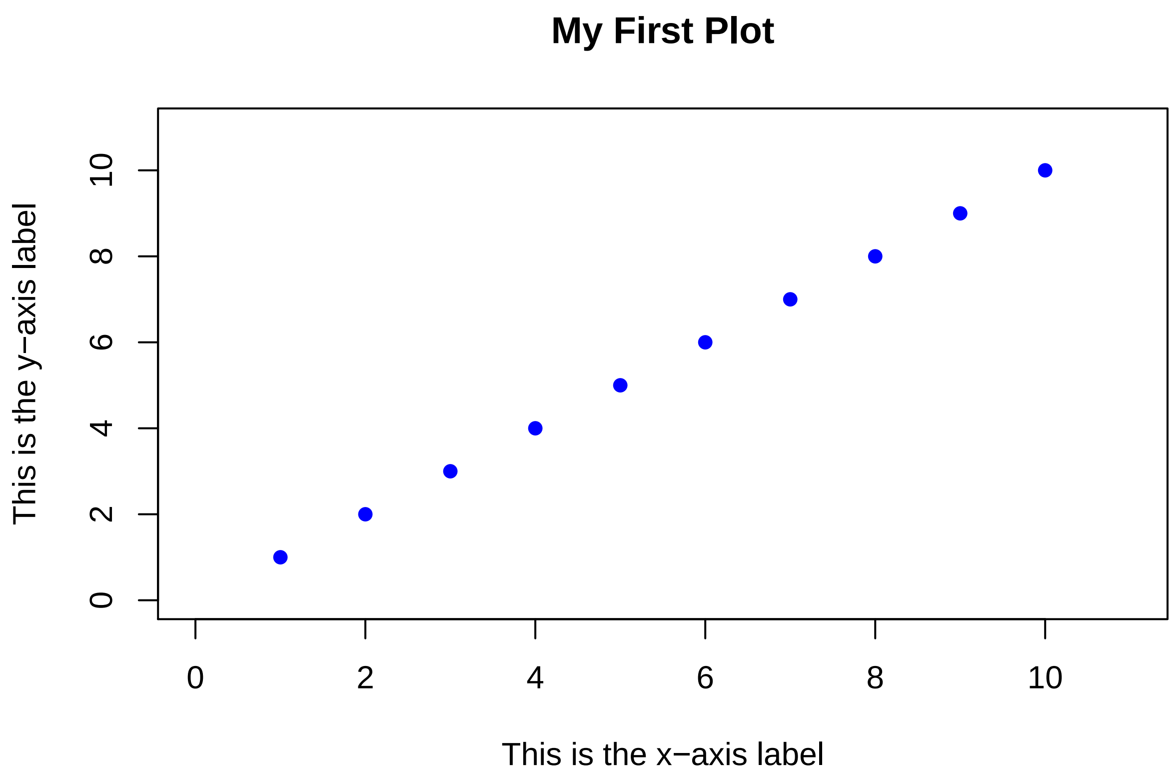
11.3 Scatterplot: `plot()`

The most common high-level plotting function is `plot(x, y)`. The `plot()` function makes a scatterplot from two vectors x and y, where the x vector indicates the x (horizontal) values of the points, and the y vector indicates the y (vertical) values.

Table 11.2: `plot()` function arguments

Argument	Description
`x, y`	Vectors of equal length specifying the x and y values of the points
`type`	Type of plot. `"l"` means lines, `"p"` means points, `"b"` means lines and points, `"n"` means no plotting
`main`, `xlab`, `ylab`	Strings giving labels for the plot title, and x and y axes
`xlim`, `ylim`	Limits to the axes. For example, `xlim = c(0, 100)` will set the minimum and maximum of the x-axis to 0 and 100.
`pch`	An integer indicating the type of plotting symbols (see `?points` and section below), or a string specifying symbols as text. For example, `pch = 21` will create a two-color circle, while `pch = "P"` will plot the character `"P"`. To see all the different symbol types, run `?points`.
`col`	Main color of the plotting symbols. For example `col = "red"` will create red symbols.
`cex`	A numeric vector specifying the size of the symbols (from 0 to Inf). The default size is 1. `cex = 4` will make the points very large, while `cex = .5` will make them very small.

```
plot(x = 1:10,                          # x-coordinates
     y = 1:10,                          # y-coordinates
     type = "p",                        # Just draw points (no lines)
     main = "My First Plot",
     xlab = "This is the x-axis label",
     ylab = "This is the y-axis label",
     xlim = c(0, 11),                   # Min and max values for x-axis
     ylim = c(0, 11),                   # Min and max values for y-axis
     col = "blue",                      # Color of the points
     pch = 16,                          # Type of symbol (16 means Filled circle)
     cex = 1)                            # Size of the symbols
```



Aside from the x and y arguments, all of the arguments are optional. If you don't specify a specific argument, then R will use a default value, or try to come up with a value that makes sense. For example, if you don't specify the `xlim` and `ylim` arguments, R will set the limits so that all the points fit inside the plot.

11.3.1 Symbol types: `pch`

When you create a plot with `plot()` (or points with `points()`), you can specify the type of symbol with the `pch` argument. You can specify the symbol type in one of two ways: with an integer, or with a string. If you use a string (like `"p"`), R will use that text as the plotting symbol. If you use an integer value, you'll get the symbol that correspond to that number. See Figure for all the symbol types you can specify with an integer.

Symbols differ in their shape and how they are colored. Symbols 1 through 14 only have borders and are always empty, while symbols 15 through 20 don't have a border and are always filled. Symbols 21 through 25 have both a border and a filling. To specify the border color or background for symbols 1 through 20, use the `col` argument. For symbols 21 through 25, you set the color of the border with `col`, and the color of the background using `bg`

Let's look at some different symbol types in action when applied to the same data:

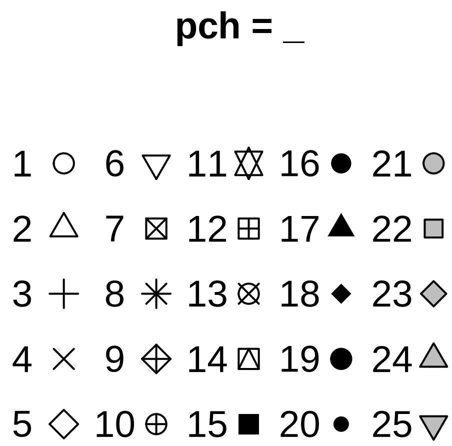
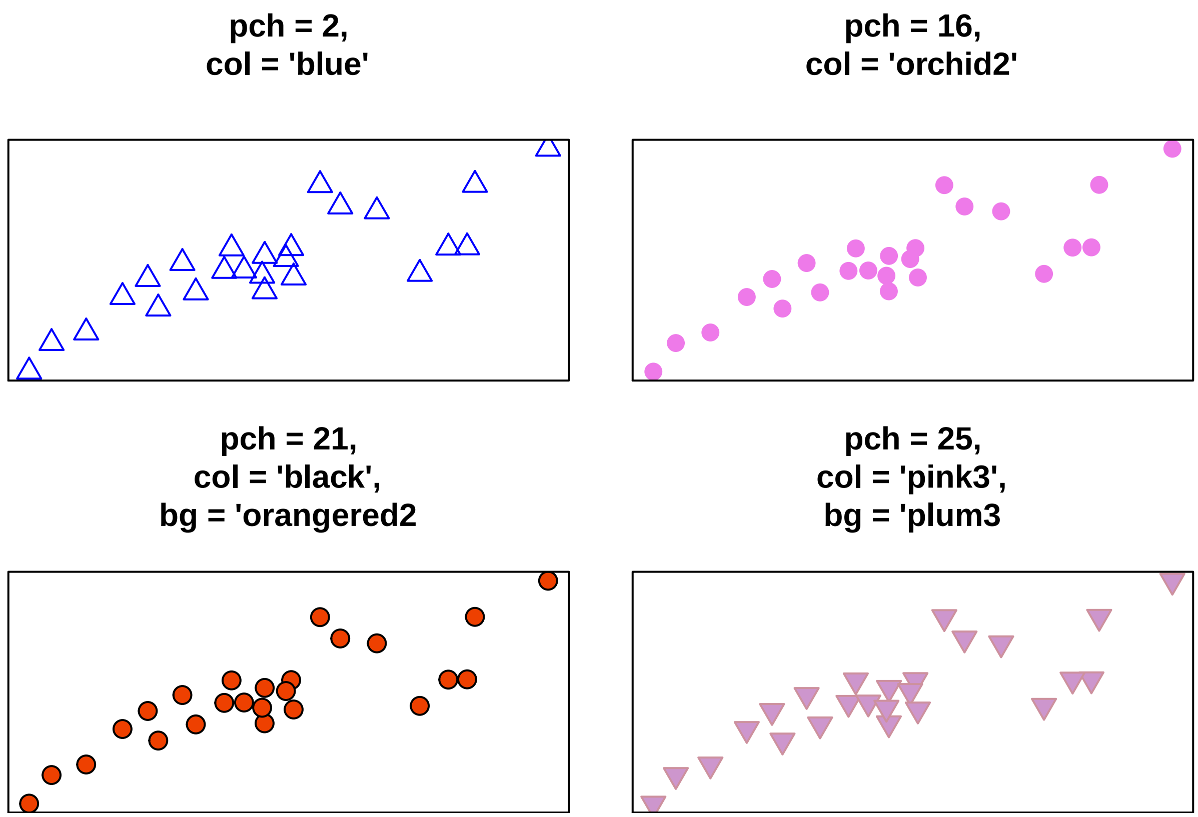


Figure 11.4: The symbol types associated with the pch plotting parameter.



11.4 Histogram: `hist()`

Table 11.3: `hist()` function arguments

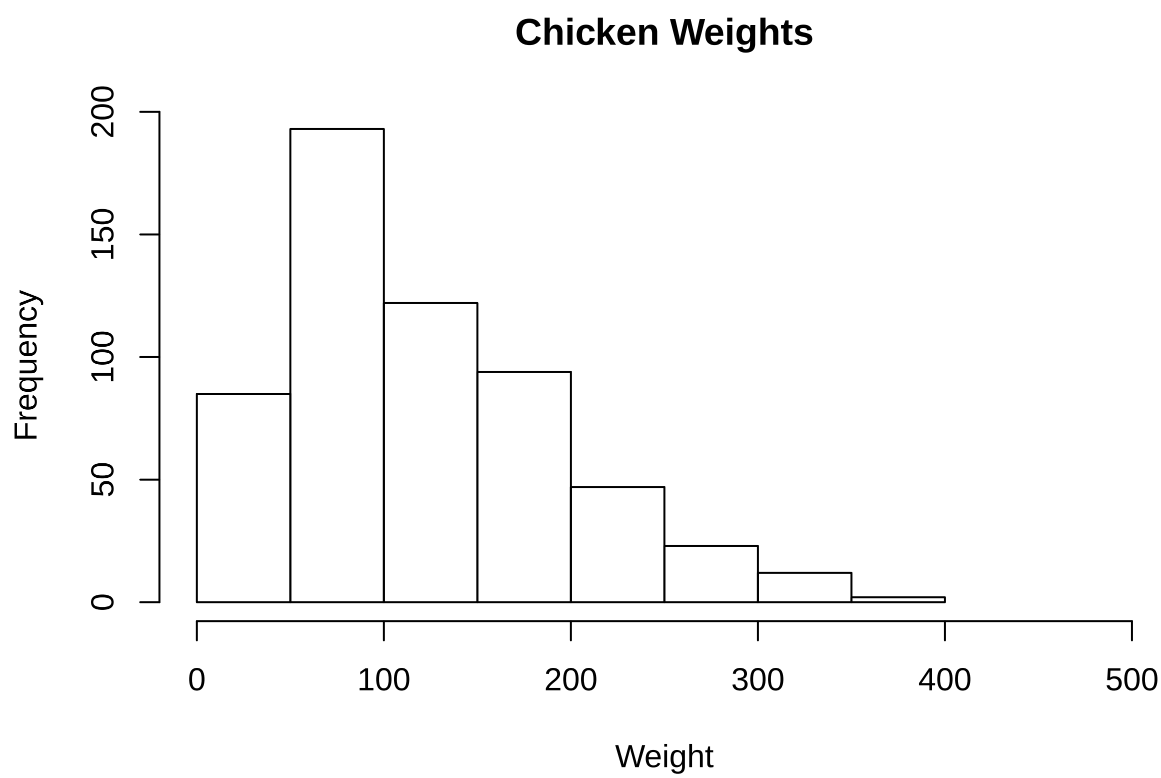
Argument	Description
`x`	Vector of values
`breaks`	How should the bin sizes be calculated? Can be specified in many ways (see `?hist` for details)

Argument	Description
`freq`	Should frequencies or probabilities be plotted? `freq = TRUE` shows frequencies, `freq = FALSE` shows probabilities.
`col`, `border`	Colors of the bin filling (`col`) and border (`border`)

Histograms are the most common way to plot a vector of numeric data. To create a histogram we'll use the `hist()` function. The main argument to `hist()` is a `x`, a vector of numeric data. If you want to specify how the histogram bins are created, you can use the `breaks` argument. To change the color of the border or background of the bins, use `col` and `border`:

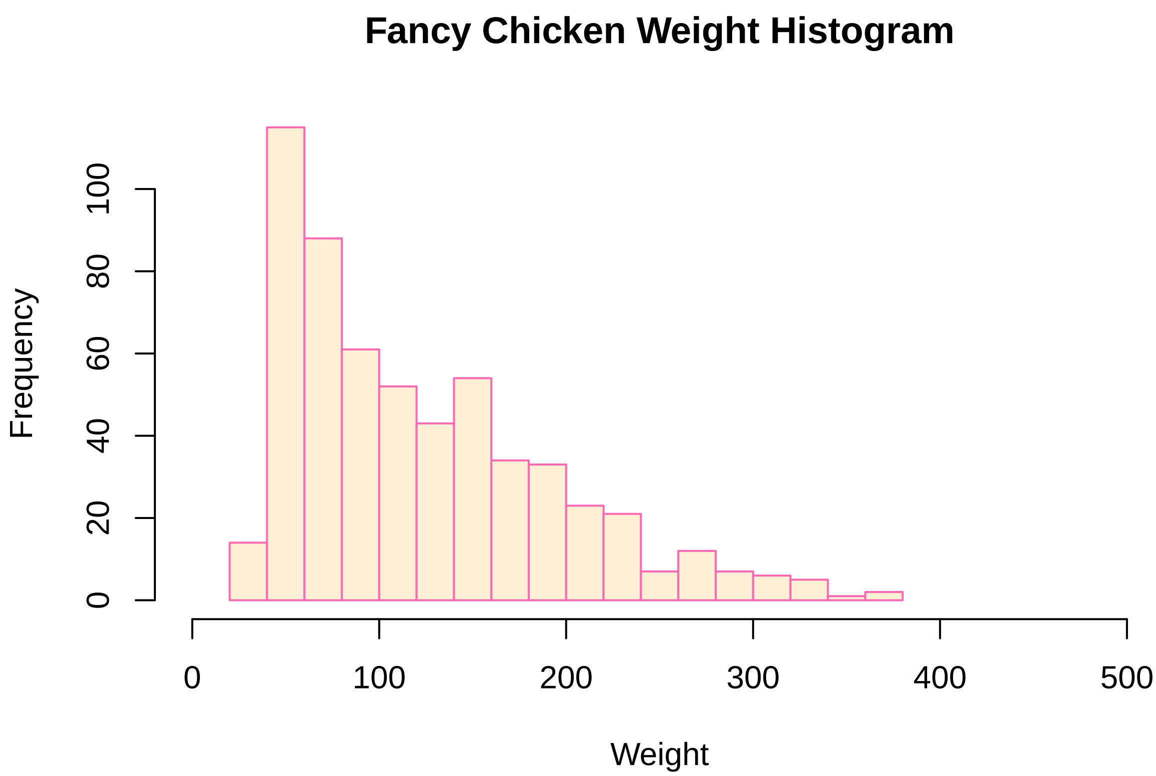
Let's create a histogram of the weights in the ChickWeight dataset:

```
hist(x = ChickWeight$weight,
     main = "Chicken Weights",
     xlab = "Weight",
     xlim = c(0, 500))
```



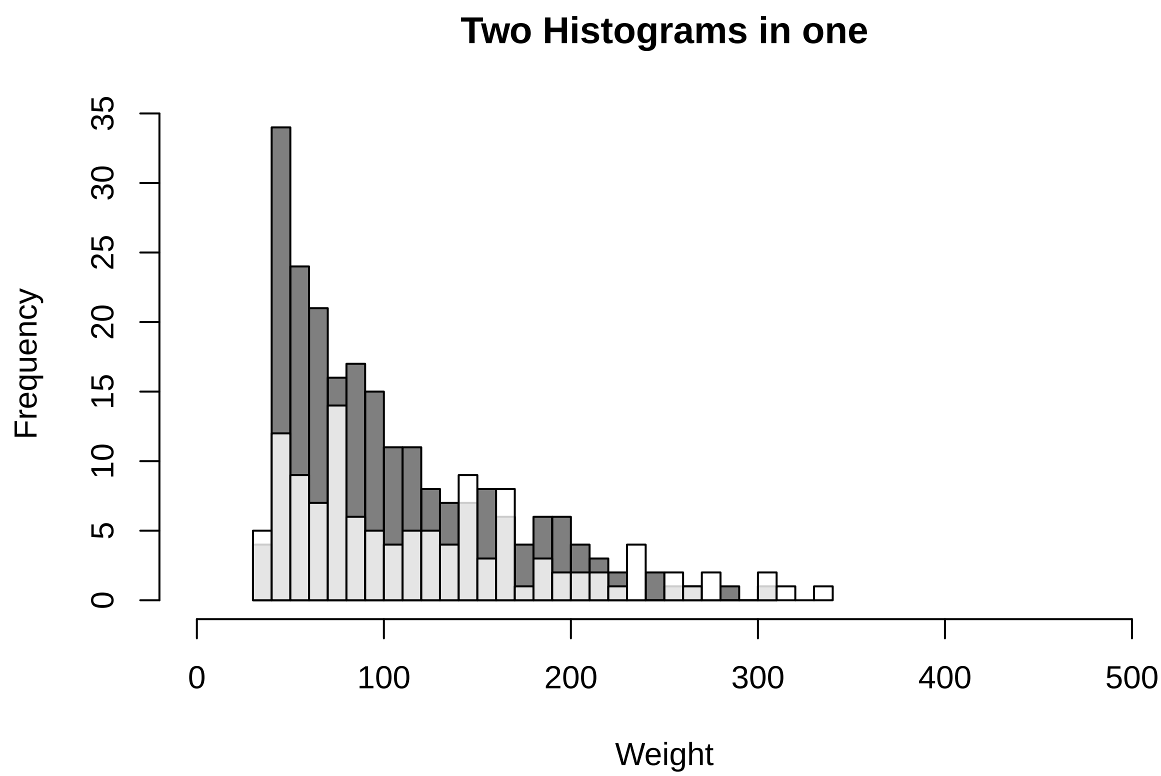
We can get more fancy by adding additional arguments like `breaks = 20` to force there to be 20 bins, and `col = "papayawhip"` and `bg = "hotpink"` to make it a bit more colorful:

```
hist(x = ChickWeight$weight,
     main = "Fancy Chicken Weight Histogram",
     xlab = "Weight",
     ylab = "Frequency",
     breaks = 20, # 20 Bins
     xlim = c(0, 500),
     col = "papayawhip", # Filling Color
     border = "hotpink") # Border Color
```



If you want to plot two histograms on the same plot, for example, to show the distributions of two different groups, you can use the `add = TRUE` argument to the second plot.

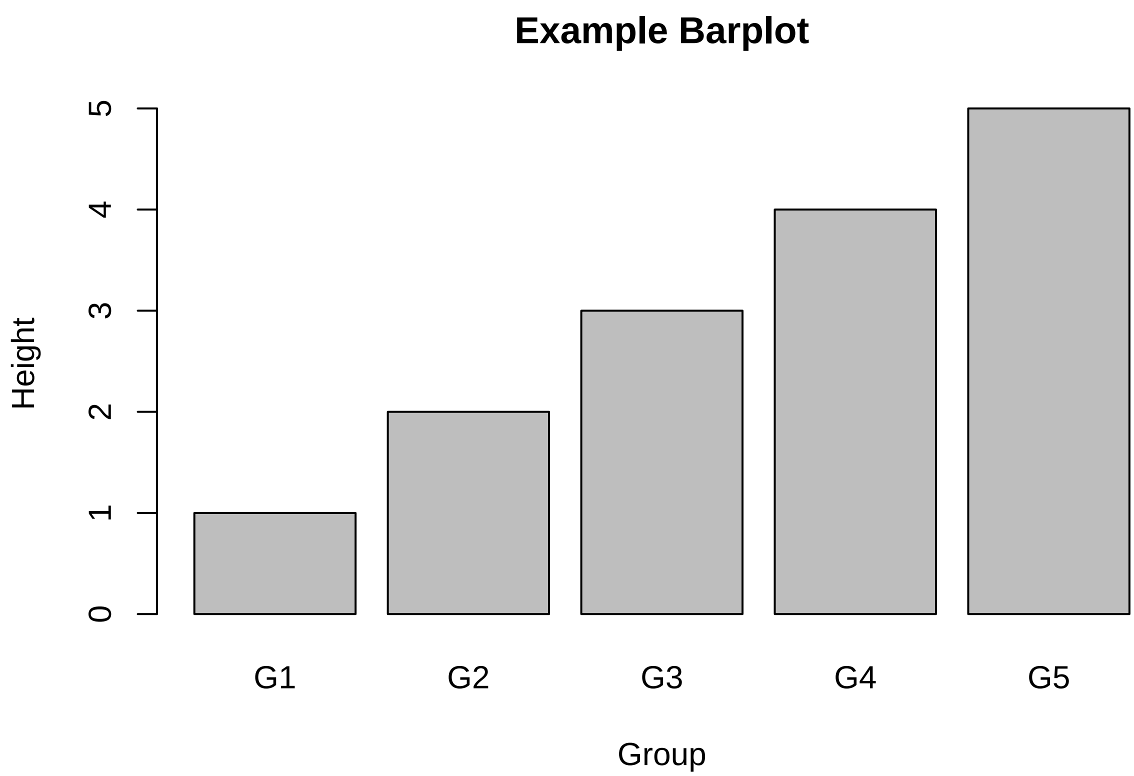
```
hist(x = ChickWeight$weight[ChickWeight$Diet == 1],
     main = "Two Histograms in one",
     xlab = "Weight",
     ylab = "Frequency",
     breaks = 20,
     xlim = c(0, 500),
     col = gray(0, .5))

hist(x = ChickWeight$weight[ChickWeight$Diet == 2],
     breaks = 30,
     add = TRUE, # Add plot to previous one!
     col = gray(1, .8))
```



11.5 Barplot: `barplot()`

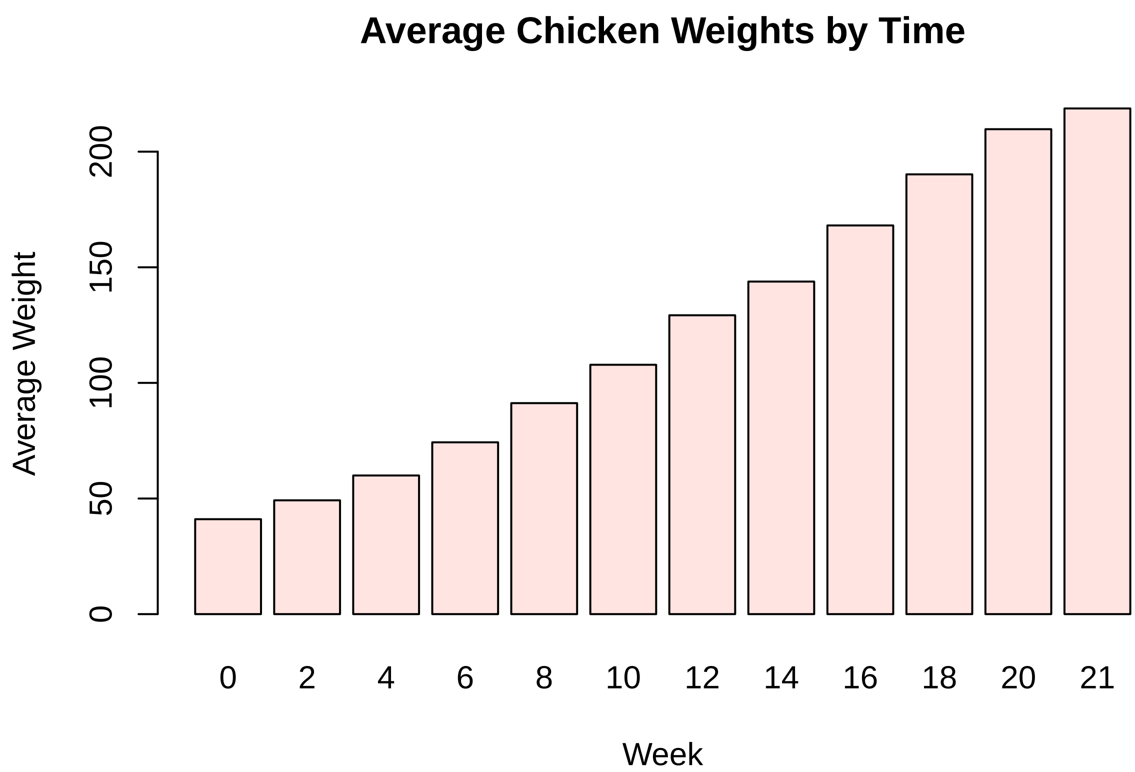
A barplot typically shows summary statistics for different groups. The primary argument to a barplot is `height`: a vector of numeric values which will generate the height of each bar. To add names below the bars, use the `names.arg` argument. For additional arguments specific to `barplot()`, look at the help menu with `?barplot`:

```
barplot(height = 1:5,  # A vector of heights
        names.arg = c("G1", "G2", "G3", "G4", "G5"), # A vector of names
        main = "Example Barplot",
        xlab = "Group",
        ylab = "Height")
```



Of course, you should plot more interesting data than just a vector of integers with a barplot. In the plot below, I create a barplot with the average weight of chickens for each week:

```
# Calculate mean weights for each time period
diet.weights <- aggregate(weight ~ Time,
                          data = ChickWeight,
                          FUN = mean)

# Create barplot
barplot(height = diet.weights$weight,
        names.arg = diet.weights$Time,
        xlab = "Week",
        ylab = "Average Weight",
        main = "Average Chicken Weights by Time",
        col = "mistyrose")
```



11.5.1 Clustered barplot

If you want to create a clustered barplot, with different bars for different groups of data, you can enter a matrix as the argument to `height`. R will then plot each column of the matrix as a separate set of bars. For example, let's say I conducted an experiment where I compared how fast pirates can swim under four conditions: Wearing clothes versus being naked, and while being chased by a shark versus not being chased by a shark. Let's say I conducted this experiment and calculated the following average swimming speed:

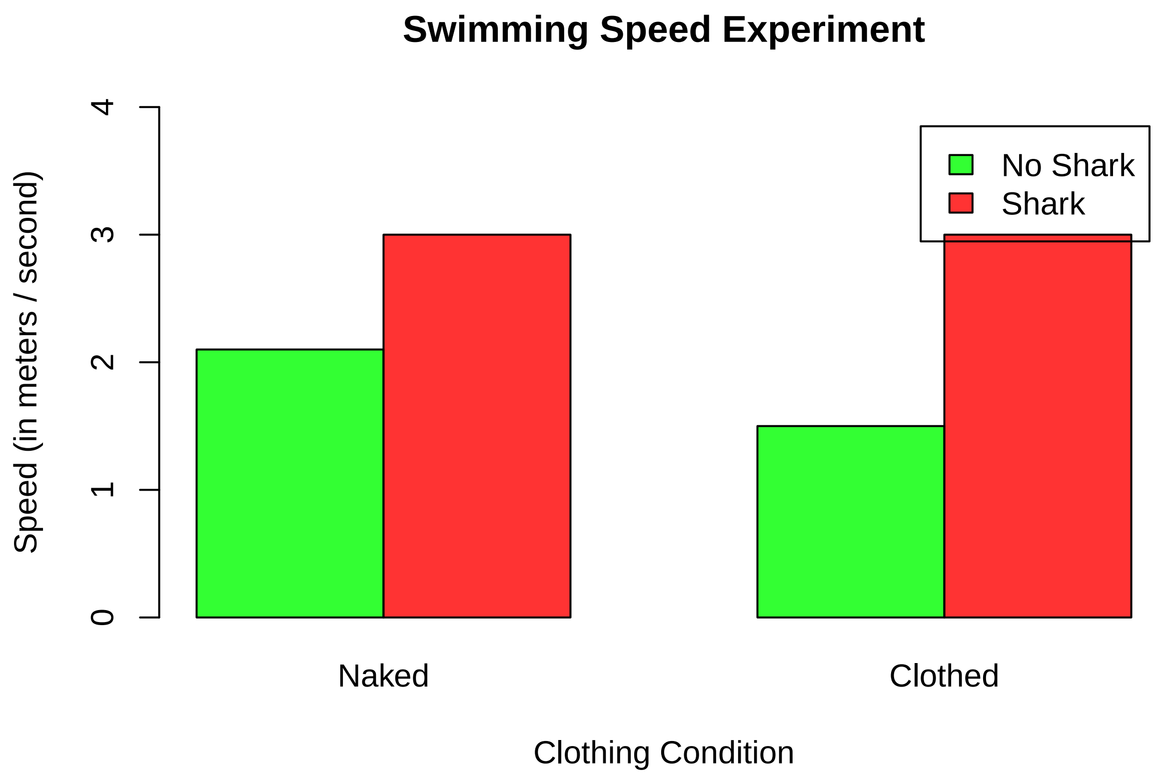
	Naked	Clothed
No Shark	2.1	1.5
Shark	3.0	3.0

I can represent these data in a matrix as follows. In order for the final barplot to include the condition names, I'll add row and column names to the matrix with `colnames()` and `rownames()`

```
swim.data <- cbind(c(2.1, 3), # Naked Times
                   c(1.5, 3)) # Clothed Times

colnames(swim.data) <- c("Naked", "Clothed")
rownames(swim.data) <- c("No Shark", "Shark")

# Print result
swim.data
##          Naked Clothed
## No Shark   2.1     1.5
## Shark      3.0     3.0
```

Now, when I enter this matrix as the `height = swim.data` argument to `barplot()`, I'll get multiple bars.

```
barplot(height = swim.data,
        beside = TRUE,                          # Put the bars next to each other
        legend.text = TRUE,                     # Add a legend
        col = c(transparent("green", .2),
                transparent("red", .2)),
        main = "Swimming Speed Experiment",
        ylab = "Speed (in meters / second)",
        xlab = "Clothing Condition",
        ylim = c(0, 4))
```



11.6 pirateplot()

Table 11.4: `pirateplot()` function arguments

Argument	Description
`formula`	A formula specifying a y-axis variable as a function of 1, 2 or 3 x-axis variables. For example, `formula = weight ~ Diet + Time` will plot `weight` as a function of `Diet` and `Time`
`data`	A dataframe containing the variables specified in `formula`
`theme`	A plotting theme, can be an integer from 1 to 4. Setting `theme = 0` will turn off all plotting elements so you can then turn them on individually.
`pal`	The color palette. Can either be a named color palette from the `piratepal()` function (e.g. `"basel"`, `"xmen"`, `"google"`) or a standard R color. For example, make a black and white plot, set `pal = "black"`
`cap.beans`	If `cap.beans = TRUE`, beans will be cut off at the maximum and minimum data values

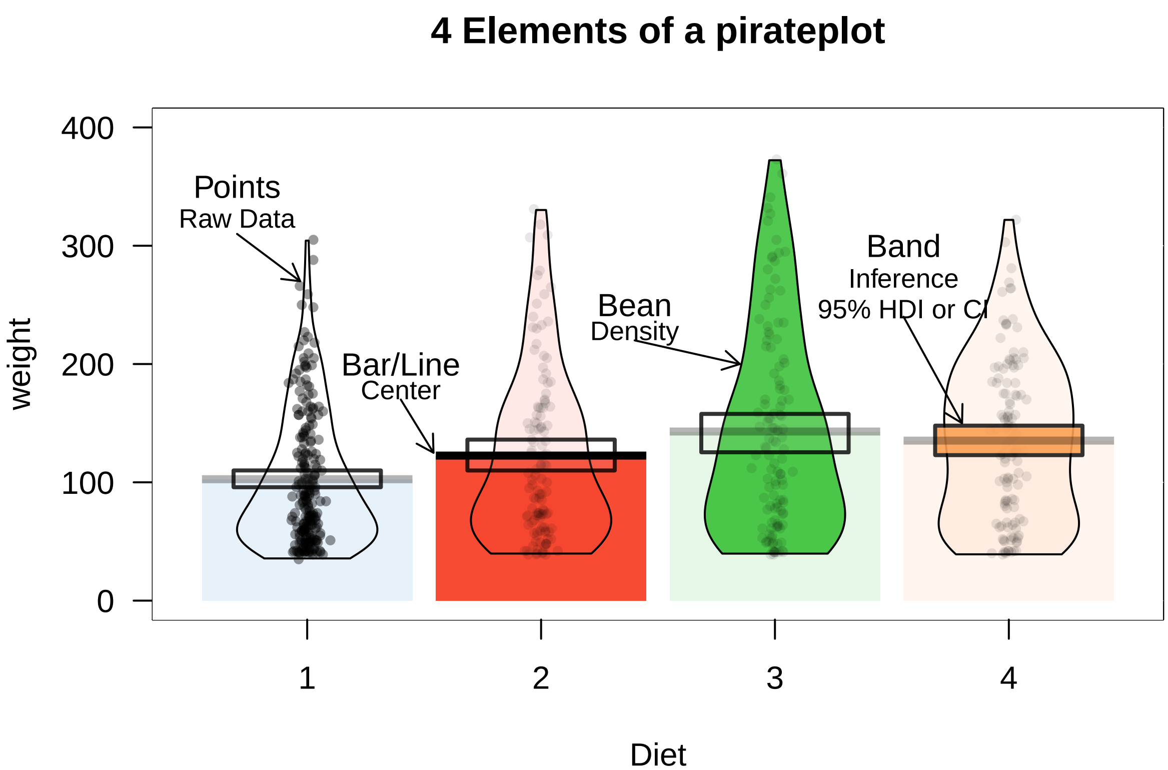


Figure 11.5: The pirateplot(), an R pirate's favorite plot!

A pirateplot a plot contained in the `yarrr` package written specifically by, and for R pirates The pirateplot is an easy-to-use function that, unlike barplots and boxplots, can easily show raw data, descriptive statistics, and inferential statistics in one plot. Figure 11.5 shows the four key elements in a pirateplot:

Table 11.5: 4 elements of a `pirateplot()`

Element	Description
Points	**Raw** data.
Bar / Line	**Descriptive** statistic, usually the mean or median
Bean	Smoothed density curve showing the full data distribution.
Band	**Inference** around the mean, either a Bayesian Highest Density Interval (HDI), or a Confidence Interval (CI)

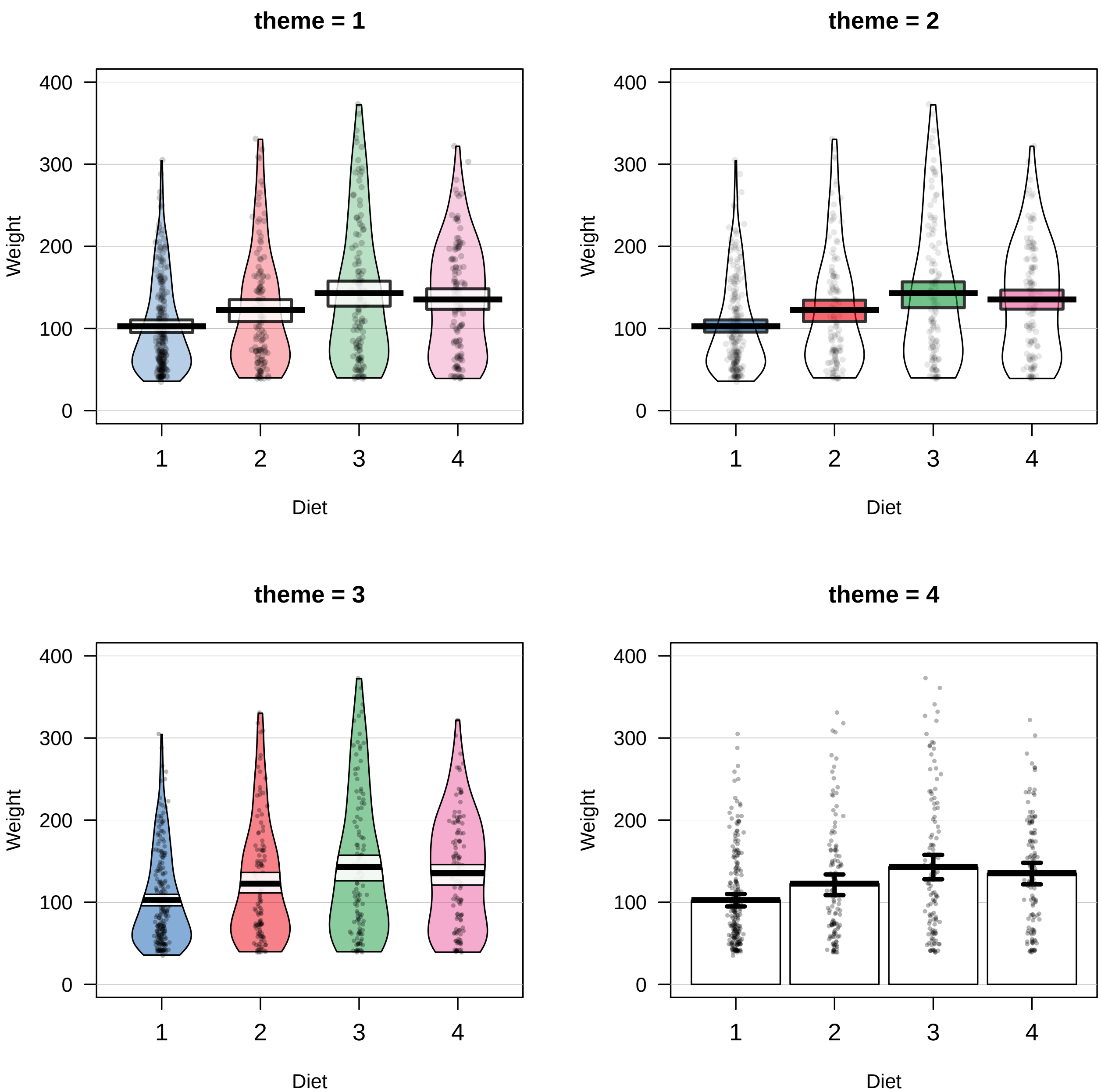
The two main arguments to `pirateplot()` are `formula` and `data`. In `formula`, you specify plotting variables in the form `y ~ x`, where `y` is the name of the dependent variable, and `x` is the name of the independent variable. In `data`, you specify the name of the dataframe object where the variables are stored.

Let's create a pirateplot of the ChickWeight data. I'll set the dependent variable to `weight`, and the independent variable to `Time` using the argument `formula = weight ~ Time`:

```
yarrr::pirateplot(formula = weight ~ Time, # dv is weight, iv is Diet
                   data = ChickWeight,
                   main = "Pirateplot of chicken weights",
                   xlab = "Diet",
                   ylab = "Weight")
```

11.6.1 Pirateplot themes

There are many different pirateplot themes, these themes dictate the overall look of the plot. To specify a theme, just use the `theme = x` argument, where `x` is the theme number:

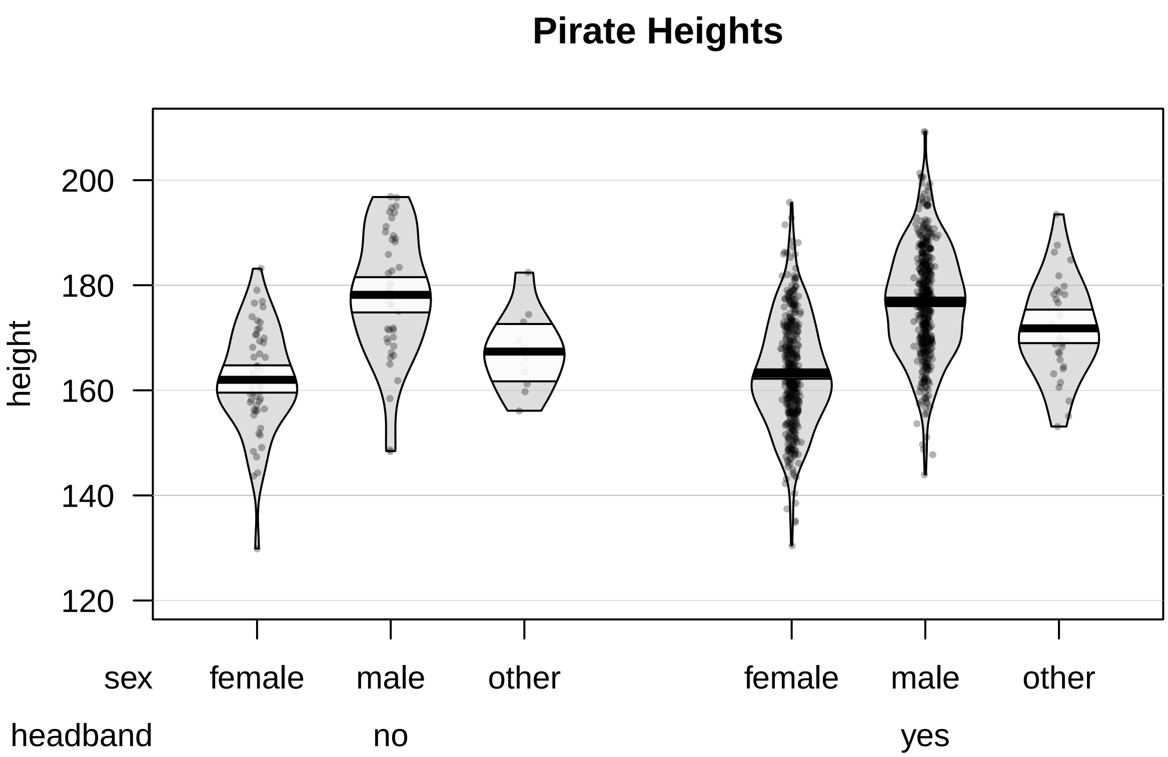


For example, here is a pirateplot height data from the `pirates` dataframe using `theme = 3`. Here, I'll plot pirates' heights as a function of their sex and whether or not they wear a headband. I'll also make the plot all grayscale by using the `pal = "gray"` argument:

```
yarrr::pirateplot(formula = height ~ sex + headband,     # DV = height, IV1 = sex, IV2 = headband
                  data = pirates,
                  theme = 3,
                  main = "Pirate Heights",
                  pal = "gray")
```

Table 11.6: Customising plotting elements

element	color	opacity
points	point.col, point.bg	point.o
beans	bean.f.col, bean.b.col	bean.f.o, bean.b.o
bar	bar.f.col, bar.b.col	bar.f.o, bar.b.o
inf	inf.f.col, inf.b.col	inf.f.o, inf.b.o
avg.line	avg.line.col	avg.line.o



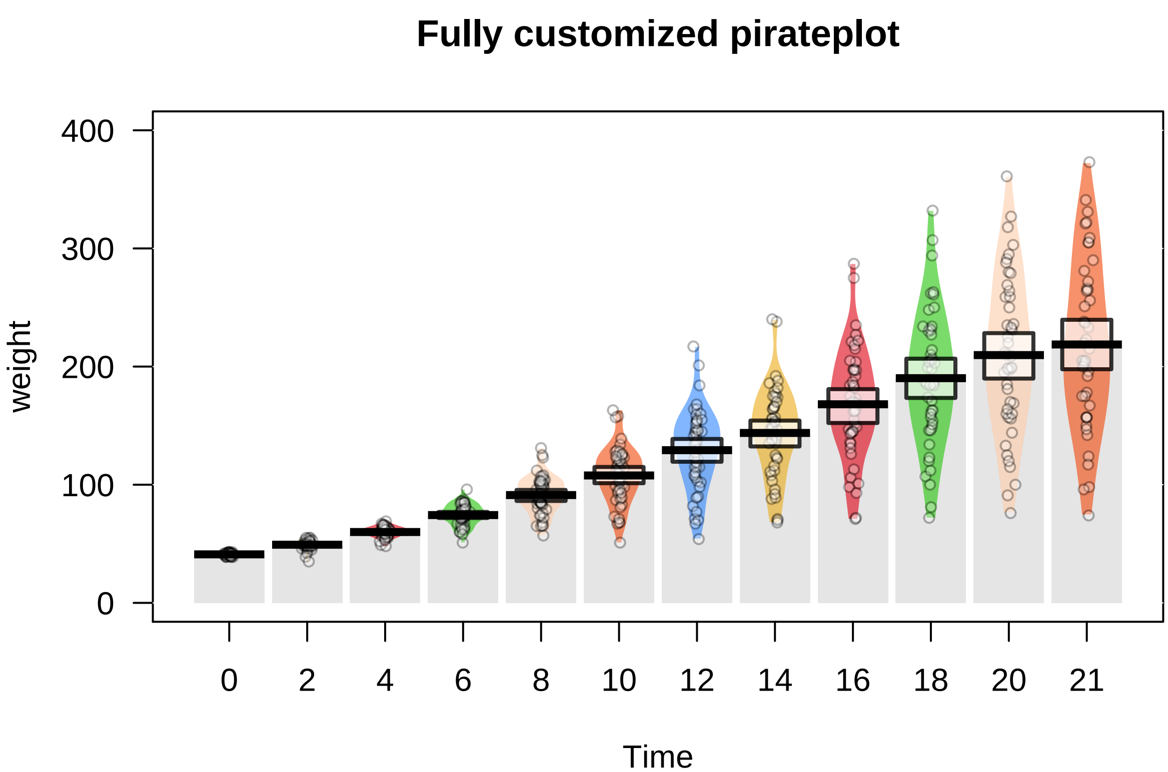
11.6.2 Customizing pirateplots

Regardless of the theme you use, you can always customize the color and opacity of graphical elements. To do this, specify one of the following arguments. Note: Arguments with `.f.` correspond to the *filling* of an element, while `.b.` correspond to the *border* of an element:

For example, I could create the following pirateplots using `theme = 0` and specifying elements explicitly:

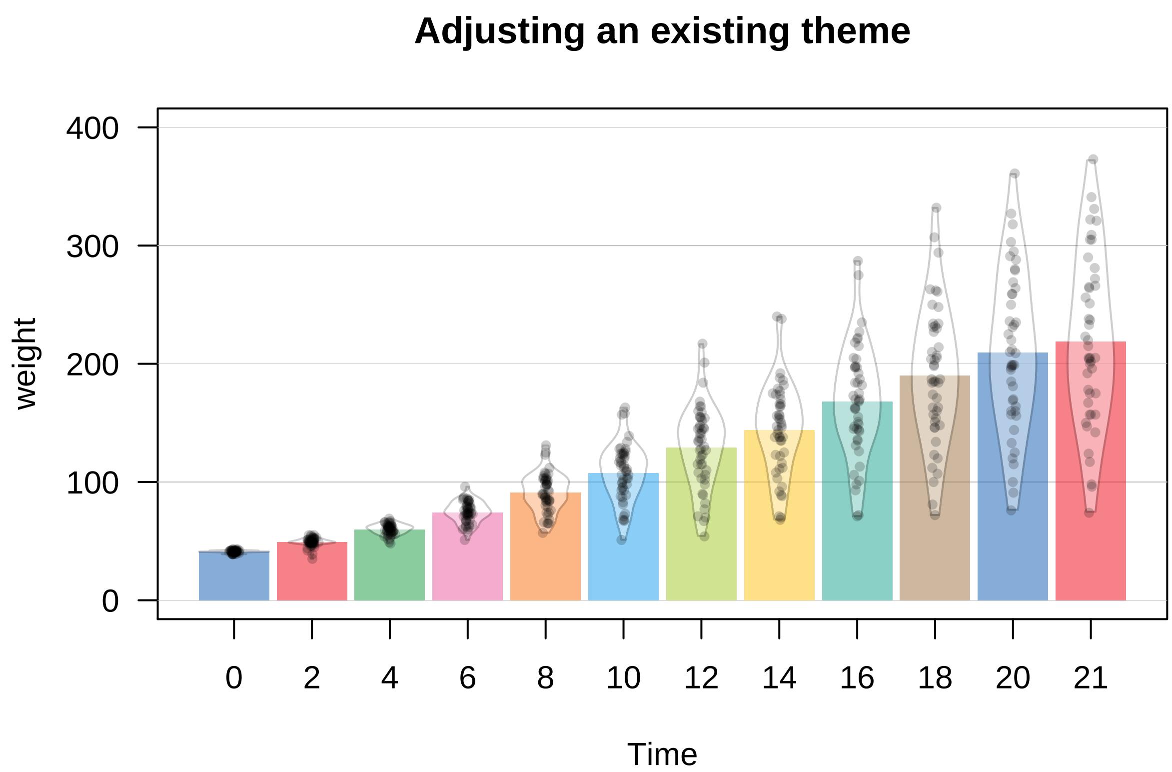
```
pirateplot(formula = weight ~ Time,
           data = ChickWeight,
           theme = 0,
           main = "Fully customized pirateplot",
           pal = "southpark", # southpark color palette
           bean.f.o = .6, # Bean fill
           point.o = .3, # Points
           inf.f.o = .7, # Inference fill
           inf.b.o = .8, # Inference border
           avg.line.o = 1, # Average line
           bar.f.o = .5, # Bar
```

```
            inf.f.col = "white", # Inf fill col
            inf.b.col = "black", # Inf border col
            avg.line.col = "black", # avg line col
            bar.f.col = gray(.8), # bar filling color
            point.pch = 21,
            point.bg = "white",
            point.col = "black",
            point.cex = .7)
```



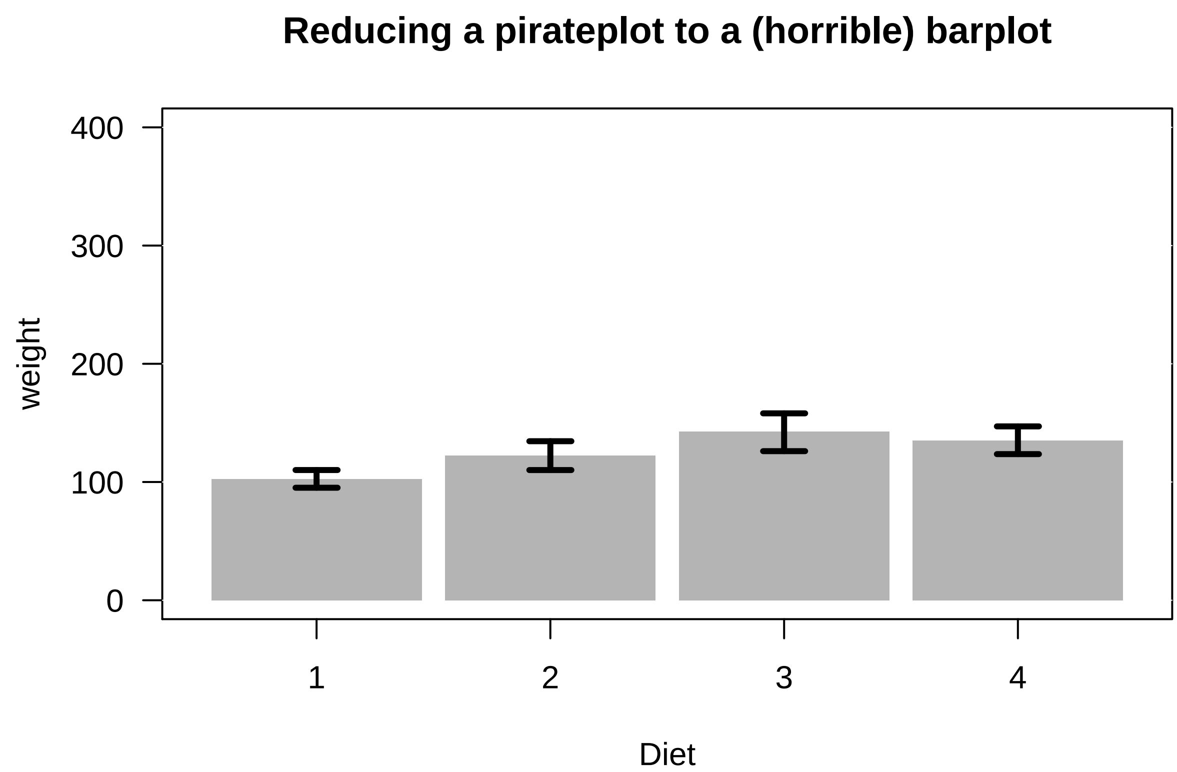
If you don't want to start from scratch, you can also start with a theme, and then make selective adjustments:

```
pirateplot(formula = weight ~ Time,
           data = ChickWeight,
           main = "Adjusting an existing theme",
           theme = 2,  # Start with theme 2
           inf.f.o = 0, # Turn off inf fill
           inf.b.o = 0, # Turn off inf border
           point.o = .2,   # Turn up points
           bar.f.o = .5, # Turn up bars
           bean.f.o = .4, # Light bean filling
           bean.b.o = .2, # Light bean border
           avg.line.o = 0, # Turn off average line
           point.col = "black") # Black points
```



Just to drive the point home, as a barplot is a special case of a pirateplot, you can even reduce a pirateplot into a horrible barplot:

```
# Reducing a pirateplot to a (at least colorful) barplot
pirateplot(formula = weight ~ Diet,
           data = ChickWeight,
           main = "Reducing a pirateplot to a (horrible) barplot",
           theme = 0,                                    # Start from scratch
           pal = "black",
           inf.disp = "line",                            # Use a line for inference
           inf.f.o = 1,                                  # Turn up inference opacity
           inf.f.col = "black",                          # Set inference line color
           bar.f.o = .3)
```



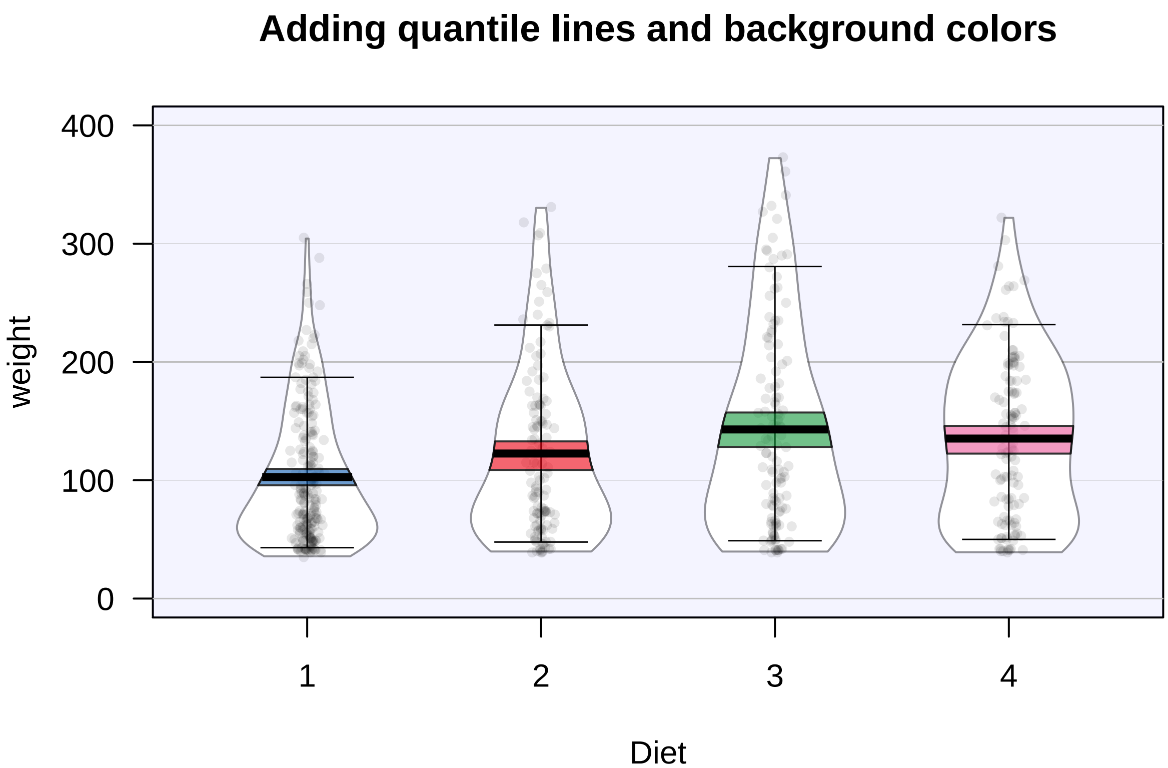
There are many additional arguments to `pirateplot()` that you can use to complete customize the look of your plot. To see them all, look at the help menu with `?pirateplot` or look at the vignette at

Table 11.7: Additional `pirateplot()` customizations.

Element	Argument	Examples
Background color	back.col	`back.col = 'gray(.9, .9)'`
Gridlines	gl.col, gl.lwd, gl.lty	`gl.col = 'gray', gl.lwd = c(.75, 0), gl.lty = 1`
Quantiles	quant, quant.lwd, quant.col	`quant = c(.1, .9), quant.lwd = 1, quant.col = 'black'`
Average line	avg.line.fun	`avg.line.fun = median`
Inference Calculation	inf.method	`inf.method = 'hdi', inf.method = 'ci'`
Inference Display	inf.disp	`inf.disp = 'line', inf.disp = 'bean', inf.disp = 'rect'`

```
# Additional pirateplot customizations
pirateplot(formula = weight ~ Diet,
           data = ChickWeight,
           main = "Adding quantile lines and background colors",
           theme = 2,
           cap.beans = TRUE,
           back.col = transparent("blue", .95), # Add light blue background
           gl.col = "gray", # Gray gridlines
           gl.lwd = c(.75, 0),
           inf.f.o = .6, # Turn up inf filling
           inf.disp = "bean", # Wrap inference around bean
```

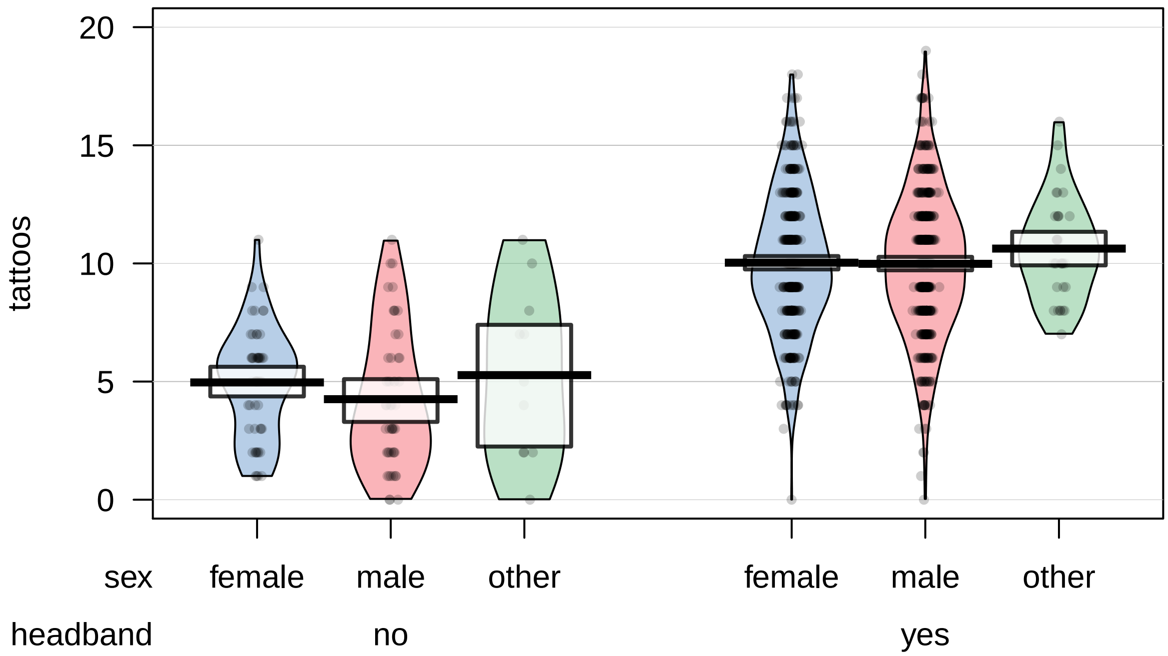
```
           bean.b.o = .4, # Turn down bean borders
           quant = c(.1, .9), # 10th and 90th quantiles
           quant.col = "black") # Black quantile lines
```



11.6.3 Saving output

If you include the `plot = FALSE` argument to a pirateplot, the function will return some values associated with each bean in the plot. In the next chunk, I'll

```
# Create a pirateplot
pirateplot(formula = tattoos ~ sex + headband,
           data = pirates)
```




```r
# Save data from the pirateplot to an object
tattoos.pp <- pirateplot(formula = tattoos ~ sex + headband,
                         data = pirates,
                         plot = FALSE)
```

Now I can access the summary and inferential statistics from the plot in the `tattoos.pp` object. The most interesting element is `$summary` which shows summary statistics for each bean (aka, group):

```r
# Show me statistics from groups in the pirateplot
tattoos.pp
## $summary
##      sex headband bean.num   n       avg   inf.lb    inf.ub
## 1 female       no        1  55  4.963636 4.274457  5.491925
## 2   male       no        2  47  4.255319 3.230407  4.975205
## 3  other       no        3  11  5.272727 2.511369  7.207242
## 4 female      yes        4 409 10.031785 9.769694 10.318491
## 5   male      yes        5 443  9.984199 9.694375 10.268986
## 6  other      yes        6  35 10.628571 9.874442 11.350058
##
## $avg.line.fun
## [1] "mean"
##
## $inf.method
## [1] "hdi"
##
## $inf.p
## [1] 0.95
```

Once you've created a plot with a high-level plotting function, you can add additional elements with *low-level* functions. For example, you can add data points with `points()`, reference lines with `abline()`, text with `text()`, and legends with `legend()`.

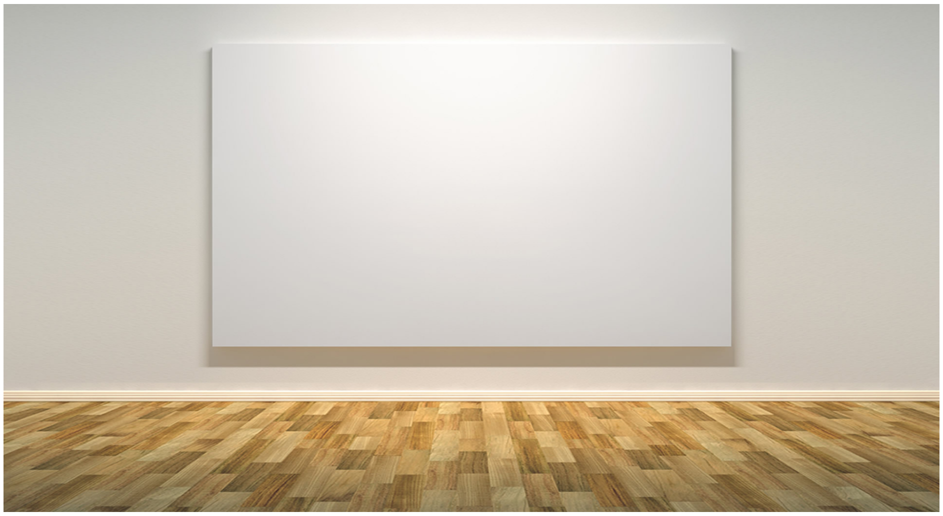


Figure 11.6: Sometimes it's nice to start with a blank plotting canvas, and then add each element individually with low-level plotting commands

11.7 Low-level plotting functions

Low-level plotting functions allow you to add elements, like points, or lines, to an existing plot. Here are the most common low-level plotting functions:

Table 11.8: Common low-level plotting functions.

Function	Outcome
`points(x, y)`	Adds points
`abline()`, `segments()`	Adds lines or segments
`arrows()`	Adds arrows
`curve()`	Adds a curve representing a function
`rect()`,`polygon()`	Adds a rectangle or arbitrary shape
`text()`, `mtext()`	Adds text within the plot, or to plot margins
`legend()`	Adds a legend
`axis()`	Adds an axis

11.7.1 Starting with a blank plot

Before you start adding elements with low-level plotting functions, it's useful to start with a blank plotting space like the one I have in Figure 11.7. To do this, execute the `plot()` function, but use the `type = "n"` argument to tell R that you don't want to plot anything yet. Once you've created a blank plot, you can additional elements with low-level plotting commands.

```
# Create a blank plotting space
plot(x = 1,
     xlab = "X Label",
     ylab = "Y Label",
     xlim = c(0, 100),
     ylim = c(0, 100),
     main = "Blank Plotting Canvas",
     type = "n")
```

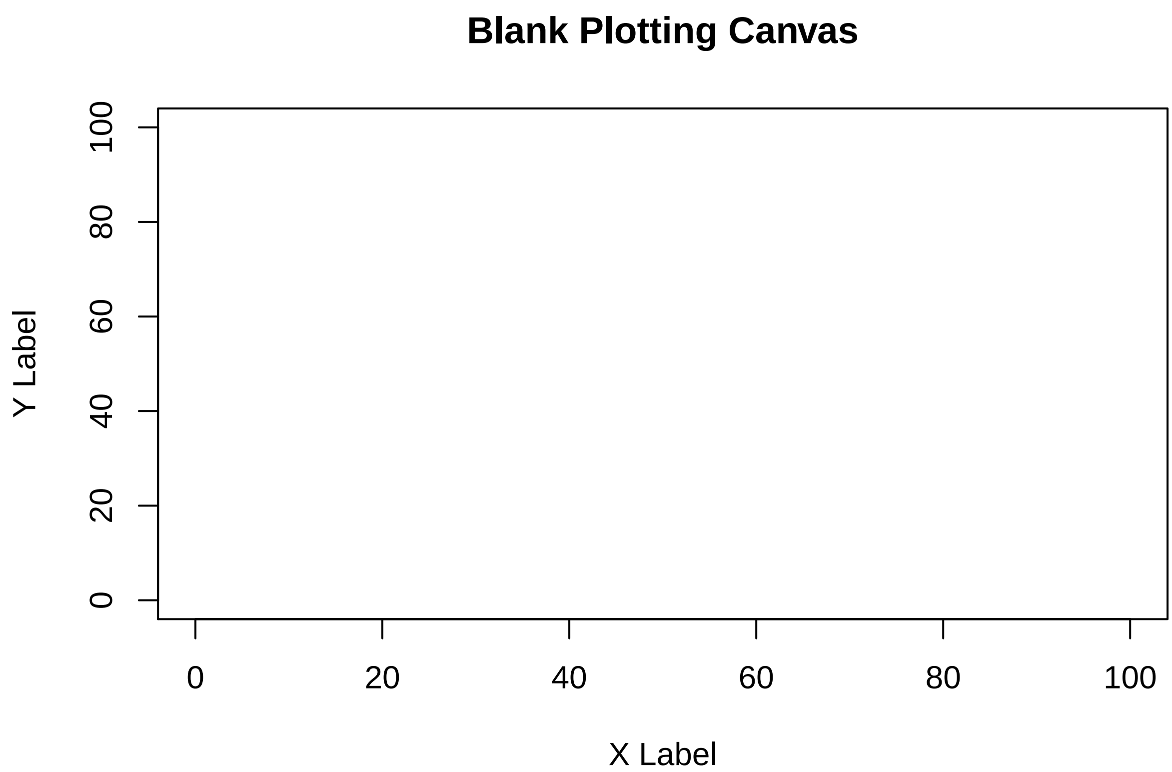


Figure 11.7: A blank plotting space, ready for additional elements!

11.7.2 points()

To add new points to an existing plot, use the `points()` function. The `points` function has many similar arguments to the `plot()` function, like `x` (for the x-coordinates), `y` (for the y-coordinates), and parameters like `col` (border color), `cex` (point size), and `pch` (symbol type). To see all of them, look at the help menu with `?points()`.

Let's use `points()` to create a plot with different symbol types for different data. I'll use the pirates dataset and plot the relationship between a pirate's age and the number of tattoos he/she has. I'll create separate points for male and female pirates:

```
# Create a blank plot
plot(x = 1,
     type = "n",
     xlim = c(100, 225),
     ylim = c(30, 110),
     pch = 16,
     xlab = "Height",
     ylab = "Weight",
     main = "Adding points to a plot with points()")

# Add coral2 points for male data
points(x = pirates$height[pirates$sex == "male"],
       y = pirates$weight[pirates$sex == "male"],
       pch = 16,
```

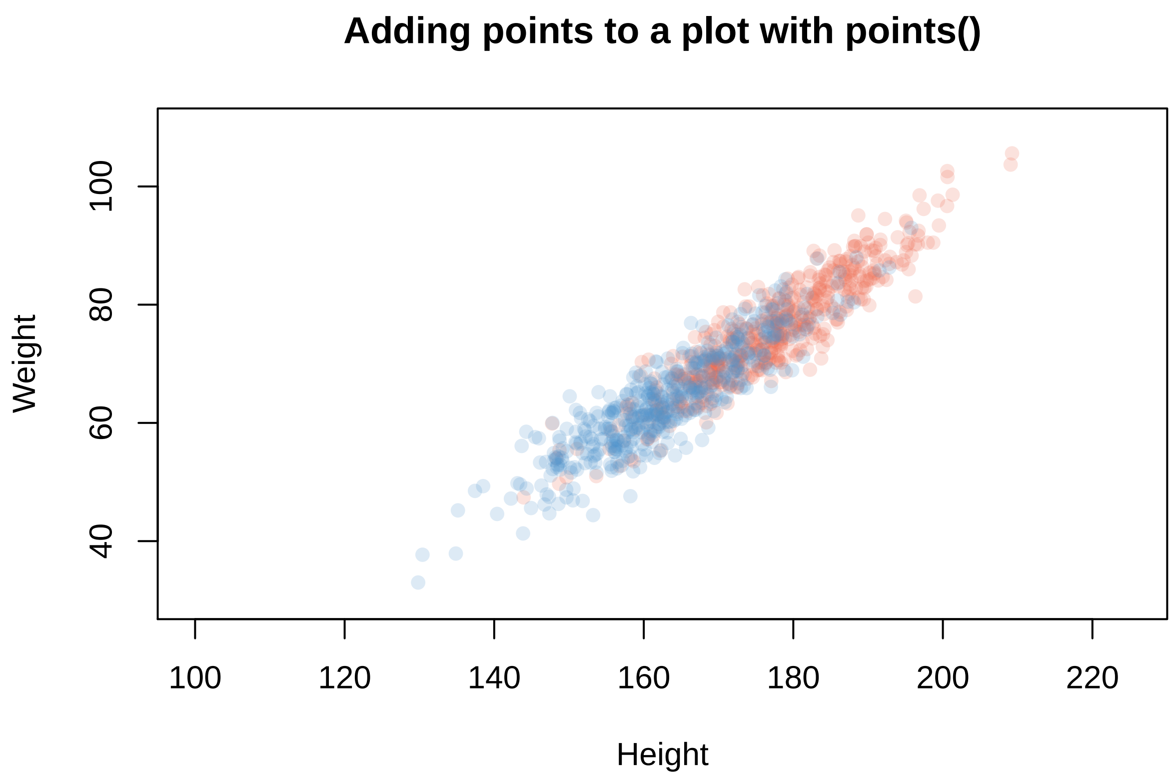


Figure 11.8: Using points() to add points with different colors

```
       col = transparent("coral2", trans.val = .8))

# Add steelblue points for female data
points(x = pirates$height[pirates$sex == "female"],
       y = pirates$weight[pirates$sex == "female"],
       pch = 16,
       col = transparent("steelblue3", trans.val = .8))
```

11.7.3 abline(), segments(), grid()

Table 11.9: Arguments to `abline()` and `segments()`

Argument	Outcome
`h, v`	Locations of horizontal and vertical lines (for `abline()` only)
`x0, y0, x1, y1`	Starting and ending coordinates of lines (for `segments()` only)
`lty`	Line type. 1 = solid, 2 = dashed, 3 = dotted, ...
`lwd`	Width of the lines specified by a number. 1 is the default (.2 is very thin, 5 is very thick)
`col`	Line color

To add straight lines to a plot, use `abline()` or `segments()`. `abline()` will add a line across the entire plot, while `segments()` will add a line with defined starting and end points.

For example, we can add reference lines to a plot with `abline()`. In the following plot, I'll add vertical and horizontal reference lines showing the means of the variables on the x and y axes, for the horizontal line, I'll specify `h = mean(pirates$height)`, for the vertical line, I'll specify `v = mean(pirates$weight)`

```
plot(x = pirates$weight,
     y = pirates$height,
```

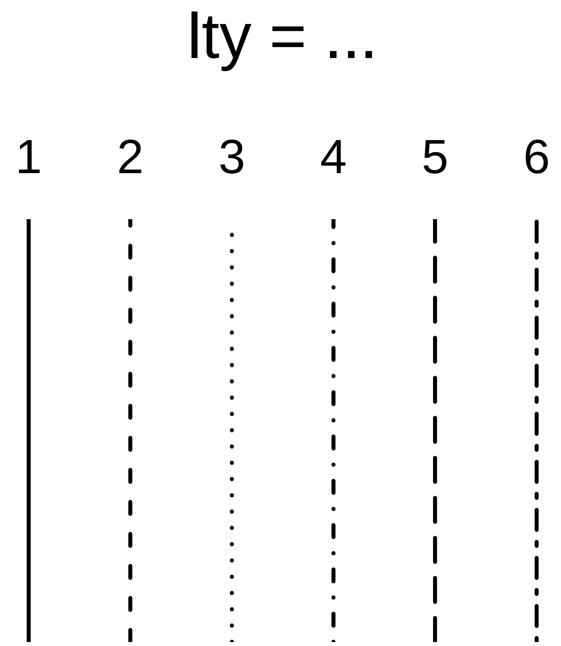
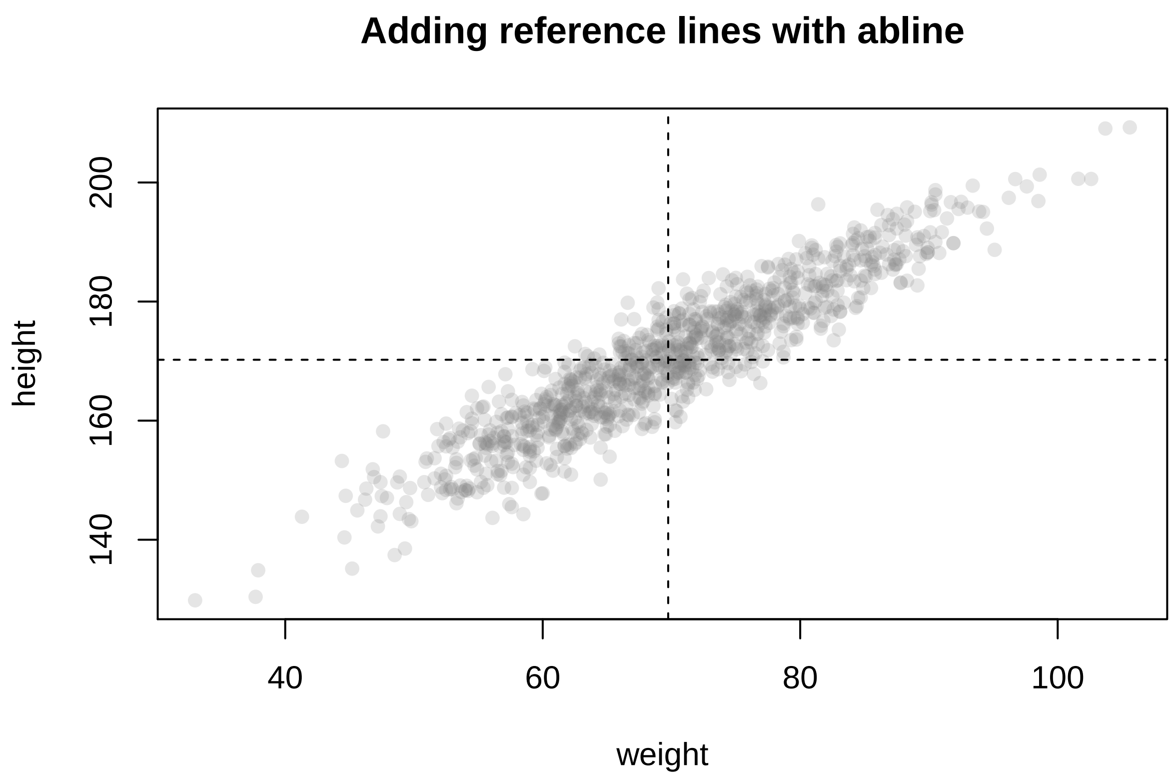


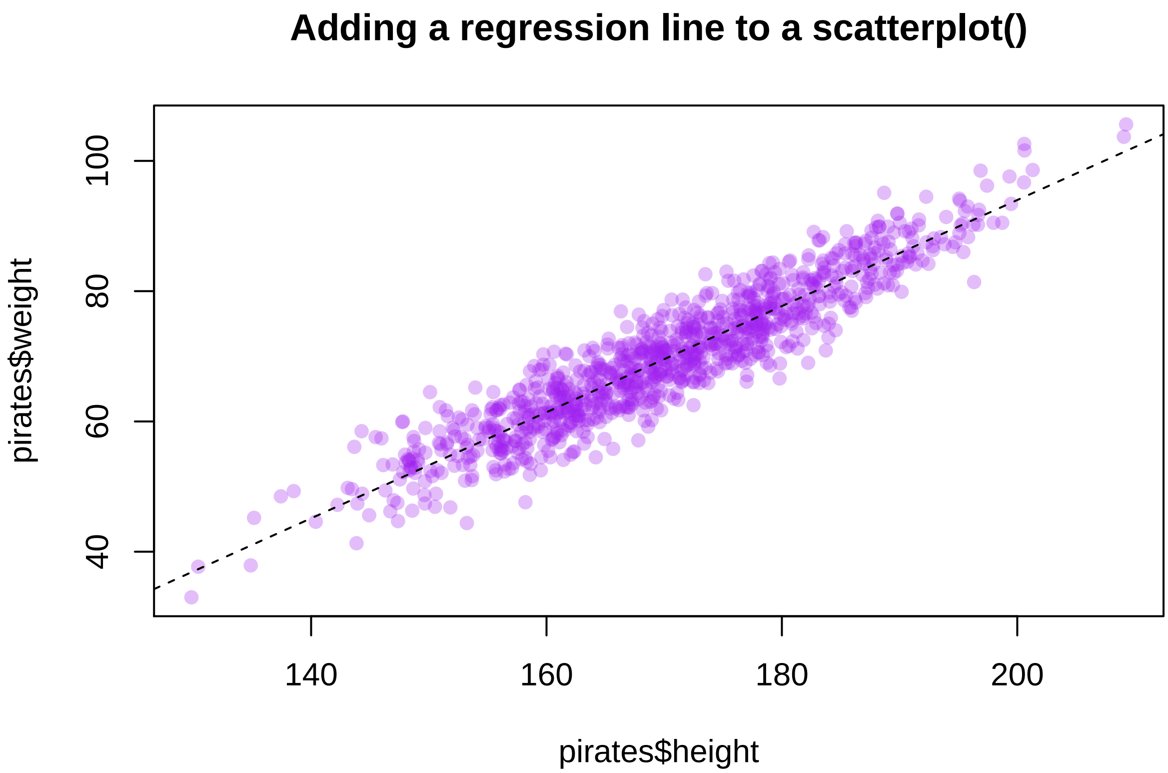
Figure 11.9: Changing line type with the lty argument.



To change the look of your lines, use the `lty` argument, which changes the type of line (see Figure 11.9), `lwd`, which changes its thickness, and `col` which changes its color

You can also add a regression line (also called a line of best fit) to a scatterplot by entering a regression object created with `lm()` as the main argument to `abline()`:

```
# Add a regression line to a scatterplot
plot(x = pirates$height,
     y = pirates$weight,
     pch = 16,
     col = transparent("purple", .7),
     main = "Adding a regression line to a scatterplot()")

# Add the regression line
abline(lm(weight ~ height, data = pirates),
       lty = 2)
```



The `segments()` function works very similarly to `abline()` – however, with the `segments()` function, you specify the beginning and end points of the segments with the arguments `x0`, `y0`, `x1`, and `y1`. In Figure 11.10 I use `segments()` to connect two vectors of data:

```
# Before and after data
before <- c(2.1, 3.5, 1.8, 4.2, 2.4, 3.9, 2.1, 4.4)
after <- c(7.5, 5.1, 6.9, 3.6, 7.5, 5.2, 6.1, 7.3)

# Create plotting space and before scores
plot(x = rep(1, length(before)),
     y = before,
     xlim = c(.5, 2.5),
     ylim = c(0, 11),
     ylab = "Score",
     xlab = "Time",
     main = "Using segments() to connect points",
     xaxt = "n")

# Add after scores
```

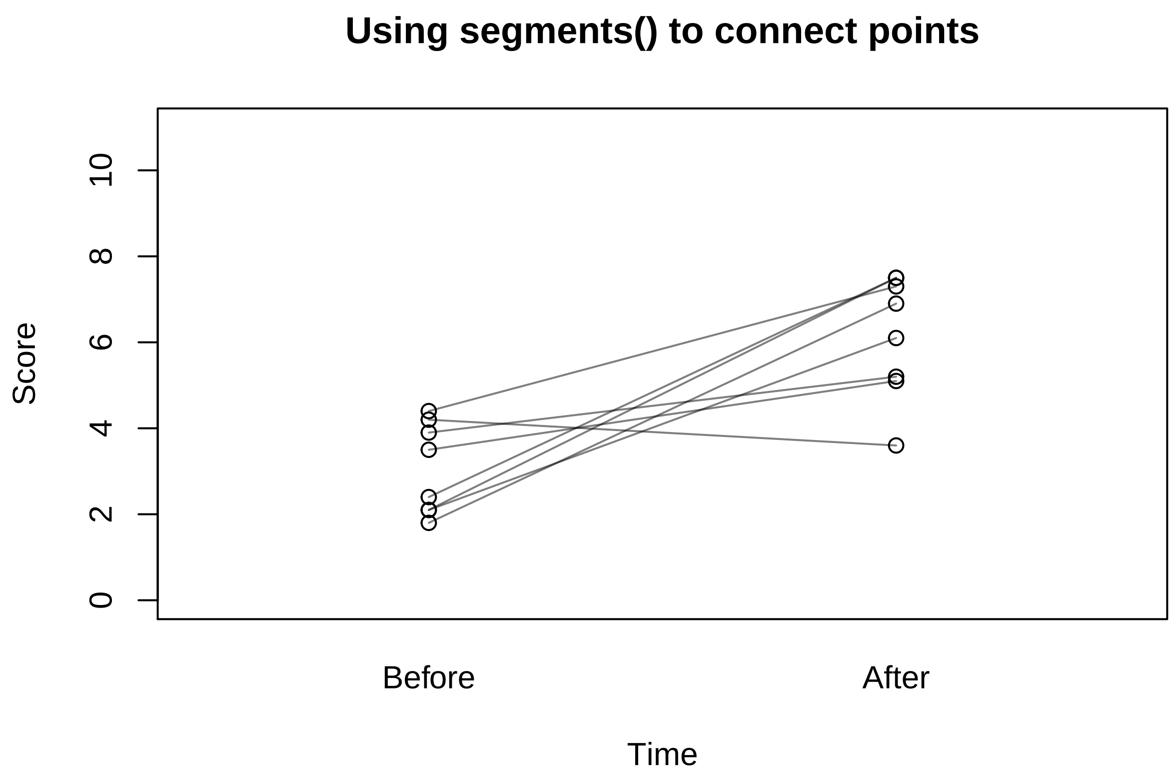
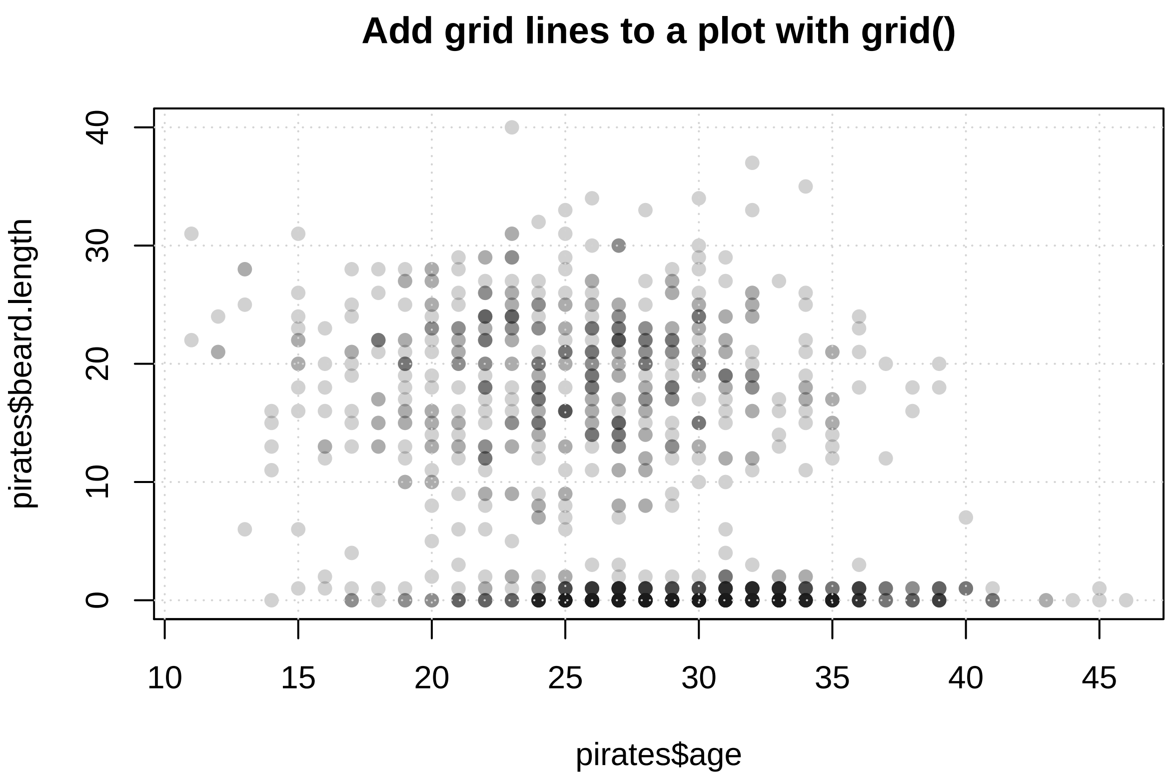


Figure 11.10: Connecting points with segments().

```
points(x = rep(2, length(after)), y = after)

# Add connections with segments()
segments(x0 = rep(1, length(before)),
         y0 = before,
         x1 = rep(2, length(after)),
         y1 = after,
         col = gray(0, .5))

# Add labels
mtext(text = c("Before", "After"),
      side = 1, at = c(1, 2), line = 1)
```

The `grid()` function allows you to easily add grid lines to a plot (you can customize your grid lines further with `lty`, `lwd`, and `col` arguments):

```
# Add gridlines to a plot with grid()
plot(pirates$age,
     pirates$beard.length,
     pch = 16,
     col = gray(.1, .2), main = "Add grid lines to a plot with grid()")

# Add gridlines
grid()
```



11.7.4 `text()`

Table 11.10: Arguments to `text()`

Argument	Outcome
`x, y`	Coordinates of the labels
`labels`	Labels to be plotted
`cex`	Size of the labels
`adj`	Horizontal text adjustment. `adj = 0` is left justified, `adj = .5` is centered, and `adj = 1` is right-justified
`pos`	Position of the labels relative to the coordinates. `pos = 1`, puts the label below the coordinates, while 2, 3, and 4 put it to the left, top and right of the coordinates respectively

With `text()`, you can add text to a plot. You can use `text()` to highlight specific points of interest in the plot, or to add information (like a third variable) for every point in a plot. For example, the following code adds the three words "Put", "Text", and "Here" at the coordinates (1, 9), (5, 5), and (9, 1) respectively. See Figure 11.11 for the plot:

```
plot(1,
     xlim = c(0, 10),
     ylim = c(0, 10),
     type = "n")

text(x = c(1, 5, 9),
     y = c(9, 5, 1),
     labels = c("Put", "text", "here"))
```

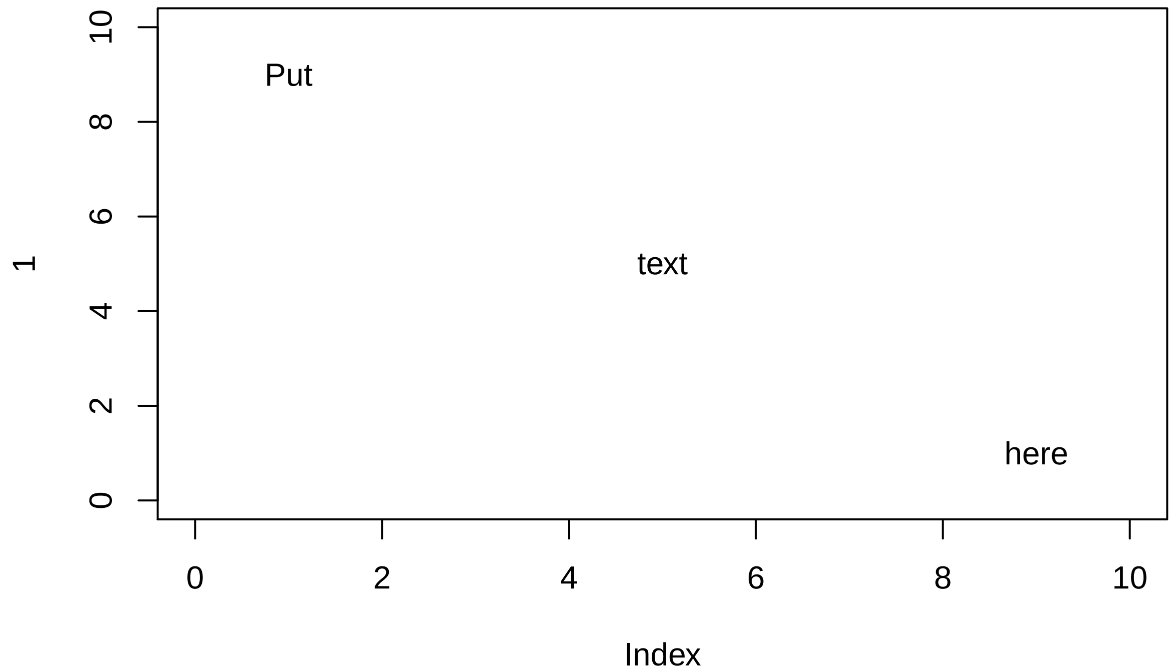


Figure 11.11: Adding text to a plot with text()

You can do some cool things with `text()`, in Figure 11.12 I create a scatterplot of data, and add data labels above each point by including the `pos = 3` argument:

```
# Create data vectors
height <- c(156, 175, 160, 172, 159, 165, 178)
weight <- c(65, 74, 69, 72, 66, 75, 75)
id <- c("andrew", "heidi", "becki", "madisen", "david", "vincent", "jack")

# Plot data
plot(x = height,
     y = weight,
     xlim = c(155, 180),
     ylim = c(65, 80),
     pch = 16,
     col = yarrr::piratepal("xmen"))

# Add id labels
text(x = height,
     y = weight,
     labels = id,
     pos = 3)             # Put labels above the points
```

When entering text in the `labels` argument, keep in mind that R will, by default, plot the entire text in one line. However, if you are adding a long text string (like a sentence), you may want to separate the text into separate lines. To do this, add the text `\n` where you want new lines to start. Look at Figure 11.13 for an example.

```
plot(1,
     type = "n",
     main = "The \\n tag",
     xlab = "", ylab = "")
```

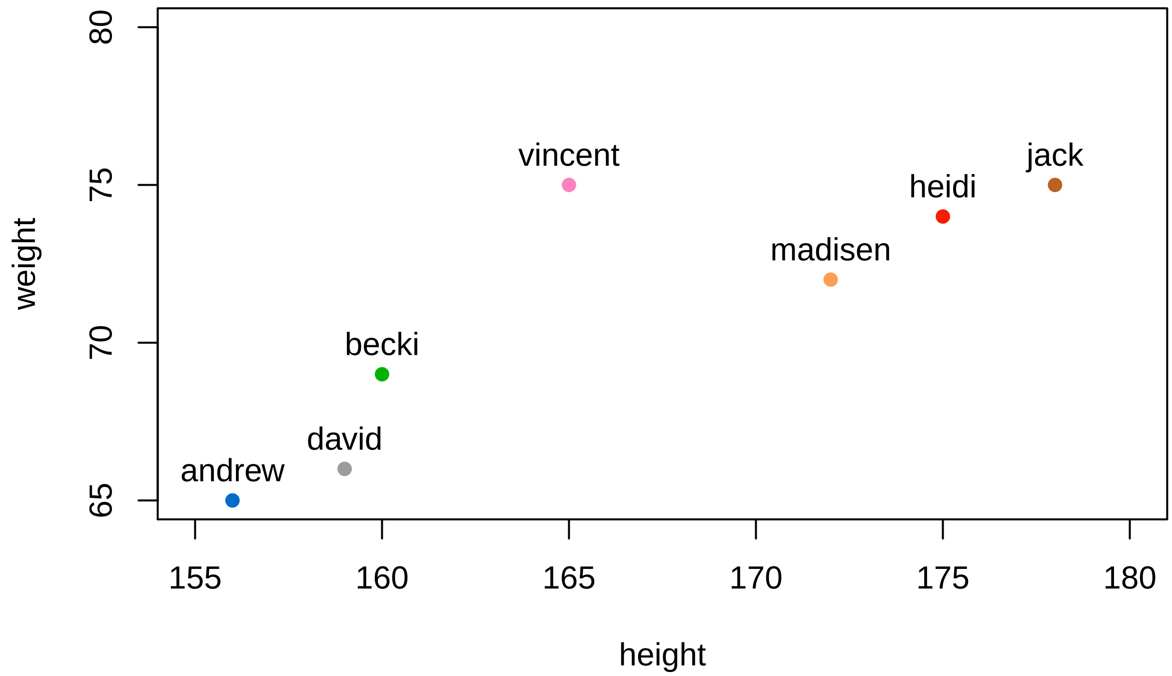


Figure 11.12: Adding labels to points with text()

```
# Text withoutbreaks
text(x = 1, y = 1.3, labels = "Text without \\n", font = 2)
text(x = 1, y = 1.2,
     labels = "Haikus are easy. But sometimes they don't make sense. Refrigerator",
     font = 3) # italic font

abline(h = 1, lty = 2)
# Text with  breaks
text(x = 1, y = .92, labels = "Text with \\n", font = 2)
text(x = 1, y = .7,
     labels = "Haikus are easy\nBut sometimes they don't make sense\nRefrigerator",
     font = 3)   # italic font
```

11.7.5 Combining text and numbers with paste()

A common way to use text in a plot, either in the main title of a plot or using the `text()`function, is to combine text with numerical data. For example, you may want to include the text "Mean = 3.14" in a plot to show that the mean of the data is 3.14. But how can we combine numerical data with text? In R, we can do this with the `paste()` function:

The paste function will be helpful to you anytime you want to combine either multiple strings, or text and strings together. For example, let's say you want to write text in a plot that says `The mean of these data are XXX`, where XXX is replaced by the group mean. To do this, just include the main text and the object referring to the numerical mean as arguments to `paste()`. In Figure X I plot the chicken weights over time, and add text to the plot specifying the overall mean of weights.

```
# Create the plot
plot(x = ChickWeight$Time,
```

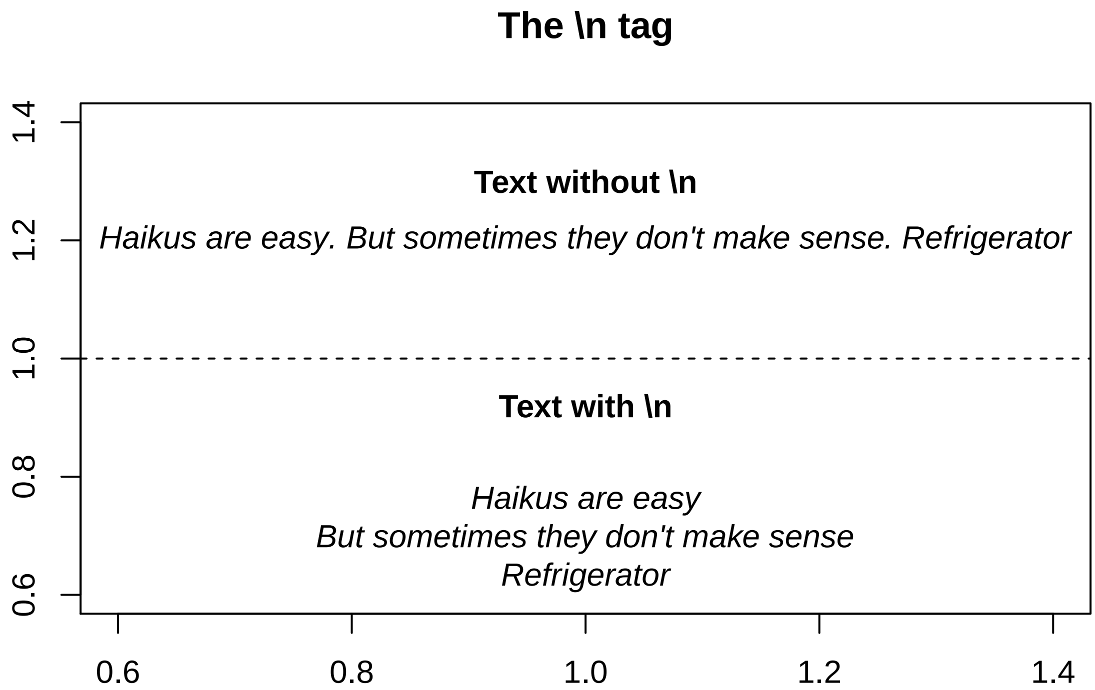
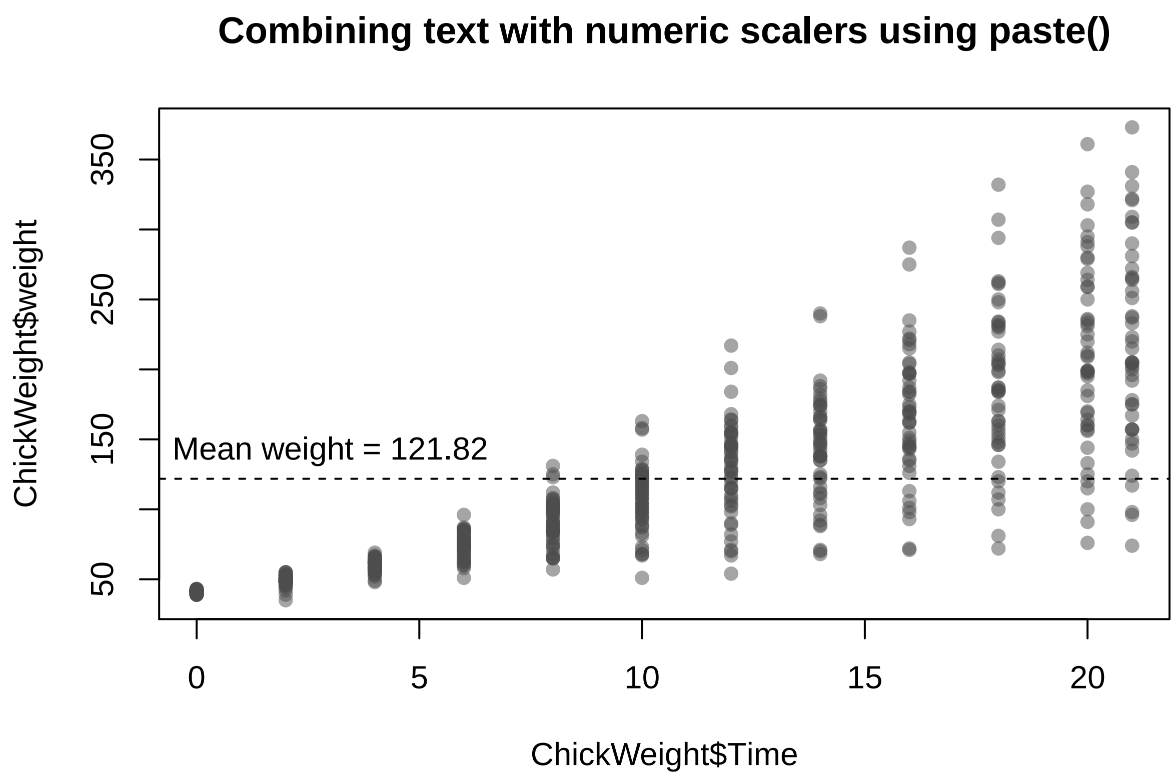


Figure 11.13: Break up lines in text with .

```
     y = ChickWeight$weight,
     col = gray(.3, .5),
     pch = 16,
     main = "Combining text with numeric scalers using paste()")

# Add reference line
abline(h = mean(ChickWeight$weight),
       lty = 2)

# Add text
text(x = 3,
     y = mean(ChickWeight$weight),
     labels = paste("Mean weight =",
                    round(mean(ChickWeight$weight), 2)),
     pos = 3)
```



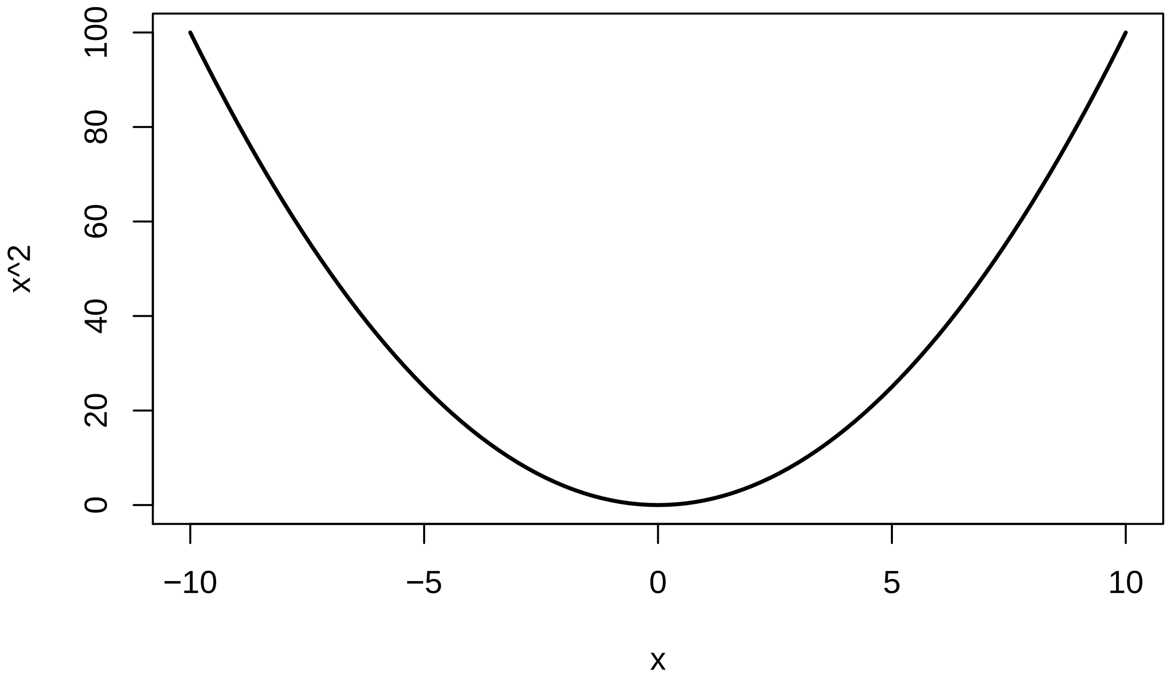
11.7.6 `curve()`

Table 11.11: Arguments to `curve()`

Argument	Outcome
`expr`	The name of a function written as a function of `x` that returns a single vector. You can either use base functions in R like `expr = $x^2$`, `expr = x + 4 - 2`, or use your own custom functions such as `expr = my.fun`, where `my.fun` is previously defined (e.g.; `my.fun <- function(x) {dnorm(x, mean = 10, sd = 3))`
`from, to`	The starting (`from`) and ending (`to`) value of x to be plotted.
`add`	A logical value indicating whether or not to add the curve to an existing plot. If `add = FALSE`, then `curve()` will act like a high-level plotting function and create a new plot. If `add = TRUE`, then `curve()` will act like a low-level plotting function.
`lty, lwd, col`	Additional standard line arguments

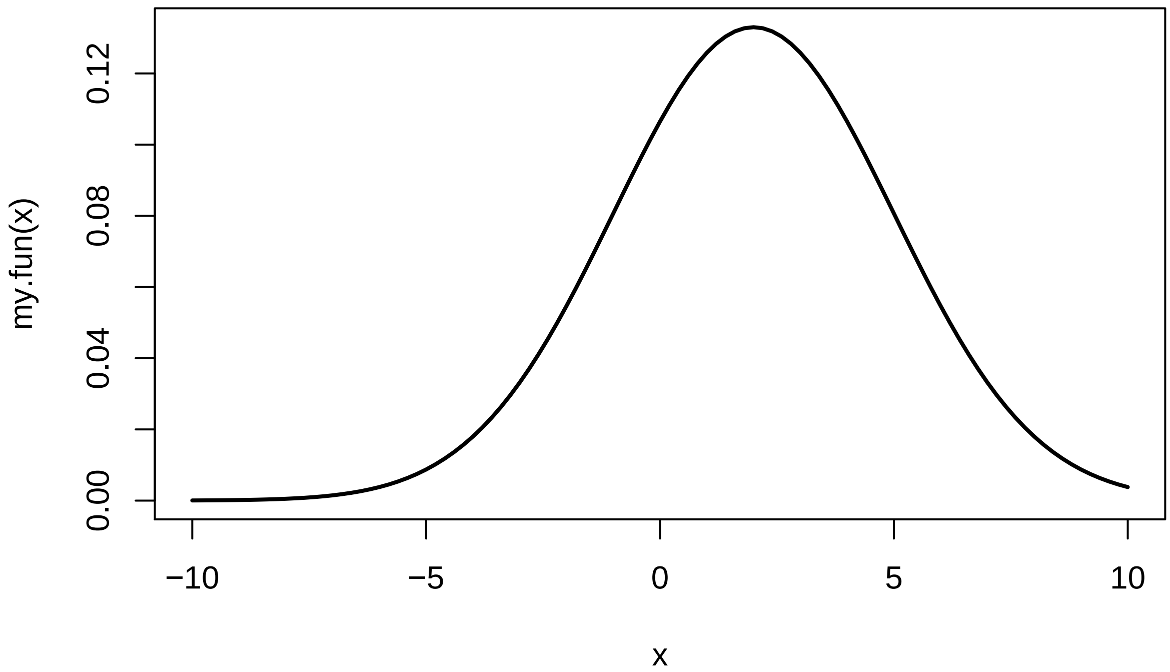
The `curve()` function allows you to add a line showing a specific function or equation to a plot. For example, to add the function x^2 to a plot from the x-values -10 to 10, you can run the code:

```
# Plot the function x^2 from -10 to +10
curve(expr = x^2,
      from = -10,
      to = 10, lwd = 2)
```



If you want to add a custom function to a plot, you can define the function and then use that function name as the argument to `expr`. For example, to plot the normal distribution with a mean of 10 and standard deviation of 3, you can use this code:

```
# Plot the normal distribution with mean = 22 and sd = 3

# Create a function
my.fun <- function(x) {dnorm(x, mean = 2, sd = 3)}

curve(expr = my.fun,
      from = -10,
      to = 10, lwd = 2)
```



In Figure~11.14, I use the `curve()` function to create curves of several mathematical formulas.

```
# Create plotting space
plot(1,
     xlim = c(-5, 5), ylim = c(-5, 5),
     type = "n",
     main = "Plotting function lines with curve()",
     ylab = "", xlab = "")

# Add x and y-axis lines
abline(h = 0)
abline(v = 0)

# set up colors
col.vec <- piratepal("google")

# x ^ 2
curve(expr = x^2, from = -5, to = 5,
      add = TRUE, lwd = 3, col = col.vec[1])

# sin(x)
curve(expr = sin, from = -5, to = 5,
      add = TRUE, lwd = 3, col = col.vec[2])

# dnorm(mean = 2, sd = .2)
my.fun <- function(x) {return(dnorm(x, mean = 2, sd = .2))}
curve(expr = my.fun,
      from = -5, to = 5,
      add = TRUE,
      lwd = 3, col = col.vec[3])

# Add legend
legend("bottomright",
```

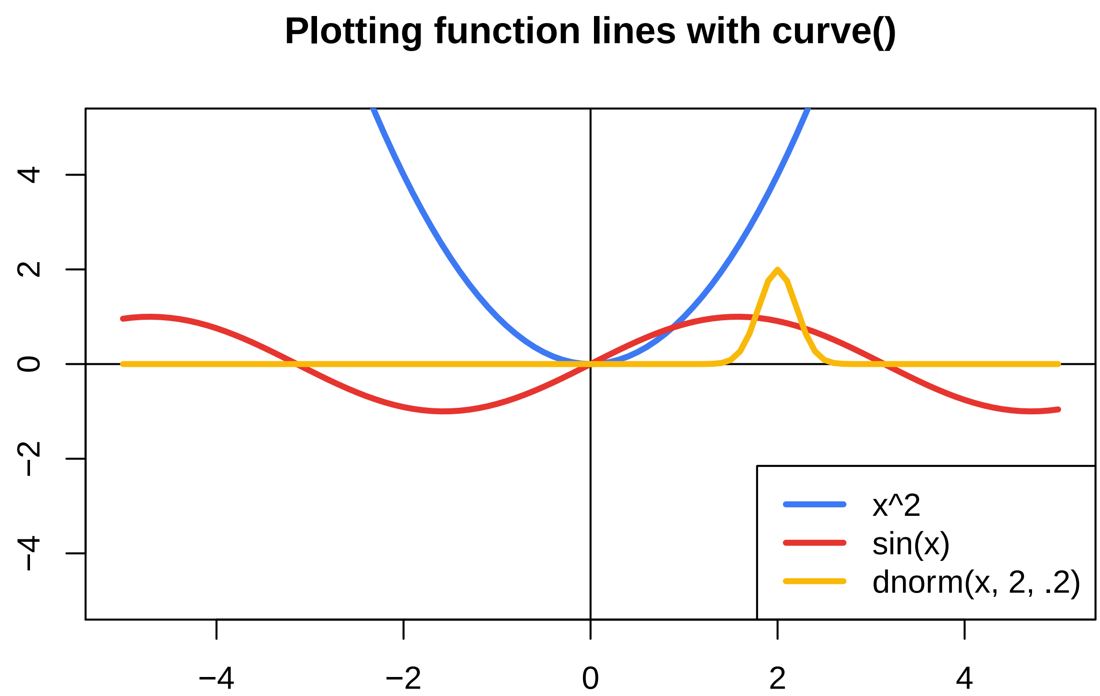


Figure 11.14: Drawing function lines with curve()

```
       legend = c("x^2", "sin(x)", "dnorm(x, 2, .2)"),
       col = col.vec[1:3],
       lwd = 3)
```

11.7.7 legend()

Table 11.12: Arguments to `legend()`

Argument	Outcome
`x, y`	Coordinates of the legend - for example, `x = 0, y = 0` will put the text at the coordinates (0, 0). Alternatively, you can enter a string indicating where to put the legend (i.e.; `"topright"`, `"topleft"`). For example, `"bottomright"` will always put the legend at the bottom right corner of the plot.
`labels`	A string vector specifying the text in the legend. For example, `legend = c("Males, "Females")` will create two groups with names Males and Females.
`pch, lty, lwd, col, pt.bg, ...`	Additional arguments specifying symbol types (`pch`), line types (`lty`), line widths (`lwd`), background color of symbol types 21 through 25 (`pt.bg`) and several other optional arguments. See `?legend` for a complete list

The last low-level plotting function that we'll go over in detail is `legend()` which adds a legend to a plot. For example, to add a legend to to bottom-right of an existing graph where data from females are plotted in blue circles and data from males are plotted in pink circles, you'd use the following code:

```
# Add a legend to the bottom right of a plot

legend("bottomright",                 # Put legend in bottom right of graph
       legend = c("Females", "Males"), # Names of groups
       col = c("blue", "orange"),      # Colors of symbols
       pch = c(16, 16))                # Symbol types
```

In Figure 11.15 I use this code to add a legend to plot containing data from males and females:

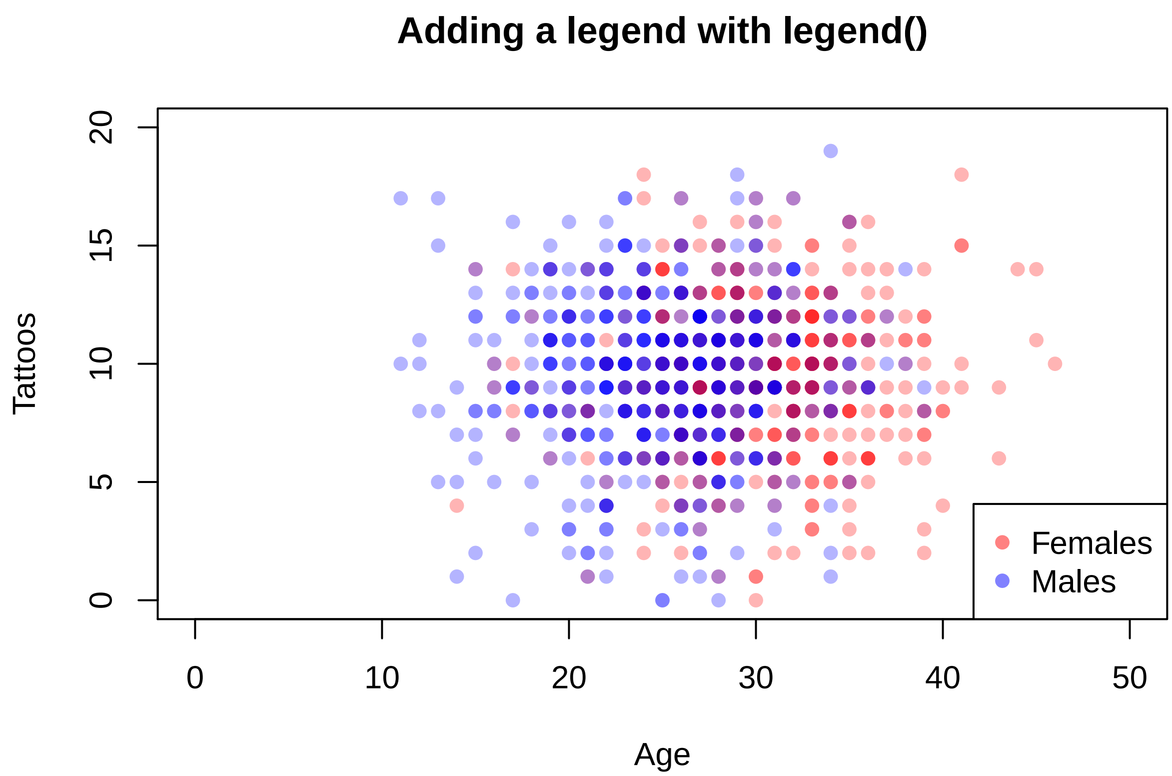


Figure 11.15: Adding a legend to a plot with legend().

```
       pch = c(16, 16),
       bg = "white")
```

There are many more low-level plotting functions that can add additional elements to your plots. Here are some I use. To see examples of how to use each one, check out their associated help menus.

```
plot(1, xlim = c(1, 100), ylim = c(1, 100),
     type = "n", xaxt = "n", yaxt = "n",
     ylab = "", xlab = "", main = "Adding simple figures to a plot")

text(25, 95, labels = "rect()")
rect(xleft = 10, ybottom = 70,
     xright = 40, ytop = 90, lwd = 2, col = "coral")

text(25, 60, labels = "polygon()")
polygon(x = runif(6, 15, 35),
        y = runif(6, 40, 55),
        col = "skyblue")

text(25, 30, labels = "segments()")
segments(x0 = runif(5, 10, 40),
         y0 = runif(5, 5, 25),
         x1 = runif(5, 10, 40),
         y1 = runif(5, 5, 25),
         lwd = 2)

text(75, 95, labels = "symbols(circles)")
```

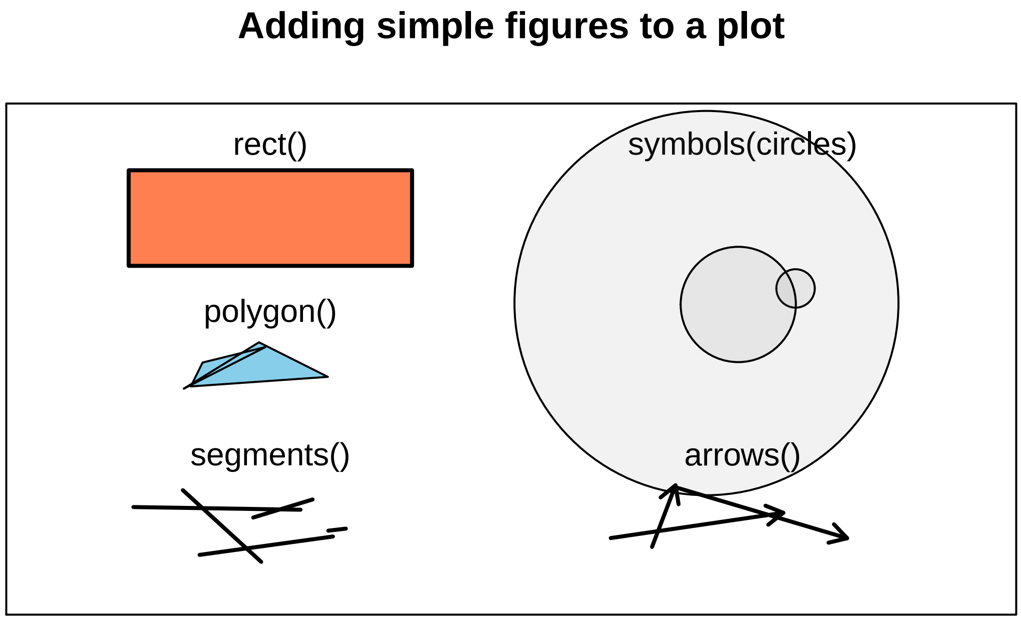


Figure 11.16: Additional figures one can add to a plot with rect(), polygon(), segments(), symbols(), and arrows().

```
symbols(x = runif(3, 60, 90),
        y = runif(3, 60, 70),
        circles = c(1, .1, .3),
        add = TRUE, bg = gray(.5, .1))

text(75, 30, labels = "arrows()")
arrows(x0 = runif(3, 60, 90),
       y0 = runif(3, 10, 25),
       x1 = runif(3, 60, 90),
       y1 = runif(3, 10, 25),
       length = .1, lwd = 2)
```

11.8 Saving plots to a file with `pdf()`, `jpeg()` and `png()`

Once you've created a plot in R, you may wish to save it to a file so you can use it in another document. To do this, you'll use either the `pdf()`, `png()` or `jpeg()` functions. These functions will save your plot to either a .pdf, .jpg, or .png file.

Table 11.13: Arguments to `pdf()`, `jpeg()` and `png()`

Argument	Outcome
`file`	The directory and name of the final plot entered as a string. For example, to put a plot on my desktop, I'd write `file = "/Users/nphillips/Desktop/plot.pdf"` when creating a pdf, and `file = "/Users/nphillips/Desktop/plot.jpg"` when creating a jpeg.
`width, height`	The width and height of the final plot in inches.

Argument	Outcome
`dev.off()`	This is *not* an argument to `pdf()` and `jpeg()`. You just need to execute this code after creating the plot to finish creating the image file (see examples).

To use these functions to save files, you need to follow 3 steps:

1. Execute the `pdf()` or `jpeg()` functions with `file, width, height` arguments.
2. Execute all your plotting code (e.g.; `plot(x = 1:10, y = 1:10)`)
3. Complete the file by executing the command `dev.off()`. This tells R that you're done creating the file.

The chunk below shows an example of the three steps in creating a pdf:

```
# Step 1: Call the pdf command to start the plot
pdf(file = "/Users/ndphillips/Desktop/My Plot.pdf",   # The directory you want to save the file in
    width = 4, # The width of the plot in inches
    height = 4) # The height of the plot in inches

# Step 2: Create the plot with R code
plot(x = 1:10,
     y = 1:10)
abline(v = 0) # Additional low-level plotting commands
text(x = 0, y = 1, labels = "Random text")

# Step 3: Run dev.off() to create the file!
dev.off()
```

You'll notice that after you close the plot with `dev.off()`, you'll see a message in the prompt like "null device". That's just R telling you that you can now create plots in the main R plotting window again.

The functions `pdf()`, `jpeg()`, and `png()` all work the same way, they just return different file types. If you can, use `pdf()` it saves the plot in a high quality format.

11.9 Examples

Figure 11.17 shows a modified version of a scatterplot I call a `balloonplot`:

```
# Turn a boring scatterplot into a  balloonplot!

# Create some random correlated data
x <- rnorm(50, mean = 50, sd = 10)
y <- x + rnorm(50, mean = 20, sd = 8)

# Set up the plotting space
plot(1,
     bty = "n",
     xlim = c(0, 100),
     ylim = c(0, 100),
     type = "n", xlab = "", ylab = "",
     main = "Turning a scatterplot into a balloon plot!")

# Add gridlines
grid()
```

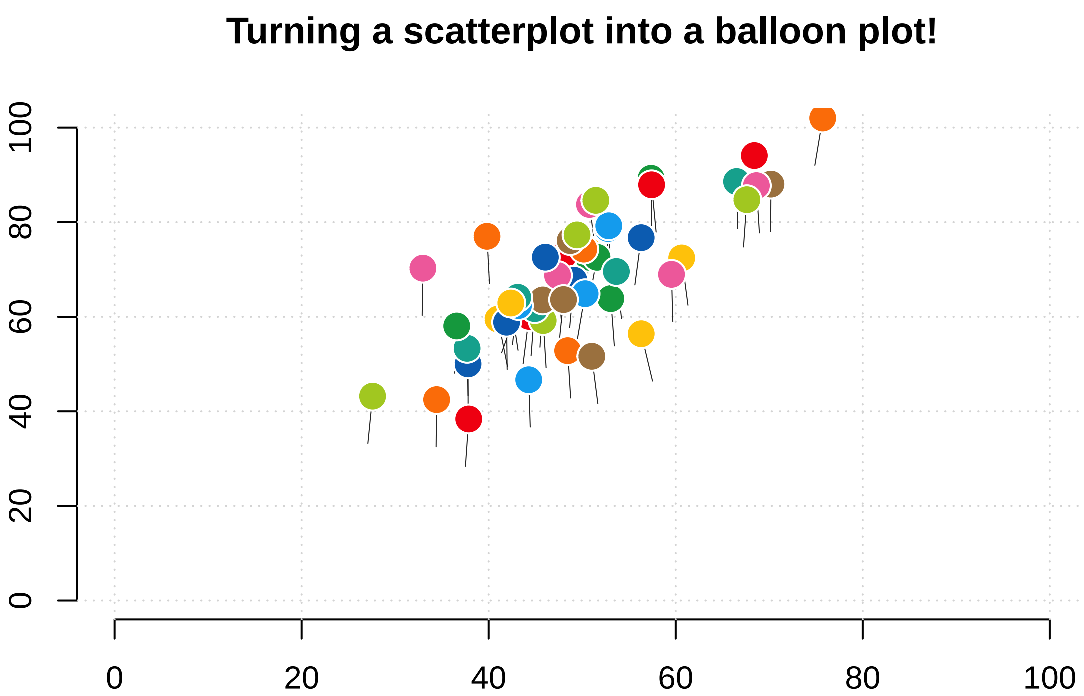


Figure 11.17: A balloon plot

```
# Add Strings with segments()
segments(x0 = x + rnorm(length(x), mean = 0, sd = .5),
         y0 = y - 10,
         x1 = x,
         y1 = y,
         col = gray(.1, .95),
         lwd = .5)

# Add balloons
points(x, y,
       cex = 2, # Size of the balloons
       pch = 21,
       col = "white", # white border
       bg = yarrr::piratepal("basel"))  # Filling color
```

You can use colors and point sizes in a scatterplot to represent third variables. In Figure 11.18, I'll plot the relationship between pirate height and weight, but now I'll make the size and color of each point reflect how many tattoos the pirate has

```
# Just the first 100 pirates
pirates.r <- pirates[1:100,]

plot(x = pirates.r$height,
     y = pirates.r$weight,
     xlab = "height",
     ylab = "weight",
     main = "Specifying point sizes and colors with a 3rd variable",
     cex = pirates.r$tattoos  / 8,          # Point size reflects how many tattoos they have
     col = gray(1 - pirates.r$tattoos / 20)) # color reflects tattoos
```

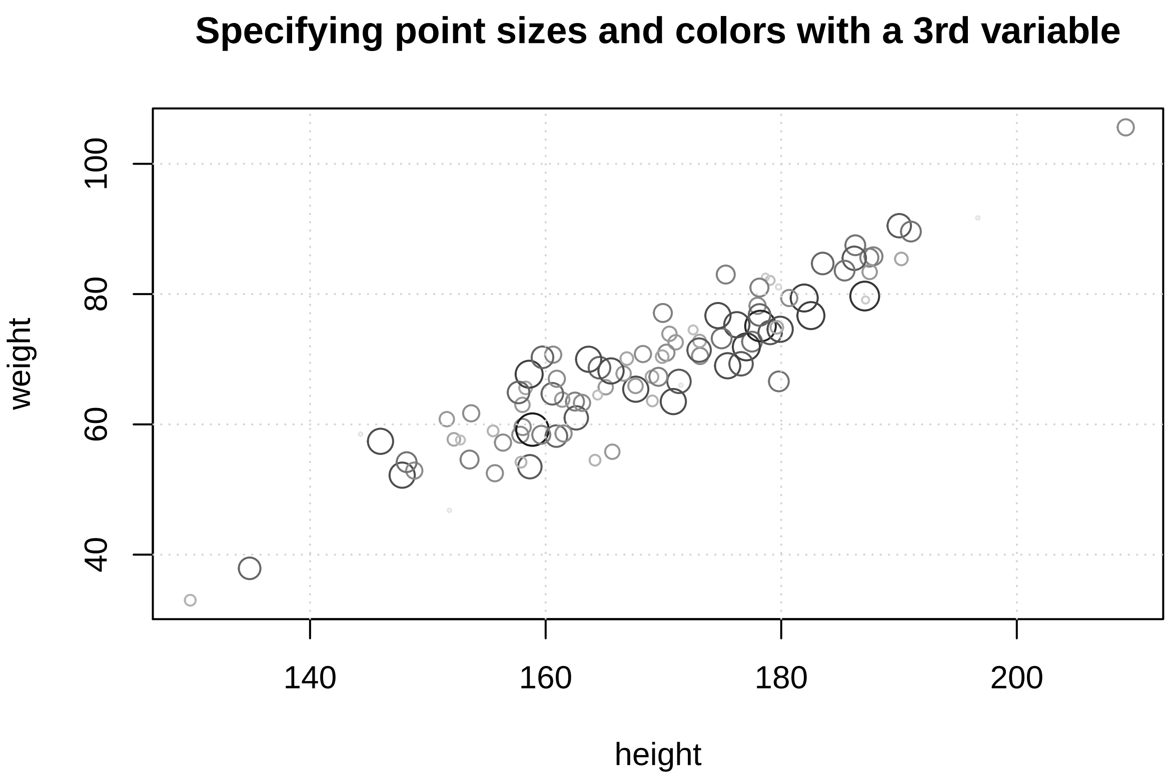
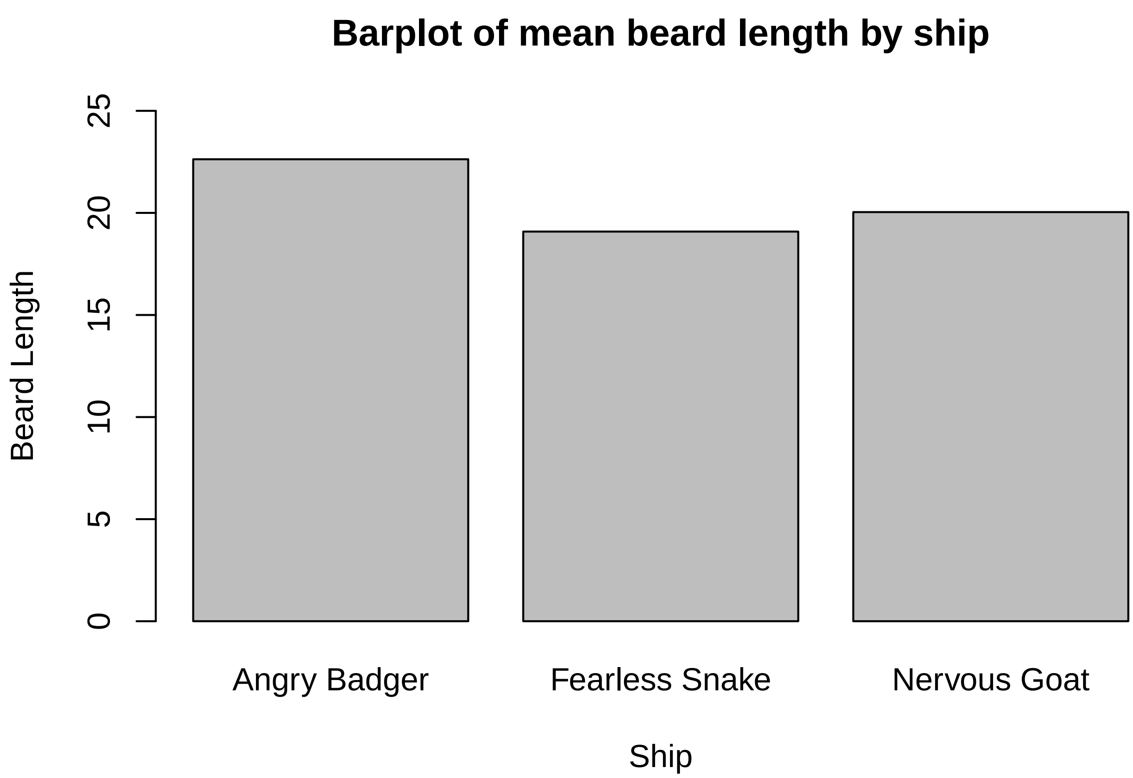


Figure 11.18: Specifying the size and color of points with a third variable.

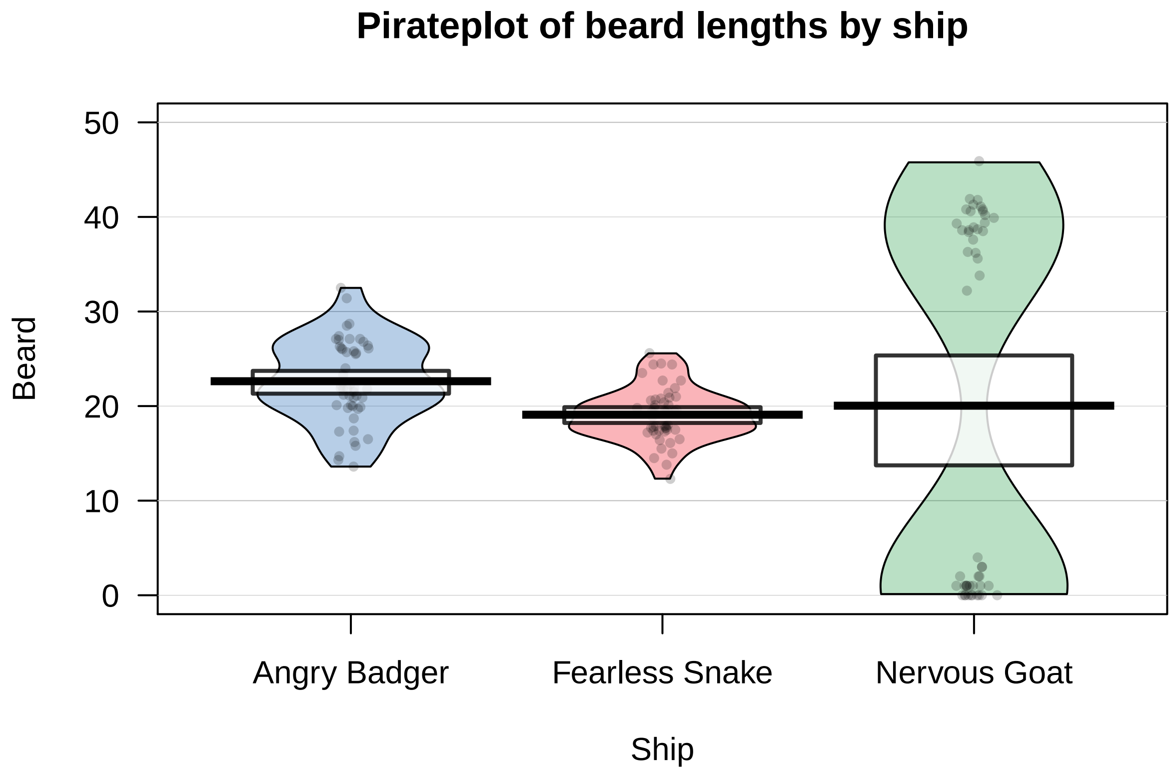
```
grid()
```

11.10 Test your R might! Purdy pictures

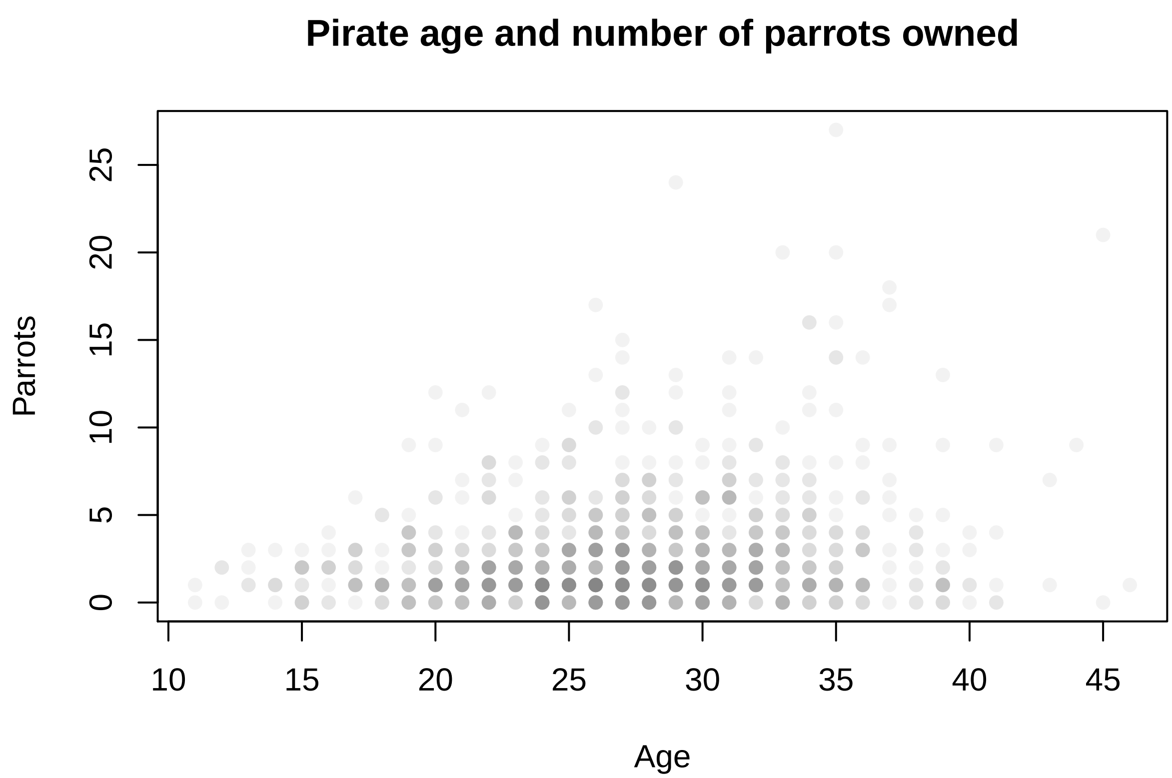
1. The `BeardLengths` dataframe (contained in the `yarrr` package or online at https://github.com/ndphillips/ThePiratesGuideToR/raw/master/data/BeardLengths.txt) contains data on the lengths of beards from 3 different pirate ships. Calculate the average beard length for each ship using `aggregate()`, then create the following barplot:



2. Now using the entire `BeardLengths` dataframe, create the following pirateplot:



3. Using the `pirates` dataset, create the following scatterplot showing the relationship between a pirate's age and how many parrot's (s)he has owned (hint: to make the points solid and transparent, use `pch = 16`, and `col = gray(level = .5, alpha = .1)`).



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Plotting (II)

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Placeholder

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