

Creating objects in R

Objects vs. variables

Comments

Challenge

Functions and their arguments

Vectors and data types

Challenge

Subsetting vectors

Conditional subsetting

Missing data

Challenge

Introduction to R

Data Carpentry contributors

Creating objects in R

You can get output from R simply by typing math in the console:

```
3 + 5  
12 / 7
```

However, to do useful and interesting things, we need to assign *values* to *objects*. To create an object, we need to give it a name followed by the assignment operator `<-`, and the value we want to give it:

```
weight_kg <- 55
```

`<-` is the assignment operator. It assigns values on the right to objects on the left. So, after executing `x <- 3`, the value of `x` is `3`. The arrow can be read as **3 goes into x**. For historical reasons, you can also use `=` for assignments, but not in every context. Because of the slight

(<http://blog.revolutionanalytics.com/2008/12/use-equals-or-arrow-for->

assignment.html) differences (<http://r.789695.n4.nabble.com/Is-there-any-difference-between-and-tp878594p878598.html>) in syntax, it is good practice to always use `<-` for assignments.

In RStudio, typing `Alt + -` (push `Alt` at the same time as the `-` key) will write `<-` in a single keystroke in a PC, while typing `Option + -` (push `Option` at the same time as the `-` key) does the same in a Mac.

Objects can be given any name such as `x`, `current_temperature`, or `subject_id`. You want your object names to be explicit and not too long. They cannot start with a number (`2x` is not valid, but `x2` is). R is case sensitive (e.g., `weight_kg` is different from `Weight_kg`). There are some names that cannot be used because they are the names of fundamental functions in R (e.g., `if`, `else`, `for`, see here (<https://stat.ethz.ch/R-manual/R-devel/library/base/html/Reserved.html>) for a complete list). In general, even if it's allowed, it's best to not use other function names (e.g., `c`, `T`, `mean`, `data`, `df`, `weights`). If in doubt, check the help to see if the name is already in use. It's also best to avoid dots (`.`) within an object name as in `my.dataset`. There are many functions in R with dots in their names for historical reasons, but because dots have a special meaning in R (for methods) and other programming languages, it's best to avoid them. It is also recommended to use nouns for object names, and verbs for function names. It's important to be consistent in the styling of your code (where you put spaces, how you name objects, etc.). Using a consistent coding style makes your code clearer to read for your future self and your collaborators. In R, three popular style guides are Google's (<https://google.github.io/styleguide/Rguide.xml>), Jean Fan's (<http://jef.works/R-style-guide/>) and the tidyverse's (<http://style.tidyverse.org/>). The tidyverse's is very comprehensive and may seem overwhelming at first. You can install the **lintr** (<https://github.com/jimhester/lintr>) package to automatically check for issues in the styling of your code.

Objects vs. variables

What are known as `objects` in R are known as `variables` in many other programming languages. Depending on the context, `object` and `variable` can have drastically different meanings. However, in this lesson, the two words are used synonymously. For more information see: <https://cran.r-project.org/doc/manuals/r-release/R-lang.html#Objects> (<https://cran.r-project.org/doc/manuals/r-release/R-lang.html#Objects>)

When assigning a value to an object, R does not print anything. You can force R to print the value by using parentheses or by typing the object name:

```
weight_kg <- 55      # doesn't print anything
(weight_kg <- 55)    # but putting parenthesis around the call print
                    # the value of `weight_kg`
weight_kg           # and so does typing the name of the object
```

Now that R has `weight_kg` in memory, we can do arithmetic with it. For instance, we may want to convert this weight into pounds (weight in pounds is 2.2 times the weight in kg):

```
2.2 * weight_kg
```

We can also change an object's value by assigning it a new one:

```
weight_kg <- 57.5
2.2 * weight_kg
```

This means that assigning a value to one object does not change the values of other objects. For example, let's store the animal's weight in pounds in a new object, `weight_lb`:

```
weight_lb <- 2.2 * weight_kg
```

and then change `weight_kg` to 100.

```
weight_kg <- 100
```

What do you think is the current content of the object `weight_lb`? 126.5 or 220?

Comments

The comment character in R is `#`, anything to the right of a `#` in a script will be ignored by R. It is useful to leave notes and explanations in your scripts. RStudio makes it easy to comment or uncomment a paragraph: after selecting the lines you want to comment, press at the same time on your keyboard `Ctrl + Shift + C`. If you only want to comment out one line, you can put the cursor at any location of that line (i.e. no need to select the whole line), then press `Ctrl + Shift + C`.

Challenge

What are the values after each statement in the following?

```
mass <- 47.5           # mass?  
age  <- 122            # age?  
mass <- mass * 2.0      # mass?  
age  <- age - 20        # age?  
mass_index <- mass/age  # mass_index?
```

Answer

Functions and their arguments

Functions are “canned scripts” that automate more complicated sets of commands including operations assignments, etc. Many functions are predefined, or can be made available by importing R *packages* (more on that later). A function usually takes one or more inputs called *arguments*. Functions often (but not always) return a *value*. A typical example would be the function `sqrt()`. The input (the argument) must be a number, and the return value (in fact, the output) is the square root of that number. Executing a function (‘running it’) is called *calling* the function. An example of a function call is:

```
b <- sqrt(a)
```

Here, the value of `a` is given to the `sqrt()` function, the `sqrt()` function calculates the square root, and returns the value which is then assigned to the object `b`. This function is very simple, because it takes just one argument.

The return ‘value’ of a function need not be numerical (like that of `sqrt()`), and it also does not need to be a single item: it can be a set of things, or even a dataset. We’ll see that when we read data files into R.

Arguments can be anything, not only numbers or filenames, but also other objects. Exactly what each argument means differs per function, and must be looked up in the documentation (see below). Some functions take arguments which may either be specified by the user, or, if left out, take on a *default* value: these are called *options*. Options are typically used to alter the way the function operates, such as whether it ignores ‘bad values’, or what symbol to use in a plot. However, if you want something specific, you can specify a value of your choice which will be used instead of the default.

Let’s try a function that can take multiple arguments: `round()`.

```
round(3.14159)
```

```
#> [1] 3
```

Here, we've called `round()` with just one argument, `3.14159`, and it has returned the value `3`. That's because the default is to round to the nearest whole number. If we want more digits we can see how to do that by getting information about the `round` function. We can use `args(round)` to find what arguments it takes, or look at the help for this function using `?round`.

```
args(round)
```

```
#> function (x, digits = 0)
#> NULL
```

```
?round
```

We see that if we want a different number of digits, we can type `digits = 2` or however many we want.

```
round(3.14159, digits = 2)
```

```
#> [1] 3.14
```

If you provide the arguments in the exact same order as they are defined you don't have to name them:

```
round(3.14159, 2)
```

```
#> [1] 3.14
```

And if you do name the arguments, you can switch their order:

```
round(digits = 2, x = 3.14159)
```

```
#> [1] 3.14
```

It's good practice to put the non-optional arguments (like the number you're rounding) first in your function call, and to then specify the names of all optional arguments. If you don't, someone reading your code might have to look up the definition of a function with unfamiliar arguments to understand what you're doing.

Vectors and data types

A vector is the most common and basic data type in R, and is pretty much the workhorse of R. A vector is composed by a series of values, which can be either numbers or characters. We can assign a series of values to a vector using the `c()` function. For example we can create a vector of animal weights and assign it to a new object `weight_g`:

```
weight_g <- c(50, 60, 65, 82)
weight_g
```

A vector can also contain characters:

```
animals <- c("mouse", "rat", "dog")
animals
```

The quotes around “mouse”, “rat”, etc. are essential here. Without the quotes R will assume objects have been created called `mouse`, `rat` and `dog`. As these objects don't exist in R's memory, there will be an error message.

There are many functions that allow you to inspect the content of a vector. `length()` tells you how many elements are in a particular vector:

```
length(weight_g)
length(animals)
```

An important feature of a vector, is that all of the elements are the same type of data. The function `class()` indicates the class (the type of element) of an object:

```
class(weight_g)
class(animals)
```

The function `str()` provides an overview of the structure of an object and its elements. It is a useful function when working with large and complex objects:

```
str(weight_g)
str(animals)
```

You can use the `c()` function to add other elements to your vector:

```
weight_g <- c(weight_g, 90) # add to the end of the vector
weight_g <- c(30, weight_g) # add to the beginning of the vector
weight_g
```

In the first line, we take the original vector `weight_g`, add the value `90` to the end of it, and save the result back into `weight_g`. Then we add the value `30` to the beginning, again saving the result back into `weight_g`.

We can do this over and over again to grow a vector, or assemble a dataset. As we program, this may be useful to add results that we are collecting or calculating.

An **atomic vector** is the simplest R **data type** and is a linear vector of a single type. Above, we saw 2 of the 6 main **atomic vector** types that R uses: "character" and "numeric" (or "double"). These are the basic building blocks that all R objects are built from. The other 4 **atomic vector** types are:

- "logical" for TRUE and FALSE (the boolean data type)
- "integer" for integer numbers (e.g., `2L`, the `L` indicates to R that it's an integer)
- "complex" to represent complex numbers with real and imaginary parts (e.g., `1 + 4i`) and that's all we're going to say about them
- "raw" for bitstreams that we won't discuss further

You can check the type of your vector using the `typeof()` function and inputting your vector as the argument.

Vectors are one of the many **data structures** that R uses. Other important ones are lists (`list`), matrices (`matrix`), data frames (`data.frame`), factors (`factor`) and arrays (`array`).

Challenge

1. Create a vector `height_mm` that contains the following heights of animals 100,150,99,87 in mm respectively.

Answer

2. What is the total height of these animals in mm? (*Hint: use function `sum`*)

Answer

3. Another animal was measured and its height is 220mm. Add this to the beginning of the vector `height_mm` and save the total height of the new set of animals in the `total_height` variable. What is the new total_height?

Answer

```
height_mm <- c(220, height_mm)
total_height <- sum(height_mm)
```

Subsetting vectors

If we want to extract one or several values from a vector, we must provide one or several indices in square brackets. For instance:

```
animals <- c("mouse", "rat", "dog", "cat")
animals[2]
```

```
#> [1] "rat"
```

```
animals[c(3, 2)]
```

```
#> [1] "dog" "rat"
```

We can also repeat the indices to create an object with more elements than the original one:

```
more_animals <- animals[c(1, 2, 3, 2, 1, 4)]
more_animals
```

```
#> [1] "mouse" "rat"   "dog"   "rat"   "mouse" "cat"
```


R indices start at 1. Programming languages like Fortran, MATLAB, Julia, and R start counting at 1, because that's what human beings typically do. Languages in the C family (including C++, Java, Perl, and Python) count from 0 because that's simpler for computers to do.

Conditional subsetting

Another common way of subsetting is by using a logical vector. `TRUE` will select the element with the same index, while `FALSE` will not:

```
weight_g <- c(21, 34, 39, 54, 55)
weight_g[c(TRUE, FALSE, TRUE, TRUE, FALSE)]
```

```
#> [1] 21 39 54
```

Typically, these logical vectors are not typed by hand, but are the output of other functions or logical tests. For instance, if you wanted to select only the values above 50:

```
weight_g > 50    # will return logicals with TRUE for the indices
                  that meet the condition
```

```
#> [1] FALSE FALSE FALSE  TRUE  TRUE
```

```
## so we can use this to select only the values above 50
weight_g[weight_g > 50]
```

```
#> [1] 54 55
```

You can combine multiple tests using `&` (both conditions are true, AND) or `|` (at least one of the conditions is true, OR):

```
weight_g[weight_g < 30 | weight_g > 50]
```

```
#> [1] 21 54 55
```

```
weight_g[weight_g >= 30 & weight_g == 21]
```

```
#> numeric(0)
```

Here, `<` stands for “less than”, `>` for “greater than”, `>=` for “greater than or equal to”, and `==` for “equal to”. The double equal sign `==` is a test for numerical equality between the left and right hand sides, and should not be confused with the

`single = sign`, which performs variable assignment (similar to `<-`).

A common task is to search for certain strings in a vector. One could use the “or” operator `|` to test for equality to multiple values, but this can quickly become tedious. The function `%in%` allows you to test if any of the elements of a search vector are found:

```
animals <- c("mouse", "rat", "dog", "cat")
animals[animals == "cat" | animals == "rat"] # returns both rat and cat
```

```
#> [1] "rat" "cat"
```

```
animals %in% c("rat", "cat", "dog", "duck", "goat")
```

```
#> [1] FALSE  TRUE  TRUE  TRUE
```

```
animals[animals %in% c("rat", "cat", "dog", "duck", "goat")]
```

```
#> [1] "rat" "dog" "cat"
```

Missing data

As R was designed to analyze datasets, it includes the concept of missing data (which is uncommon in other programming languages). Missing data are represented in vectors as `NA`.

When doing operations on numbers, most functions will return `NA` if the data you are working with include missing values. This feature makes it harder to overlook the cases where you are dealing with missing data. You can add the argument `na.rm = TRUE` to calculate the result while ignoring the missing values.

```
heights <- c(2, 4, 4, NA, 6)
mean(heights)
max(heights)
mean(heights, na.rm = TRUE)
max(heights, na.rm = TRUE)
```

If your data include missing values, you may want to become familiar with the functions `is.na()`, `na.omit()`, and `complete.cases()`. See below for examples.

```
## Extract those elements which are not missing values.  
heights[!is.na(heights)]  
  
## Returns the object with incomplete cases removed. The returned  
object is an atomic vector of type `"numeric"` (or `"double"`).  
na.omit(heights)  
  
## Extract those elements which are complete cases. The returned o  
bject is an atomic vector of type `"numeric"` (or `"double"`).  
heights[complete.cases(heights)]
```

Recall that you can use the `typeof()` function to find the type of your atomic vector.

Challenge

1. Using this vector of heights in inches, create a new vector, `heights_no_na`, with the NAs removed.

```
heights <- c(63, 69, 60, 65, NA, 68, 61, 70, 61, 59, 64,
             69, 63, 63, NA, 72, 65, 64, 70, 63, 65)
```

2. Use the function `median()` to calculate the median of the `heights` vector.
3. How many people in the set are taller than 67 inches.

Answer

```
heights <- c(63, 69, 60, 65, NA, 68, 61, 70, 61, 59,
             64, 69, 63, 63, NA, 72, 65, 64, 70, 63, 65)

# 1.
heights_no_na <- heights[!is.na(heights)]
# or
heights_no_na <- na.omit(heights)
# or
heights_no_na <- heights[complete.cases(heights)]

# 2.
median(heights, na.rm = TRUE)

# 3.
heights_above_67 <- heights_no_na[heights_no_na > 67]
length(heights_above_67)
```

