

## programming structures in R

R is a block-structured language in the context of the ALGOL-descendant family (C, C++, Python, Perl, etc.). Blocks are identified by braces [ ]; however, braces optional if a block contains a single statement. Statements are separated by newline characters or by semicolons (optional).

## loops in R

Assume the following illustration that returns the squared value of each element **n** in vector **x**:

```
1 > x <- c(5,12,13)
2 > for (n in x) print(n^2)
3 [1] 25
4 [1] 144
5 [1] 169
```

Concretely, **for** every element **n** in vector **x**, the function **print(n^2)** returns the squared value of each element individually until the entire vector is passed through. The latter is achieved through looped iterations—the first iteration returns the function **print(n^2)** applied against **n = x[1]**, the second iteration returns the function **print(n^2)** applied against **n = x[2]**, and the third iterations returns the **n = [3]**.

Equally available for looping in R is with the **while** and **repeat** functions; completed with **break** (causing control to exit the loop). The follow illustrates the use of the latter three functions:

```
1 i <- 1
2 > while (i <= 10) i <- i+4    #i is assigned 1, 5, 9, and then 13 before breaking
3 > i
4 [1] 13
5
6 > i <- 1
7 > while(TRUE) {              #break plays a key role to break the loop after i > 10 = TRUE
8 +   i <- i+4
9 +   if (i > 10) break
10 + }
11 > i
12 [1] 13
13
14 > i <- 1
15 > repeat {                   #Note the lack of Boolean exit condition with repeat (break is required
16 +   i <- i+4
17 +   if (i > 10) break
18 + }
19 > i
20 [1] 13
```

Additionally, the **next** function can be used to **skip** the remainder of the current iteration of a loop and proceed as follows. The advantage lies in avoiding complexity in nested **if-then-else** statements that can make code overly verbose.

The **for** constructs applies to **any** vector, regardless of class (mode). For example, filenames can be looped over to read their respective contents and perform a function or series of operations on.

## looping over nonvector sets in R

R does not directly support iterative functions over nonvector sets. Some examples of indirect iterations to nonvector sets are as follows:

- ... **lapply()** is applicable, assuming the iterations of the loop are independent of each other; allowing the order of operation to be irrelevant.
- ... **get()** takes a character string as an argument representative of the name of some object and returns the object of the representative name.

Assuming two given matrices **u** and **v**, containing statistical data to become the object of R's linear regression function **lm()** to each of the latter:

```
1 > u <- matrix(c(1,2,3,1,2,4), nrow = 3)
2 > v <- matrix(c(8,12,20,15,10,2), nrow = 3)
3 > u
4      [,1] [,2]
5 [1,]    1    1
6 [2,]    2    2
7 [3,]    3    4
8
9 > v
10     [,1] [,2]
11 [1,]    8   15
12 [2,]   12   10
13 [3,]   20    2
14
15 > for(m in c("u", "v")) {
16 +   z <- get(m)
17 +   print(lm(z[,2] ~ z[,1]))
18 + }
19
20 Call:
21 lm(formula = z[, 2] ~ z[, 1])
22
23 Coefficients:
24 (Intercept)      z[, 1]
25   -0.6667       1.5000
26
27 Call:
28 lm(formula = z[, 2] ~ z[, 1])
29
30 Coefficients:
31 (Intercept)      z[, 1]
32   23.286      -1.071
```

The above illustration initially sets **m** equal to **u**; the lines then assign matrix **u** to **z**, allowing **lm()** call on **u**.

```
1 > z <- get(m)
2 > print(lm(z[,2] ~ z[,1]))
3
4 Call:
5 lm(formula = z[, 2] ~ z[, 1])
6
7 Coefficients:
8 (Intercept)      z[, 1]
9   23.286      -1.071
```

The loop is then iterated over on matrix **v**, performing the same set of operations; calling **lm()** on **v**.

## if-else statements in R

The **if-else** syntax can be found as follows:

```
1 > if (r == 4) {  
2 +   x <- 1  
3 + } else {  
4 +   x <- 3  
5 +   y <- 4  
6 + }
```

Simplicity aside, it is noted that there is just a **single statement** within the **if** function (**x <- 1**). It is thus implied that the braces **{ }** around the initial **if** statement are unnecessary. However, the right brace **}** is used by the R parser to identify the statement as an **if-else**, rather than an **if** alone. An **if-else** statement works as a call to a function, returning the last value assigned:

```
1 > v <- if(cond) expression1 else expression2if (r == 4)
```

The above sets **v** to the result of **expression1** or **expression2** depending on whether **cond** is **TRUE**.

```
1 > x <- 2  
2 > y <- if(x == 2) x else x+1  
3 > y  
4 [1] 2  
5  
6 > x <- 3  
7 > y <- if(x == 2) x else x+1  
8 > y  
9 [1] 4
```

As applications become more complex, **expression1** and **expression2** are likely to take on calls to functions. It is noted to not allow compactness to take priority over clarity. When applying **if-else** statements to vectors, the **ifelse( )** function should be applied to produce faster running code.

## arithmetic and boolean operators and values in R

a list of basic operators in R programming:

Operation	Description
<b>x + y</b>	Addition
<b>x - y</b>	Subtraction
<b>x * y</b>	Multiplication
<b>x / y</b>	Division
<b>x ^ y</b>	Exponentiation
<b>x %% y</b>	Modular arithmetic
<b>x %/% y</b>	Integer division
<b>x == y</b>	Test for equality
<b>x &lt;= y</b>	Test for less than or equal to
<b>x &gt;= y</b>	Test for greater than or equal to
<b>x &amp;&amp; y</b>	Boolean AND for scalars
<b>x    y</b>	Boolean OR for scalars
<b>x &amp; y</b>	Boolean AND for vectors (vector x, y, result)
<b>x   y</b>	Boolean OR for vectors (vector x, y, result)
<b>!x</b>	Boolean negation

R technically does not employ scalar data types; scalars are treated as one-element vectors. However, the above illustrates various Boolean operators for both scalar and vector cases. The example on the proceeding page illustrates the need for the latter distinction:

```

1 > x <- c(TRUE, FALSE, TRUE)      #create logical vector x
2 > y <- c(TRUE, TRUE, FALSE)      #create logical vector y
3 > x
4 [1] TRUE FALSE TRUE
5
6 > y
7 [1] TRUE TRUE FALSE
8
9 > x & y                          #test Boolean AND for vectors x AND y
10 [1] TRUE FALSE FALSE
11
12 > x[1] && y[1]                  #test Boolean AND for scalars in x[1] AND y[1]
13 [1] TRUE
14
15 > x && y                        #looks at just the first elements in vector x AND y
16 [1] TRUE
17
18 > if( x[1] && y[1]) print("both TRUE")
19 [1] "both TRUE"
20
21 > if(x & y) print("both TRUE")
22 [1] "both TRUE"
23 Warning message:
24 In if (x & y) print("both TRUE") :
25   the condition has length > 1 and only the first element will be used
26 > if(x & y) print("both TRUE")

```

The illustration above demonstrates the unique property of an **if** function *requiring a single Boolean* in evaluation, opposed to a vector of Booleans. The **warning** result in example where **&** is applied is proof.

The Boolean logicals **TRUE** and **FALSE** can be abbreviated as **T** and **F** (capitalized). When applied in arithmetic, the values of **T** and **F** are represented as **1** and **0**:

```

1 > 1 < 2                          #1 is less than 2
2 [1] TRUE
3
4 > (1 < 2) * (3 < 4)              #1 is less than 2 and 3 is less than 4 (T * T = 1 * 1 = 1)
5 [1] 1
6
7 > (1 < 2) * (3 < 4) * (5 < 1)    #(T * T * F = 1 * 1 * 0 = 0)
8 [1] 0
9
10 > (1 < 2) == TRUE               #1 is less than 2 = TRUE, thus TRUE = TRUE
11 [1] TRUE
12
13 > (1 < 2) == 1                  #1 is less than 2 = TRUE = 1, thus 1 = TRUE
14 [1] TRUE

```

## default values for arguments **=** in R

R employs the use of **named arguments** and **lazy evaluation** in context. **Named arguments** refer to the optional arguments that exist within a given function. **Lazy evaluation** refers to how R does not evaluate an argument until/unless the argument is necessary. Therefore, **named arguments** may, or may not, be used:

```

1 read.csv(file, header = TRUE, sep = ",", quote = "\"",
  dec = ".", fill = TRUE, comment.char = "", ...)

```

The above example of the **read.csv()** function illustrates the number of **default values** assigned as arguments when the function is called, unless stated otherwise in the code.

## return values in R

The return value of a function can be any R object. Values are printed directly to the caller with the **return()** function. By default, the value of the last executed statement is returned regardless. It is common in practice to avoid the use of the **return()** function call; there is possibility of lengthening execution time as such. However, for the purpose of tracking function control returning to the caller, the insertion of **return()** can make the code clearer and maintainable.

Considering the return value can be any R object, **complex objects** are equally applicable:

```
1 > g                                     #print the function g()
2 function() {
3     t <- function(x) return(x^2)
4     return(t)
5 }
6 > g()                                   #print the environment of function g()
7 function(x) return(x^2)
8 <environment: 0x0000000005f36210>
```

Functions with **multiple return values** should be placed in a **list**, or other applicable container.

## functions are objects in R

Functions in R are referred to as **first-class objects** (of class "function"); they can be used like most objects.

```
1 > g <- function(x) {                  #standard function syntax in R
2 +   return(x+1)
3 + }
```

Concretely, the **function()** is a **function** that serves to create **functions**. The two arguments in the above function are **x**—the formal argument—and the body **return(x + 1)** of class "expression". The illustration above creates a function object which is then assigned to **g**. The brace "**{**" is even a function in itself:

As defined by R – For **{**, the result of the last expression evaluated. This has the visibility of the last evaluation.

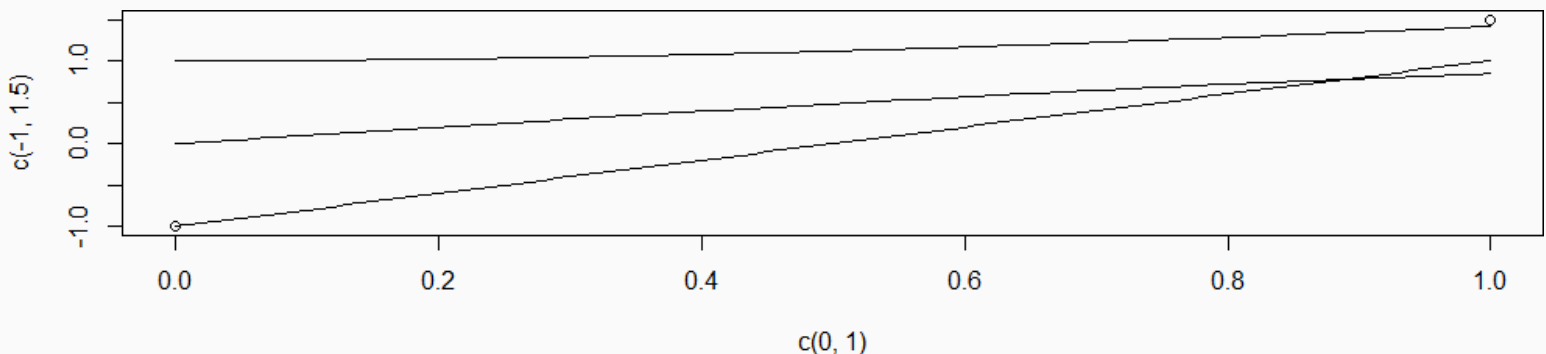
The arguments of the above example can be accessed as follows via the **formals()** and **body()** functions.

Because functions are R objects, they can be printed directly to the console by simply calling the function.

For longer functions that need examination, the **page()** function can be used to export the function to text.

Additionally, functions can be assigned to variables and used as arguments in other functions. Functions can be looped through a list of multiple functions equally. Looping through several functions to plot a graph:

```
1 > g1 <- function(x) return(sin(x))
2 > g2 <- function(x) return(sqrt(x^2 + 1))
3 > g3 <- function(x) return(2*x - 1)
4 > plot(c(0,1),c(-1,1.5))
5 > for(f in c(g1, g2, g3)) plot(f, 0, 1, add = TRUE)
```



The **formals()** and **body()** functions can equally be used to assign/replace functions (discussed more later).

## environment and scope issues in R

Along with **functions** consisting of its arguments and body, the function's environment is also stored; made up of the collection of objects present at creation.

### The Top-Level Environment

```
1 > w <- 12
2 > f <- function(y) {           #function f() created at the Top-Level Environment
3 +   d <- 8                     #aka the interpreter command prompt
4 +   h <- function() {
5 +       return(d*(w+y))
6 +   }
7 +   return(h())
8 + }
9 > environment(f)
10 <environment: R_GlobalEnv
```

The top-level environment in R is referred to as **R\_GlobalEnv** in the output but **.GlobalEnv** in the code.

```
1 > ls()                         #lists the objects within the Top-Level environment
2 [1] "f" "w"
3
4 > ls.str()                     #lists structure of Top-Level objects with more detail
5 f : function (y)
6 w : num 12
```

Within the **scope hierarchy** of R, the environments to variables are defined similar to that of the C programming language; variable **w** is **global** to **f()**, while variable **d** is **local** to **f()**. The difference in R results from an expanded focus on the **hierarchy**. Unlike C, R can have functions defined within functions—remembering that functions in R are objects and objects can be defined anywhere in R. Taking the above:

**h()** is **local** to **f()**

**d** is **local** to **f()**

**d** is **global** to **h()**

**y** is **local** to **f()** → arguments are considered **locals** in R

**w()** is **global** to **f()**

**w()** is **global** to **h()**

**\*h()**'s environment consists of any arguments defined when **h()** comes into existence; upon assignment

```
1 > h <- function() {
2 +   return(d*(w+y))
3 + }
```

When **f()** is called multiple times, **h()** comes into existence multiple times and is then removed each time **f()** returns. Therefore, **h()**'s environment are the objects **d** and **y** created within **f()**; **plus f()**'s environment (**w**). Concretely, if one function is defined within another, the inner function's environment includes the environment of the outer function's, including any **locals** created thus far in the out function's environment.

***With multiple nested functions, there is a nested sequence of larger and larger environments; the "root" environment consists of the top-level objects.***

Applying the latter logic to calling the function **f()** as follows:

```
1 > f(2)
2 [1] 112
```

```
1 > h
2 Error: object 'h' not found
```

Calling **f(2)** sets **local d** to **8** and then calls **h()** → **d\*(w+y) = 8\*(12+2)** resulting in **112**. Note that **w** does not explicitly exist within **h()** and thus, R ascended the hierarchy (to the Top-Level) to find **w <- 12**.

As discussed above, **h()** is **local** to **f()** and thus not visible at the Top-Level Environment.

## function side-effects in R

A property of functional programming is that functions do not change **nonlocal** variables (generally no side-effects). The code within a function has read access to **nonlocal** variables (not write access). Assumptions of reassignments are merely copies made during execution of a given function.

```
1  > w <- 12                #Top-Level Environment variable w remains unchanged as follows
2  > f
3  function(y) {
4      d <- 8
5      w <- w + 1
6      y <- y - 2
7      print(w)
8      h <- function() {
9          return(d*(w+y))
10     }
11     return(h())
12 }
13
14 > t <- 4                  #Top-Level Environment variable t remains unchanged as above
15 > f(t)
16 [1] 13
17 [1] 120
18
19 > w
20 [1] 12
21
22 > t
23 [1] 4
```

Concretely as illustrated above, references to the **local** variable **w** are sent to the same memory location as the **global** variable **w** until the **local** variable **w** changes; in this case, a new memory location is used. An exception to the read-only nature of **globals** is with the **superassignment** operator (discussed later).

## no pointers in R

R does not have **pointers** or **references** similar to those of programming languages like **C**. In Python, functions are available that directly change the arguments themselves:

```
1  >>> x = [13, 5, 12]
2  >>> x.sort()
3  >>> x
4  [5, 12, 13]
```

To produce the same result, assigning the sorted values of vector **x** to **x**, a **reassignment** is necessary:

```
1  > x <- c(13, 5, 12)
2  > sort(x)                #sorting vector x
3  [1]  5 12 13
4
5  > x                      #vector x is not assigned the arguments of sort()
6  [1] 13  5 12
7
8  > x <- sort(x)           #vector x must be reassigned to maintain the latter arguments
9  > x
10 [1]  5 12 13
```

The above logic can be applied to functions with multiple arguments equally; although with more complexity in the syntax as the arguments and nature of the function itself, expands.

## writing upstairs 🌐 in R

Although code within a certain level of environmental hierarchy has read access to the variables in levels above, direct write access to upper level variables is not possible with the standard assignment `<-` operator.

In order to write a variable to another in an environmental level higher than the variable of focus, the **superassignment** `<<-` operator, or the **assign()** function, must be applied.

### Writing to nonlocals with the superassignment operator

```
1 > two <- function(u) {
2 +   u <<- 2*u
3 +   z <- 2*z
4 + }
5 > x <- 1
6 > z <- 3
7 > u                                     #u is not assigned in the global environment
8 Error: object 'u' not found
9
10 > two(x)                             #execute function(u) as assigned to variable two
11 > x                                    #global variable x maintains original assignment
12 [1] 1
13
14 > z                                    #global variable z maintains original assignment
15 [1] 3
16
17 > u                                    #u is superassigned as a top-level variable
18 [1] 2
```

Although the **superassignment** `<<-` operator is used to write top-level variables, its function is more discrete. The `<<-` operator performs an upward search in the environment hierarchy, stopping at the first level where a variable of that name is identified; the selected level becomes global in nature.

In the above illustration, **inc()** is defined within **f()**. Because there is no assignment to **x** upward in the hierarchy, the **x** within **inc()** is the one the value is then written to; not **x** at the top-level.

### Writing to nonlocals with the assign() function

```
1 > two                                     #variation of two( ) above; using assign( ) instead of <<-
2 function(u) {
3   assign("u", 2*u, pos = .GlobalEnv)
4   z <- 2*z
5 }
6
7 > two(x)
8 > x                                     #x is not within two( ) and maintains its global value
9 [1] 1
10
11 > u                                     #u is not within two( ) but is superassigned with assign( ) top-level
12 [1] 2
```



## when to use global variables 🚫 in R

The use of **global variables** within the discipline of programming is widely debated. Many experts advocate for the banishment of **global variables** under any and all circumstances possible. There are certain circumstances where **global variables** provide value in the context of R programming. In the following text, the term **global variable**, or **globals** is used to refer to any variable located higher in the environment hierarchy than the level of the given code within context (focus).

Within the R compiled code and binary constructions, **globals** are used widely; both in C code and R routines. For example, the **superassignment** `<-` operator can be found in many R libraries. **Threaded code** and **GPU** code used for writing fast programs, typically use **globals** aggressively in practice; this allows communication avenues between parallel actions/actors.

```
1 > f
2 function(lxyy) {                                #lzyy is a list containing x and y
3     ...
4     lxyy$x <- ...
5     lxyy$y <- ...
6     return(lxyy)
7 }
8 > lxy$x <- ...                                  #set global variable x
9 > lxy$y <- ...                                  #set global variable y
10 > lxy <- f(lxy)
11 > ... <- lxy$x                                  #use new x
12 > ... <- lxy$y                                  #use new y
```

The above code can become unreliable as the variables become more complex, say as list classes. An alternate method of applying **globals** within the function are as follows:

```
1 > f
2 function() {
3     ...
4     x <- ...                                     #set global variable x
5     y <- ...                                     #set global variable y
6 }
7 > x <- ...
8 > y <- ...
9 > f()                                           #variables x and y are changed within the function execution
10 > ... <- x                                     #use new x
11 > ... <- y                                     #use new y
```

The latter example results in more clear, concise, and manageable code for maintenance and debugging—choosing to use global variables opposed to returning lists. In this theory, the use of **globals** become acceptable if they are considered to be **truly global**; being used broadly within the program's environment.

The alter argument to using **globals** for simplified code occurs with the cost of simplicity gained; debugging code down the line will become difficult when trying to track the local of **global** variable assignments, or reassignments. It is noted, however, that the optimization of text editors allow 'find' functions to locate and identify text within a space (ctrl + f); this make sense, considering the original publication calling for abandonment of **globals** was written in the 1970s.

An additional argument in the use of **globals** is found when certain functions **f()** are called in multiple independent segments of a program. Each call might require its own value of variables **x** and **y**. The solution would be to set up vectors for **x** and **y** values for each value as a corresponding element in the vector. The ultimate solution, however, loses some of the simplicity gained from the use of **globals**.

**Specifically, in R**, a concern with **globals** exists at the **Top-Level Environment**. Code using **globals** runs the risk of overwriting unrelated variables consisting of the same name, or naming convention. A solution to protecting the integrity of **globals** at the **Top-Level** would be to employ application-specific assignments:

<b>The below (left)</b>	→	<b>is replaced by the below (right)</b>
<pre>1 &gt; sim &lt;- list()</pre>		<pre>1 &gt; assign("simenv", new.env(), envir = .GlobalEnv)</pre>

The above creates a new environment to capture **globals** at the top-level; accessed with **get( )** or **assign( )**:

<b>The below (left)</b>	→	<b>is replaced by the below (right)</b>
<pre>1 &gt; if(is.null(sim\$evnts)) { 2 +   sim\$evnts &lt;- newevnt 3 + }</pre>		<pre>1 &gt; if(is.null(get("evnts", envir = simenv))) { 2 +   assign("evnts", newevnt, envir = simenv) 3 + }</pre>

The above illustrations loses simplicity for the sake of **global** variable integrity, but still remains more manageable than other circumstances (lists of lists of lists) and mitigates unintended reassignments.

## closures {} in R

R **closures** consist of a function's arguments and body together with its **environment** at the time of a call. Including the **environment** is exploiting a type of programming with a feature **also known as a closure**. A **closure** consists of a function that sets up a local variable and creates *another* function to access the variable.

```
1 > counter
2 function() {
3   ctr <- 0
4   f <- function() {
5     ctr <- ctr + 1
6     cat("this count currently has value", ctr, "\n")
7   }
8   return(f)
9 }
```

Illustrating the operation of a single function in multiple programming environments as follows:

```
1 > c1 <- counter()           #assigning counter() to variable c1
2 > c2 <- counter()           #assigning counter() to variable c2
3 > c1                         #c1 calls counter() in its own environment
4 function() {
5   ctr <- ctr + 1
6   cat("this count currently has value", ctr, "\n")
7 }
8 <environment: 0x000000003cfbb30>
9 > c2                         #c2 calls counter() in its own environment
10 function() {
11   ctr <- ctr + 1
12   cat("this count currently has value", ctr, "\n")
13 }
14 <environment: 0x0000000035ed130>
15 > c1()                       #call to counter with c1, registers "1"
16 this count currently has value 1
17 > c1()                       #call to counter with c1, registers "2"
18 this count currently has value 2
19 > c2()                       #call to counter with c2, registers "1"
20 this count currently has value 1
21 > c2()                       #call to counter with c2, registers "2"
22 this count currently has value 2
23 > c2()                       #call to counter with c2, registers "3"
24 this count currently has value 3
25 > c1()                       #note counter() operates in separate environments
26 this count currently has value 3
```

## recursion ↻ in R

A **recursive** function in R is one that calls itself; the intuition behind **recursion** is relatively simple:

To solve a problem of type **X** by writing a **recursive** function **f()**:

- ... Break the original problem of type **X** into one or more smaller problems of type **X**.
- ... Within function **f()**, call function **f()** on each smaller problem segment.
- ... Within function **f()**, converge the results of each call to **f()**; solving the original problem.

An famously illustrative example of **recursion** is found in the [Towers of Hanoi Problem](#).

### Illustrative recursion through a Quicksort implementation

**Quicksort** is an algorithm used to sort a vector of numbers from smallest to largest. The implementation in R can be explained as with the vector (5,4,12,13,3,8,88):

All elements (4,12,13,3,8,88) are compared to element 5 and two subvectors are formed

- ... Subvector1 → all elements < 5 → (4,3)
- ... Subvector2 → all elements >= 5 → (12,13,8,88)
- ... The function is then called upon the subvectors, returning (3,4) and (8,12,13,88)
- ... The returns are stringed together with element 5, resulting in (3,4,5,8,12,13,88)

The following example is for illustrative purposes, considering R's **sort()** function is compiled in C (faster):

```
1  > qs
2  function(x) {
3    if(length(x) <= 1) return(x)
4    pivot <- x[1]
5    therest <- x[-1]
6    sv1 <- therest[therest < pivot]
7    sv2 <- therest[therest >= pivot]
8    sv1 <- qs(sv1)
9    sv2 <- qs(sv2)
10   return(c(sv1, pivot, sv2))
11 }
12 > x <- c(5,4,12,13,3,8,88)
13 > qs(x)
14 [1] 3 4 5 8 12 13 88
```

Noting the **termination condition**:

```
1    if(length(x) <= 1) return(x)
```

Without the above constraint, R would endlessly call upon itself with empty vectors (until R interpreter fails).

Two potential reservations about **recursion** in R:

- ... **Recursion** can be fairly abstract when implemented
- ... **Recursion** can be memory-intensive when operating on larger problems

## replacement functions in R

```
1 > x <- c(1,2,4)
2 > names(x)
3 NULL
4
5 > names(x) <- c("a","b","ab")
6 > names(x)
7 [1] "a" "b" "ab"
8
9 > x
10  a  b ab
11  1  2  4
```

Recalling an example introduced earlier:

Focusing on **line 5**, appears rather dormant. However, note that a value is assigned to the result of a function call.

The availability of such an action in R is due to R's **replacement function** property. Below is the actual result of executing the script in **line 5**:

```
1 > x <- "names<-"(x, value = c("a","b","ab"))
```

Concretely, the call is function **names<-()**.

Any assignment statement where the left side is **not just** an identifier (variable name) is considered a **replacement function**. Concretely, when R is fed the following syntax, note the behavior:

<b>The below (left)</b>	<b>→</b>	<b>is computed by R as below (right)</b>
1 > g(u) <- v		1 > u <- "g<-"(u, value = v)

Note that function **g(u)** has to be defined in the current R environment prior to the call being successful.

Another example of **replacement functions** can be found through **subscripting** operations (also functions):

```
1 > x <- c(8,88,5,12,13)
2 > x
3 [1] 8 88 5 12 13
4
5 > x[3]
6 [1] 5
7
8 > "["(x,3)
9 [1] 5
10
11 > x <- "["(x, 2:3, value = 99:100)
12 > x
13 [1] 8 99 100 12 13
```

As illustrated before, the call in **line 11** is performing the backend calculations in R when the code is executed: **1 > x[2:3] <- 99:100** which is ultimately verified as follows:

```
1 > x <- c(8,88,5,12,13)
2 > x[2:3] <- 99:100
3 > x
4 [1] 8 99 100 12 13
```

## tools for function composition in R

Functions can be written directly in the terminal session console (not advised for longer functions):

```
1 > g <- function() {
2 +   return(x+1)
3 + }
```

Text editors (like Notepad) can be used and directly from the R Console through the **source()** function:

```
1 > source("xyz.R")
```

Another option for quick edits to functions is through the **edit()** function:

```
1 > f1 <- edit(f1)
```

The **edit()** function can be used to edit **data structures** equally.

## creating binary operations $\oplus$ in R

Similar to creating functions, **binary operations** can also be created in R:

```
1 > "%a2b%" <- function(a,b) return(a+2*b)
2 > 3 %a2b% 5
3 [1] 13
```

## anonymous functions in R

In R, the purpose of the **function()** function is to create functions. Considering the following code:

```
1 > inc <- function(x) return(x+1)
2 > inc
3 function(x) return(x+1)
```

The above illustration instructs R to create a function that adds 1 to its argument and then assigns that function to variable **inc**. However, the assignment is not always taken; it is available to use the function object created by the call to **function()** without naming the object. Functions in the context are referred to as **anonymous** since they are unnamed. The proceeding example illustrates the latter:

```
1 > z <- matrix(1:6, nrow = 3)           #create matrix z
2 > z
3      [,1] [,2]
4 [1,]    1    4
5 [2,]    2    5
6 [3,]    3    6
7
8 > f <- function(x) x/c(2,8)           #create function(x) assigned to f
9 > y <- apply(z,1,f)                   #apply function f to matrix z as variable y
10 > y
11      [,1] [,2] [,3]
12 [1,]  0.5 1.000 1.500
13 [2,]  0.5 0.625 0.750
```

The following bypasses the **assignment** to **f** by using an **anonymous** function without the call to **apply()**:

```
1 > y <- apply(z,1,function(x) x/c(2,8))
2 > y
3      [,1] [,2] [,3]
4 [1,]  0.5 1.000 1.500
5 [2,]  0.5 0.625 0.750
```

The third **formal argument** to **apply()** is required to be a function. This is represented in the above illustration considering that the return value of **function()** is a function. Sometimes, it is more clear to write the code using **anonymous functions** opposed to defining functions **externally**. However, more complex functions would be less like to benefit from the above application.