Introduction to the R Language

Control Structures

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Control Structures

Control structures in R allow you to control the flow of execution of the program, depending on runtime conditions. Common structures are

- `if`, `else`: testing a condition
- `for`: execute a loop a fixed number of times
- `while`: execute a loop *while* a condition is true
- `repeat`: execute an infinite loop
- `break`: break the execution of a loop
- `next`: skip an interation of a loop
- `return`: exit a function

Most control structures are not used in interactive sessions, but rather when writing functions or longer expresisons.

Control Structures: if

```
if(<condition>) {
        ## do something
} else {
        ## do something else
}
if(<condition1>) {
        ## do something
} else if(<condition2>)  {
        ## do something different
} else {
        ## do something different
}
```

if

This is a valid if/else structure.

```
if(x > 3) {
        y <- 10
} else {
        y <- 0
}
```

So is this one.

```
y <- if(x > 3) {
        10
} else {
        0
}
```

if

Of course, the else clause is not necessary.

```
if(<condition1>) {

}

if(<condition2>) {

}
```

for

`for` loops take an interator variable and assign it successive values from a sequence or vector. For loops are most commonly used for iterating over the elements of an object (list, vector, etc.)

```
for(i in 1:10) {
        print(i)
}
```

This loop takes the `i` variable and in each iteration of the loop gives it values 1, 2, 3, ..., 10, and then exits.

for

These three loops have the same behavior.

```
x <- c("a", "b", "c", "d")

for(i in 1:4) {
        print(x[i])
}

for(i in seq_along(x)) {
        print(x[i])
}

for(letter in x) {
        print(letter)
}

for(i in 1:4) print(x[i])
```

Nested for loops

`for` loops can be nested.

```
x <- matrix(1:6, 2, 3)

for(i in seq_len(nrow(x))) {
        for(j in seq_len(ncol(x))) {
                print(x[i, j])
        }
}
```

Be careful with nesting though. Nesting beyond 2–3 levels is often very difficult to read/understand.

while

While loops begin by testing a condition. If it is true, then they execute the loop body. Once the loop body is executed, the condition is tested again, and so forth.

```
count <- 0
while(count < 10) {
        print(count)
        count <- count + 1
}
```

While loops can potentially result in infinite loops if not written properly. Use with care!

while

Sometimes there will be more than one condition in the test.

```
z <- 5

while(z >= 3 && z <= 10) {
        print(z)
        coin <- rbinom(1, 1, 0.5)

        if(coin == 1) {  ## random walk
                z <- z + 1
        } else {
                z <- z - 1
        }
}
```

Conditions are always evaluated from left to right.

repeat

Repeat initiates an infinite loop; these are not commonly used in statistical applications but they do have their uses. The only way to exit a `repeat` loop is to call `break`.

```
x0 <- 1
tol <- 1e-8

repeat {
        x1 <- computeEstimate()

        if(abs(x1 - x0) < tol) {
                break
        } else {
                x0 <- x1
        }
}
```

repeat

The loop in the previous slide is a bit dangerous because there's no guarantee it will stop. Better to set a hard limit on the number of iterations (e.g. using a for loop) and then report whether convergence was achieved or not.

next, return

`next` is used to skip an iteration of a loop

```
for(i in 1:100) {
        if(i <= 20) {
                ## Skip the first 20 iterations
                next
        }
        ## Do something here
}
```

`return` signals that a function should exit and return a given value

Control Structures

Summary

- Control structures like `if`, `while`, and `for` allow you to control the flow of an R program
- Infinite loops should generally be avoided, even if they are theoretically correct.
- Control structures mentiond here are primarily useful for writing programs; for command-line interactive work, the *apply functions are more useful.

Functions

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Functions

Functions are created using the `function()` directive and are stored as R objects just like anything else. In particular, they are R objects of class “function”.

```
f <- function(<arguments>) {
        ## Do something interesting
}
```

Functions in R are “first class objects”, which means that they can be treated much like any other R object. Importantly,

- Functions can be passed as arguments to other functions
- Functions can be nested, so that you can define a function inside of another function
- The return value of a function is the last expression in the function body to be evaluated.

Function Arguments

Functions have *named arguments* which potentially have *default values*.

- The *formal arguments* are the arguments included in the function definition
- The `formals` function returns a list of all the formal arguments of a function
- Not every function call in R makes use of all the formal arguments
- Function arguments can be *missing* or might have default values

Argument Matching

R functions arguments can be matched positionally or by name. So the following calls to `sd` are all equivalent

```
> mydata <- rnorm(100)
> sd(mydata)
> sd(x = mydata)
> sd(x = mydata, na.rm = FALSE)
> sd(na.rm = FALSE, x = mydata)
> sd(na.rm = FALSE, mydata)
```

Even though it's legal, I don't recommend messing around with the order of the arguments too much, since it can lead to some confusion.

Argument Matching

You can mix positional matching with matching by name. When an argument is matched by name, it is "taken out" of the argument list and the remaining unnamed arguments are matched in the order that they are listed in the function definition.

```
> args(lm)
function (formula, data, subset, weights, na.action,
          method = "qr", model = TRUE, x = FALSE,
          y = FALSE, qr = TRUE, singular.ok = TRUE,
          contrasts = NULL, offset, ...)
```

The following two calls are equivalent.

```
lm(data = mydata, y ~ x, model = FALSE, 1:100)
lm(y ~ x, mydata, 1:100, model = FALSE)
```

Argument Matching

- Most of the time, named arguments are useful on the command line when you have a long argument list and you want to use the defaults for everything except for an argument near the end of the list
- Named arguments also help if you can remember the name of the argument and not its position on the argument list (plotting is a good example).

Argument Matching

Function arguments can also be *partially* matched, which is useful for interactive work. The order of operations when given an argument is

1. Check for exact match for a named argument
2. Check for a partial match
3. Check for a positional match

Defining a Function

```
f <- function(a, b = 1, c = 2, d = NULL) {


}
```

In addition to not specifying a default value, you can also set an argument value to `NULL`.

Lazy Evaluation

Arguments to functions are evaluated *lazily*, so they are evaluated only as needed.

```
f <- function(a, b) {
    a^2
}
f(2)
```

```
## [1] 4
```

This function never actually uses the argument `b`, so calling `f(2)` will not produce an error because the 2 gets positionally matched to `a`.

Lazy Evaluation

```
f <- function(a, b) {
    print(a)
    print(b)
}
f(45)
```

```
## [1] 45
```

```
## Error: argument "b" is missing, with no default
```

Notice that “45” got printed first before the error was triggered. This is because `b` did not have to be evaluated until after `print(a)`. Once the function tried to evaluate `print(b)` it had to throw an error.

The "..." Argument

The ... argument indicate a variable number of arguments that are usually passed on to other functions.

- ... is often used when extending another function and you don't want to copy the entire argument list of the original function

```
myplot <- function(x, y, type = "l", ...) {
        plot(x, y, type = type, ...)
}
```

- Generic functions use ... so that extra arguments can be passed to methods (more on this later).

```
> mean
function (x, ...)
UseMethod("mean")
```

The "..." Argument

The ... argument is also necessary when the number of arguments passed to the function cannot be known in advance.

```
> args(paste)
function (..., sep = " ", collapse = NULL)

> args(cat)
function (..., file = "", sep = " ", fill = FALSE,
    labels = NULL, append = FALSE)
```

Arguments Coming After the "..." Argument

One catch with ... is that any arguments that appear *after* ... on the argument list must be named explicitly and cannot be partially matched.

```
> args(paste)
function (..., sep = " ", collapse = NULL)

> paste("a", "b", sep = ":")
[1] "a:b"

> paste("a", "b", se = ":")
[1] "a b :"
```

Introduction to the R Language

Scoping Rules

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A Diversion on Binding Values to Symbol

How does R know which value to assign to which symbol? When I type

```
> lm <- function(x) { x * x }
> lm
function(x) { x * x }
```

how does R know what value to assign to the symbol `lm`? Why doesn't it give it the value of `lm` that is in the *stats* package?

A Diversion on Binding Values to Symbol

When R tries to bind a value to a symbol, it searches through a series of `environments` to find the appropriate value. When you are working on the command line and need to retrieve the value of an R object, the order is roughly

1. Search the global environment for a symbol name matching the one requested.
2. Search the namespaces of each of the packages on the search list

The search list can be found by using the `search` function.

```
> search()
[1] ".GlobalEnv"        "package:stats"     "package:graphics"
[4] "package:grDevices" "package:utils"     "package:datasets"
[7] "package:methods"   "Autoloads"         "package:base"
```

Binding Values to Symbol

- The *global environment* or the user's workspace is always the first element of the search list and the *base* package is always the last.
- The order of the packages on the search list matters!
- User's can configure which packages get loaded on startup so you cannot assume that there will be a set list of packages available.
- When a user loads a package with `library` the namespace of that package gets put in position 2 of the search list (by default) and everything else gets shifted down the list.
- Note that R has separate namespaces for functions and non-functions so it's possible to have an object named c and a function named c.

Scoping Rules

The scoping rules for R are the main feature that make it different from the original S language.

- The scoping rules determine how a value is associated with a free variable in a function
- R uses *lexical scoping* or *static scoping*. A common alternative is *dynamic scoping*.
- Related to the scoping rules is how R uses the search *list* to bind a value to a symbol
- Lexical scoping turns out to be particularly useful for simplifying statistical computations

Lexical Scoping

Consider the following function.

```
f <- function(x, y) {
        x^2 + y / z
}
```

This function has 2 formal arguments `x` and `y`. In the body of the function there is another symbol `z`. In this case `z` is called a *free variable*. The scoping rules of a language determine how values are assigned to free variables. Free variables are not formal arguments and are not local variables (assigned insided the function body).

Lexical Scoping

Lexical scoping in R means that

the values of free variables are searched for in the environment in which the function was defined.

What is an environment?

- An *environment* is a collection of (symbol, value) pairs, i.e. `x` is a symbol and `3.14` might be its value.
- Every environment has a parent environment; it is possible for an environment to have multiple "children"
- the only environment without a parent is the empty environment
- A function + an environment = a *closure* or *function closure*.

Lexical Scoping

Searching for the value for a free variable:

- If the value of a symbol is not found in the environment in which a function was defined, then the search is continued in the *parent environment*.
- The search continues down the sequence of parent environments until we hit the *top-level environment*; this usually the global environment (workspace) or the namespace of a package.
- After the top-level environment, the search continues down the search list until we hit the *empty environment*. If a value for a given symbol cannot be found once the empty environment is arrived at, then an error is thrown.