# The R Inferno

Patrick Burns[1]

30th April 2011

[1]This document resides in the tutorial section of http://www.burns-stat.com. More elementary material on R may also be found there. S+ is a registered trademark of TIBCO Software Inc. The author thanks D. Alighieri for useful comments.

# Contents

# List of Figures

# List of Tables

# Preface

**Abstract:** If you are using R and you think you're in hell, this is a map for you.


WANDERED through
http://www.r-project.org.

To state the good I found there, I'll also say what else I saw.

Having abandoned the true way, I fell into a deep sleep and awoke in a deep dark wood. I set out to escape the wood, but my path was blocked by a lion. As I fled to lower ground, a figure appeared before me. "Have mercy on me, whatever you are," I cried, "whether shade or living human."

"Not a man, though once I was. My parents were from Lombardy. I was born *sub Julio* and lived in Rome in an age of false and lying gods."

"Are you Virgil, the fountainhead of such a volume?"

"I think it wise you follow me. I'll lead you through an eternal place where you shall hear despairing cries and see those ancient souls in pain as they grieve their second death."

After a journey, we arrived at an archway. Inscribed on it: "Through me the way into the suffering city, through me the way among the lost." Through the archway we went.

Now sighing and wails resounded through the starless air, so that I too began weeping. Unfamiliar tongues, horrendous accents, cries of rage—all of these whirled in that dark and timeless air.

# Circle 1

# Falling into the Floating Point Trap

Once we had crossed the Acheron, we arrived in the first Circle, home of the virtuous pagans. These are people who live in ignorance of the Floating Point Gods. These pagans expect

```
.1 == .3 / 3
```

to be true.

The virtuous pagans will also expect

```
seq(0, 1, by=.1) == .3
```

to have exactly one value that is true.

But *you* should not expect something like:

```
unique(c(.3, .4 - .1, .5 - .2, .6 - .3, .7 - .4))
```

to have length one.

I wrote my first program in the late stone age. The task was to program the quadratic equation. Late stone age means the medium of expression was punchcards. There is no backspace on a punchcard machine—once the holes are there, there's no filling them back in again. So a typo at the end of a line means that you have to throw the card out and start the line all over again. A procedure with which I became all too familiar.

Joy ensued at the end of the long ordeal of acquiring a pack of properly punched cards. Short-lived joy. The next step was to put the stack of cards into an in-basket monitored by the computer operator. Some hours later the (large) paper output from the job would be in a pigeonhole. There was of course an error in the program. After another struggle with the punchcard machine (relatively brief this time), the card deck was back in the in-basket.

It didn't take many iterations before I realized that it only ever told me about the *first* error it came to. Finally on the third day, the output featured no messages about errors. There was an answer—a *wrong* answer. It was a simple quadratic equation, and the answer was clearly 2 and 3. The program said it was 1.999997 and 3.000001. All those hours of misery and it can't even get the right answer.

I can write an R function for the quadratic formula somewhat quicker.

```
> quadratic.formula
function (a, b, c)
{
        rad <- b^2 - 4 * a * c
        if(is.complex(rad) || all(rad >= 0)) {
                rad <- sqrt(rad)
        } else {
                rad <- sqrt(as.complex(rad))
        }
        cbind(-b - rad, -b + rad) / (2 * a)
}
> quadratic.formula(1, -5, 6)
     [,1] [,2]
[1,]    2    3
> quadratic.formula(1, c(-5, 1), 6)
                [,1]           [,2]
[1,]  2.0+0.000000i  3.0+0.000000i
[2,] -0.5-2.397916i -0.5+2.397916i
```

It is more general than that old program, and more to the point it gets the right answer of 2 and 3. Except that it doesn't. R merely prints so that most numerical error is invisible. We can see how wrong it actually is by subtracting the right answer:

```
> quadratic.formula(1, -5, 6) - c(2, 3)
     [,1] [,2]
[1,]    0    0
```

Well okay, it gets the right answer in this case. But there *is* error if we change the problem a little:

```
> quadratic.formula(1/3, -5/3, 6/3)
     [,1] [,2]
[1,]    2    3
> print(quadratic.formula(1/3, -5/3, 6/3), digits=16)
[1,] 1.999999999999999 3.000000000000001
> quadratic.formula(1/3, -5/3, 6/3) - c(2, 3)
               [,1]         [,2]
[1,] -8.881784e-16 1.332268e-15
```

That R prints answers nicely is a blessing. And a curse. R is good enough at hiding numerical error that it is easy to forget that it is there. Don't forget.

Whenever floating point operations are done—even simple ones, you should assume that there will be numerical error. If by chance there is no error, regard that as a happy accident—not your due. You can use the `all.equal` function instead of `'=='` to test equality of floating point numbers.

If you have a case where the numbers are logically integer but they have been computed, then use `round` to make sure they really are integers.

Do not confuse numerical error with an error. An error is when a computation is wrongly performed. Numerical error is when there is visible noise resulting from the finite representation of numbers. It is numerical error—not an error—when one-third is represented as 33%.

We've seen another aspect of virtuous pagan beliefs—what is printed is all that there is.

```
> 7/13 - 3/31
[1] 0.4416873
```

R prints—by default—a handy abbreviation, not all that it knows about numbers:

```
> print(7/13 - 3/31, digits=16)
[1] 0.4416873449131513
```

Many summary functions are even more restrictive in what they print:

```
> summary(7/13 - 3/31)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.4417  0.4417  0.4417  0.4417  0.4417  0.4417
```

Numerical error from finite arithmetic can not only fuzz the answer, it can fuzz the question. In mathematics the rank of a matrix is some specific integer. In computing, the rank of a matrix is a vague concept. Since eigenvalues need not be clearly zero or clearly nonzero, the rank need not be a definite number.

We descended to the edge of the first Circle where Minos stands guard, gnashing his teeth. The number of times he wraps his tail around himself marks the level of the sinner before him.

# Circle 2

# Growing Objects

We made our way into the second Circle, here live the gluttons.

Let's look at three ways of doing the same task of creating a sequence of numbers. Method 1 is to grow the object:

```
vec <- numeric(0)
for(i in 1:n) vec <- c(vec, i)
```

Method 2 creates an object of the final length and then changes the values in the object by subscripting:

```
vec <- numeric(n)
for(i in 1:n) vec[i] <- i
```

Method 3 directly creates the final object:

```
vec <- 1:n
```

Table 2.1 shows the timing in seconds on a particular (old) machine of these three methods for a selection of values of $n$. The relationships for varying $n$ are all roughly linear on a log-log scale, but the timings are drastically different.

You may wonder why growing objects is so slow. It is the computational equivalent of suburbanization. When a new size is required, there will not be

Table 2.1: Time in seconds of methods to create a sequence.

| n | grow | subscript | colon operator |
|---|---|---|---|
| 1000 | 0.01 | 0.01 | .00006 |
| 10,000 | 0.59 | 0.09 | .0004 |
| 100,000 | 133.68 | 0.79 | .005 |
| 1,000,000 | 18,718 | 8.10 | .097 |

enough room where the object is; so it needs to move to a more open space. Then that space will be too small, and it will need to move again. It takes a lot of time to move house. Just as in physical suburbanization, growing objects can spoil all of the available space. You end up with lots of small pieces of available memory, but no large pieces. This is called fragmenting memory.

A more common—and probably more dangerous—means of being a glutton is with `rbind`. For example:

```
my.df <- data.frame(a=character(0), b=numeric(0))
for(i in 1:n) {
    my.df <- rbind(my.df, data.frame(a=sample(letters, 1),
        b=runif(1)))
}
```

Probably the main reason this is more common is because it is more likely that each iteration will have a different number of observations. That is, the code is more likely to look like:

```
my.df <- data.frame(a=character(0), b=numeric(0))
for(i in 1:n) {
    this.N <- rpois(1, 10)
    my.df <- rbind(my.df, data.frame(a=sample(letters,
        this.N, replace=TRUE), b=runif(this.N)))
}
```

Often a reasonable upper bound on the size of the final object is known. If so, then create the object with that size and then remove the extra values at the end. If the final size is a mystery, then you can still follow the same scheme, but allow for periodic growth of the object.

```
current.N <- 10 * n
my.df <- data.frame(a=character(current.N),
    b=numeric(current.N))
count <- 0
for(i in 1:n) {
    this.N <- rpois(1, 10)
    if(count + this.N > current.N) {
        old.df <- my.df
        current.N <- round(1.5 * (current.N + this.N))
        my.df <- data.frame(a=character(current.N),
            b=numeric(current.N))
        my.df[1:count,] <- old.df[1:count, ]
    }
    my.df[count + 1:this.N,] <- data.frame(a=sample(letters,
        this.N, replace=TRUE), b=runif(this.N))
    count <- count + this.N
}
my.df <- my.df[1:count,]
```

Figure 2.1: The giants by Sandro Botticelli.

Often there is a simpler approach to the whole problem—build a list of pieces and then scrunch them together in one go.

```
my.list <- vector('list', n)
for(i in 1:n) {
   this.N <- rpois(1, 10)
   my.list[[i]] <- data.frame(a=sample(letters, this.N
       replace=TRUE), b=runif(this.N))
}
my.df <- do.call('rbind', my.list)
```

There are ways of cleverly hiding that you are growing an object. Here is an example:

```
hit <- NA
for(i in 1:one.zillion) {
    if(runif(1) < 0.3) hit[i] <- TRUE
}
```

Each time the condition is true, `hit` is grown.

Eliminating the growth of objects can be one of the easiest and most dramatic ways of speeding up R code.

If you use too much memory, R will complain. The key issue is that R holds all the data in RAM. This is a limitation if you have huge datasets. The up-side is flexibility—in particular, R imposes no rules on what data are like.

You can get a message, all too familiar to some people, like:

```
Error: cannot allocate vector of size 79.8 Mb.
```

This is often misinterpreted along the lines of: "I have xxx gigabytes of memory, why can't R even allocate 80 megabytes?" It is because R has already allocated a lot of memory successfully. The error message is about how much memory R was going after at the point where it failed.

The user who has seen this message logically asks, "What can I do about it?" There are some easy answers:

1. Don't be a glutton by using bad programming constructs.
2. Get a bigger computer.
3. Reduce the problem size.

If you've obeyed the first answer and can't follow the second or third, then your alternatives are harder. One is to restart the R session, but this is often ineffective.

Another of those hard alternatives is to explore where in your code the memory is growing. One method (on at least one platform) is to insert lines like:

```
cat('point 1 mem', memory.size(), memory.size(max=TRUE), '\n')
```

throughout your code. This shows the memory that R currently has and the maximum amount R has had in the current session.

However, probably a more efficient and informative procedure would be to use Rprof with memory profiling. Rprof also profiles time use.

Another way of reducing memory use is to store your data in a database and only extract portions of the data into R as needed. While this takes some time to set up, it can become quite a natural way to work.

A "database" solution that only uses R is to save (as in the `save` function) objects in individual files, then use the files one at a time. So your code using the objects might look something like:

```
for(i in 1:n) {
   objname <- paste('obj.', i, sep='')
   load(paste(objname, '.rda', sep=''))
   the_obj <- get(objname)
   rm(list=objname)
   # use the_obj
}
```

Are tomorrow's bigger computers going to solve the problem? For some people, yes—their data will stay the same size and computers will get big enough to hold it comfortably. For other people it will only get worse—more powerful computers means extraordinarily larger datasets. If you are likely to be in this latter group, you might want to get used to working with databases now.

If you have one of those giant computers, you may have the capacity to attempt to create something larger than R can handle. See:

```
?'Memory-limits'
```

for the limits that are imposed.

# Circle 3

# Failing to Vectorize

We arrive at the third Circle, filled with cold, unending rain. Here stands Cerberus barking out of his three throats. Within the Circle were the blasphemous wearing golden, dazzling cloaks that inside were all of lead—weighing them down for all of eternity. This is where Virgil said to me, "Remember your science—the more perfect a thing, the more its pain or pleasure."

Here is some sample code:

```
lsum <- 0
for(i in 1:length(x)) {
   lsum <- lsum + log(x[i])
}
```

No. No. No.

This is speaking R with a C accent—a strong accent. We can do the same thing much simpler:

```
lsum <- sum(log(x))
```

This is not only nicer for your carpal tunnel, it is computationally much faster. (As an added bonus it avoids the bug in the loop when `x` has length zero.)

The command above works because of vectorization. The `log` function is vectorized in the traditional sense—it does the same operation on a vector of values as it would do on each single value. That is, the command:

```
log(c(23, 67.1))
```

has the same result as the command:

```
c(log(23), log(67.1))
```

The `sum` function is vectorized in a quite different sense—it takes a vector and produces something based on the whole vector. The command `sum(x)` is equivalent to:

```
x[1] + x[2] + ... + x[length(x)]
```

The `prod` function is similar to `sum`, but does products rather than sums. Products can often overflow or underflow (a suburb of Circle 1)—taking logs and doing sums is generally a more stable computation.

You often get vectorization for free. Take the example of `quadratic.formula` in Circle 1 (page 9). Since the arithmetic operators are vectorized, the result of this function is a vector if any or all of the inputs are. The only slight problem is that there are two answers per input, so the call to `cbind` is used to keep track of the pairs of answers.

In binary operations such as:

```
c(1,4) + 1:10
```

recycling automatically happens along with the vectorization.

Here is some code that combines both this Circle and Circle 2 (page 12):

```
ans <- NULL
for(i in 1:507980) {
   if(x[i] < 0) ans <- c(ans, y[i])
}
```

This can be done simply with:

```
ans <- y[x < 0]
```

A double `for` loop is often the result of a function that has been directly translated from another language. Translations that are essentially verbatim are unlikely to be the best thing to do. Better is to rethink what is happening with R in mind. Using direct translations from another language may well leave you longing for that other language. Making good translations may well leave you marvelling at R's strengths. (The catch is that you need to know the strengths in order to make the good translations.)

If you are translating code into R that has a double `for` loop, think.

If your function is not vectorized, then you can possibly use the `Vectorize` function to make a vectorized version. But this is vectorization from an external point of view—it is not the same as writing inherently vectorized code. The `Vectorize` function performs a loop using the original function.

Some functions take a function as an argument and demand that the function be vectorized—these include `outer` and `integrate`.

There is another form of vectorization:

```
> max(2, 100, -4, 3, 230, 5)
[1] 230
> range(2, 100, -4, 3, 230, 5, c(4, -456, 9))
[1] -456 230
```

Figure 3.1: The hypocrites by Sandro Botticelli.

This form of vectorization is to treat the collection of arguments as the vector. This is NOT a form of vectorization you should expect, it is essentially foreign to R—`min`, `max`, `range`, `sum` and `prod` are rare exceptions. In particular, `mean` does not adhere to this form of vectorization, and unfortunately does not generate an error from trying it:

```
> mean(2, -100, -4, 3, -230, 5)
[1] 2
```

But you get the correct answer if you add three (particular) keystrokes:

```
> mean(c(2, -100, -4, 3, -230, 5))
[1] -54
```

One reason for vectorization is for computational speed. In a vector operation there is always a loop. If the loop is done in C code, then it will be much faster than if it is done in R code. In some cases, this can be very important. In other cases, it isn't—a loop in R code now is as fast as the same loop in C on a computer from a few years ago.

Another reason to vectorize is for clarity. The command:

```
volume <- width * depth * height
```

Table 3.1: Summary of subscripting with `[`.

| subscript | effect |
|---|---|
| positive numeric vector | selects items with those indices |
| negative numeric vector | selects all but those indices |
| character vector | selects items with those names (or dimnames) |
| logical vector | selects the `TRUE` (and `NA`) items |
| missing | selects all |

clearly expresses the relation between the variables. This same clarity is present whether there is one item or a million. Transparent code is an important form of efficiency. Computer time is cheap, human time (and frustration) is expensive. This fact is enshrined in the maxim of Uwe Ligges.

**Uwe's Maxim Computers are cheap, and thinking hurts.**

A fairly common question from new users is: "How do I assign names to a group of similar objects?" Yes, you can do that, but you probably don't want to—better is to vectorize your thinking. Put all of the similar objects into one list. Subsequent analysis and manipulation is then going to be much smoother.

## 3.1 Subscripting

Subscripting in R is extremely powerful, and is often a key part of effective vectorization. Table 3.1 summarizes subscripting.

The dimensions of arrays and data frames are subscripted independently.

Arrays (including matrices) can be subscripted with a matrix of positive numbers. The subscripting matrix has as many columns as there are dimensions in the array—so two columns for a matrix. The result is a vector (not an array) containing the selected items.

Lists are subscripted just like (other) vectors. However, there are two forms of subscripting that are particular to lists: `$` and `[[`. These are almost the same, the difference is that `$` expects a name rather than a character string.

```
> mylist <- list(aaa=1:5, bbb=letters)
> mylist$aaa
[1] 1 2 3 4 5
> mylist[['aaa']]
[1] 1 2 3 4 5
> subv <- 'aaa'; mylist[[subv]]
[1] 1 2 3 4 5
```

You shouldn't be too surprised that I just lied to you. Subscripting with `[[` can be done on atomic vectors as well as lists. It can be the safer option when

a single item is demanded. If you are using `[[` and you want more than one item, you are going to be disappointed.

We've already seen (in the `lsum` example) that subscripting can be a symptom of not vectorizing.

As an example of how subscripting can be a vectorization tool, consider the following problem: We have a matrix `amat` and we want to produce a new matrix with half as many rows where each row of the new matrix is the product of two consecutive rows of `amat`.

It is quite simple to create a loop to do this:

```
bmat <- matrix(NA, nrow(amat)/2, ncol(amat))
for(i in 1:nrow(bmat)) bmat[i,] <- amat[2*i-1,] * amat[2*i,]
```

Note that we have avoided Circle 2 (page 12) by preallocating `bmat`.

Later iterations do not depend on earlier ones, so there is hope that we can eliminate the loop. Subscripting is the key to the elimination:

```
> bmat2 <- amat[seq(1, nrow(amat), by=2),] *
+     amat[seq(2, nrow(amat), by=2),]
> all.equal(bmat, bmat2)
[1] TRUE
```

## 3.2 Vectorized if

Here is some code:

```
if(x < 1) y <- -1 else y <- 1
```

This looks perfectly logical. And if `x` has length one, then it does as expected. However, if `x` has length greater than one, then a warning is issued (often ignored by the user), and the result is not what is most likely intended. Code that fulfills the common expectation is:

```
y <- ifelse(x < 1, -1, 1)
```

Another approach—assuming `x` is never exactly 1—is:

```
y <- sign(x - 1)
```

This provides a couple of lessons:

1. The condition in `if` is one of the few places in R where a vector (of length greater than 1) is not welcome (`the` `:` operator is another).
2. `ifelse` is what you want in such a situation (though, as in this case, there are often more direct approaches).

Recall that in Circle 2 (page 12) we saw:

```
hit <- NA
for(i in 1:one.zillion) {
    if(runif(1) < 0.3) hit[i] <- TRUE
}
```

One alternative to make this operation efficient is:

```
ifelse(runif(one.zillion) < 0.3, TRUE, NA)
```

If there is a mistake between `if` and `ifelse`, it is almost always trying to use `if` when `ifelse` is appropriate. But ingenuity knows no bounds, so it is also possible to try to use `ifelse` when `if` is appropriate. For example:

```
ifelse(x, character(0), '')
```

The result of `ifelse` is ALWAYS the length of its first (formal) argument. Assuming that `x` is of length 1, the way to get the intended behavior is:

```
if(x) character(0) else ''
```

Some more caution is warranted with `ifelse`: the result gets not only its length from the first argument, but also its attributes. If you would like the answer to have attributes of the other two arguments, you need to do more work. In Circle 8.2.7 we'll see a particular instance of this with factors.

## 3.3 Vectorization impossible

Some things are not possible to vectorize. For instance, if the present iteration depends on results from the previous iteration, then vectorization is usually not possible. (But some cases are covered by `filter`, `cumsum`, etc.)

If you need to use a loop, then make it lean:

- Put as much outside of loops as possible. One example: if the same or a similar sequence is created in each iteration, then create the sequence first and reuse it. Creating a sequence is quite fast, but appreciable time can accumulate if it is done thousands or millions of times.
- Make the number of iterations as small as possible. If you have the choice of iterating over the elements of a factor or iterating over the levels of the factor, then iterating over the levels is going to be better (almost surely).

The following bit of code gets the sum of each column of a matrix (assuming the number of columns is positive):

```
sumxcol <- numeric(ncol(x))
for(i in 1:ncol(x)) sumxcol[i] <- sum(x[,i])
```

A more common approach to this would be:

```
sumxcol <- apply(x, 2, sum)
```

Since this is a quite common operation, there is a special function for doing this that does not involve a loop in R code:

```
sumxcol <- colSums(x)
```

There are also `rowSums`, `colMeans` and `rowMeans`.

Another approach is:

```
sumxcol <- rep(1, nrow(x)) %*% x
```

That is, using matrix multiplication. With a little ingenuity a lot of problems can be cast into a matrix multiplication form. This is generally quite efficient relative to alternatives.

# Circle 4

# Over-Vectorizing

We skirted past Plutus, the fierce wolf with a swollen face, down into the fourth Circle. Here we found the lustful.

It is a good thing to want to vectorize when there is no effective way to do so. It is a bad thing to attempt it anyway.

A common reflex is to use a function in the apply family. This is not vectorization, it is loop-hiding. The `apply` function has a `for` loop in its definition. The `lapply` function buries the loop, but execution times tend to be roughly equal to an explicit `for` loop. (Confusion over this is understandable, as there is a significant difference in execution speed with at least some versions of S+.) Table 4.1 summarizes the uses of the apply family of functions.

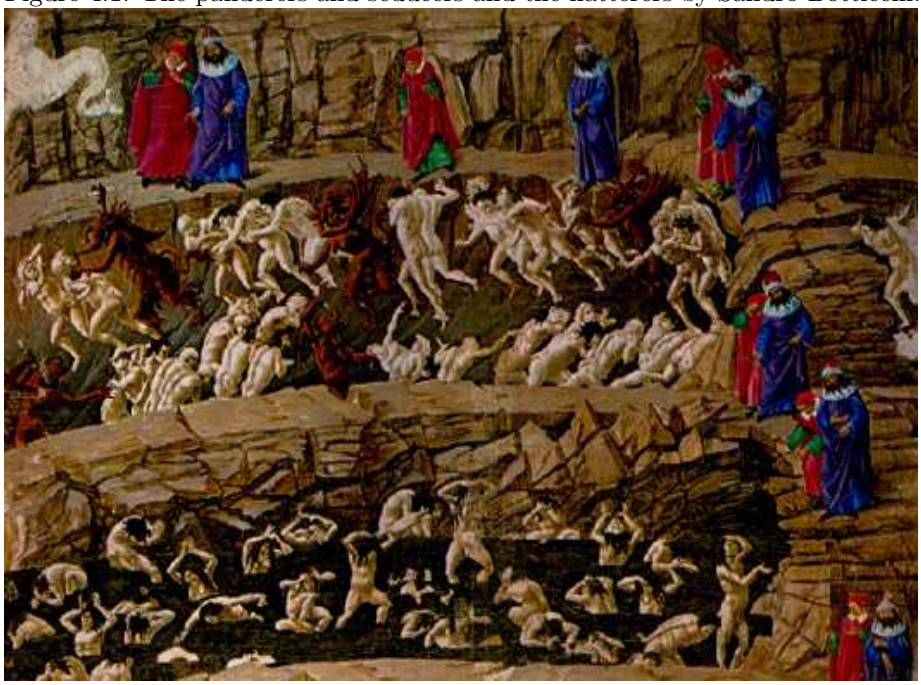
Base your decision of using an apply function on Uwe's Maxim (page 20). The issue is of human time rather than silicon chip time. Human time can be wasted by taking longer to write the code, and (often much more importantly) by taking more time to understand subsequently what it does.

A command applying a complicated function is unlikely to pass the test.

Table 4.1: The apply family of functions.

| function | input | output | comment |
|---|---|---|---|
| `apply` | matrix or array | vector or array or list | |
| `lapply` | list or vector | list | |
| `sapply` | list or vector | vector or matrix or list | simplify |
| `vapply` | list or vector | vector or matrix or list | safer simplify |
| `tapply` | data, categories | array or list | ragged |
| `mapply` | lists and/or vectors | vector or matrix or list | multiple |
| `rapply` | list | vector or list | recursive |
| `eapply` | environment | list | |
| `dendrapply` | dendogram | dendogram | |
| `rollapply` | data | similar to input | package `zoo` |

Figure 4.1: The panderers and seducers and the flatterers by Sandro Botticelli.



Use an explicit `for` loop when each iteration is a non-trivial task. But a simple loop can be more clearly and compactly expressed using an apply function.

There is at least one exception to this rule. We will see in Circle 8.1.56 that if the result will be a list and some of the components can be `NULL`, then a `for` loop is trouble (big trouble) and `lapply` gives the expected answer.

The `tapply` function applies a function to each bit of a partition of the data. Alternatives to `tapply` are `by` for data frames, and `aggregate` for time series and data frames. If you have a substantial amount of data and speed is an issue, then `data.table` may be a good solution.

Another approach to over-vectorizing is to use too much memory in the process. The `outer` function is a wonderful mechanism to vectorize some problems. It is also subject to using a lot of memory in the process.

Suppose that we want to find all of the sets of three positive integers that sum to 6, where the order matters. (This is related to partitions in number theory.) We can use `outer` and `which`:

```
the.seq <- 1:4
which(outer(outer(the.seq, the.seq, '+'), the.seq, '+') == 6,
      arr.ind=TRUE)
```

This command is nicely vectorized, and a reasonable solution to this particular

problem. However, with larger problems this could easily eat all memory on a machine.

Suppose we have a data frame and we want to change the missing values to zero. Then we can do that in a perfectly vectorized manner:

```
x[is.na(x)] <- 0
```

But if x is large, then this may take a lot of memory. If—as is common—the number of rows is much larger than the number of columns, then a more memory efficient method is:

```
for(i in 1:ncol(x)) x[is.na(x[,i]), i] <- 0
```

Note that "large" is a relative term; it is usefully relative to the amount of available memory on your machine. Also note that memory efficiency can also be time efficiency if the inefficient approach causes swapping.

One more comment: if you really want to change `NA`s to 0, perhaps you should rethink what you are doing—the new data are fictional.

It is not unusual for there to be a tradeoff between space and time.

Beware the dangers of premature optimization of your code. Your first duty is to create clear, correct code. Only consider optimizing your code when:

- Your code is debugged and stable.
- Optimization is likely to make a significant impact. Spending an hour or two to save a millisecond a month is not best practice.

# Circle 5

# Not Writing Functions

We came upon the River Styx, more a swamp really. It took some convincing, but Phlegyas eventually rowed us across in his boat. Here we found the treasoners.

## 5.1 Abstraction

A key reason that R is a good thing is because it is a language. The power of language is abstraction. The way to make abstractions in R is to write functions.

Suppose we want to repeat the integers 1 through 3 twice. That's a simple command:

```
c(1:3, 1:3)
```

Now suppose we want these numbers repeated six times, or maybe sixty times. Writing a function that abstracts this operation begins to make sense. In fact, that abstraction has already been done for us:

```
rep(1:3, 6)
```

The `rep` function performs our desired task and a number of similar tasks.

Let's do a new task. We have two vectors; we want to produce a single vector consisting of the first vector repeated to the length of the second and then the second vector repeated to the length of the first. A vector being repeated to a shorter length means to just use the first part of the vector. This is quite easily abstracted into a function that uses `rep`:

```
repeat.xy <- function(x, y)
{
    c(rep(x, length=length(y)), rep(y, length=length(x)))
}
```

The `repeat.xy` function can now be used in the same way as if it came with R.

```
repeat.xy(1:4, 6:16)
```

The ease of writing a function like this means that it is quite natural to move gradually from just using R to programming in R.

In addition to abstraction, functions crystallize knowledge. That $\pi$ is approximately 3.14159265358979323846264338327950288419716939937510582097494459230 78 is knowledge.

The function:

```
circle.area <- function(r) pi * r ^ 2
```

is both knowledge and abstraction—it gives you the (approximate) area for whatever circles you like.

This is not the place for a full discussion on the structure of the R language, but a comment on a detail of the two functions that we've just created is in order. The statement in the body of `repeat.xy` is surrounded by curly braces while the statement in the body of `circle.area` is not. The body of a function needs to be a single expression. Curly braces turn a number of expressions into a single (combined) expression. When there is only a single command in the body of a function, then the curly braces are optional. Curly braces are also useful with loops, `switch` and `if`.

Ideally each function performs a clearly specified task with easily understood inputs and return value. Very common novice behavior is to write one function that does everything. Almost always a better approach is to write a number of smaller functions, and then a function that does everything by using the smaller functions. Breaking the task into steps often has the benefit of making it more clear what really should be done. It is also much easier to debug when things go wrong.[1] The small functions are much more likely to be of general use.

A nice piece of abstraction in R functions is default values for arguments. For example, the `na.rm` argument to `sd` has a default value of `FALSE`. If that is okay in a particular instance, then you don't have to specify `na.rm` in your call. If you want to remove missing values, then you should include `na.rm=TRUE` as an argument in your call. If you create your own copy of a function just to change the default value of an argument, then you're probably not appreciating the abstraction that the function gives you.

Functions return a value. The return value of a function is almost always the reason for the function's existence. The last item in a function definition is returned. Most functions merely rely on this mechanism, but the `return` function forces what to return.

The other thing that a function can do is to have one or more side effects. A side effect is some change to the system other than returning a value. The philosophy of R is to concentrate side effects into a few functions (such as `print`, `plot` and `rm`) where it is clear that a side effect is to be expected.

[1] Notice "when" not "if".

Table 5.1: Simple objects.

| object | type | examples |
|---|---|---|
| logical | atomic | `TRUE FALSE NA` |
| numeric | atomic | `0 2.2 pi NA Inf -Inf NaN` |
| complex | atomic | `3.2+4.5i NA Inf NaN` |
| character | atomic | `'hello world' '' NA` |
| list | recursive | `list(1:3, b='hello', C=list(3, c(TRUE, NA)))` |
| NULL | | `NULL` |
| function | | `function(x, y) x + 2 * y` |
| formula | | `y ~ x` |

Table 5.2: Some not so simple objects.

| object | primary | attributes | comment |
|---|---|---|---|
| data frame | list | `class row.names` | a generalized matrix |
| matrix | vector | `dim dimnames` | special case of array |
| array | vector | `dim dimnames` | usually atomic, not always |
| factor | integer | `levels class` | tricky little devils |

The things that R functions talk about are objects. R is rich in objects. Table 5.1 shows some important types of objects.

You'll notice that each of the atomic types have a possible value `NA`, as in "Not Available" and called "missing value". When some people first get to R, they spend a lot of time trying to get rid of `NA`s. People probably did the same sort of thing when zero was first invented. `NA` is a wonderful thing to have available to you. It is seldom pleasant when your data have missing values, but life is much better with `NA` than without.

R was designed with the idea that nothing is important. Let's try that again: "nothing" is important. Vectors can have length zero. This is another stupid thing that turns out to be incredibly useful—that is, not so stupid after all. We're not so used to dealing with things that aren't there, so sometimes there are problems—we'll see examples in Circle 8, Circle 8.1.15 for instance.

A lot of the wealth of objects has to do with attributes. Many attributes change how the object is thought about (both by R and by the user). An attribute that is common to most objects is `names`. The attribute that drives object orientation is `class`. Table 5.2 lists a few of the most important types of objects that depend on attributes. Formulas, that were listed in the simple table, have class `"formula"` and so might more properly be in the not-so-simple list.

A common novice problem is to think that a data frame is a matrix. They look the same. They are not that same. See, for instance, Circle 8.2.37.

The word "vector" has a number of meanings in R:

1. an atomic object (as opposed to a list). This is perhaps the most common

usage.

2. an object with no attributes (except possibly `names`). This is the definition implied by `is.vector` and `as.vector`.

3. an object that can have an arbitrary length (includes lists).

Clearly definitions 1 and 3 are contradictory, but which meaning is implied should be clear from the context. When the discussion is of vectors as opposed to matrices, it is definition 2 that is implied.

The word "list" has a technical meaning in R—this is an object of arbitrary length that can have components of different types, including lists. Sometimes the word is used in a non-technical sense, as in "search list" or "argument list".

Not all functions are created equal. They can be conveniently put into three types.

There are anonymous functions as in:

```
apply(x, 2, function(z) mean(z[z > 0]))
```

The function given as the third argument to `apply` is so transient that we don't even give it a name.

There are functions that are useful only for one particular project. These are your one-off functions.

Finally there are functions that are persistently valuable. Some of these could well be one-off functions that you have rewritten to be more abstract. You will most likely want a file or package containing your persistently useful functions.

In the example of an anonymous function we saw that a function can be an argument to another function. In R, functions are objects just as vectors or matrices are objects. You are allowed to think of functions as data.

A whole new level of abstraction is a function that returns a function. The empirical cumulative distribution function is an example:

```
> mycumfun <- ecdf(rnorm(10))
> mycumfun(0)
[1] 0.4
```

Once you write a function that returns a function, you will be forever immune to this Circle.

In Circle 2 (page 12) we briefly met `do.call`. Some people are quite confused by `do.call`. That is both unnecessary and unfortunate—it is actually quite simple and is very powerful. Normally a function is called by following the name of the function with an argument list:

```
sample(x=10, size=5)
```

The `do.call` function allows you to provide the arguments as an actual list:

```
do.call("sample", list(x=10, size=5))
```

Simple.

At times it is useful to have an image of what happens when you call a function. An environment is created by the function call, and an environment is created for each function that is called by that function. So there is a stack of environments that grows and shrinks as the computation proceeds.

Let's define some functions:

```
ftop <- function(x)
{
   # time 1
   x1 <- f1(x)
   # time 5
   ans.top <- f2(x1)
   # time 9
   ans.top
}
f1 <- function(x)
{
   # time 2
   ans1 <- f1.1(x)
   # time 4
   ans1
}
f2 <- function(x)
{
   # time 6
   ans2 <- f2.1(x)
   # time 8
   ans2
}
```

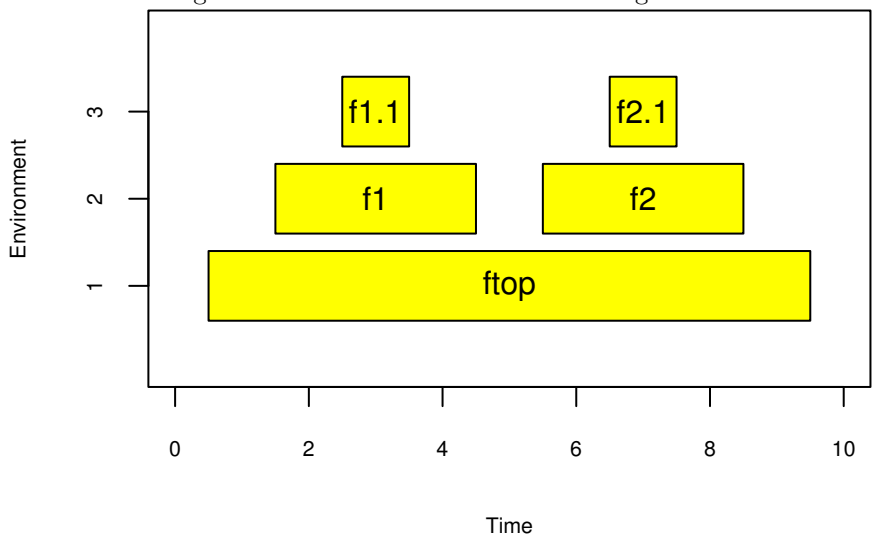
And now let's do a call:

```
# time 0
ftop(myx)
# time 10
```

Figure 5.1 shows how the stack of environments for this call changes through time. Note that there is an `x` in the environments for `ftop`, `f1` and `f2`. The `x` in `ftop` is what we call `myx` (or possibly a copy of it) as is the `x` in `f1`. But the `x` in `f2` is something different.

When we discuss debugging, we'll be looking at this stack at a specific point in time. For instance, if an error occurred in `f2.1`, then we would be looking at the state of the stack somewhere near time 7.

Figure 5.1: Stack of environments through time.




R is a language rich in objects. That is a part of its strength. Some of those objects are elements of the language itself—calls, expressions and so on. This allows a very powerful form of abstraction often called computing on the language. While messing with language elements seems extraordinarily esoteric to almost all new users, a lot of people moderate that view.

## 5.2 Simplicity

Make your functions as simple as possible. Simple has many advantages:

- Simple functions are likely to be human efficient: they will be easy to understand and to modify.
- Simple functions are likely to be computer efficient.
- Simple functions are less likely to be buggy, and bugs will be easier to fix.
- (Perhaps ironically) simple functions may be more general—thinking about the heart of the matter often broadens the application.

If your solution seems overly complex for the task, it probably is. There may be simple problems for which R does not have a simple solution, but they are rare.

Here are a few possibilities for simplifying:

- Don't use a list when an atomic vector will do.

- Don't use a data frame when a matrix will do.
- Don't try to use an atomic vector when a list is needed.
- Don't try to use a matrix when a data frame is needed.

Properly formatting your functions when you write them should be standard practice. Here "proper" includes indenting based on the logical structure, and putting spaces between operators. Circle 8.1.30 shows that there is a particularly good reason to put spaces around logical operators.

A semicolon can be used to mark the separation of two R commands that are placed on the same line. Some people like to put semicolons at the end of all lines. This highly annoys many seasoned R users. Such a reaction seems to be more visceral than logical, but there is some logic to it:

- The superfluous semicolons create some (imperceptible) inefficiency.
- The superfluous semicolons give the false impression that they are doing something.

One reason to seek simplicity is speed. The `Rprof` function is a very convenient means of exploring which functions are using the most time in your function calls. (The name `Rprof` refers to time profiling.)

## 5.3 Consistency

Consistency is good. Consistency reduces the work that your users need to expend. Consistency reduces bugs.

One form of consistency is the order and names of function arguments. Surprising your users is not a good idea—even if the universe of your users is of size 1.

A rather nice piece of consistency is always giving the correct answer. In order for that to happen the inputs need to be suitable. To insure that, the function needs to check inputs, and possibly intermediate results. The tools for this job include `if`, `stop` and `stopifnot`.

Sometimes an occurrence is suspicious but not necessarily wrong. In this case a warning is appropriate. A warning produces a message but does not interrupt the computation.

There is a problem with warnings. No one reads them. People have to read error messages because no food pellet falls into the tray after they push the button. With a warning the machine merely beeps at them but they still get their food pellet. Never mind that it might be poison.

The appropriate reaction to a warning message is:

1. Figure out what the warning is saying.

2. Figure out why the warning is triggered.
3. Figure out the effect on the results of the computation (via deduction or experimentation).
4. Given the result of step 3, decide whether or not the results will be erroneous.

You want there to be a minimal amount of warning messages in order to increase the probability that the messages that are there will be read. If you have a complex function where a large number of suspicious situations is possible, you might consider providing the ability to turn off some warning messages. Without such a system the user may be expecting a number of warning messages and hence miss messages that are unexpected and important.

The `suppressWarnings` function allows you to suppress warnings from specific commands:

```
> log(c(3, -1))
[1] 1.098612 NaN
Warning message:
In log(c(3, -1)) : NaNs produced
> suppressWarnings(log(c(3, -1)))
[1] 1.098612 NaN
```

We want our functions to be correct. Not all functions *are* correct. The results from specific calls can be put into 4 categories:

1. Correct.
2. An error occurs that is clearly identified.
3. An obscure error occurs.
4. An incorrect value is returned.

We like category 1. Category 2 is the right behavior if the inputs do not make sense, but not if the inputs are sensible. Category 3 is an unpleasant place for your users, and possibly for you if the users have access to you. Category 4 is by far the worst place to be—the user has no reason to believe that anything is wrong. Steer clear of category 4.

You should consistently write a help file for each of your persistent functions. If you have a hard time explaining the inputs and/or outputs of the function, then you should change the function. Writing a good help file is an excellent way of debugging the function. The `prompt` function will produce a template for your help file.

An example is worth a thousand words, so include examples in your help files. Good examples are gold, but any example is much better than none. Using data from the `datasets` package allows your users to run the examples easily.

# Circle 6

# Doing Global Assignments

Heretics imprisoned in flaming tombs inhabit Circle 6.

A global assignment can be performed with `'<<-'`:

```
> x <- 1
> y <- 2
> fun
function () {
   x <- 101
   y <<- 102
}
> fun()
> x
[1] 1
> y
[1] 102
```

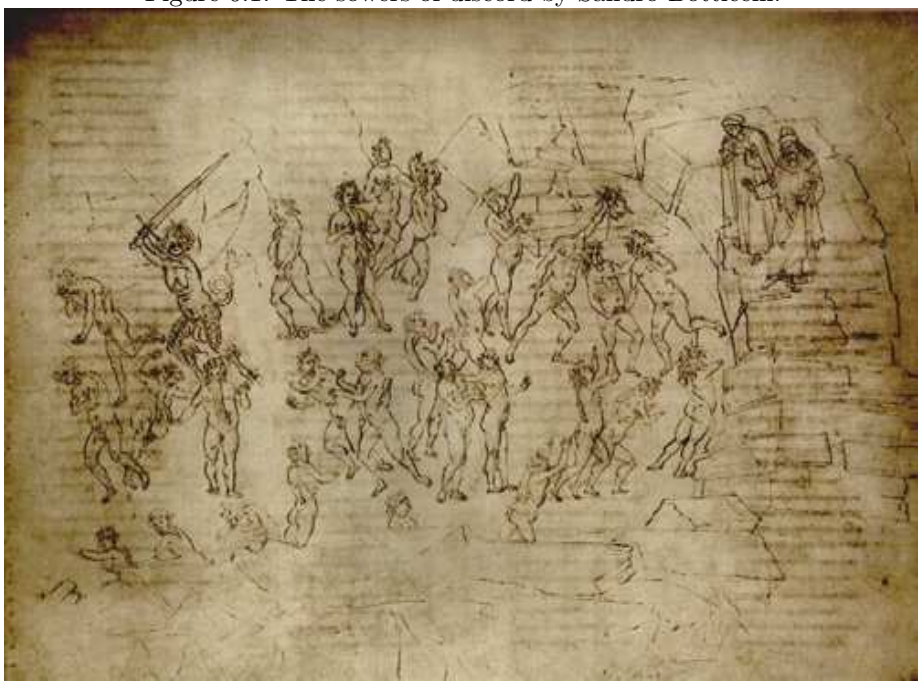
This is life beside a volcano.

If you think you need `'<<-'`, think again. If on reflection you still think you need `'<<-'`, think again. Only when your boss turns red with anger over you not doing anything should you temporarily give in to the temptation. There have been proposals (no more than half-joking) to eliminate `'<<-'` from the language. That would not eliminate global assignments, merely force you to use the `assign` function to achieve them.

What's so wrong about global assignments? Surprise.
Surprise in movies and novels is good. Surprise in computer code is bad.

Except for a few functions that clearly have side effects, it is expected in R that a function has no side effects. A function that makes a global assignment violates this expectation. To users unfamiliar with the code (and even to the writer of the code after a few weeks) there will be an object that changes seemingly by magic.

Figure 6.1: The sowers of discord by Sandro Botticelli.



A particular case where global assignment is useful (and not so egregious) is in memoization. This is when the results of computations are stored so that if the same computation is desired later, the value can merely be looked up rather than recomputed. The global variable is not so worrisome in this case because it is not of direct interest to the user. There remains the problem of name collisions—if you use the same variable name to remember values for two different functions, disaster follows.

In R we can perform memoization by using a locally global variable. ("locally global" is meant to be a bit humorous, but it succinctly describes what is going on.) In this example of computing Fibonacci numbers, we are using the `<<-` operator but using it safely:

```
fibonacci <- local({
   memo <- c(1, 1, rep(NA, 100))
   f <- function(x) {
      if(x == 0) return(0)
      if(x < 0) return(NA)
      if(x > length(memo))
         stop("'x' too big for implementation")
      if(!is.na(memo[x])) return(memo[x])
      ans <- f(x-2) + f(x-1)
      memo[x] <<- ans
```

```
        ans
    }
})
```

So what is this mumbo jumbo saying? We have a function that is just implementing memoization in the naive way using the `'<<-'` operator. But we are hiding the memo object in the environment local to the function. And why is `fibonacci` a function? The return value of something in curly braces is whatever is last. When defining a function we don't generally name the object we are returning, but in this case we need to name the function because it is used recursively.

Now let's use it:

```
> fibonacci(4)
[1] 3
> head(get('memo', envir=environment(fibonacci)))
[1] 1 1 2 3 NA NA
```

From computing the Fibonacci number for 4, the third and fourth elements of `memo` have been filled in. These values will not need to be computed again, a mere lookup suffices.

R always passes by value. It never passes by reference.

There are two types of people: those who understand the preceding paragraph and those who don't.

If you don't understand it, then R is right for you—it means that R is a safe place (notwithstanding the load of things in this document suggesting the contrary). Translated into humanspeak it essentially says that it is dreadfully hard to corrupt data in R. But ingenuity knows no bounds ...

If you do understand the paragraph in question, then you've probably already caught on that the issue is that R is heavily influenced by functional programming—side effects are minimized. You may also worry that this implies hideous memory inefficiency. Well, of course, the paragraph in question is a lie. If it were literally true, then objects (which may be very large) would always be copied when they are arguments to functions. In fact, R attempts to only copy objects when it is necessary, such as when the object is changed inside the function. The paragraph is conceptually true, but not literally true.

# Circle 7

# Tripping on Object Orientation

We came upon a sinner in the seventh Circle. He said, "Below my head is the place of those who took to simony before me—they are stuffed into the fissures of the stone." Indeed, with flames held to the soles of their feet.

It turns out that versions of S (of which R is a dialect) are color-coded by the cover of books written about them. The books are: the brown book, the blue book, the white book and the green book.

## 7.1 S3 methods

S3 methods correspond to the white book.

The concept in R of attributes of an object allows an exceptionally rich set of data objects. S3 methods make the `class` attribute the driver of an object-oriented system. It is an optional system. Only if an object has a `class` attribute do S3 methods really come into effect.

There are some functions that are *generic*. Examples include `print`, `plot`, `summary`. These functions look at the class attribute of their first argument. If that argument does have a class attribute, then the generic function looks for a *method* of the generic function that matches the class of the argument. If such a match exists, then the method function is used. If there is no matching method or if the argument does not have a class, then the default method is used.

Let's get specific. The `lm` (linear model) function returns an object of class `"lm"`. Among the methods for `print` are `print.lm` and `print.default`. The result of a call to `lm` is printed with `print.lm`. The result of `1:10` is printed with `print.default`.

S3 methods are simple and powerful. Objects are printed and plotted and summarized appropriately, with no effort from the user. The user only needs to know `print`, `plot` and `summary`.

There is a cost to the free lunch. That `print` is generic means that what you see is not what you get (sometimes). In the printing of an object you may see a number that you want—an R-squared for example—but don't know how to grab that number. If your mystery number is in `obj`, then there are a few ways to look for it:

```
print.default(obj)
print(unclass(obj))
str(obj)
```

The first two print the object as if it had no class, the last prints an outline of the structure of the object. You can also do:

```
names(obj)
```

to see what components the object has—this can give you an overview of the object.

### 7.1.1 generic functions

Once upon a time a new user was appropriately inquisitive and wanted to know how the median function worked. So, logically, the new user types the function name to see it:

```
> median
function (x, na.rm = FALSE)
UseMethod("median")
<environment: namespace:stats>
```

The new user then asks, "How can I find the code for `median`?"

The answer is, "You *have* found the code for `median`." `median` is a generic function as evidenced by the appearance of `UseMethod`. What the new user meant to ask was, "How can I find the default method for `median`?"

The most sure-fire way of getting the method is to use `getS3method`:

```
getS3method('median', 'default')
```

### 7.1.2 methods

The `methods` function lists the methods of a generic function. Alternatively given a class it returns the generic functions that have methods for the class. This statement needs a bit of qualification:

- It is listing what is currently attached in the session.
- It is looking at names—it will list objects in the format of *generic.class*. It is reasonably smart, but it can be fooled into listing an object that is not really a method.

A list of all methods for `median` (in the current session) is found with:

```
methods(median)
```

and methods for the `"factor"` class are found with:

```
methods(class='factor')
```

### 7.1.3 inheritance

Classes can inherit from other classes. For example:

```
> class(ordered(c(90, 90, 100, 110, 110)))
[1] "ordered" "factor"
```

Class `"ordered"` inherits from class `"factor"`. Ordered factors are factors, but not all factors are ordered. If there is a method for `"ordered"` for a specific generic, then that method will be used when the argument is of class `"ordered"`. However, if there is not a method for `"ordered"` but there is one for `"factor"`, then the method for `"factor"` will be used.

Inheritance should be based on similarity of the structure of the objects, not similarity of the concepts for the objects. Matrices and data frames have similar concepts. Matrices are a specialization of data frames (all columns of the same type), so conceptually inheritance makes sense. However, matrices and data frames have completely different implementations, so inheritance makes no practical sense. The power of inheritance is the ability to (essentially) reuse code.

## 7.2 S4 methods

S4 methods correspond to the green book.

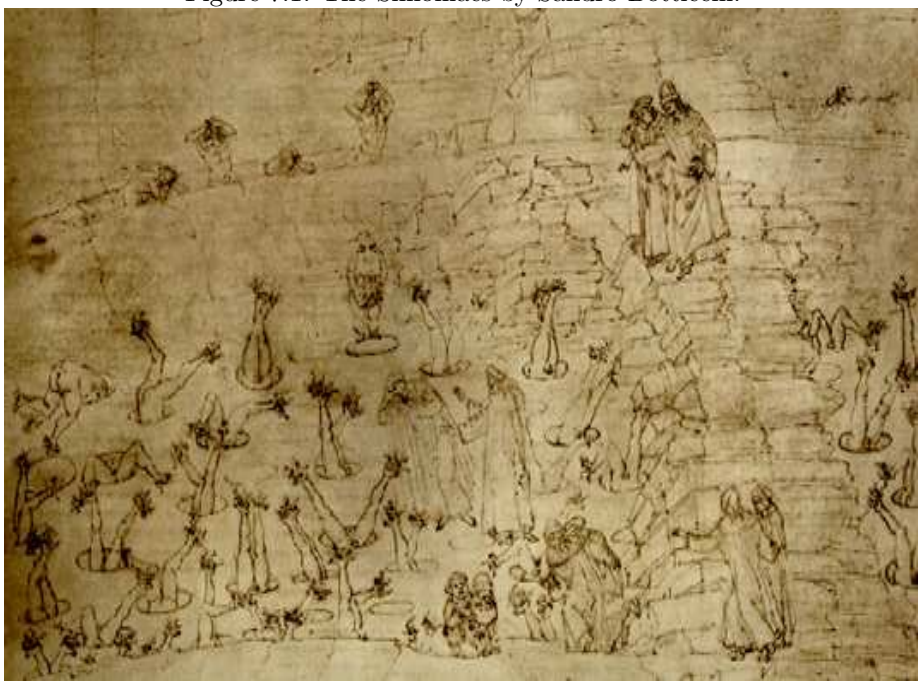
S3 methods are simple and powerful, and a bit *ad hoc*. S4 methods remove the *ad hoc*—they are more strict and more general. The S4 methods technology is a stiffer rope—when you hang yourself with it, it surely will not break. But that is basically the point of it—the programmer is restricted in order to make the results more dependable for the user. That's the plan anyway, and it often works.

### 7.2.1 multiple dispatch

One feature of S4 methods that is missing from S3 methods (and many other object-oriented systems) is multiple dispatch. Suppose you have an object of class `"foo"` and an object of class `"bar"` and want to perform function `fun` on these objects. The result of

```
fun(foo, bar)
```

Figure 7.1: The Simoniacs by Sandro Botticelli.



may or may not to be different from

```
fun(bar, foo)
```

If there are many classes or many arguments to the function that are sensitive to class, there can be big complications. S4 methods make this complicated situation relatively simple.

We saw that `UseMethod` creates an S3 generic function. S4 generic functions are created with `standardGeneric`.

### 7.2.2 S4 structure

S4 is quite strict about what an object of a specific class looks like. In contrast S3 methods allow you to merely add a `class` attribute to any object—as long as a method doesn't run into anything untoward, there is no penalty. A key advantage in strictly regulating the structure of objects in a particular class is that those objects can be used in C code (via the `.Call` function) without a copious amount of checking.

Along with the strictures on S4 objects comes some new vocabulary. The pieces (components) of the object are called *slots*. Slots are accessed by the `` `@` `` operator. So if you see code like:

```
x@Data
```

that is an indication that `x` is an S4 object.

By now you will have noticed that S4 methods are driven by the `class` attribute just as S3 methods are. This commonality perhaps makes the two systems appear more similar than they are. In S3 the decision of what method to use is made in real-time when the function is called. In S4 the decision is made when the code is loaded into the R session—there is a table that charts the relationships of all the classes. The `showMethods` function is useful to see the layout.

S4 has inheritance, as does S3. But, again, there are subtle differences. For example, a concept in S4 that doesn't resonate in S3 is *contains*. If S4 class `"B"` has all of the slots that are in class `"A"`, then class `"B"` contains class `"A"`.

### 7.2.3 discussion

Will S4 ever totally supplant S3? Highly unlikely. One reason is backward compatibility—there is a whole lot of code that depends on S3 methods. Additionally, S3 methods are convenient. It is very easy to create a `plot` or `summary` method for a specific computation (a simulation, perhaps) that expedites analysis.

So basically S3 and S4 serve different purposes. S4 is useful for large, industrial-strength projects. S3 is useful for *ad hoc* projects.

If you are planning on writing S4 (or even S3) methods, then you can definitely do worse than getting the book *Software for Data Analysis: Programming with R* by John Chambers. Don't misunderstand: this book can be useful even if you are not using methods.

Two styles of object orientation are hardly enough. Luckily, there are the `OOP`, `R.oo` and `proto` packages that provide three more.

## 7.3 Namespaces

Namespaces don't really have much to do with object-orientation. To the casual user they are related in that both seem like an unwarranted complication. They are also related in the sense that that seeming complexity is actually simplicity in disguise.

Suppose that two packages have a function called `recode`. You want to use a particular one of these two. There is no guarantee that the one you want will always be first on the search list. That is the problem for which namespaces are the answer.

To understand namespaces, let's consider an analogy of a function that returns a named list. There are some things in the environment of the function that you get to see (the components that it returns), and possibly some objects that you can't see (the objects created in the function but not returned). A

namespace exports one or more objects so that they are visible, but may have some objects that are private.

The way to specify an object from a particular namespace is to use the `::` operator:

```
> stats::coef
function (object, ...)
UseMethod("coef")
<environment: namespace:stats>
```

This operator fails if the name is not exported:

```
> stats::coef.default
Error: 'coef.default' is not an exported object
  from 'namespace:stats'
```

There are ways to get the non-exported objects, but you have to promise not to use them except to inspect the objects. You can use `:::` or the `getAnywhere` function:

```
> stats:::coef.default
function (object, ...)
object$coefficients
<environment: namespace:stats>
> getAnywhere('coef.default')
A single object matching 'coef.default' was found
It was found in the following places
  registered S3 method for coef from namespace stats
  namespace:stats
with value
function (object, ...)
object$coefficients
<environment: namespace:stats>
```

There can be problems if you want to modify a function that is in a namespace. Functions `assignInNamespace` and `unlockBinding` can be useful in this regard.

The existence of namespaces, S3 methods, and especially S4 methods makes R more suitable to large, complex applications than it would otherwise be. But R is not the best tool for every application. And it doesn't try to be. One of the design goals of R is to make it easy to interact with other software to encourage the best tool being used for each task.

# Circle 8

# Believing It Does as Intended

In this Circle we came across the fraudulent—each trapped in their own flame.

This Circle is wider and deeper than one might hope. Reasons for this include:

- Backwards compatibility. There is roughly a two-decade history of compatibility to worry about. If you are a new user, you will think that rough spots should be smoothed out no matter what. You will think differently if a new version of R breaks your code that has been working. The larger splinters have been sanded down, but this still leaves a number of annoyances to adjust to.
- R is used both interactively and programmatically. There is tension there. A few functions make special arrangements to make interactive use easier. These functions tend to cause trouble if used inside a function. They can also promote false expectations.
- R does a lot.

In this Circle we will meet a large number of ghosts, chimeras and devils. These can often be exorcised using the `browser` function. Put the command:

```
browser()
```

at strategic locations in your functions in order to see the state of play at those points. A close alternative is:

```
recover()
```

`browser` allows you to look at the objects in the function in which the `browser` call is placed. `recover` allows you to look at those objects as well as the objects in the caller of that function and all other active functions.

Liberal use of `browser`, `recover`, `cat` and `print` while you are writing functions allows your expectations and R's expectations to converge.

A very handy way of doing this is with `trace`. For example, if browsing at the end of the `myFun` function is convenient, then you can do:

```
trace(myFun, exit=quote(browser()))
```

You can customize the tracing with a command like:

```
trace(myFun, edit=TRUE)
```

If you run into an error, then debugging is the appropriate action. There are at least two approaches to debugging. The first approach is to look at the state of play at the point where the error occurs. Prepare for this by setting the `error` option. The two most likely choices are:

```
options(error=recover)
```

or

```
options(error=dump.frames)
```

The difference is that with `recover` you are automatically thrown into debug mode, but with `dump.frames` you start debugging by executing:

```
debugger()
```

In either case you are presented with a selection of the frames (environments) of active functions to inspect.

You can force R to treat warnings as errors with the command:

```
options(warn=2)
```

If you want to set the error option in your `.First` function, then you need a trick since not everything is in place at the time that `.First` is executed:

```
options(error=expression(recover()))
```

or

```
options(error=expression(dump.frames()))
```

The second idea for debugging is to step through a function as it executes. If you want to step through function `myfun`, then do:

```
debug(myfun)
```

and then execute a statement involving `myfun`. When you are done debugging, do:

```
undebug(myfun)
```

A more sophisticated version of this sort of debugging may be found in the `debug` package.

## 8.1 Ghosts

### 8.1.1 differences with S+

There are a number of differences between R and S+.

The differences are given in the R FAQ (http://cran.r-project.org/faqs.html). A few, but not all, are also mentioned here.

### 8.1.2 package functionality

Suppose you have seen a command that you want to try, such as

```
fortune('dog')
```

You try it and get the error message:

```
Error: could not find function "fortune"
```

You, of course, think that your installation of R is broken. I don't have evidence that your installation is not broken, but more likely it is because your current R session does not include the package where the `fortune` function lives. You can try:

```
require(fortune)
```

Whereupon you get the message:

```
Error in library(package, ...) :
      there is no package called 'fortune'
```

The problem is that you need to install the package onto your computer. Assuming you are connected to the internet, you can do this with the command:

```
install.packages('fortune')
```

After a bit of a preamble, you will get:

```
Warning message:
package 'fortune' is not available
```

Now the problem is that we have the wrong name for the package. Capitalization as well as spelling is important. The successful incantation is:

```
install.packages('fortunes')
require(fortunes)
fortune('dog')
```

Installing the package only needs to be done once, attaching the package with the `require` function needs to be done in every R session where you want the functionality.

The command:

```
library()
```

shows you a list of packages that are in your standard location for packages.

Figure 8.1: The falsifiers: alchemists by Sandro Botticelli.

### 8.1.3 precedence

It is a sin to assume that code does what is intended. The following command clearly intends to produce a sequence from one to one less than $n$:

```
1:n-1
```

From the presence of the example here, you should infer that is not what you get.

Here is another way to make a similar mistake:

```
10^2:6
```

If you do:

```
-2.3 ^ 4.5
```

you will get a nice, pleasing number. If you do:

```
x <- -2.3
x ^ 4.5
```

you will get not-a-number, written as `NaN`. While you may think the two commands are the same, they are not—operator precedence has struck again. If the latter operation is really what you want, then you need to do:

```
as.complex(x) ^ 4.5
```

Pay attention to the precedence of operators. If you are at all unsure, then parentheses can force the command to do what you want.

You can see R's precedence table by doing:

```
> ?Syntax
```

### 8.1.4 equality of missing values

The following can not possibly work to test for missing values in `x`:

```
x == NA
```

Why not?

Here's a hint:

```
3 == c(3, 1, 3, NA)
```

Instead, do:

```
is.na(x)
```

### 8.1.5 testing NULL

Likewise there is `is.null` for testing if an object is `NULL`.

```
> xnull <- NULL
> xnull == NULL
logical(0)
> xnotnull <- 42
> xnotnull == NULL
logical(0)
> is.null(xnull)
[1] TRUE
```

However, it is often better to test if the length of the object is zero—`NULL` is not the only zero length object.

```
> is.null(numeric(0))
[1] FALSE
```

### 8.1.6 membership

Another common wish for the `` `==` `` operator is to indicate which elements of a vector are in some other vector. If you are lucky it will work, but generally does not. (Actually you will be unlucky if you are writing a function and it does work—you'll miss the bug you just put in your function.)

```
> x1 <- 10:1
> x1 == c(4, 6)
[1] FALSE FALSE FALSE FALSE FALSE FALSE  TRUE FALSE
[9] FALSE FALSE
```

The command above fails to give the locations in `x1` that are equal to 4 and 6.

Use `` `%in%` `` for situations like this:

```
> x1 %in% c(4, 6)
[1] FALSE FALSE FALSE FALSE  TRUE FALSE  TRUE FALSE
[9] FALSE FALSE
```

### 8.1.7 multiple tests

If you want to do multiple tests, you don't get to abbreviate. With the `x1` from just above:

```
> x1 == 4 | 6
[1]  TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[10] TRUE
> x1 == (4 | 6)
[1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[9] FALSE TRUE
```

In a second we'll discuss what is really happening in these two statements. It would be a good exercise for you to try to figure it out on your own.

But first, the way to actually do the intended operation is:

```
> x1 == 4 | x1 == 6
[1] FALSE FALSE FALSE FALSE TRUE FALSE TRUE FALSE
[9] FALSE FALSE
```

or (better for the more general case):

```
> x1 %in% c(4, 6)
[1] FALSE FALSE FALSE FALSE TRUE FALSE TRUE FALSE
[9] FALSE FALSE
```

Now, what are our bogus attempts doing?

```
x1 == 4 | 6
```

is evaluated as

```
(x1 == 4) | 6
```

(otherwise the two statements would get the same answer). This last statement is the same as:

```
6 | (x1 == 4)
```

since "or" is commutative. The `|` operator coerces its arguments to be logical. Any non-zero number coerces to `TRUE`, and so all elements of the resulting command will be `TRUE` since 6 is coerced to `TRUE`.

The other statement has a different result but follows a somewhat similar cascade of coercions.

```
4 | 6
```

is the same as

```
TRUE | TRUE
```

which is `TRUE`. So then R is being asked:

```
x1 == TRUE
```

The `==` operator coerces not to logical, but to the most general type, numeric in this case. `TRUE` coerced to numeric is 1.

### 8.1.8 coercion

Automatic coercion is a good thing. However, it can create surprises. There is an ordering of the modes for coercion—most specific to least specific—as shown below.

```
> modes <- c('logical', 'numeric', 'complex', 'character')
> modarr <- array(vector('list',16), c(4,4), list(modes,modes))
> for(i in 1:4) for(j in 1:4) {
+    modarr[[i, j]] <- c(vector(modes[i], 0),
+      vector(modes[j], 0))
+ }
> modarr
          logical     numeric     complex     character
logical   Logical,0   Numeric,0   Complex,0   Character,0
numeric   Numeric,0   Numeric,0   Complex,0   Character,0
complex   Complex,0   Complex,0   Complex,0   Character,0
character Character,0 Character,0 Character,0 Character,0
```

This example leaves out the integer subtype of numeric. Integers go between logical and (general) numeric. You are highly unlikely to need to care (or even know) if an object is stored as integer or the more general numeric.

Here is the full list of atomic (storage) modes from most specific to most general:

- `logical`
- `integer`
- `numeric`
- `complex`
- `character`

Comment: This example uses a matrix that is a list. Notice the use of `` `[[` `` for the matrix. Some people arrive at such a matrix by accident—an event that may lead to confusion.

### 8.1.9 comparison under coercion

Be careful when doing comparisons where coercion might come into play:

```
> 50 < '7'
[1] TRUE
```

### 8.1.10 parentheses in the right places

You want to put parentheses in the right places so that it is the desired operations that are done:

```
> length(mylist != 1)
Error: (list) object cannot be coerced to double
> length(mylist) != 1
[1] TRUE
```

In this example we are lucky enough to get an error so we know something is wrong.

### 8.1.11 excluding named items

Negative subscripts allow you to say which items you don't want:

```
> xlet <- 1:6
> names(xlet) <- letters[1:6]
> xlet[-c(3,4)]
a b e f
1 2 5 6
```

Sometimes you would like to do the excluding with names rather than numbers, but this does not work (naturally enough):

```
> xlet[-c('c', 'd')]
Error in -c("c", "d") : Invalid argument to unary operator
```

There is a reasonable way to get the behavior though:

```
> xlet[!(names(xlet) %in% c('c', 'd'))]
a b e f
1 2 5 6
```

Actually parentheses are not needed:

```
> xlet[!names(xlet) %in% c('c', 'd')]
a b e f
1 2 5 6
```

But it seems like magic to me that this works—I feel more comfortable with the parentheses. Uwe's Maxim (page 20) comes into this for me: I need to think less when the parentheses are there.

The negative of a character string does work in some circumstances in `subset`, but note that there are warnings coming up about using `subset`.

### 8.1.12 excluding missing values

```
> xna <- c(1, NA, 3, 2, 4, 2)
> xna[xna == 2]
[1] NA 2 2
```

As you can see, if you only wanted the values that are for sure 2, then you would be disappointed. If that is what you want, then you need to say so:

```
> xna[!is.na(xna) & xna == 2]
[1] 2 2
```

Or more compactly:

```
> xna[which(xna == 2)]
[1] 2 2
```

### 8.1.13 negative nothing is something

```
> x2 <- 1:4
> x2[-which(x2 == 3)]
[1] 1 2 4
```

The command above returns all of the values in `x2` not equal to 3.

```
> x2[-which(x2 == 5)]
numeric(0)
```

The hope is that the above command returns all of `x2` since no elements are equal to 5. Reality will dash that hope. Instead it returns a vector of length zero.

There is a subtle difference between the two following statements:

```
x[]
x[numeric(0)]
```

Subtle difference in the input, but no subtlety in the difference in the output.

There are at least three possible solutions for the original problem.

```
out <- which(x2 == 5)
if(length(out)) x2[-out] else x2
```

Another solution is to use logical subscripts:

```
x2[!(x2 %in% 5)]
```

Or you can, in a sense, work backwards:

```
x2[ setdiff(seq_along(x2), which(x2 == 5)) ]
```

### 8.1.14 but zero can be nothing

```
> x3 <- 1:3
> x3[c(0, 4)] <- c(-1, 9)
Warning message: number of items to replace is not
a multiple of replacement length
> x3
[1] 1 2 3 -1
```

This is an instance where you don't want to ignore the warning message because the fourth element does not get its intended value.

### 8.1.15 something plus nothing is nothing

```
> 1 + NULL
numeric(0)
```

This computation goes through without error or warning. It works because the recycling rule says that the length of the result should be 0. Sometimes you would prefer to be warned.

### 8.1.16 sum of nothing is zero

Some people are surprised by:

```
> sum(numeric(0))
[1] 0
```

And perhaps even more by:

```
> prod(numeric(0))
[1] 1
```

The counterparts in logicland are:

```
> any(logical(0))
[1] FALSE
> all(logical(0))
[1] TRUE
```

Surprising or not, these are the correct answers. We demand that

```
sum(c(1, 3, 5, 7))
```

equals

```
sum(c(1, 3)) + sum(c(5, 7))
```

So we should also demand that it equals:

```
sum(c(1, 3, 5, 7)) + sum(numeric(0))
```

Similar behavior occurs with min and max, although there are warnings with these:

```
> min(NULL)
[1] Inf
Warning message:
In min(NULL) : no finite arguments to min; returning Inf
> max(NULL)
[1] -Inf
Warning message:
In max(NULL) : no finite arguments to max; returning -Inf
```

### 8.1.17 the methods shuffle

While a matrix and a data frame can represent the same data and may look the same, they are different. In particular, generic functions can and do give different results.

Let's start by making some data:

```
> mat1 <- cbind(1:3, 7:9)
> df1 <- data.frame(1:3, 7:9)
```

Now, notice:

```
> mean(mat1)
[1] 5
> mean(df1)
X1.3 X7.9
   2    8
> median(mat1)
[1] 5
> median(df1)
[1] 2 8
> sum(mat1)
[1] 30
> sum(df1)
[1] 30
```

The example of `median` with data frames is a troublesome one. As of R version 2.13.0 there is not a data frame method of `median`. In this particular case it gets the correct answer, but that is an accident. In other cases you get bizarre answers.

Unless and until there is such a method, you can get what I imagine you expect with:

```
> sapply(df1, median)
X1.3 X7.9
   2    8
```

### 8.1.18 first match only

`match` only matches the first occurrence:

```
> match(1:2, rep(1:4, 2))
[1] 1 2
```

If that is not what you want, then change what you do:

```
> which(rep(1:4, 2) %in% 1:2)
[1] 1 2 5 6
```

### 8.1.19 first match only (reprise)

If names are not unique, then subscripting with characters will only give you the first match:

```
> x4 <- c(a=1, b=2, a=3)
> x4["a"]
a
1
```

If this is not the behavior you want, then you probably want to use `%in%`:

```
> x4[names(x4) %in% 'a']
a a
1 3
```

### 8.1.20 partial matching can partially confuse

Partial matching happens in function calls and some subscripting.

The two following calls are the same:

```
> mean(c(1:10, 1000), trim=.25)
[1] 6
> mean(c(1:10, 1000), t=.25)
[1] 6
```

The `trim` argument is the only argument to `mean.default` which starts with "t" so R knows that you meant "trim" when you only said "t". This is helpful, but some people wonder if it is too helpful by a half.

```
> l1 <- list(aa=1:3, ab=2:4, b=3:5, bb=4:6, cc=5:7)
> l1$c
[1] 5 6 7
> l1[['c']]
NULL
> l1[['c', exact=FALSE]]
[1] 5 6 7
> l1$a
NULL
> myfun1 <- function(x, trim=0, treat=1) {
+    treat * mean(x, trim=trim)
+ }
> myfun1(1:4, tr=.5)
Error in myfun1(1:4, tr = .05) :
  argument 2 matches multiple formal arguments
```

The `$` operator always allows partial matching. The `[[` operator, which is basically synonymous with `$` on lists, does not allow partial matching by default (in recent versions of R). An ambiguous match results in `NULL` for lists, but results in an error in function calls. The `myfun1` example shows why an error is warranted. For the full details on subscripting, see:

```
?Extract
```

Here are the rules for argument matching in function calls, but first some vocabulary: A *formal argument* is one of the argument names in the definition of the function. The `mean.default` function has 4 formal arguments (`x`, `trim`, `na.rm` and `'...'`). A *tag* is the string used in a call to indicate which formal argument is meant. We used "t" as a tag in a call to `mean` (and hence to `mean.default`). There is a partial match if all the characters of the tag match the start of the formal argument.

- If a tag matches a formal argument exactly, then the two are bound.
- Unmatched tags are partially matched to unmatched formal arguments.
- An error occurs if any tag partially matches more than one formal argument not already bound.
- (Positional matching) Unmatched formal arguments are bound to unnamed (no tag) arguments in the call, based on the order in the call and of the formal arguments.
- If `'...'` is among the formal arguments, any formal arguments after `'...'` are only matched exactly.
- If `'...'` is among the formal arguments, any unmatched arguments in the call, tagged or not, are taken up by the `'...'` formal argument.
- An error occurs if any supplied arguments in the call are unmatched.

The place where partial matching is most likely to bite you is in calls that take a function as an argument and you pass in additional arguments for the function. For example:

```
apply(xmat, 2, mean, trim=.2)
```

If the `apply` function had an argument that matched or partially matched "trim", then `apply` would get the `trim` value, not `mean`.

There are two strategies in general use to reduce the possibility of such collisions:

- The apply family tends to have arguments that are in all capitals, and hence unlikely to collide with arguments of other functions that tend to be in lower case.
- Optimization functions tend to put the `'...'` (which is meant to be given to the function that is an argument) among the first of its arguments. Thus additional arguments to the optimizer (as opposed to the function being optimized) need to be given by their full names.

Neither scheme is completely satisfactory—you can still get unexpected collisions in various ways. If you do (and you figure out what is happening), then you can include all of the arguments in question in your call.

### 8.1.21 no partial match assignments

One of the most pernicious effects of partial matching in lists is that it can fool you when making replacements:

```
> ll2 <- list(aa=1:3, bb=4:6)
> ll2$b
[1] 4 5 6
> ll2$b <- 7:9
> ll2
$aa
[1] 1 2 3
$bb
[1] 4 5 6
$b
[1] 7 8 9
```

This applies to data frames as well (data frames are lists, after all).

### 8.1.22 cat versus print

If you `print` a vector that does not have names, there is an indication of the index of the first element on each line:

```
> options(width=20)
> 1:10
[1]  1  2  3  4  5
[6]  6  7  8  9 10
```

Alternatively, `cat` just prints the contents of the vector:

```
> cat(1:10)
1 2 3 4 5 6 7 8 9 10>
```

Notice that there is not a newline after the results of `cat`, you need to add that yourself:

```
cat(1:10, '\n')
```

There is a more fundamental difference between `print` and `cat`—`cat` actually interprets character strings that it gets:

```
> xc <- 'blah\\blah\tblah\n'
> print(xc)
[1] "blah\\blah\tblah\n"
> cat(xc)
blah\blah       blah
>
```

Table 8.1: A few of the most important backslashed characters.

| character | meaning |
|---|---|
| \\ | backslash |
| \n | newline |
| \t | tab |
| \" | double quote (used when this is the string delimiter) |
| \' | single quote (used when this is the string delimiter) |

Strings are two-faced. One face is what the string actually says (this is what `cat` gives you). The other face is a representation that allows you to see all of the characters—how the string is actually built—this is what `print` gives you. Do not confuse the two.

Reread this item—it is important. Important in the sense that if you don't understand it, you are going to waste a few orders of magnitude more time fumbling around than it would take to understand.

### 8.1.23 backslashes

Backslashes are the escape character for R (and for Unix and C).

Since backslash doesn't mean backslash, there needs to be a way to mean backslash. Quite logically that way is backslash-backslash:

```
> cat('\\')
\>
```

Sometimes the text requires a backslash after the text has been interpreted. In the interpretation each pair of backslashes becomes one backslash. Backslashes grow in powers of two.

There are two other very common characters involving backslash: `\t` means tab and `\n` means newline. Table 8.1 shows the characters using backslash that you are most likely to encounter. You can see the entire list via:

```
?Quotes
```

Note that `nchar` (by default) gives the number of logical characters, not the number of keystrokes needed to create them:

```
> nchar('\\')
[1] 1
```

### 8.1.24 internationalization

It may surprise some people, but not everyone writes with the same alphabet. To account for this R allows string encodings to include latin1 and UTF-8.

There is also the possibility of using different locales. The locale can affect the order in which strings are sorted into.

The freedom of multiple string encodings and multiple locales gives you the chance to spend hours confusing yourself by mixing them.

For more information, do:

```
> ?Encoding
> ?locales
```

### 8.1.25 paths in Windows

Quite unfortunately Windows uses the backslash to separate directories in paths. Consider the R command:

```
attach('C:\tmp\foo')
```

This is confusing the two faces of strings. What that string actually contains is: C, colon, tab, m, p, formfeed, o, o. No backslashes at all. What should really be said is:

```
attach('C:\\tmp\\foo')
```

However, in all (or at least virtually all) cases R allows you to use slashes in place of backslashes in Windows paths—it does the translation under the hood:

```
attach('C:/tmp/foo')
```

If you try to copy and paste a Windows path into R, you'll get a string (which is wrong) along with some number of warnings about unrecognized escapes. One approach is to paste into a command like:

```
scan('', '', n=1)
```

### 8.1.26 quotes

There are three types of quote marks, and a cottage industry has developed in creating R functions that include the string "quote". Table 8.2 lists functions that concern quoting in various ways. The `bquote` function is generally the most useful—it is similar to `substitute`.

Double-quotes and single-quotes—essentially synonymous—are used to delimit character strings. If the quote that is delimiting the string is inside the string, then it needs to be escaped with a backslash.

```
> '"'
[1] "\""
```

A backquote (also called "backtick") is used to delimit a name, often a name that breaks the usual naming conventions of objects.

Table 8.2: Functions to do with quotes.

| function | use |
|---|---|
| bquote | substitute items within .() |
| noquote | print strings without surrounding quotes |
| quote | language object of unevaluated argument |
| Quote | alias for quote |
| dQuote | add double left and right quotes |
| sQuote | add single left and right quotes |
| shQuote | quote for operating system shell |

```
> '3469'
[1] "3469"
> `3469`
Error: Object "3469" not found
> `2` <- 2.5
> `2` + `2`
[1] 5
```

### 8.1.27 backquotes

Backquotes are used for names of list components that are reserved words and other "illegal" names. No need to panic.

```
> ll3 <- list(A=3, NA=4)
Error: unexpected '=' in "ll3 <- list(A=3, NA="
> ll3 <- list(A=3, 'NA'=4)
> ll3 <- list(A=3, 'NA'=4, 'for'=5)
> ll3
$A
[1] 3
$`NA`
[1] 4
$`for`
[1] 5
> ll3$'for'
[1] 5
```

Although the component names are printed using backquotes, you can access the components using either of the usual quotes if you like. The initial attempt to create the list fails because the NA was expected to be the data for the second (nameless) component.

### 8.1.28 disappearing attributes

Most coercion functions strip the attributes from the object. For example, the result of:

```
as.numeric(xmat)
```

will not be a matrix. A command that does the coercion but keeps the attributes is:

```
storage.mode(xmat) <- 'numeric'
```

### 8.1.29 disappearing attributes (reprise)

```
> x5 <- 1
> attr(x5, 'comment') <- 'this is x5'
> attributes(x5)
$comment
[1] "this is x5"
> attributes(x5[1])
NULL
```

Subscripting almost always strips almost all attributes.

If you want to keep attributes, then one solution is to create a class for your object and write a method for that class for the `[` function.

### 8.1.30 when space matters

Spaces, or their lack, seldom make a difference in R commands. Except that spaces can make it much easier for humans to read (recall Uwe's Maxim, page 20).

There is an instance where space does matter to the R parser. Consider the statement:

```
x<-3
```

This could be interpreted as either

```
x <- 3
```

or

```
x < -3
```

This should prompt you to use the spacebar on your keyboard. Most important to make code legible to humans is to put spaces around the `<-` operator. Unfortunately that does not solve the problem in this example—it is in comparisons that the space is absolutely required.

### 8.1.31 multiple comparisons

```
0 < x < 1
```

seems like a reasonable way to test if `x` is between 0 and 1. R doesn't think so. The command that R agrees with is:

```
0 < x & x < 1
```

### 8.1.32 name masking

By default `T` and `F` are assigned to `TRUE` and `FALSE`, respectively. However, they can be used as object names (but in S+ they can not be). This leads to two suggestions:

1. It is extremely good practice to use `TRUE` and `FALSE` rather than `T` and `F`.
2. It is good practice to avoid using `T` and `F` as object names in order not to collide with those that failed to follow suggestion 1.

It is also advisable to avoid using the names of common functions as object names. Two favorites are `c` and `t`.

And don't call your matrix `matrix`, see:

```
fortune('dog')
```

Usually masking objects is merely confusing. However, if you mask a popular function name with your own *function*, it can verge on suicidal.

```
> c <- function(x) x * 100
> par(mfrow=c(2, 2))
Error in c(2, 2) : unused argument(s) (2)
```

If you get an extraordinarily strange error, it may be due to masking. Evasive action after the fact includes:

```
find('c')
```

if you know which function is the problem. To find the problem, you can try:

```
conflicts(detail=TRUE)
```

Another possibility for getting out of jail is to start R with `--vanilla`.

### 8.1.33 more sorting than sort

The `order` function is probably what you are looking for when `sort` doesn't do the sorting that you want. Uses of `order` include:

- sorting the rows of a matrix or data frame.
- sorting one vector based on values of another.
- breaking ties with additional variables.

### 8.1.34 sort.list not for lists

Do not be thinking that `sort.list` is to sort lists. You silly fool.

In fact sorting doesn't work on lists:

```
> sort(as.list(1:20))
Error in sort.int(x, na.last = na.last, ...) :
  'x' must be atomic
> sort.list(as.list(1:20))
Error in sort.list(as.list(1:20)) : 'x' must be atomic
Have you called 'sort' on a list?
```

If you have lists that you want sorted in some way, you'll probably need to write your own function to do it.

### 8.1.35 search list shuffle

`attach` and `load` are very similar in purpose, but different in effect. `attach` creates a new item in the search list while `load` puts its contents into the global environment (the first place in the search list).

Often `attach` is the better approach to keep groups of objects separate. However, if you change directory into a location and want to have the existing `.RData`, then `load` is probably what you want.

Here is a scenario (that you don't want):

- There exists a `.RData` in directory `project1`.
- You start R in some other directory and then change directory to `project1`.
- The global environment is from the initial directory.
- You attach `.RData` (from `project1`).
- You do some work, exit and save the workspace.
- You have just wiped out the original `.RData` in `project1`, losing the data that was there.

### 8.1.36 source versus attach or load

Both `attach` and `load` put R objects onto the search list. The `source` function does that as well, but when the starting point is code to create objects rather than actual objects.

There are conventions to try to keep straight which you should do. Files of R code are often the extension "`.R`". Other extensions for this include "`.q`", "`.rt`", "`.Rscript`".

Extension for files of R objects include "`.rda`" and "`.RData`".

### 8.1.37 string not the name

If you have a character string that contains the name of an object and you want the object, then use `get`:

```
funs <- c('mean', 'median')
get(funs[2])(data)
```

If you found `as.name` and thought that would solve your problem, you were right but you need one more step:

```
eval(as.name(funs[2]))(data)
```

### 8.1.38 get a component

The `get` function is extremely powerful, but it is not clairvoyant. If you say:

```
get('myobj$comp')
```

it thinks (quite rightly) you are asking for an object named 'myobj$comp'. If you want the `comp` component of `myobj`, you have to say:

```
get('myobj')$comp
```

### 8.1.39 string not the name (encore)

If you have a character string that contains the name of a component that you want to extract from a list, then you can not use the `` `$` `` operator. You need to use `` `[[` ``:

```
> mylist <- list(aaa=1:5, bbb=letters)
> subv <- 'aaa'
> mylist$subv
NULL
> # the next three lines are all the same
> mylist$aaa
[1] 1 2 3 4 5
> mylist[['aaa']]
[1] 1 2 3 4 5
> mylist[[subv]]
[1] 1 2 3 4 5
```

### 8.1.40 string not the name (yet again)

If you create a character string with `paste` and you want that to be the name of an object, you can not use that on the left of an assignment:

```
> paste('x', 1, sep='') <- 3:5
Error: Target of assignment expands to non-language object
```

But `assign` will do this:

```
for(i in 1:n) assign(paste('obj', i, sep='.'), mylist[[i]])
```

WARNING: An operation like this can land you in Circle 3 ([page 17] failing to vectorize—this example is anti-vectorizing) and/or the heresy of Circle 6 (page 35).

As we have just seen with `get`, assigning to a name like `'myobj$comp'` is not going to get you where you want to go—it will create an object with a non-standard name rather than modifying the `comp` component of `myobj`. Create a copy of the object, change the component in the copy, then assign the name to the copy.

### 8.1.41 string not the name (still)

A formula can easily be created out of a character string:

```
> myvars <- paste('V', 1:9, sep='')
> myvars
[1] "V1" "V2" "V3" "V4" "V5" "V6" "V7" "V8" "V9"
> as.formula(paste('y ~ ', paste(myvars[c(3,5,8)],
+    collapse=' + ')))
y ~ V3 + V5 + V8
```

### 8.1.42 name not the argument

You may want to produce a plot or other output that states the dataset that was used. You might try something like:

```
myfun <- function(x, ...)
{
   plot(x, main=x, ...)
}
```

But that is going to produce a less than pleasing main title. The `substitute` function along with `deparse` is probably what you are looking for.

```
myfun2 <- function(x, ...)
{
   plot(x, main=deparse(substitute(x)), ...)
}
```

### 8.1.43 unexpected else

```
Error: unexpected 'else' in "else"
```

If you aren't expecting 'else' in 'else', then where would you expect it?

While you may think that R is ludicrous for giving you such an error message, R thinks you are even more ludicrous for expecting what you did to work.

R takes input until it gets a complete statement, evaluates that statement, then takes more input. Here is how to get that error:

```
if(any(abs(x) > 1)) atan(x)
else asin(x)
```

When R gets to the end of the first line, it has a perfectly complete statement so it evaluates it. Now it finds a statement starting with 'else'—this makes no sense. Proper formatting is the key. If it is convenient, you can put the whole statement on one line:

```
if(any(abs(x) > 1)) atan(x) else asin(x)
```

Alternatively, use curly braces (and a well-placed 'else'):

```
if(any(abs(x) > 1)) {
    atan(x)
} else {
    asin(x)
}
```

### 8.1.44 dropping dimensions

```
> xmat <- array(1:4, c(2,2))
> xmat[1,] # simple vector, not a matrix
[1] 1 3
> xmat[1, , drop=FALSE] # still a matrix
     [,1] [,2]
[1,]    1    3
```

By default dimensions of arrays are dropped when subscripting makes the dimension length 1. Subscripting with `drop=FALSE` overrides the default.

NOTE: Failing to use `drop=FALSE` inside functions is a major source of bugs. You only test the function when the subscript has length greater than 1. The function fails once it hits a situation where the subscript is length 1—somewhere downstream a matrix is expected and there is a simple vector there instead.

NOTE: Failing to use `drop=FALSE` inside functions is a major source of bugs.

### 8.1.45 drop data frames

The `drop` function has no effect on a data frame. If you want dropping to be done in a data frame, you need to use the `drop` argument in subscripting.

Dropping in data frames can be surprising (but it is logical).

```
> xdf <- data.frame(a=1:2, b=c('v', 'w'))
> xdf[1,] # data frame
  a b
1 1 v
> drop(xdf[1,]) # data frame
  a b
1 1 v
> xdf[1, , drop=TRUE] # list
$a
[1] 1
$b
[1] v
Levels: v w
> xdf[,1] # numeric vector
[1] 1 2
> xdf[, 1, drop=FALSE] # data frame
  a
1 1
2 2
> drop(xdf[, 1, drop=FALSE]) # data frame
  a
1 1
2 2
```

### 8.1.46 losing row names

The row names of a data frame are lost through dropping:

```
> xdf2 <- data.frame(a=1:4, b=42:45,
+   row.names=LETTERS[1:4])
> xdf2[, 1]
[1] 1 2 3 4
> as.matrix(xdf2)[, 1]
A B C D
1 2 3 4
```

Coercing to a matrix first will retain the row names, but possibly at the expense of not getting the right values if the column types of the data frame are mixed.

```
> xdf2b <- data.frame(a=1:4, b=letters[21:24],
+   row.names=LETTERS[1:4])
```

```
> as.matrix(xdf2b)[,1]
  A   B   C   D
"1" "2" "3" "4"
> drop(as.matrix(xdf2b[, 1, drop=FALSE]))
A B C D
1 2 3 4
```

The final incantation, though a bit complicated, will give you the right thing.

### 8.1.47 apply function returning a vector

If you use `apply` with a function that returns a vector, that becomes the first dimension of the result. This is likely not what you naively expect if you are operating on rows:

```
> matrix(15:1, 3)
     [,1] [,2] [,3] [,4] [,5]
[1,]   15   12    9    6    3
[2,]   14   11    8    5    2
[3,]   13   10    7    4    1
> apply(matrix(15:1, 3), 1, sort)
     [,1] [,2] [,3]
[1,]    3    2    1
[2,]    6    5    4
[3,]    9    8    7
[4,]   12   11   10
[5,]   15   14   13
```

The naive expectation is really arrived at with:

```
t(apply(matrix(15:1, 3), 1, sort))
```

But note that no transpose is required if you operate on columns—the naive expectation holds in that case.

### 8.1.48 empty cells in tapply

If there are combinations of levels that do not appear, then `tapply` gives `NA` as the answer (or `NULL` if `simplify=FALSE`):

```
> tapply(9, factor(1, levels=1:2), sum)
 1  2
 9 NA
> tapply(9, factor(1, levels=1:2), sum, simplify=FALSE)
$`1`
[1] 9
$`2`
NULL
```

`by` copies the `tapply` behavior:

```
> by(9, factor(1, levels=1:2), sum)
factor(1, levels = 1:2): 1
[1] 9
------------------------------------------------------------
factor(1, levels = 1:2): 2
[1] NA
```

`aggregate` drops the empty cell:

```
> aggregate(9, list(factor(1, levels=1:2)), sum)
Group.1 x
1       1 9
```

You can get the "right" answer for the empty cell via `split` and `sapply`:

```
> sapply(split(9, factor(1, levels=1:2)), sum)
1 2
9 0
```

This behavior depends on the default value of `drop=FALSE` in `split`.

### 8.1.49 arithmetic that mixes matrices and vectors

To do matrix multiplication between a matrix and a vector you do:

```
xmat %*% yvec
```

or

```
yvec %*% xmat
```

R is smart enough to orient the vector in the way that makes sense. There is no need to coerce the vector to a matrix.

If you want to multiply each row of a matrix by the corresponding element of a vector, then do:

```
xmat * yvec
```

or

```
yvec * xmat
```

This works because of the order in which the elements of the matrix are stored in the underlying vector.

But what to do if you want to multiply each column by the corresponding element of a vector? If you do:

```
xmat * yvec
```

R does not check that the length of `yvec` matches the number of columns of `xmat` and do the multiplication that you want. It does a multiplication that you don't want. There are a few ways to get your multiplication, among them are:

```
xmat * rep(yvec, each=nrow(xmat))
```

and

```
sweep(xmat, 2, yvec, '*')
```

The `sweep` function is quite general—make friends with it. The `scale` function can be useful for related problems.

### 8.1.50 single subscript of a data frame or array

Be careful of the number of commas when subscripting data frames and matrices. It is perfectly acceptable to subscript with no commas—this treats the object as its underlying vector rather than a two dimensional object. In the case of a data frame, the underlying object is a list and the single subscript refers to the columns of the data frame. For matrices the underlying object is a vector with length equal to the number of rows times the number of columns.

### 8.1.51 non-numeric argument

```
> median(x)
Error in median.default(x) : need numeric data
```

If you get an error like this, it could well be because x is a factor.

### 8.1.52 round rounds to even

The `round` function rounds to even if it is rounding off an exact 5.

Some people are surprised by this. I'm surprised that they are surprised—rounding to even is the sensible thing to do. If you want a function that rounds up, write it yourself (possibly using the `ceiling` and `floor` functions, or by slightly increasing the size of the numbers).

Some times there is the surprise that an exact 5 is not rounded to even. This will be due to Circle 1 (page 9)—what is apparently an exact 5 probably isn't.

### 8.1.53 creating empty lists

You create a numeric vector of length 500 with:

```
numeric(500)
```

So obviously you create a list of length 500 with:

```
list(500)
```

Right?

No. A touch of finesse is needed:

```
vector('list', 500)
```

Note that this command hints at the fact that lists are vectors in some sense. When "vector" is used in the sense of an object that is not a list, it is really shorthand for "atomic vector".

### 8.1.54 list subscripting

```
my.list <- list('one', rep(2, 2))
```

There is a difference between

```
my.list[[1]]
```

and

```
my.list[1]
```

The first is likely what you want—the first component of the list. The second is a list of length one whose component is the first component of the original list.

```
> my.list[[1]]
[1] "one"
> my.list[1]
[[1]]
[1] "one"
> is.list(my.list[[1]])
[1] FALSE
> is.list(my.list[1])
[1] TRUE
```

Here are some guidelines:

- single brackets always give you back the same type of object – a list in this case.
- double brackets need not give you the same type of object.
- double brackets always give you one item.
- single brackets can give you any number of items.

### 8.1.55 NULL or delete

If you have a list `xl` and you want component `comp` not to be there any more, you have some options. If `comp` is the index of the component in question, then the most transparent approach is:

```
xl <- xl[-comp]
```

In any case you can do:

```
xl[[comp]] <- NULL
```

or

```
xl[comp] <- NULL
```

The first two work in S+ as well, but the last one does not—it has no effect in S+.

If you want the component to stay there but to be `NULL`, then do:

```
xl[comp] <- list(NULL)
```

Notice single brackets, not double brackets.

### 8.1.56 disappearing components

A `for` loop can drop components of a list that it is modifying.

```
> xl.in <- list(A=c(a=3, z=4), B=NULL, C=c(w=8), D=NULL)
> xl.out <- vector('list', 4); names(xl.out) <- names(xl.in)
> for(i in 1:4) xl.out[[i]] <- names(xl.in[[i]])
> xl.out # not right
$A
[1] "a" "z"
$C
NULL
$D
[1] "w"
> xl.out2 <- lapply(xl.in, names)
> xl.out2
$A
[1] "a" "z"
$B
NULL
$C
[1] "w"
$D
NULL
```

Note that the result from our `for` loop is MOST decidedly not what we want. Possibly not even what we could have dreamed we could get.

Take care when `NULL` can be something that is assigned into a component of a list. Using `lapply` can be a good alternative.

### 8.1.57 combining lists

Some people are pleasantly surprised that the c function works with lists. Then they go on to abuse it.

```
> xlis <- list(A=1:4, B=c('a', 'x'))
> c(xlis, C=6:5)
$A
[1] 1 2 3 4
$B
[1] "a" "x"
$C1
[1] 6
$C2
[1] 5
```

Probably not what was intended. Try:

```
c(xlis, list(C=6:5))
```

### 8.1.58 disappearing loop

Consider the loop:

```
for(i in 1:10) i
```

It is a common complaint that this loop doesn't work, that it doesn't do anything. Actually it works perfectly well. The problem is that no real action is involved in the loop. You probably meant something like:

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

Automatic printing of unassigned objects only happens at the top level.

### 8.1.59 limited iteration

One of my favorite tricks is to only give the top limit of iteration rather than the sequence:

```
for(i in trials) { ... }
```

rather than

```
for(i in 1:trials) { ... }
```

Then I wonder why the results are so weird.

### 8.1.60 too much iteration

```
for(i in 1:length(x)) { ... }
```

is fine if x has a positive length. However, if its length is zero, then R wants to do two iterations. A safer idiom is:

```
for(i in seq_along(x)) { ... }
```

or if you want to be compatible with S+:

```
for(i in seq(along=x)) { ... }
```

### 8.1.61 wrong iterate

The `for` iterate can be from any vector. This makes looping much more general than in most other languages, but can allow some users to become confused:

```
nums <- seq(-1, 1, by=.01)
ans <- NULL
for(i in nums) ans[i] <- i^2
```

This has two things wrong with it. You should recognize that we have tried (but failed) to visit Circle 2 (page 12) here, and the index on `ans` is not what the user is expecting. Better would be:

```
nums <- seq(-1, 1, by=.01)
ans <- numeric(length(nums))
for(i in seq(along=nums)) ans[i] <- nums[i]^2
```

Even better, of course, would be to avoid a loop altogether. That is possible in this case, perhaps not in a real application.

### 8.1.62 wrong iterate (encore)

A loop like:

```
for(i in 0:9) {
   this.x <- x[i]
   ...
```

does not do as intended. While C and some other languages index from 0, R indexes from 1. The unfortunate thing in this case is that an index of 0 is allowed in R, it just doesn't do what is wanted.

### 8.1.63 wrong iterate (yet again)

```
> nam <- c(4, 7)
> vec <- rep(0, length(nam))
> names(vec) <- nam
> for(i in nam) vec[i] <- 31
> vec
4  7
0  0 NA 31 NA NA 31
```

### 8.1.64 iterate is sacrosanct

In the following loop there are two uses of 'i'.

```
> for(i in 1:3) {
+    cat("i is", i, "\n")
+    i <- rpois(1, lambda=100)
+    cat("end iteration", i, "\n")
+ }
i is 1
end iteration 93
i is 2
end iteration 91
i is 3
end iteration 101
```

The `i` that is created in the body of the loop is used during that iteration but does not change the `i` that starts the next iteration. This is unlike a number of other languages (including S+).

This is proof that R is hard to confuse, but such code will definitely confuse humans. So avoid it.

### 8.1.65 wrong sequence

```
> seq(0:10)
[1]  1  2  3  4  5  6  7  8  9 10 11
> 0:10
[1]  0  1  2  3  4  5  6  7  8  9 10
> seq(0, 10)
[1]  0  1  2  3  4  5  6  7  8  9 10
```

What was meant was either the second or third command, but mixing them together gets you the wrong result.

### 8.1.66 empty string

Do not confuse

```
character(0)
```

with

```
""
```

The first is a vector of length zero whose elements would be character if it had any. The second is a vector of length one, and the element that it has is the empty string.

The result of `nchar` on the first object is a numeric vector of length zero, while the result of `nchar` on the second object is 0—that is, a vector of length one whose first and only element is zero.

```
> nchar(character(0))
numeric(0)
> nchar("")
[1] 0
```

### 8.1.67 NA the string

There is a missing value for character data. In normal printing (with quotes around strings) the missing value is printed as NA; but when quotes are not used, it is printed as <NA>. This is to distinguish it from the string 'NA':

```
> cna <- c('missing value'=NA, 'real string'='NA')
> cna
missing value  real string
           NA         "NA"
> noquote(cna)
missing value  real string
         <NA>           NA
```

NA the string really does happen. It is Nabisco in finance, North America in geography, and possibly sodium in chemistry. There are circumstances—particularly when reading data into R—where NA the string becomes NA the missing value. Having a name or dimname that is accidentally a missing value can be an unpleasant experience.

If you have missing values in a character vector, you may want to take some evasive action when operating on the vector:

```
> people <- c('Alice', NA, 'Eve')
> paste('hello', people)
[1] "hello Alice" "hello NA"    "hello Eve"
> ifelse(is.na(people), people, paste('hello', people))
[1] "hello Alice" NA            "hello Eve"
```

### 8.1.68 capitalization

Some people have a hard time with the fact that R is case-sensitive. Being case-sensitive is a good thing. The case of letters REALLy doEs MakE a diFFerencE.

### 8.1.69 scoping

Scoping problems are uncommon in R because R uses scoping rules that are intuitive in almost all cases. An issue with scoping is most likely to arise when moving S+ code into R.

Perhaps you want to know what "scoping" means. In the evaluator if at some point an object of a certain name, `z` say, is needed, then we need to know where to look for `z`. Scoping is the set of rules of where to look.

Here is a small example:

```
> z <- 'global'
> myTopFun
function () {
   subfun <- function() {
      paste('used:', z)
   }
   z <- 'inside_myTopFun'
   subfun()
}
> myTopFun()
[1] "used: inside_myTopFun"
```

The `z` that is used is the one inside the function. Let's think a bit about what is *not* happening. At the point in time that `subfun` is defined, the only `z` about is the one in the global environment. *When* the object is assigned is not important. *Where* the object is assigned is important. Also important is the state of the relevant environments when the function is evaluated.

### 8.1.70 scoping (encore)

The most likely place to find a scoping problem is with the modeling functions.

Let's explore with some examples.

```
> scope1
function () {
   sub1 <- function(form) coef(lm(form))
   xx <- rnorm(12)
   yy <- rnorm(12, xx)
   form1 <- yy ~ xx
   sub1(form1)
}
> scope1()
```

```
(Intercept)         xx
-0.07609548 1.33319273
> scope2
function () {
   sub2 <- function() {
      form2 <- yy ~ xx
      coef(lm(form2))
   }
   xx <- rnorm(12)
   yy <- rnorm(12, xx)
   sub2()
}
> scope2()
(Intercept)       xx
-0.1544372 0.2896239
```

The `scope1` and `scope2` functions are sort of doing the same thing. But `scope3` is different—it is stepping outside of the natural nesting of environments.

```
> sub3
function () {
   form3 <- yy ~ xx
   coef(lm(form3))
}
> scope3
function () {
   xx <- rnorm(12)
   yy <- rnorm(12, xx)
   sub3()
}
> scope3()
Error in eval(expr, envir, enclos) : Object "yy" not found
```

One lesson here is that the environment of the calling function is not (necessarily) searched. (In technical terms that would be dynamic scope rather than the lexical scope that R uses.)

There are of course solutions to this problem. `scope4` solves the problem by saying where to look for the data to which the formula refers.

```
> sub4
function (data) {
   form4 <- yy ~ xx
   coef(lm(form4, data=data))
}
> scope4
function ()  {
   xx <- rnorm(12)
```

```
   yy <- rnorm(12, xx)
   sub4(sys.nframe())
}
> scope4()
(Intercept)          xx
  0.6303816   1.0930864
```

Another possibility is to change the environment of the formula, as `scope5` does:

```
> sub5
function (data) {
   form5 <- eval(substitute(yy ~ xx), envir=data)
   coef(lm(form5))
}
> scope5
function () {
   xx <- rnorm(12)
   yy <- rnorm(12, xx)
   sub5(sys.nframe())
}
> scope5()
(Intercept)        xx
  0.1889312 1.4208295
```

Some caution with solutions is warranted—not all modeling functions follow the same scoping rules for their arguments.

## 8.2 Chimeras

"What brings you into such pungent sauce?"

There is no other type of object that creates as much trouble as factors. Factors are an implementation of the idea of categorical data. (The name 'factor' might cause trouble in itself—the term arrives to us via designed experiments.)

The core data of a factor is an integer vector. The `class` attribute is `"factor"`, and there is a `levels` attribute that is a character vector that provides the identity of each category. You may be able to see trouble coming already—a numeric object that conceptually is not at all numeric.

But R tries to save you from yourself:

```
> is.numeric(factor(1:4))
[1] FALSE
```

Factors can be avoided in some settings by using character data instead. Sometimes this is a reasonable idea.

Figure 8.2: The treacherous to kin and the treacherous to country by Sandro Botticelli.

### 8.2.1 numeric to factor to numeric

While in general factors do not refer to numbers, they may do. In which case we have even more room for confusion.

```
> as.numeric(factor(101:103))
[1] 1 2 3
```

If you were expecting:

```
[1] 101 102 103
```

shame on you.

If your factor represents numbers and you want to recover those numbers from the factor, then you need a more circuitous route to get there:

```
as.numeric(as.character(factor(101:103)))
```

Slightly more efficient, but harder to remember is:

```
as.numeric(levels(f))[f]
```

where `f` is the factor.

### 8.2.2 cat factor

Using `cat` on any factor will just give the core data:

```
> cat(factor(letters[1:5]))
1 2 3 4 5>
```

### 8.2.3 numeric to factor accidentally

When using `read.table` or its friends, it is all too common for a column of data that is meant to be numeric to be read as a factor. This happens if `na.strings` is not properly set, if there is a bogus entry in the column, and probably many other circumstances.

This is dynamite.

The data are thought to be numeric. They are in fact numeric (at least sort of), but decidedly not with the numbers that are intended. Hence you can end up with data that 'works' but produces complete garbage.

When processing the data, the construct:

```
as.numeric(as.character(x))
```

guards you against this occurring. If `x` is already the correct numbers, then nothing happens except wasting a few microseconds. If `x` is accidentally a factor, then it becomes the correct numbers (at least mostly—depending on why it became a factor there may be some erroneously missing values).

### 8.2.4 dropping factor levels

```
> ff <- factor(c('AA', 'BA', 'CA'))
> ff
[1] AA BA CA
Levels: AA BA CA
> ff[1:2]
[1] AA BA
Levels: AA BA CA
```

Notice that there are still three levels even though only two appear in the vector. It is in general a good thing that levels are not automatically dropped—the factor then has the possible levels it can contain rather than merely the levels it happens to contain.

There are times when you want levels dropped that do not appear. Here are two ways of doing that:

```
> ff[1:2, drop=TRUE]
[1] AA BA
Levels: AA BA
> factor(ff[1:2])
[1] AA BA
Levels: AA BA
```

If `f0` is a factor that already has levels that are not used that you want to drop, then you can just do:

```
f0 <- f0[drop=TRUE]
```

### 8.2.5 combining levels

Bizarre things have been known to happen from combining levels. A safe approach is to create a new factor object. Here we change from individual letters to a vowel-consonant classification:

```
> flet <- factor(letters[c(1:5, 1:2)])
> flet
[1] a b c d e a b
Levels: a b c d e
> ftrans <- c(a='vowel', b='consonant', c='consonant',
+    d='consonant', e='vowel')
> fcv <- factor(ftrans[as.character(flet)])
> fcv
[1] vowel consonant consonant consonant vowel vowel consonant
Levels: consonant vowel
```

Probably more common is to combine some levels, but leave others alone:

```
> llet <- levels(flet)
> names(llet) <- llet
> llet
  a   b   c   d   e
"a" "b" "c" "d" "e"
> llet[c('a', 'b')] <- 'ab'
> llet
   a    b    c    d    e
"ab" "ab"  "c"  "d"  "e"
> fcom <- factor(llet[as.character(flet)])
> fcom
[1] ab ab c  d  e ab ab
Levels: ab c d e
```

### 8.2.6 do not subscript with factors

```
> x6 <- c(s=4, j=55, f=888)
> x6[c('s', 'f')]
s f
4 888
> x6[factor(c('s', 'f'))]
j s
55 4
```

### 8.2.7 no go for factors in ifelse

```
> ifelse(c(TRUE, FALSE, TRUE), factor(letters),
+   factor(LETTERS))
[1] 1 2 3
> ifelse(c(TRUE, FALSE, TRUE), factor(letters), LETTERS)
[1] "1" "B" "3"
```

(Recall that the length of the output of `ifelse` is always the length of the first argument. If you were expecting the first argument to be replicated, you shouldn't have.)

### 8.2.8 no c for factors

```
c(myfac1, myfac2)
```

just gives you the combined vector of integer codes. Certainly a method for `c` could be written for factors, but note it is going to be complicated—the levels of the factors need not match. It would be horribly messy for very little gain. This is a case in which R is not being overly helpful. Better is for you to do the combination that makes sense for the specific case at hand.

Another reason why there is not a `c` function for factors is that `c` is used in other contexts to simplify objects:

```
> c(matrix(1:4, 2))
[1] 1 2 3 4
```

The operation that `c` does on factors is consistent with this.

A generally good solution is:

```
c(as.character(myfac1), as.character(myfac2))
```

Or maybe more likely `factor` of the above expression. Another possibility is:

```
unlist(list(myfac1, myfac2))
```

For example:

```
> unlist(list(factor(letters[1:3]), factor(LETTERS[7:8])))
[1] a b c G H
Levels: a b c G H
```

This last solution does not work for ordered factors.

### 8.2.9 ordering in ordered

You need a bit of care when creating ordered factors:

```
> ordered(c(100, 90, 110, 90, 100, 110))
[1] 100 90 110 90 100 110
Levels: 90 < 100 < 110
> ordered(as.character(c(100, 90, 110, 90, 100, 110)))
[1] 100 90 110 90 100 110
Levels: 100 < 110 < 90
```

The automatic ordering is done lexically for characters. This makes sense in general, but not in this case. (Note that the ordering may depend on your locale.) You can always specify `levels` to have direct control.

You can have essentially this same problem if you try to sort a factor.

### 8.2.10 labels and excluded levels

The number of labels must equal the number of levels. Seems like a good rule. These can be the same going into the function, but need not be in the end. The issue is values that are excluded.

```
> factor(c(1:4,1:3), levels=c(1:4,NA), labels=1:5)
Error in factor(c(1:4, 1:3), levels = c(1:4, NA), ... :
invalid labels; length 5 should be 1 or 4
> factor(c(1:4,1:3), levels=c(1:4,NA), labels=1:4)
```

```
[1] 1 2 3 4 1 2 3
Levels: 1 2 3 4
> factor(c(1:4,1:3), levels=c(1:4,NA), labels=1:5,
+    exclude=NULL)
[1] 1 2 3 4 1 2 3
Levels: 1 2 3 4 5
```

And of course I lied to you. The number of labels can be 1 as well as the number of levels:

```
> factor(c(1:4,1:3), levels=c(1:4,NA), labels='Blah')
[1] Blah1 Blah2 Blah3 Blah4 Blah1 Blah2 Blah3
Levels: Blah1 Blah2 Blah3 Blah4
```

### 8.2.11 is missing missing or missing?

Missing values of course make sense in factors. It is entirely possible that we don't know the category into which a particular item falls.

```
> f1 <- factor(c('AA', 'BA', NA, 'NA'))
> f1
[1] AA BA <NA> NA
Levels: AA BA NA
> unclass(f1)
[1]  1  2 NA  3
attr(,"levels")
[1] "AA" "BA" "NA"
```

As we saw in Circle 8.1.67, there is a difference between a missing value and the string `'NA'`. In `f1` there is a category that corresponds to the string `'NA'`. Values that are missing are indicated not by the usual `NA`, but by `<NA>` (to distinguish them from `'NA'` the string when quotes are not used).

It is also possible to have a category that is missing values. This is achieved by changing the `exclude` argument from its default value:

```
> f2 <- factor(c('AA', 'BA', NA, 'NA'), exclude=NULL)
> f2
[1] AA BA <NA> NA
Levels: AA BA NA NA
> unclass(f2)
[1] 1 2 4 3
attr(,"levels")
[1] "AA" "BA" "NA" NA
```

Unlike in `f1` the core data of `f2` has no missing values.

Let's now really descend into the belly of the beast.

```
> f3 <- f2
> is.na(f3)[1] <- TRUE
> f3
[1] <NA> BA <NA> NA
Levels: AA BA NA NA
> unclass(f3)
[1] NA 2 4 3
attr(,"levels")
[1] "AA" "BA" "NA" NA
```

Here we have a level that is missing values, we also have a missing value in the core data.[1]

To summarize, there are two ways that missing values can enter a factor:

- Missing means we don't know what category the item falls into.
- Missing is the category of items that (originally) had missing values.

### 8.2.12 data frame to character

```
> xdf3 <- data.frame(a=3:2, b=c('x', 'y'))
> as.character(xdf3[1,])
[1] "3" "1"
```

This is a hidden version of coercing a factor to character. One approach to get the correct behavior is to use `as.matrix`:

```
> as.character(as.matrix(xdf3[1,]))
[1] "3" "x"
```

I'm not sure if it is less upsetting or more upsetting if you try coercing more than one row of a data frame to character:

```
> as.character(xdf3)
[1] "c(3, 2)" "c(1, 2)"
```

If the columns of the data frame include factors or characters, then converting to a matrix will automatically get you a characters:

```
> as.matrix(xdf3)
     a   b
[1,] "3" "x"
[2,] "2" "y"
```

[1] The author would be intrigued to hear of an application where this makes sense—an item for which it is unknown if it is missing or not.

### 8.2.13 nonexistent value in subscript

When a subscript contains values that are not present in the object, the results vary depending on the context:

```
> c(b=1)[c('a', 'b')]
<NA> b
  NA 1
> list(b=1)[c('a', 'b')]
$<NA>
NULL
$b
[1] 1
> matrix(1:2, 2, 1, dimnames=list(NULL, 'b'))[,c('a', 'b')]
Error: subscript out of bounds
> matrix(1:2, 1, 2, dimnames=list('b', NULL))[c('a', 'b'),]
Error: subscript out of bounds
> data.frame(b=1:2)[, c('a', 'b')]
Error in "[.data.frame"(data.frame(b = 1:2), , c("a", "b")) :
  undefined columns selected
> data.frame(V1=1, V2=2, row.names='b')[c('a', 'b'),]
   V1 V2
NA NA NA
b   1  2
```

Some people wonder why the names of the extraneous items show up as `NA` and not as `"a"`. An answer is that then there would be no indication that `"a"` was not a name in the object.

The examples here are for character subscripts, similar behavior holds for numeric and logical subscripts.

### 8.2.14 missing value in subscript

Here are two vectors that we will use:

```
> a <- c(rep(1:4, 3), NA, NA)
> b <- rep(1:2, 7)
> b[11:12] <- NA
> a
[1] 1 2 3 4 1 2 3 4 1 2 3 4 NA NA
> b
[1] 1 2 1 2 1 2 1 2 1 2 NA NA 1 2
```

We now want to create `anew` so that it is like `a` except it has `101` in the elements where `a` is less than 2 or greater than 3, and `b` equals 1.

```
> anew <- a
```

```
> anew[(a < 2 | a > 3) & b == 1] <- 101
> anew
[1] 101 2 3 4 101 2 3 4 101 2 3 4 NA NA
```

There were three values changed in `anew`; let's try again but give different values to those three:

```
> anew2 <- a
> anew2[(a < 2 | a > 3) & b == 1] <- 101:103
Error: NAs are not allowed in subscripted assignments
```

Now we get an error. Since the value being assigned into the vector has length greater than 1, the assignment with missing values in the subscripts is ambiguous. R wisely refuses to do it (frustrating as it may be). There is a simple solution, however:

```
> anew2[which((a < 2 | a > 3) & b == 1)] <- 101:103
> anew2
[1] 101 2 3 4 102 2 3 4 103 2 3 4 NA NA
```

The `which` function effectively treats `NA` as `FALSE`.

But we still have a problem in both `anew` and `anew2`. The 12th element of `a` is 4 (and hence greater than 3) while the 12th element of `b` is `NA`. So we don't know if the 12th element of `anew` should be changed or not. The 12th element of `anew` should be `NA`:

```
> anew[is.na(b) & (a < 2 | a > 3)] <- NA
> anew
[1] 101 2 3 4 101 2 3 4 101 2 3 NA NA NA
```

### 8.2.15 all missing subscripts

```
> letters[c(2,3)]
[1] "b" "c"
> letters[c(2,NA)]
[1] "b" NA
> letters[c(NA,NA)]
 [1] NA NA NA NA NA NA NA NA NA NA NA NA
[13] NA NA NA NA NA NA NA NA NA NA NA NA
[25] NA NA
```

What is happening here is that by default `NA` is logical—that is the most specific mode (see Circle 8.1.8) so the last command is subscripting with logical values instead of numbers. Logical subscripts are automatically replicated to be the length of the object.

### 8.2.16 missing value in if

```
if(NA) { # creates error
```

It is a rather common error for an `if` condition to be `NA`. When this occurs, it is common for the problem to be non-obvious. Debugging is called for in that case.

### 8.2.17 and and andand

An alternative title here could have been 'or or oror'.

There are two 'and' operators and two 'or' operators:

- `&&` and `||` go with `if`
- `&` and `|` go with `ifelse`

`&&` and `||`, like `if`, expect single element inputs. Because they only deal with single elements, they can do shortcuts. If the answer is known with the first (left) argument, then there is no need to evaluate the second.

```
> if(TRUE || stop()) 4 else 5
[1] 4
> if(TRUE && stop()) 4 else 5
Error:
> if(FALSE || stop()) 4 else 5
Error:
> if(FALSE && stop()) 4 else 5
[1] 5
```

This can be used to make sure that it is safe to perform a test, as in:

```
> if(ncol(x) > 6) { ...
Error in if (ncol(x) > 6) : argument is of length zero
> if(is.matrix(x) && ncol(x) > 6) { ... # okay
```

Note that in the last line `x` is excluded from being a data frame. If you want to allow both data frames and matrices, then testing the length of `dim(x)` would be an approach.

### 8.2.18 equal and equalequal

Just because `&&` and `&` have similar purposes, don't go thinking that `==` and `=` are similar. Completely different.

Fortunately R keeps you from making this error in a key context:

```
> if(x = 7) { ...
Error: unexpected '=' in "if(x ="
> if(x == 7) { ... # okay
```

The difference is:

- `==` is a logical operator that tests equality.
- `=` is an assignment operator similar to `<-` (but see Circle 8.2.26).

### 8.2.19 is.integer

`is.integer` is a test of how the data are stored, it does not test if the numbers are logically integers:

```
> is.integer(c(4, 0, 3))
[1] FALSE
```

The key thing to say here is that, almost surely, you do not care if an object is stored as integer. It is important if you are sending the data to C or Fortran. Otherwise you can bask in the ease of letting R take care of details so you can think about the big picture.

If you really want integers (that is, stored in integer format), then use "L":

```
> is.integer(c(4L, 0L, 3L))
[1] TRUE
> is.integer(c(4L, 0L, 3))
[1] FALSE
```

The `:` operator is one of the few places in R where integers are produced :

```
> is.integer(1:3)
[1] TRUE
> is.integer(c(1:3, 4))
[1] FALSE
> is.integer(c(1:3, 4:4))
[1] TRUE
```

Given experience with other languages, you may expect:

```
> is.integer( 4. )
[1] FALSE
> is.integer( 4 )
[1] FALSE
```

the first comand above to be `FALSE` and the second to be `TRUE`. That is, that using a decimal point signifies that you want a floating point number as opposed to an integer. As you see R has a fondness for floating point numbers.

You can coerce to integer, but (as always) be careful what you ask for:

```
> as.integer(c(0, 1, -2.99, 2.99))
[1]  0  1 -2  2
```

### 8.2.20 is.numeric, as.numeric with integers

An integer vector tests `TRUE` with `is.numeric`. However, `as.numeric` changes it from storage mode integer to storage mode double. If you care about it being integer, then you want to use `as.integer`.

```
> is.integer(c(4L, 0L))
[1] TRUE
> is.numeric(c(4L, 0L))
[1] TRUE
> is.integer(as.numeric(c(4L, 0L)))
[1] FALSE
```

### 8.2.21 is.matrix

The `is.matrix` function can cause surprises, not least because it can give different answers in R and S+.

```
> is.matrix(1:3)
[1] FALSE
> is.matrix(array(1:3, c(3,1)))
[1] TRUE
> is.matrix(array(1:3, c(3,1,1)))
[1] FALSE
> is.matrix(array(1:3, 3))
[1] FALSE
> is.matrix(data.frame(1:3))
[1] FALSE # would be TRUE in S+
> is.matrix(t(1:3))
[1] TRUE
```

The definition of "matrix" that `is.matrix` uses is that it is an array with a `dim` attribute of length 2. Note that the `t` function coerces a non-array to be a (column) matrix and then does the transpose.

Some people want objects to be matrices by default. It isn't going to happen. R is a language of general objects, not a matrix language.

### 8.2.22 max versus pmax

I care not to try to count the number of times I've got this wrong, nor to tally the hours I've spent tracking down the problem. And I'm only thinking of the time after I knew very well the difference between `max` and `pmax` (and `min` and `pmin`).

Recall from Circle 3 (page 17) that there are two senses of vectorization. `max` and `pmax` are each vectorized but in opposite senses.

- `max` returns the single number that is the largest of all the input.
- `pmax` returns a vector that for each index location is the maximum across inputs.

```
> max(1:5, 6:2)
[1] 6
```

```
> pmax(1:5, 6:2)
[1] 6 5 4 4 5
```

The 'p' in `pmax` stands for 'parallel'.

### 8.2.23 all.equal returns a surprising value

We met `all.equal` in Circle 1 (page 9) as an alternative to `'=='`. Numerical error causes `'=='` not to provide a useful result in many cases.

```
if(all(x == y)) { # wrong if there is numerical error
if(all.equal(x, y)) { # WRONG, not FALSE when not equal
if(isTRUE(all.equal(x, y)) { # right
```

### 8.2.24 all.equal is not identical

The purpose of `all.equal` is to compare items that may have some fuzziness to them. Sometimes the fuzziness that `all.equal` sees can be surprising:

```
> all.equal(as.numeric(NA), 0/0)
[1] TRUE
```

The `identical` function allows for no fuzziness at all:

```
> identical(as.numeric(NA), 0/0)
[1] FALSE
```

### 8.2.25 identical really really means identical

```
> xi <- 1:10
> yi <- 1:10
> identical(xi, yi[1:10])
[1] TRUE
> yi[11] <- 11
> identical(xi, yi[1:10])
[1] FALSE
> zi <- 1:10
> zi[11] <- 11L
> identical(xi, zi[1:10])
[1] TRUE
```

`xi` is stored as type integer. But once `yi` has been given one double value, it is stored as double.

As has already been stated, you are unlikely to need to care about how numbers are stored. If you think you care without a specific instance of why it matters, you should probably get over it.

Though identical is very strict about what objects that it considers to be the same, it doesn't go as far as insisting that they share the same place in memory. That is basically a foreign concept to R.

### 8.2.26 = is not a synonym of <-

The `'='` operator can mean the same thing as `'<-'` in a lot of circumstances, but there are times when it is different.

Consider the command:

```
foo(93, a = 47)
```

versus

```
foo(93, a <- 47)
```

These two commands may lead to entirely different results. You clearly do not want to use `'<-'` when you want to set an argument of a function.

A common occurrence where you don't want to use `'='` where `'<-'` is meant is:

```
system.time(result <- my.test.function(100))
```

If you used `'='` in the command above, R would think you were trying to set the `result` argument of `system.time`, which doesn't exist. (If using `system.time` is not a common occurrence for you, perhaps it should be.)

Standard advice is to avoid using `'='` when you mean `'<-'` even though it takes an extra keystroke. However, it is largely a matter of taste (as long as you know the differences).

### 8.2.27 complex arithmetic

The precedence with complex numbers may well not be what you expect. Consider the command:

```
> 1+3i - 3+5i
[1] -2+8i
```

### 8.2.28 complex is not numeric

```
> is.numeric(1+3i)
[1] FALSE
```

Complex numbers are numbers, but they are not numeric in R's sense. To test for numbers in the broader sense, you need:

```
is.numeric(x) || is.complex(x)
```

### 8.2.29 nonstandard evaluation

There are a few functions that allow names of objects as well as a character string of the name. For example:

```
help(subset)
```

works where

```
help('subset')
```

is what really makes sense.

The functions that do this are meant for interactive use. The intention of allowing names is to be helpful. Such helpfulness seems like a mixed blessing. It is hard to tell what the net time savings is of removing two keystrokes versus the periodic confusion that it causes.

If the named object contains a character string of what is really wanted, some of these functions give you what you want while others (often of necessity) do not.

```
foo <- 'subset'
help(foo) # gets help on subset
getAnywhere(foo) # finds foo, not subset
do.call('getAnywhere', list(foo)) # finds subset
```

A partial list of functions that have non-standard evaluation of arguments are: `help`, `rm`, `save`, `attach`, `require`, `library`, `subset`, `replicate`.

The `require` function has a program-safety mechanism in the form of the `character.only` argument.

```
require(foo) # load package foo
require(foo, character.only=FALSE) # load package foo
require(foo, character.only=TRUE) # load package named by foo
```

The same is true of `library`.

### 8.2.30 help for for

The logical thing to do to get help for `for` is:

```
?for
```

That doesn't work. Using the `help` function breaks in a seemingly different way:

```
help(for)
```

Instead do (for instance):

```
?'for'
help('for')
```

### 8.2.31 subset

The `subset` function is meant to provide convenience in interactive use. It often causes inconvenience and confusion when used inside functions. Use usual subscripting, not `subset`, when writing functions.

Patient: Doc, it hurts when I do this.
Doctor: Don't do that.

Here is an example of `subset` in action:

```
> xdf5 <- data.frame(R=1:2, J=3:4, E=5:6, K=7:8)
> subset(xdf5, select=J:K)
  J E K
1 3 5 7
2 4 6 8
> subset(xdf5, select=-E)
  R J K
1 1 3 7
2 2 4 8
```

The `select` argument allows VERY non-standard use of the `':'` and `'-'` operators. This can be a handy shortcut for interactive use. There is a grave danger of users expecting such tricks to work in other contexts. Even in interactive use there is the danger of expecting `J:K` to pertain to alphabetic order rather than order within the data frame.

Note also that `subset` returns a data frame even if only one column is selected.

### 8.2.32 = vs == in subset

There is a big difference between:

```
subset(Theoph, Subject = 1)
```

and

```
subset(Theoph, Subject == 1)
```

The latter is what is intended, the former does not do any subsetting at all.

### 8.2.33 single sample switch

The `sample` function has a helpful feature that is not always helpful. Its first argument can be either the population of items to sample from, or the number of items in the population. There's the rub.

```
> sample(c(4.9, 8.6), 9, replace=TRUE)
[1] 4.9 4.9 8.6 4.9 8.6 4.9 8.6 4.9 8.6
> sample(c(4.9), 9, replace=TRUE)
[1] 2 3 3 2 4 4 3 4 1
```

If the population is numeric, at least 1 and of size one (due, say, to selection within a function), then it gets interpreted as the size of the population. Note in the example above the size is rounded down to the nearest integer.

There is a kludgy workaround, which is to make the population character:

```
> as.numeric(sample(as.character(c(4.9)), 9, replace=TRUE))
[1] 4.9 4.9 4.9 4.9 4.9 4.9 4.9 4.9 4.9
```

### 8.2.34 changing names of pieces

R does an extraordinary job of ferreting out replacement statements. For example, the following actually does what is intended:

```
names(mylist$b[[1]]) <- letters[1:10]
```

It is possible to get it wrong though. Here is an example:

```
> right <- wrong <- c(a=1, b=2)
> names(wrong[1]) <- 'changed'
> wrong
a b
1 2
> names(right)[1] <- 'changed'
> right
changed       b
      1       2
```

What goes wrong is that we change names on something that is then thrown away. So to change the first two names in our ridiculous example, we would do:

```
names(mylist$b[[1]])[1:2] <- LETTERS[1:2]
```

### 8.2.35 a puzzle

```
> class(dfxy)
[1] "data.frame"
> length(dfxy)
[1] 8
> length(as.matrix(dfxy))
[1] 120
```

What is

```
nrow(dfxy)
```

### 8.2.36 another puzzle

If the following is a valid command:

```
weirdFun()()()
```

what does `weirdFun` return?

Write an example.

### 8.2.37 data frames vs matrices

A matrix and a data frame look the same when printed. That is good—they are conceptually very similar. However, they are implemented entirely differently.

Objects that are conceptually similar but implemented differently are a good source of confusion.

```
> x %*% y
Error in x %*% y : requires numeric matrix/vector arguments
```

The problem here is that while `x` looks like a matrix, it is actually a data frame. A solution is to use `as.matrix`, or possibly `data.matrix`,

In theory the actual implementation of data frames should not matter at all to the user. Theory often has some rough edges.

### 8.2.38 apply not for data frames

One rough edge is applying a function to a data frame. The `apply` function often doesn't do what is desired because it coerces the data frame to a matrix before proceeding.

```
apply(myDataFrame, 2, class) # not right
```

Data frames are actually implemented as a list with each component of the list being a column of the data frame. Thus:

```
lapply(myDataFrame, class)
```

does what was attempted above.

### 8.2.39 data frames vs matrices (reprise)

Consider the command:

```
array(sample(x), dim(x))
```

This permutes the elements of a matrix. If `x` is a data frame, the command will work but the result will most assuredly not be what you want.

It is possible to get a column of a data frame with a command like:

```
x$B
```

If you try this with a matrix you'll get an error similar to:

```
Error in x$B : $ operator is invalid for atomic vectors
```

If your x might be either a data frame or a matrix, it will be better to use:

```
x[, 'B']
```

On the other hand, if you want to rule out the possibility of a matrix then `$` might be the better choice.

Operations with data frames can be slower than the same operation on the corresponding matrix. In one real-world case, switching from data frames to matrices resulted in about four times the speed.

Simpler is better.

### 8.2.40 names of data frames and matrices

The `names` of a data frame are not the same as the `names` of the corresponding matrix. The `names` of a data frame are the column names while the `names` of a matrix are the names of the individual elements.

Items that are congruent are:

- `rownames`
- `colnames`
- `dimnames`

### 8.2.41 conflicting column names

Here is an example where expectations are frustrated:

```
> one.col.mat <- cbind(matname=letters[1:3])
> one.col.mat
     matname
[1,] "a"
[2,] "b"
[3,] "c"
> data.frame(x=one.col.mat)
  matname
1       a
2       b
3       c
> data.frame(x=cbind(letters[1:3]))
  x
1 a
2 b
3 c
```

When the call to `data.frame` uses a tag (name) for an item, it is expected that the corresponding column of the output will have that name. However, column names that are already there take precedence.

Notice also that the data frames contain a factor column rather than character.

### 8.2.42 cbind favors matrices

If you `cbind` two matrices, you get a matrix. If you `cbind` two data frames, you get a data frame. If you `cbind` two vectors, you get a matrix:

```
> is.matrix(cbind(x=1:10, y=rnorm(10)))
[1] TRUE
```

If you want a data frame, then use the `data.frame` function:

```
> dfxy <- data.frame(x=1:10, y=rnorm(10))
```

### 8.2.43 data frame equal number of rows

A data frame is implemented as a list. But not just any list will do—each component must represent the same number of rows. If you work hard enough, you might be able to produce a data frame that breaks the rule. More likely your frustration will be that R stops you from getting to such an absurd result.

### 8.2.44 matrices in data frames

Let's make two data frames:

```
> ymat <- array(1:6, c(3,2))
> xdf6 <- data.frame(X=101:103, Y=ymat)
> xdf7 <- data.frame(X=101:103)
> xdf7$Y <- ymat
> xdf6
    X Y.1 Y.2
1 101   1   4
2 102   2   5
3 103   3   6
> xdf7
    X Y.1 Y.2
1 101   1   4
2 102   2   5
3 103   3   6
> dim(xdf6)
[1] 3 3
> dim(xdf7)
[1] 3 2
```

They print exactly the same. But clearly they are not the same since they have different dimensions.

```
> xdf6[, 'Y.1']
[1] 1 2 3
> xdf7[, 'Y.1']
Error in "[.data.frame"(xdf7, , "Y.1") :
  undefined columns selected
> xdf6[, 'Y']
Error in "[.data.frame"(xdf6, , "Y") :
  undefined columns selected
> xdf7[, 'Y']
     [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6
```

`xdf6` includes components `Y.1` and `Y.2`. `xdf7` does not have such components (in spite of how it is printed)—it has a `Y` component that is a two-column matrix.

You will surely think that allowing a data frame to have components with more than one column is an abomination. That will be your thinking unless, of course, you've had occasion to see it being useful. The feature is worth the possible confusion, but perhaps a change to printing could reduce confusion.

## 8.3 Devils

The most devilish problem is getting data from a file into R correctly.

### 8.3.1 read.table

The `read.table` function is the most common way of getting data into R. Reading its help file three times is going to be very efficient time management if you ever use `read.table`. In particular the `header` and `row.names` arguments control what (if anything) in the file should be used as column and row names.

Another great time management tool is to inspect the result of the data you have read before attempting to use it.

### 8.3.2 read a table

The `read.table` function does not create a table—it creates a data frame. You don't become a book just because you read a book. The `table` function returns a table.

The idea of `read.table` and relatives is that they read data that are in a rectangular format.

### 8.3.3 the missing, the whole missing and nothing but the missing

Misreading missing values is an efficacious way of producing garbage. Missing values can become non-missing, non-missing values can become missing, logically numeric columns can become factors.

The `na.strings` argument to `read.table` needs to be set properly. An example might be:

```
na.strings=c('.', '-999')
```

### 8.3.4 misquoting

A quite common file format is to have a column of names followed by some number of columns of data. If there are any apostrophes in those names, then you are likely to get an error reading the file unless you have set the `quote` argument to `read.table`. A likely value for `quote` is:

```
quote=''
```

This sounds like easy advise, but almost surely it is not going to be apparent that quotes are the problem. You may get an error that says there was the wrong number of items in a line. When you get such an error, it is often a good idea to use `count.fields` to get a sense of what R thinks about your file. Something along the lines of:

```
foo.cf <- count.fields('foo.txt', sep='\t')
table(foo.cf)
```

### 8.3.5 thymine is TRUE, female is FALSE

You are reading in DNA bases identified as A, T, G and C. The columns are read as factors. Except for the column that is all T—that column is logical.

Similarly, a column for gender that is all F for female will be logical.

The solution is to use the `read.table` argument:

```
colClasses='character'
```

or

```
colClasses='factor'
```

as you like.

If there are columns of other sorts of data, then you need to give `colClasses` a vector of appropriate types for the columns in the file.

Using `colClasses` can also make the call much more efficient.

Figure 8.3: The treacherous to country and the treacherous to guests and hosts by Sandro Botticelli.

### 8.3.6 whitespace is white

Whitespace is invisible, and we have a predilection to believe that invisible means non-existent.

```
> factor(c('A ', 'A', 'B'))
[1] A  A  B
Levels: A A  B
```

It is extraordinarily easy to get factors like this when reading in data. Setting the `strip.white` argument of `read.table` to `TRUE` can prevent this.

### 8.3.7 extraneous fields

When a file has been created in a spreadsheet, there are sometimes extraneous empty fields in some of the lines of the file. In such a case you might get an error similar to:

```
> mydat <- read.table('myfile', header=TRUE, sep='\t')
Error in scan(file, what, nmax, sep, dec, quote, skip, :
  line 10 did not have 55 elements
```

This, of course, is a perfect instance to use `count.fields` to see what is going on. If extraneous empty fields do seem to be the problem, then one solution is:

```
> mydat <- read.table('myfile', header=TRUE, sep='\t',
+    fill=TRUE)
> mydat <- mydat[, 1:53]
```

At this point, it is wiser than usual to carefully inspect the results to see that the data are properly read and aligned.

### 8.3.8 fill and extraneous fields

When the `fill` argument is `TRUE` (which is the default for `read.csv` and `read.delim` but not for `read.table`), there can be trouble if there is a variable number of fields in the file.

```
> writeLines(c("A,B,C,D",
+              "1,a,b,c",
+              "2,d,e,f",
+              "3,a,i,j",
+              "4,a,b,c",
+              "5,d,e,f",
+              "6,g,h,i,j,k,l,m,n"),
+   con=file("test.csv"))
> read.csv("test.csv")
  A B C D
```

```
1 1 a b c
2 2 d e f
3 3 a i j
4 4 a b c
5 5 d e f
6 6 g h i
7 j k l m
8 n
> read.csv("test.csv", fill=FALSE)
Error in scan(file = file, what = what, ...  :
 line 6 did not have 4 elements
```

The first 5 lines of the file are checked for consistency of the number of fields. Use `count.fields` to check the whole file.

### 8.3.9 reading messy files

`read.table` and its relatives are designed for files that are arranged in a tabular form. Not all files are in tabular form. Trying to use `read.table` or a relative on a file that is not tabular is folly—you can end up with mangled data.

Two functions used to read files with a more general layout are `scan` and `readLines`.

### 8.3.10 imperfection of writing then reading

Do not expect to write data to a file (such as with `write.table`), read the data back into R and have that be precisely the same as the original. That is doing two translations, and there is often something lost in translation.

You do have some choices to get the behavior that you want:

- Use `save` to store the object and use `attach` or `load` to use it. This works with multiple objects.
- Use `dput` to write an ASCII representation of the object and use `dget` to bring it back into R.
- Use `serialize` to write and `unserialize` to read it back. (But the help file warns that the format is subject to change.)

### 8.3.11 non-vectorized function in integrate

The `integrate` function expects a vectorized function. When it gives an argument of length 127, it expects to get an answer that is of length 127. It shares its displeasure if that is not what it gets:

```
> fun1 <- function(x) sin(x) + sin(x-1) + sin(x-2) + sin(x-3)
```

```
> integrate(fun1, 0, 2)
-1.530295 with absolute error < 2.2e-14
> fun2 <- function(x) sum(sin(x - 0:3))
> integrate(fun2, 0, 2)
Error in integrate(fun2, 0, 2) :
evaluation of function gave a result of wrong length
In addition: Warning message:
longer object length
   is not a multiple of shorter object length in: x - 0:3
> fun3 <- function(x) rowSums(sin(outer(x, 0:3, '-')))
> integrate(fun3, 0, 2)
-1.530295 with absolute error < 2.2e-14
```

`fun1` is a straightforward implementation of what was wanted, but not easy to generalize. `fun2` is an ill-conceived attempt at mimicking `fun1`. `fun3` is a proper implementation of the function using `outer` as a step in getting the vectorization correct.

### 8.3.12 non-vectorized function in outer

The function given to `outer` needs to be vectorized (in the usual sense):

```
> outer(1:3, 4:1, max)
Error in dim(robj) <- c(dX, dY) :
  dims [product 12] do not match the length of object [1]
> outer(1:3, 4:1, pmax)
     [,1] [,2] [,3] [,4]
[1,]    4    3    2    1
[2,]    4    3    2    2
[3,]    4    3    3    3
> outer(1:3, 4:1, Vectorize(function(x, y) max(x, y)))
     [,1] [,2] [,3] [,4]
[1,]    4    3    2    1
[2,]    4    3    2    2
[3,]    4    3    3    3
```

The `Vectorize` function can be used to transform a function (by essentially adding a loop—it contains no magic to truly vectorize the function).

### 8.3.13 ignoring errors

You have a loop in which some of the iterations may produce an error. You would like to ignore any errors and proceed with the loop. One solution is to use `try`.

The code:

```
ans <- vector('list', n)
for(i in seq(length.out=n)) {
    ans[[i]] <- rpois(round(rnorm(1, 5, 10)), 10)
}
```

will fail when the number of Poisson variates requested is negative. This can be modified to:

```
ans <- vector('list', n)
for(i in seq(length.out=n)) {
    this.ans <- try(rpois(round(rnorm(1, 5, 10)), 10))
    if(!inherits(this.ans, 'try-error')) {
        ans[[i]] <- this.ans
    }
}
```

Another approach is to use `tryCatch` rather than `try`:

```
ans <- vector('list', n)
for(i in seq(length.out=n)) {
    ans[[i]] <- tryCatch(rpois(round(rnorm(1, 5, 10)), 10),
        error=function(e) NaN)
}
```

### 8.3.14 accidentally global

It is possible for functions to work where they are created, but not to work in general. Objects within the function can be global accidentally.

```
> myfun4 <- function(x) x + y
> myfun4(30)
[1] 132
> rm(y)
> myfun4(30)
Error in myfun4(30) : Object "y" not found
```

The `findGlobals` function can highlight global objects:

```
> library(codetools)
> findGlobals(myfun4)
[1] "+" "y"
```

### 8.3.15 handling ...

The `'...'` construct can be a slippery thing to get hold of until you know the trick. One way is to package it into a list:

```
function(x, ...) {
   dots <- list(...)
   if('special.arg' %in% names(dots)) {
   # rest of function
}
```

Another way is to use `match.call`:

```
function(x, ...) {
   extras <- match.call(expand.dots=FALSE)$...
   # rest of function
}
```

If your function processes the arguments, then you may need to use `do.call`:

```
function(x, ...) {
    # ...
    dots <- list(...)
    ans <- do.call('my.other.fun', c(list(x=x),
        dots[names(dots) %in% spec]))
    # ...
}
```

### 8.3.16 laziness

R uses lazy evaluation. That is, arguments to functions are not evaluated until they are required. This can save both time and memory if it turns out the argument is not required.

In extremely rare circumstances something is not evaluated that should be. You can use `force` to get around the laziness.

```
> xr <- lapply(11:14, function(i) function() i^2)
> sapply(1:4, function(j) xr[[j]]())
[1] 196 196 196 196
> xf <- lapply(11:14, function(i) {force(i); function() i^2})
> sapply(1:4, function(j) xf[[j]]())
[1] 121 144 169 196
```

Extra credit for understanding what is happening in the `xr` example.

### 8.3.17 lapply laziness

`lapply` does not evaluate the calls to its `FUN` argument. Mostly you don't care. But it can have an effect if the function is generic. It is safer to say:

```
lapply(xlist, function(x) summary(x))
```

than to say:

```
lapply(xlist, summary)
```

### 8.3.18 invisibility cloak

In rare circumstances the visibility of a result may not be as expected:

```
> myfun6 <- function(x) x
> myfun6(zz <- 7)
> .Last.value
[1] 7
> a6 <- myfun6(zz <- 9)
> a6
[1] 9
> myfun6(invisible(11))
> myfun7 <- function(x) 1 * x
> myfun7(invisible(11))
[1] 11
```

### 8.3.19 evaluation of default arguments

Consider:

```
> myfun2 <- function(x, y=x) x + y
> x <- 100
> myfun2(2)
[1] 4
> myfun2(2, x)
[1] 102
```

Some people expect the result of the two calls above to be the same. They are not. The default value of an argument to a function is evaluated inside the function, not in the environment calling the function.

Thus writing a function like the following will not get you what you want.

```
> myfun3 <- function(x=x, y) x + y
> myfun3(y=3)
Error in myfun3(y = 3) : recursive default argument reference
```

(The actual error message you get may be different in your version of R.)

The most popular error to make in this regard is to try to imitate the default value of an argument. Something like:

```
> myfun5 <- function(x, n=xlen) { xlen <- length(x); ...}
> myfun5(myx, n=xlen-2)
```

`xlen` is defined inside `myfun5` and is not available for you to use when calling `myfun5`.

### 8.3.20 sapply simplification

The `sapply` function "simplifies" the output of `lapply`. It isn't always so simple. That is, the simplification that you get may not be the simplification you expect. This uncertainty makes `sapply` not so suitable for use inside functions. The `vapply` function is sometimes a safer alternative.

### 8.3.21 one-dimensional arrays

Arrays can be of any positive dimension (modulo memory and vector length limits). In particular, one-dimensional arrays are possible. Almost always these look and act like plain vectors. Almost.

Here is an example where they don't:

```
> df2 <- data.frame(x=rep(1, 3), y=tapply(1:9,
+    factor(rep(c('A', 'B', 'C'), each=3)), sum))
> df2
  x y
A 1 6
B 1 15
C 1 24
> tapply(df2$y, df2$x, length)
1
3
> by(df2$y, df2$x, length)
INDICES: 1
[1] 1
> by(as.vector(df2$y), df2$x, length)
INDICES: 1
[1] 3
```

`tapply` returns an array, in particular it can return a one-dimensional array—which is the case with `df2$y`. The `by` function in this case when given a one-dimensional array produces the correct answer to a question that we didn't think we were asking.

One-dimensional arrays are neither matrices nor (exactly) plain vectors.

### 8.3.22 by is for data frames

The `by` function is essentially just a pretty version of `tapply` for data frames. The "for data frames" is an important restriction. If the first argument of your call to `by` is not a data frame, you may be in for trouble.

```
> tapply(array(1:24, c(2,3,4)), 1:24 %% 2, length)
0 1
12 12
> by(array(1:24, c(2,3,4)), 1:24 %% 2, length)
```

```
Error in tapply(1:2L, list(INDICES = c(1, 0, 1, 0, 1, 0, 1,  :
  arguments must have same length
```

In this example we have the good fortune of an error being triggered, we didn't have that for the problem in Circle 8.3.21.

### 8.3.23 stray backquote

A stray backquote in a function definition can yield the error message:

```
symbol print-name too long
```

The backquote is sometimes (too) close to the tab key and/or the escape key. It is also close to minimal size and hence easy to overlook.

### 8.3.24 array dimension calculation

There are times when the creation of matrices fails to be true to the intention:

```
> mf <- matrix(runif((2 - .1) / .1 * 5), ncol=5)
Warning message: data length [94] is not a sub-multiple or
  multiple of the number of rows [19] in matrix
```

Notice that the matrix is created—that is a warning not an error—the matrix is merely created inappropriately. If you ignore the warning, there could be consequences down the line.

Let's investigate the ingredients:

```
> (2 - .1) / .1
[1] 19
> (2 - .1) / .1 - 19
[1] -3.552714e-15
> as.integer((2 - .1) / .1)
[1] 18
```

When R coerces from a floating point number to an integer it truncates rather than rounds.

The moral of the story is that `round` can be a handy function to use. In a sense this problem really belongs in Circle 1 (page 9), but the subtlety makes it difficult to find.

### 8.3.25 replacing pieces of a matrix

We have two matrices:

```
> m6 <- matrix(1:6, 3)
> m4 <- matrix(101:104, 2)
> m6
```

```
     [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6
> m4
     [,1] [,2]
[1,]  101  103
[2,]  102  104
```

Our task is to create a new matrix similar to `m6` where some of the rows are replaced by the first row of `m4`. Here is the natural thing to do:

```
> m6new <- m6
> m6new[c(TRUE, FALSE, TRUE), ] <- m4[1,]
> m6new
     [,1] [,2]
[1,]  101  101
[2,]    2    5
[3,]  103  103
```

We are thinking about rows being the natural way of looking at the problem. The problem is that that isn't the R way, despite the context.

One way of getting what we want is:

```
> s6 <- c(TRUE, FALSE, TRUE)
> m6new[s6, ] <- rep(m4[1,], each=sum(s6))
> m6new
     [,1] [,2]
[1,]  101  103
[2,]    2    5
[3,]  101  103
```

### 8.3.26 reserved words

R is a language. Because of this, there are reserved words that you can not use as object names. Perhaps you can imagine the consequences if the following command actually worked:

```
FALSE <- 4
```

You can see the complete list of reserved words with:

```
?Reserved
```

### 8.3.27 return is a function

Unlike some other languages `return` is a function that takes the object meant to be returned. The following construct does NOT do what is intended:

```
return (2/5) * 3:9
```

It will return 0.4 and ignore the rest.

### 8.3.28 return is a function (still)

`return` is a function and not a reserved word.

```
> # kids, don't try this at home
> return <- function(x) 4 * x
> # notice: no error
> rm(return)
```

### 8.3.29 BATCH failure

Friday afternoon you start off a batch job happy in the knowledge that come Monday morning you will have the results of sixty-some hours of computation in your hands. Come Monday morning results are nowhere to be found. The job fell over after an hour because of a stray comma in your file of commands.

Results can't be guaranteed, but it is possible to at least test for that stray comma and its mates. Once you've written your file of commands, parse the file:

```
parse(file='batchjob.in')
```

If there is a syntax error in the file, then you'll get an error and a location for the (first) error. If there are no syntax errors, then you'll get an expression (a large expression).

### 8.3.30 corrupted .RData

There are times when R won't start in a particular location because of a corrupted `.RData` file. If what you have in the `.RData` is important, this is bad news.

Sometimes this can be caused by a package not being attached in the R session that the file depends on. Whether or not this is the problem, you can try starting R in vanilla mode (renaming the `.RData` file first is probably a good idea) and then try attaching the file.

In principle it should be possible to see what objects a `.RData` file holds and extract a selection of objects from it. However, I don't know of any tools to do that.

### 8.3.31 syntax errors

Syntax errors are one of the most common problems, especially for new users. Unfortunately there is no good way to track down the problem other than

puzzling over it. The most common problems are mismatched parentheses or square brackets, and missing commas.

Using a text editor that performs syntax highlighting can eliminate a lot of the problems.

Here is a particularly nasty error:

```
> lseq <- seq(0, 1, 1ength=10)
Error: unexpected input in "seq(0, 1, 1en"
```

Hint: the end of the error message is the important location. In fact, the last letter that it prints is the first point at which it knew something was wrong.

### 8.3.32 general confusion

If you are getting results that are totally at odds with your expectations, look where you are stepping:

- Objects may be different than you expect. You can use `str` to diagnose this possibility. (The output of `str` may not make much sense immediately, but a little study will reveal what it is saying.)
- Functions may be different than you expect. Try using `conflicts` to diagnose this.
- Pretty much the only thing left is your expectations.

Calls to `browser`, `cat` and `debugger` can help you eliminate ghosts, chimeras and devils. But the most powerful tool is your skepticism.

# Circle 9

# Unhelpfully Seeking Help

Here live the thieves, guarded by the centaur Cacus. The inhabitants are bitten by lizards and snakes.

There's a special place for those who—not being content with one of the 8 Circles we've already visited—feel compelled to drag the rest of us into hell.

The road to writing a mail message should include at least the following stops:

## 9.1 Read the appropriate documentation.

"RTFM" in the jargon. There is a large amount of documentation about R, both official and contributed, and in various formats. A large amount of documentation means that it is often nontrivial to find what you are looking for—especially when frustration is setting in and blood pressure is rising.

**Breathe.**

There are various searches that you can do. R functions for searching include `help.search`, `RSiteSearch` and `apropos`.

If you are looking for particular functionality, then check the Task Views (found on the left-side menu of CRAN).

If you have an error, then look in rather than out—debug the problem. One way of debugging is to set the `error` option, and then use the `debugger` function:

```
options(error=dump.frames)
# command that causes the error
debugger()
```

The `debugger` function then provides a menu of the stack of functions that have been called at the point of the error. You can inspect the state of the objects inside these functions, and hopefully understand what the problem is.

Figure 9.1: The thieves by Sandro Botticelli.

As Virgil said to me, "I'm pleased with all your questions, but one of them might have found its answer when you saw the red stream boiling."

## 9.2 Check the FAQ

Most occurrences of questions are frequently asked questions. Looking through the FAQ will often solve your problem. Even if it doesn't, you will probably learn some things that will avoid later frustration.

## 9.3 Update

Sometimes you are having a problem that has already been fixed. If the problem is in a contributed package, you can do:

```
update.packages()
```

But this will only give you the latest possible package given the version of R that you are running. If you are using an old version of R, then you can miss out on fixes in packages.

There can also be problems if some packages are updated while others are not.

## 9.4 Read the posting guide

This will give you another point of view about how to approach the remaining steps. In particular, it will instruct you on what types of questions belong on the various mailing lists.

Another good resource (not specific to R, but apropos) is a web page called "How to ask questions the smart way".

If you have faithfully performed the tasks up to here, you probably do not need to continue. But do continue if it is warranted.

You can do:

```
help.request()
```

on some platforms. This will create a file containing some of the important information that should be in the message. It also reminds you of steps that you should take.

## 9.5 Select the best list

Your choices are R-help, R-devel and the special interest groups. Or the Bioconductor list if your question relates to a Bioconductor package.

Pick one—cross posting is seriously discouraged.

There are some topics that should definitely be sent to a special interest group. For example, questions about garch should go to R-sig-finance. No one outside of finance knows about garch, nor will they ever. Non-finance people have no alternative but to think that a garch is someone who lives in Garching. Garch is a specifically financial model.

Sending the question to the right list is in everyone's best interest. If you send a question about garch to R-help, then:

- Some of the people most qualified to answer your question will not see it (my guess is that the vast majority of subscribers to R-sig-finance do not subscribe to R-help).
- There will be thousands of people for whom the question will be a complete waste of time.
- There will be people in the special interest group who could profit from the answers, but who will never see the answers.

If the functionality you are concerned with is from a contributed package, seriously consider writing only to the maintainer of the package. Should you deem it appropriate to write to a list, then certainly say what package or packages are involved.

Do **NOT** file a bug report unless you are absolutely sure it is a bug—bug reports entail additional work on the part of R Core. If the behavior is discussed in this document, it is not a bug. Just because something doesn't work on your machine, that does not mean it is a problem in R. If there is a question mark in your statement (or your mind), it is not (yet) a bug. It can not be a bug if you do not have a reproducible method of exhibiting the behavior. It is a bug if you have a well-reasoned argument of why the current behavior is bad, it is not documented to have the current behavior, and you have a patch to fix the problem. Patches are highly appreciated. Note that "current behavior" means the buggy behavior needs to be exhibited in the development version of R—do not consider it enough to only check whatever version of R you happen to be running. Also check to make sure the bug has not already been reported.

Even if it is clearly a bug, it may be inappropriate to file an R bug report. The bug need not be in R, but may be in some other piece of software. If in any doubt, send a message to R-devel instead. In particular do not file an R bug report for a contributed package—send your message to the package maintainer.

Another do not: Do not hijack an existing thread. That will make a mess for people viewing the list by threads. Make a new message addressed to the list.

## 9.6 Use a descriptive subject line

Recall what words you used to search the archives (which you did do) to try to find an answer to your problem, and use a selection of those. Subjects like "Problem with code" and "Help!!" are less than perfect. A legacy of your mail should be to improve things for other users—that is unlikely to happen without an explicit subject line.

With an appropriate subject, more of the right people will read your message and hence be in a position to give you an answer.

Do not include words like "urgent". The help you receive on the mailing lists is a gift, not a right. Being pushy is likely to engender worse service, not better service.

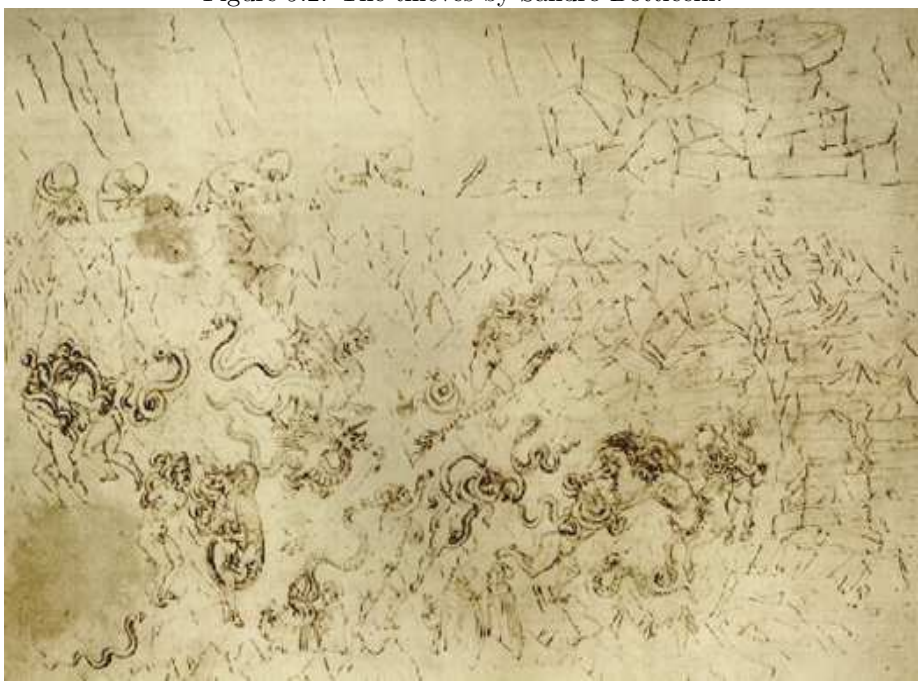
At the other end of the message there is room for your identity. Some people refuse to respond to anonymous messages. I find it hard to believe that many people refuse to respond to a message because the sender *is* identified. So on balance you may get better response if you identify yourself.

## 9.7 Clearly state your question

A statement like:

> When I use function `blahblah`, it doesn't work.

Figure 9.2: The thieves by Sandro Botticelli.



is not a clear statement of your question. We don't know what "use" means, we don't know what you expect "work" to look like, and we don't know what "doesn't work" means.

Explain:

- What function you are using (for example, there are a number of garch implementations—you need to say which one you are using).
- What you want.
- What you expected.
- Show us what happened.
- Show us the output of `str` on your data.

Sometimes background on why you are asking the question is relevant. Consider the question:

> Is there a way to order pizza with R?

The answer is, of course, "Of course there is a way to order pizza. This ***is*** R."

The question lacks both specificity and background (though it is mercifully brief). The answer to how to do the operation could depend on whether you want it delivered, and what size it should be. And do you want anchovies? If you provide background, you may get an answer that proposes a better—but entirely different—way of getting nutrients into your bloodstream.

Do not confuse a warning with an error. There are two differences:

1. warnings say "warning" and errors say "error".
2. the computation continues when there is a warning but is interrupted when there is an error.

If there really is an error, then give the results of:

```
traceback()
```

The word "crash" is very ambiguous. It would be better if you didn't use the word at all. If you do use it, you need to explain **exactly** what you mean. In addition to avoiding the use of vague words like "crash", you can be informative by displaying the results of `sessionInfo()`.

If error or warning messages are not in English and you are writing to an English mailing list, then translating pertinent messages would be in your best interest. But do show the real message as well.

If you are asking if method XYZ is implemented in R, then say that XYZ stands for Xeric Yare Zeugma (and hence not X-raY Zoometry). Give a brief explanation and a reference (preferably available online). The same technique, or something suitably similar, may well go by a different name.

Did I say you should give the results of `sessionInfo()`? The more information about the version of R you are using and your machine, the better. If the information is accurate, that's a plus.

## 9.8 Give a minimal, self-contained example

Note this does not say, "Give an example." It says to give a minimal, self-contained example. A minimal, self-contained example allows readers to reproduce the problem easily. The easier you make it for your readers, the more likely you receive help.

The word "minimal" implies an optimization. Elements of that optimization include:

- Minimize the number of packages involved. Ideal is if a vanilla session suffices.
- Minimize the number of functions involved.
- Minimize the size of any functions that are yours.

- Minimize the number and size of datasets involved. If peculiar data are required and your data are complicated, large and/or proprietary, then make up some data that exhibits the problem.

Often the process of making a **minimal** example reveals the problem. If the problem does not reveal itself, then keep these hints in mind:

- Make your example easy to cut and paste. The `dput` function is sometimes useful for this.
- If the example involves random numbers, then use `set.seed` to make the numbers non-random.
- Using data that comes with R is often the easiest for your readers.
- Format the code to be easy to understand—the space bar is an excellent resource.

Your minimal, self-contained example should **never ever** include a line of code like:

```
rm(list=ls())
```

There's a special special place for those who try to lull their would-be helpers into destroying their data.

It can not be emphasized enough that a message is putting yourself at the mercy of strangers. If someone has the wit and knowledge to answer your question, they probably have other things they would like to do. Making your message clear, concise and user-friendly gives you the best hope of at least one of those strangers diverting their attention away from their life towards your problem.

## 9.9 Wait

Don't send the message immediately. Wait some amount of time—at least 1 hour, at most 1.7348 days. Leave the room you're in.

Now reread the message from a typical list member's point of view. The answer may become apparent. More likely you may see how the question could be made more clear. Add information that only you know but which the message assumes the reader knows. Imagine yourself going through all of the steps of your problem from the beginning.

Send the message in plain text, not html.

Only send the message once. Just because you don't immediately see your message on the list does not mean it didn't go through. Seeing the same message multiple times annoys people and reduces the chances they will answer you. There seems to be positive correlation between a person's level of annoyance at this and ability to answer questions.

# Postscript

VIRGIL and I came upon the road leading to the bright world. We climbed through an opening to see once again the stars.

Most of this was stolen from the archives of R-help (thieves are consigned to Circle 9 [page 115], as you'll recall). Thanks go to Tim Triche, Jr. and especially Mark Difford for help with the table of contents and the index, and for well-placed prods. Mark's version of the source document went through an inferno of its own.

What spark of life there may be in these scribblings is due largely to the contributors of R-help, and to Beatrice.

# Index