# Rchaeology

Paul E. Johnson <pauljohn @ ku.edu>

June 12, 2012

This document was initiated on May 31, 2012. The newest copy will always be available at `http://pj.freefaculty.org/R`, either in PDF or HTML. It is also available as a vignette in the R package "rockchalk".

**Rchaeology:** The study of R programming by investigation of R source code. It is the effort to discern the programming strategies, idioms, and style of R programmers in order to better communicate with them.

**Rchaeologist:** One who practices Rchaeology.

These are Rcheological observations about the style and mannerisms of R programmers in their native habitats. Almost all of the insights here are gathered from the r-help and r-devel emails lists, the stackoverflow website pages for R, and the R source code itself. These are lessons from the "school of hard knocks."

How is this different from Rtips(`http://pj.freefaculty.org/R/Rtips.{pdf,html}`)?

1. This is oriented toward programming R, rather than using R.
2. It is more synthetic, aimed more at finding "what's right" rather than "what works."
3. It is written with Sweave (using Harrell's Sweavel style) so that code examples work.

## 1 Style Guides

The R Core Team has not been eager to write out a formal list of criteria that define "good R style." I think they don't agree among themselves about many details. The *R Internals* section "R coding standards," is quite brief. Nature abhors a vacuum, as they say. Many others have seen fit to try to fill in the gaps (Google R style guide[1]; Hadley Wickham's Style Guide[2]). In my R group at the University of Kansas, we have sought to do the same. Aaron Boulton, surveyed these efforts and we developed some guidelines for our group.

It is important to remember the following. First, any advice that does not come directly from the R Core Team has no "authority." I have advice, Hadley has advice, but none of it can be used as a trope with which to bludgeon someone who does things differently. Second, code writers can make ugly code that "runs," but they can't compel anyone else to read it. With few exceptions, coding style is not about making things "work," it is about making them work in a way that is understood by the widest possible audience.

Generally speaking, what should your code look like? Here are the two best answers I have.

1. Open the source code for R itself, and navigate to the directory src/library/stats/R. Open the file "lm.R". There's your answer.
2. Open an R session, run the following commands

```
> lm
> summary.lm
> stats:::print.summary.lm
```

[1]`http://google-styleguide.googlecode.com/svn/trunk/google-r-style.html`
[2]`https://github.com/hadley/devtools/wiki/Style`

There's your answer again.

If I'm looking over your shoulder as you write code, I may say "ach, don't do that" or "nobody is going to want to look at that." You may say, as many students have, "but this works!" And all I can say in response is, "lucky for you, you don't need help fixing it. Because nobody will want to help that." Sometimes ugly code runs, but it is hard to understand, hard to debug.

From my expertise as an Rchaeologist, I have accumulated a list of bits of style advice. These proceed in order, from things that every knowledgeable expert will accept, to matters of personal taste that are more widely accepted, to things that I like, but nobody else does.

1. Opening squiggly braces, "{" must be at the end of the line of code, rather than at the beginning. This is recommended with for statements, and it is vital after "else". This is not merely a matter of style. The following will fail in R because the system does not know that the else's work is continuing when the squiggly brace is on the next line.

   ```
   if (x < 7){
       print("so far, so good")
   }
   else
   {
       print("this is a total disaster because the squiggle is not with the else")
   }
   ```

   It should be like this:

   ```
   if (x < 7){
       print("so far, so good")
   } else {
       print("this is the "defensive" style mentioned in the R documents")
   }
   ```

   If you are a C or Java programmer, and you are used to putting your squiggly braces in different spots, you will have to stop doing that. C and Java require the author to use the semicolon to conclude every statement, so there is never any ambiguity about when a command is finished. R allows a line ending to conclude a command, opening up ambiguity about when a command is finished. To let R know that more work remains, put the squiggly brace at the end of the line.

   As far as I know, this is the only bit of R style advice on which every single qualified R programmer will agree. The placement of braces is not simply style, it is a matter of right and wrong.

   We can write it all on one line if we want to.

   ```
   if (x < 7) print("so far, so good") else print("this is else")
   ```

   The squiggly braces reduce the chance that we will make a mistake in the code, and thus I almost always use them while developing code. Perhaps, when a program is done, I'll go back and "tighten it up" so that I won't look like a novice.

2. Style for readability. If you are going to ask an R expert for help, it is vital to supply code that is as understandable as possible.

   (a) Put blank spaces on both sides of equal signs and mathematical symbols like "<","*","+", and so forth. Put one space after commas. This is purely a matter of convention and judgment, it does not affect the "rightness" of code. But every finished program by a well-qualified programmer will have this feature.

   (b) Indentation of sections is required. It allows the reader to discern "sub steps". Perhaps the R documentation is silent on many matters of style because the members of R Core are not completely in agreement with each other. Almost the only clear advice we get is the following. For indentation of subsections, use 4 spaces. Personally, I prefer 2 spaces, and until 2011 that is what I used. Now, I've changed my settings in Emacs so that indentions are 4 spaces.

3. Style for widespread comprehension.

(a) How to name functions.

i. Avoid using names that are already in use. Don't write functions named "rep" "seq" "lm", and so forth. Even though R (since 2.14) requires all package writers to use namespaces, and the system can tolerate name duplication to some extent, don't do it.

ii. Use periods to indicate classes, otherwise don't use periods in function names. Use camel case to name functions.
myFunction or getCalculatedValues are better function names than my.function or get.calculated.values.
Why do some functions have periods in the name? Browse the R source code and you find functions with names like "predict.lm" and "summary.lm". "lm" denotes the class of the input, so when a user runs the commands

```
m1 <- lm(y ~ x, data=dat)
summary(m1)
predict(m1)
```

The lm function creates an object of class "lm", and so when summary and predict are used, the R system notices that m1 is from that class, and the system then uses "summary.lm" and "predict.lm" to get the work done.
Most users don't realize that when they run "summary.lm", a new type of object is created, it is from the class "summary.lm". And in order to show that result to the user, the R system uses a function called "print.summary.lm". The function name has 3 parts, but the last two parts are the class of the object for which the function is intended. As one can see, inside the R system, the periods are VERY meaningful indicators because they are used to declare which type of object is acted upon by a function.
As a result, I suggest programmers should NEVER use periods when they name their functions, unless (of course) they are writing functions that work on classes of objects.
Instead, programmers should use camel case function names. Instead of "do.something," create a function called "doSomething". This style is very pleasant to my eye because it exactly the same style that is suggested in the Objective-C language, in which the Swarm simulation system was written. Some people, especially C++ programmers, have been trained to hate camel case.
Some parts of R, especially the old parts, were developed before "object oriented" programming had come to the forefront and, as a result, they do not comply with this advice. Nevertheless, I believe this is good advice and it is generally followed by most of the good R programmers.

(b) How to name variables (and objects and other things you need to keep track of).

i. Officially, R variable names must begin with an alphabetical character and must include only letters, numbers and the symbols "_", "-", and ".". They must not include "*","?","!","&" or other special symbols.
Please understand the history of S and R. At one time, the underscore "_" was used as the assignment symbol. That's right, instead of "<-", we used to write

```
y _ x + x^2
```

The underscore for assignment was allowed, but discouraged, when I started using R in 1998. R functions that imported data would automatically translate underscores into other symbols. Underscore for assignment has since been forbidden altogether. A while after that, the underscore was allowed in variable and function names. Because of that history, R veterans may still consider it jarring if your variables include underscores.

ii. No T or F.
This is one thing that almost everybody (99.9%) will agree with. NEVER name variables "T" or "F". These are too easily mistaken for TRUE and FALSE values. Since R uses TRUE and FALSE as vital elements of almost all commands and functions, and since users are allowed to abbreviate those as T or F, a horrible confusion can develop if variables are named T or F.

iii. Avoid declaring variables that have the same names as widely used functions. In 2001, I created a variable "rep" (for Republican party members) and nothing worked in my program.

In exasperation, I wrote to the r-help list, and learned that I had obliterated R's own function rep with my variable. That kind of mistake was common. In 2002 or so, the R system was revised so that user-declared variables cannot "step on" R system functions. Nevertheless, it is disconcerting to me (probably others) when users create variables with names like "lm", "rep", "seq", and so forth. Its distracting; its confusing.

4. Everything else is a matter of personal style and conscience.

   We should strive to have understandable code that others can understand and use. Hence, naming variables is important because it can help readers to understand our code.

   Sometimes people will have fun by naming their variables after their mothers, fathers, dogs, or favorite cities. Calling a variable "chicago" may help the author to remember that a particular regression problem was solved while in vacation in the windy city, but it will not help anybody else understand what's going on.

   Often, while I'm working on a function, I will have a variable x and then change it somehow. In the heat of the moment, I can't think of a good name, so the new thing is called xx. Then I change that and have xx2. Then I change that and have xx3. When the function works in the way it is intended, I should go back and beautify the names so they are most understandable.

I don't have a comprehensive style guide, probably never will, but I do have some advice that may help readers to understand why I name variables in certain ways. These are the objectives of my current approach.

1. Use long names for infrequently used variables. If a variable is going to be used twice, we might as well be verbose about it. If we are going to use a name 50 times in a 5 line program, we should choose a short one. For abbreviations, include a comment to remind the reader what the thing stands for.

2. Use an alphabetical scheme for naming related things so that they alway stay together in the workspace. As seen by ls(), the related bits should always be together.

   Example 1. Create a numeric variable, recode it as a factor, then create the "dummy" variables that correspond.

```
x <- runif(1000, min = 0, max = 100)
xf <- cut(x, breaks = c(-1, 20, 50, 80, 101), labels = c("cold", "luke", "warm", "hot"))
xfdummies <- contrasts(xf, contrasts = FALSE )[xf,]
colnames(xfdummies) <- c("xfcold", "xfluke", "xfwarm", "xfhot")
rownames(xfdummies) <- names(x)
dat <- data.frame(x, xf, xfdummies)
head(dat)
```

```
         x   xf xfcold xfluke xfwarm xfhot
1 24.04464 luke      0      1      0     0
2 45.25289 luke      0      1      0     0
3 87.36903  hot      0      0      0     1
4 88.44754  hot      0      0      0     1
5 86.19752  hot      0      0      0     1
6 24.86685 luke      0      1      0     0
```

   Example 2. Estimate a regression, calculate the summary, extract summary statistics.

```
set.seed(12345)
x1 <- rnorm(200, m = 400, s = 10)
x2 <- rnorm(200, m = 80, s = 30)
y <- 3 + 0.2 * x1 + 0.4 * x2 + rnorm(200, s=400)
dat <- data.frame(x1, x2, y); rm(x1,x2,y)
m1 <- lm (y ~ x1 + x2, data = dat)
m1summary <- summary(m1)
(m1se <- m1summary$sigma)
```

```
[1] 397.3396
```

```
(m1rsq <- m1summary$r.squared)
```

```
[1] 0.01245762
```

```
(m1coef <- m1summary$coef)
```

```
                 Estimate    Std. Error      t value  Pr(>|t|)
(Intercept) -826.055430 1061.6314251 -0.7781000 0.4374436
x1             2.086945    2.6434146  0.7894885 0.4307757
x2             1.307858    0.9804299  1.3339640 0.1837557
```

```
(m1aic <- AIC(m1))
```

```
[1] 2966.469
```

Example 3. Run a regression, collect mean-centered and residual centered variants of it, summarize each, and compare them.

```
library(rockchalk)
dat$y2 = with(dat, 3 + 0.2 * x1 + 0.4 * x2 + 0.35 * x1 *x2 + rnorm(200, s=4000))
m1 <- lm(y2 ~ x1 + x2, data = dat)
m1i <- lm(y2 ~ x1 * x2, data = dat)
m1ps <- plotSlopes(m1, plotx = "x1", modx = "x2")
m1ips <- plotSlopes(m1i, plotx = "x1", modx = "x2")
m1imc <- meanCenter(m1i)
m1irc <- residualCenter(m1i)
outreg(list(m1, m1i, m1imc, m1irc), tight = TRUE, modelLabels = c("Linear", "Interaction", "
    Mean Centered", "Residual Centered"))
```

| | Linear<br>Estimate<br>(S.E.) | Interaction<br>Estimate<br>(S.E.) | Mean Centered<br>Estimate<br>(S.E.) | Residual Centered<br>Estimate<br>(S.E.) |
|---|---|---|---|---|
| (Intercept) | -13280.303 | 14103.29 | 12119.134* | -13280.303 |
| | ( 10957.595) | ( 32433.267) | ( 290.315) | ( 10963.028) |
| x1 | 34.737 | -33.437 | . | 34.737 |
| | ( 27.284) | ( 80.747) | | ( 27.297) |
| x2 | 138.889* | -181.759 | . | 138.889* |
| | ( 10.119) | ( 357.567) | | ( 10.124) |
| x1:x2 | . | 0.798 | . | . |
| | | ( 0.89) | | |
| x1c | . | . | 32.426 | . |
| | | | ( 27.419) | |
| x2c | . | . | 138.598* | . |
| | | | ( 10.13) | |
| x1c:x2c | . | . | 0.798 | . |
| | | | ( 0.89) | |
| x1.X.x2 | . | . | . | 0.798 |
| | | | | ( 0.89) |
| N | 200 | 200 | 200 | 200 |
| $RMSE$ | 4101.128 | 4103.162 | 4103.162 | 4103.162 |
| $R^2$ | 0.493 | 0.495 | 0.495 | 0.495 |
| adj $R^2$ | 0.488 | 0.487 | 0.487 | 0.487 |

* $p \leq 0.05$

## 2 What's In R Guts?

### 2.1 Rewriting Formulas. My Introductory Puzzle.

On May 29, 2012, I was working on a regression problem in the rockchalk package. The functions meanCenter and residualCenter a fitted regression model and transform some variables. The non-centered variable "x1" is renamed to "x1c", and then the regression is executed with the new data. Thus it is necessary to take something that is fitted with a formula like y ~ x1*x2, and then re-fit with a formula like y ~ x1c*x2c. In the end, the answer is a single, if complicated line of code that speaks volumes about the way the advanced R user interacts with the system.

My first effort used R's update function. It is fairly easy to replace x1 with x1c in the formula, but not when x1 is logged or otherwise transformed. In exasperation, I wrote to r-help and described the problem with this working example.

```
dat <- data.frame(x1=rnorm(100,m=50), x2=rnorm(100,m=50),
 x3=rnorm(100,m=50), x4 = rnorm(100, m=50), y=rnorm(100))
m2 <- lm(y ~ log(x1) + x2*x3, data=dat)
suffixX <- function(fmla, x, s){
 upform <- as.formula(paste0(". ~ .", "-", x, "+", paste0(x, s)))
 update.formula(fmla, upform)
 }
newFmla <- formula(m2)
newFmla
suffixX(newFmla, "x2", "c")
suffixX(newFmla, "x1", "c")
```

Run that and check the last few lines of the output. See how the update misses x1 inside log(x1) or in the interaction?

```
> newFmla <- formula(m2)
> newFmla
y ~ log(x1) + x2 * x3
> suffixX(newFmla, "x2", "c")
y ~ log(x1) + x3 + x2c + x2:x3
> suffixX(newFmla, "x1", "c")
y ~ log(x1) + x2 + x3 + x1c + x2:x3
```

It gets the target if the target is all by itself, but not otherwise.

While struggling with this, I noticed this really interesting thing. The object "newFmla" is not just a text string. It is actually a list. Its parts can be probed recursively, to eventually reveal all of the individual pieces:

```
newFmla
```

```
y ~ log(x1) + x2 * x3
```

```
newFmla[[1]]
```

```
`~`
```

```
newFmla[[2]]
```

```
y
```

```
newFmla[[3]]
```

```
log(x1) + x2 * x3
```

```
newFmla[[3]][[2]]
```

```
log(x1)
```

```
newFmla[[3]][[2]][[2]]
```

```
x1
```

How could I put that information to use? I asked the members of r-help.

Lately I've had very good luck with r-help. A person who writes under the pseudonym Gabor Grothendieck wrote an answer to r-help on May 29, 2012, "Try substitute:"

```
> do.call("substitute", list(newFmla, setNames(list(as.name("x1c")), "x1")))
y ~ log(x1c) + x2 * x3
```

Bingo.

That's quintessential R. It packs together a half-dozen very deep thoughts that I will try to explain in the rest of this section. It has most of the essential secrets of R's guts, laid out in a single line. It has do.call, substitute, it interprets a formula as a list, and it shows that every command in R is, when it comes down to brass tacks, a list. I would like to take up these separate pieces in order.

## 2.2 do.call and eval

In my early work as an Rchaeologist, I had noticed eval and do.call, but did not understand their significance in the mind of the R programmers. Whenever difficult problems arose in r-help, the answer almost invariably involved do.call or eval. Maybe both.

### 2.2.1 do.call

Let's concentrate on do.call first. The syntax is like this

```
do.call("someRFunction", aListOfArgumentsToGoInTheParentheses)
```

It is as if we were telling R to run this:

```
someRFunction(aListOfArgumentsToGoInTheParentheses)
```

Let's consider an example that runs a regression the ordinary way, and then with do.call. In this example, the role of "someRFunction" will be played by lm and the list of arguments will be the parameters of the regression. The regression m1 will be constructed the ordinary way, while m2 is constructed with do.call.

```
m1 <- lm(y ~ x1*x2, data=dat)
coef(m1)
```

```
(Intercept)          x1          x2       x1:x2
334.7175924  -6.5100168  -6.8113110   0.1325085
```

```
regargs <- list(formula = y ~ x1*x2, data= quote(dat))
m2 <- do.call("lm", regargs)
coef(m2)
```

```
(Intercept)          x1          x2       x1:x2
334.7175924  -6.5100168  -6.8113110   0.1325085
```

```
all.equal(m1, m2)
```

```
[1] TRUE
```

The object regargs is a list of arguments that R can understand when they are supplied to the lm function.

do.call is a powerful, mysterious symbol. It holds flexibility; we can calculate commands and then run them. I first needed it when we had a simulation project that ran very slowly when confronted with medium or large sized problems. There's a writeup in the working examples distributed with rockchalk called stackListItems-01.R. I was using rbind over and over to join the results of simulation runs. Basically, the code was like this

```
for (i in 1:10000){
   dat <- someHugeSimulation(i)
   result <- rbind(result, dat)
}
```

That will call rbind 10000 times. I had not realized that rbind is a comparatively time-consuming task because it accesses a new chunk of memory each time it is run. On the other hand, we could collect those results in a list, then we can call rbind one time to smash together all of the results.

```
for (i in 1:10000){
   mylist[[i]] <- someHugeSimulation(i)
}
result <- do.call("rbind", mylist)
```

It is much faster to run rbind only once. It would be OK if we typed it all out like this:

```
result <- rbind(mylist[[1]], mylist[[2]], mylist[[3]], mylist[[4]], ..., mylist[[10000]])
```

But who wants to do all of that typing? How tiresome! Thanks to Erik Iverson in r-help, I understand that

```
result <- do.call("rbind", mylist)
```

is doing the EXACT same thing. “mylist” is a list of arguments. do.call is *constructing* a function call from the list of arguments. It is *as if* I had actually typed rbind with 10000 arguments.

The beauty in this is that we could design a program that can assemble the list of arguments, and also choose the function to be run, on the fly. We are not required to literally write the function in quotes, as in “rbind”. We could instead have a variable that is calculated to select one function among many, and then use do.call on that. In a very real sense, we could write a program that can write itself as it runs.

From all of this (and a peek at ?call), I arrive at an Rchaeological eureka! A call object is a quoted command plus a list of arguments for that command.

### 2.2.2 eval

Where does eval fit into the picture? As far as I can tell, do.call(”rbind”, mylist) is basically the same as eval(call(“rbind”, mylist). The call function manufactures the call object, the eval function tells it to do its work. I think of do.call as a contraction of “eval” and “call”. eval can handle evaluates any valid R expression, and a call is a valid expression. I'm leaving the question of “what is an expression” to a later time.

Here's a quick example that repeats the two regressions exercise that was completed with do.call. Now I'll create an expression regargs2. Note it is necessary for me to evaluate the expression before the lm function can understand it.

```
m3 <- lm(y ~ x1*x2, data=dat)
coef(m3)
```

```
(Intercept)          x1          x2       x1:x2
334.7175924  -6.5100168  -6.8113110   0.1325085
```

```
regargs2 <- expression(y ~ x1*x2, data = dat)
m4 <- lm(eval(regargs2))
coef(m4)
```

```
(Intercept)          x2          x3          x4           y
54.23244193  0.14541440 -0.13451021 -0.09570416  0.09045886
```

The main reason for using eval is that we can “piece together” commands and then run them after we have assembled all the pieces.

We can create a formula object implicitly (without explicitly asking for it) by using this code.

```
f1 <- y ~ x1 + x2 + x3 + log(x4)
class(f1)
```

```
[1] "formula"
```

```
m5 <- lm(f1, data = dat)
```

The object f1 is a formula object because R has created it that way. Its not just a text string. R notices the ∼ symbol and the whole line is interpreted as a formula. Observe it has separate pieces, just like newFmla in the example problem that started this section.

```
f1[[1]]
```

```
`~`
```

```
f1[[2]]
```

```
y
```

```
f1[[3]]
```

```
x1 + x2 + x3 + log(x4)
```

```
f1[[3]][[1]]
```

```
`+`
```

```
f1[[3]][[2]]
```

```
x1 + x2 + x3
```

```
f1[[3]][[3]]
```

```
log(x4)
```

Note that f1 created in this way must be a syntactically valid R formula; it cannot include any other regression options.

```
> f1 <- y ~ x1 + x2 + x3 + log(x4), data=dat
Error: unexpected ',' in "f1 <- y ~ x1 + x2 + x3 + log(x4),"
```

If can declare f1exp as an expression, then R does not re-interpret it as a formula (f1exp is an unevaluated expression, the R parser has not translated it yet). To use that as a formula in the regression, we have to evaluate it.

```
f1exp <- expression(y ~ x1 + x2 + x3 + log(x4))
class(f1exp)
```

```
[1] "expression"
```

```
m6 <- lm(eval(f1exp), data=dat)
```

When f1exp is evaluated, what do we have? Here's the answer.

```
f1expeval <- eval(f1exp)
class(f1expeval)
```

```
[1] "formula"
```

```
all.equal(f1expeval, f1)
```

```
[1] TRUE
```

```
m7 <- lm(f1expeval, data=dat)
all.equal(coef(m5), coef(m6), coef(m7))
```

```
[1] TRUE
```

The point here is that the pieces of an ordinary use command can be separated and put back together again before the work of doing calculations begins.

Now we turn back to the main theme. How is eval used in functions? Some functions take a lot of arguments. They need to pick some arguments, and send those to some functions.

Let's consider the lm code in some detail. Suppose a user submits a command like "lm(y ˜ x, data=dat, x = TRUE, y = TRUE)." Inside lm, it is necessary to pick through those arguments and then pass them off to other functions in order to build the data matrix and so forth. Here are the first lines of the lm function

```
lm <- function (formula, data, subset, weights, na.action, method = "qr",
    model = TRUE, x = FALSE, y = FALSE, qr = TRUE, singular.ok = TRUE,
    contrasts = NULL, offset, ...)
{
    ret.x <- x
    ret.y <- y
    cl <- match.call()
    mf <- match.call(expand.dots = FALSE)
    m <- match(c("formula", "data", "subset", "weights", "na.action",
        "offset"), names(mf), 0L)
    mf <- mf[c(1L, m)]
    mf$drop.unused.levels <- TRUE
    mf[[1L]] <- as.name("model.frame")
    mf <- eval(mf, parent.frame())
```

Lets consider what those lines do with a command like this.

```
m1 <- lm(y ~ x1*x2, data=dat, x = TRUE, y = TRUE)
```

The lm function notices that I supply some arguments. In line 8, the match.call function is used to grab a copy of the command that I typed. If we use R's debugging facility to stop the program at that point, we would see that mf is exactly the same as my command, except R has named the arguments:

```
> mf
lm(formula = y ~ x1 * x2, data = dat, x = TRUE, y = TRUE)
```

That's not just a string of letters, however. It is a call object, a list with individual pieces that we can revise. Lines 10 and 11 check the names of mf for the presence of certain arguments, and throw away the rest. It only wants the arguments we would be needed to run the function model.frame. Line 12 adds an argument to the list, drop.unused.levels. Up to that point, then, we can look at the individual pieces of mf:

```
> names(mf) [1] ""                    "formula"             "data" [4] "drop.unused.levels"
> mf[[1]]
lm
> mf[[2]]
y ~ x1 * x2
> mf[[3]]
dat
> mf[[4]]
[1] TRUE
```

The object mf has separate pieces that can be revised and then evaluated. Line 13 replaces the element 1 in mf with the symbol "model.frame". That's the function that will be called. Line 14 is the coup de grâce, when the revised call "mf" is sent to eval. In the end, it is *as if* lm had directly submitted the command

```
mf <- model.frame(y ~ x1 * x2, data=dat, drop.unused.levels=TRUE)
```

It would not do to simply write that into the lm function, however, because some people use variables that have names different from y, x1, and x2, and their data objects may not be called dat. lm allows users to input whatever they want for a formula and data, and then lm takes what it needs to build a model frame.

## 2.3 substitute

Most R users I know have not used substitute, except as it arises in the plotmath. In the context of plotmath, the problem is as follows. Plotmath causes the R plot functions to convert expressions into mathematical symbols in a way this is reminiscent of LaTeX. For example, a command like this:

```
text(4, 4, expression(gamma))
```

will draw the gamma symbol at the position (4,4). We can use paste to combine symbolic commands and text like so:

```
text(4, 4, expression(paste(gamma, " = 7")))
```

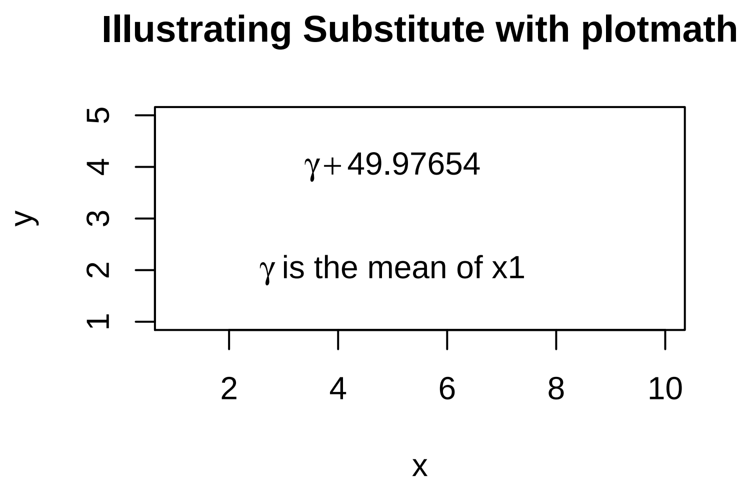
The number 7 is a nice number, but what if we want to calculate something and insert it into the expression? Your first guess might be to insert a function that makes a calculation, such as the mean, but this fails:

```
text(4, 4, expression(paste(gamma, mean(x))))
```

In order to smuggle the result of a calculation into an expression, some fancy footwork is required. In the help page for plotmath, examples using the functions bquote and substitute are offered.

For the particular purpose of blending expressions with calculation results, I find the bquote function to be more immediately understandable. In this section, I'm trying to understand the use of substitute, so let's stick with that. The plotmath help page points to syntax like this:

```
 plot(1:10, seq(1,5, length.out=10), type = "n", main="Illustrating Substitute with plotmath",
     xlab="x", ylab="y")
 text(5, 4, substitute(gamma + x1mean, list(x1mean = mean(dat$x1))))
 text(5, 2, expression(paste(gamma, " is the mean of x1")))
```



Run ?substitute and one is brought to a famous piece of Rchaeological pottery:

> 'substitute' returns the parse tree for the (unevaluated) expression 'expr', substituting any variables bound in 'env'.

Pardon me. parse tree? We've seen expressions already, that part is not so off putting. But "parse tree"? Really?

This is one of those points at which being an Rchaeologist has real benefits. The manual page gives us some insights into the R programmer, and it is his or her view of his or her own actions, but it doesn't necessarily speak to how we should understand substitute. For me, the only workable approach is to build up a sequence of increasingly complicated examples.

I start by creating the list of replacements. This replacement list can have a format like this:

```
sublist <- list(x1 = "alphabet", x2 = "zoology")
```

I want to replace x1 with alphabet and x2 with zoology. The quotes indicate that alphabet and zoology are strings, not other objects that already exist. Consider:

```
substitute(expression(x1 + x2 + log(x1) + x3), sublist)
```

```
expression("alphabet" + "zoology" + log("alphabet") + x3)
```

The special things to note are that the substitution 1) leaves other variables alone (since they are not named in sublist) and 2) it finds all valid use of the symbols x1 and x2 and replaces them.

This isn't quite what I wanted, however, because the strings have been inserted into the middle of my expression. I just want symbols. It turns out that the functions as.name and as.symbol are exactly the same, and usually I use as.symbol, but in Gabor's answer to my question, as.name is used, so I will illustrate that here.

```
sublist <- list(x1 = as.name("alphabet"), x2 = as.name("zoology"))
substitute(expression(x1 + x2 + log(x1) + x3), sublist)
```

```
expression(alphabet + zoology + log(alphabet) + x3)
```

## 2.4 setNames and names

Almost every R user has noticed that the elements of R lists can have names. In a data frame, the names of the list elements are thought of as variable names, or column names. If dat is a data frame, the names and colnames functions return the same thing, but that's not true for other types of objects.

```
dat <- data.frame(x1=1:10, x2=10:1, x3=rep(1:5,2), x4=gl(2,5))
colnames(dat)
```

```
[1] "x1" "x2" "x3" "x4"
```

```
names(dat)
```

```
[1] "x1" "x2" "x3" "x4"
```

After dat is created, we can change the names inside it with a very similar approach:

```
newnames <- c("whatever","sounds","good","tome")
colnames(dat) <- newnames
colnames(dat)
```

```
[1] "whatever" "sounds"   "good"     "tome"
```

While used interactively, this is convenient, but it is a bit tedious because we have to create dat first, and then set the names. The setNames function allows us to do this in one shot. I'll paste the data frame creating commands and the name vector in for a first try:

```
dat2 <- setNames(data.frame(x1=rnorm(10), x2=rnorm(10), x3=rnorm(10), x4=gl(2,5)), c("good","
    names","tough","find"))
head(dat2, 2)
```

```
        good       names       tough find
1 -1.6598937  0.02030747 -0.63971861    1
2 -0.2763602 -2.65139775  0.08676547    1
```

In order to make this more generally useful, the first step is to take the data-frame-creating code and set it into an expression that is not immediately evaluated (that's datcommand). When I want the data frame to be created, I use eval, and then the newnames vector is put to use.

```
newnames <- c("iVar", "uVar", "heVar", "sheVar")
datcommand <- expression(data.frame(x1=1:10, x2=10:1, x3=rep(1:5,2), x4=gl(2,5)))
eval(datcommand)
```

```
   x1 x2 x3 x4
1   1 10  1  1
2   2  9  2  1
3   3  8  3  1
4   4  7  4  1
5   5  6  5  1
6   6  5  1  2
7   7  4  2  2
8   8  3  3  2
9   9  2  4  2
10 10  1  5  2
```

```
dat3 <- setNames(eval(datcommand), newnames)
```

The whole point of this exercise is that we can write code that creates the names, and creates the data frame, and then they all come together.

What if we have just one element in a list? In Gabor's answer to my question, there is this idiom

```
setNames(list(as.name("x1c")), "x1")))
```

Consider this from the inside out.

1. as.name("x1c") is an R symbol object,
2. list(as.name("x1c")) is an list with just one object, which is that symbol object.
3. Use setNames. The object has no name! We would like to name it "x1".

It is as if we had run the command list(x1 = x1c). The big difference, of course, is that this way is much more flexible because we can calculate replacements.

### 2.5 The Big Finish

In the meanCenter function in rockchalk, some predictors are mean-centered and their names are revised. A variable named “age” becomes “agec” or “x1” becomes “x1c”. So the user’s regression formula that uses variables agec or x1 must be revised. This is a function that takes a formula “fmla” and replaces a symbol xname with newname.

```
formulaReplace <- function(fmla, xname, newname){
do.call("substitute", list(fmla, setNames(list(as.name(newname)), xname)))
}
```

This is put to use in meanCenter. Suppose a vector of variable names called nc (stands for “needs centering”) has already been calculated. The function std creates a centered variable.

```
newFmla <- mc$formula
for (i in seq_along(nc)){
    icenter <- std(stddat[, nc[i]])
    newname <- paste0(as.character(nc[i]), "c")
    newFmla <- formulaReplace(newFmla,  as.character(nc[i]), newname)
    nc[i] <- newname
}
```

If one has a copy of rockchalk 1.6 or newer, the evidence of the success of this approach should be evident in the output of the command example(meanCenter).

## 3 Do This, Not That (Stub)

R novices sometimes use Google to search for R advice and they find it, good or bad. They may find their way to the r-help email list, where advice is generally good, or to the StackOverflow pages for R, which may be better. A lot of advice is offered by people like me, who may have good intentions, but are simply not qualified to offer advice.

One of the few bits of advice that seems to grab widespread support is that “for loops are bad.” One can write an lapply statement in one line, while a for loop can take 3 lines. The code is shorter, but it won’t necessarily run more quickly. I recall being jarred by this revelation in John Chambers’s book, *Software for Data Analysis*. The members of the apply family (apply, lapply, sapply, etc) can make for more readable code, but they aren’t always faster. “However, none of the apply mechanisms changes the number of times the supplied function is called, so serious improvements will be limited to iterating simple calculations many times. Otherwise, the n evaluations of the function can be expected to be the dominant fraction of the computation”(Chambers, 2008, 213).

Todo: insert discussion of stackListItems-001.

Insert alternative methods of measuring executation time and measuring performance

Balance time spent optimizing code versus time spent running program.

## References

Chambers, John M. 2008. *Software for data analysis: programming with R.* Statistics and computing New York ; London: Springer. 3