Statistics 360: Advanced R for Data Science

Lecture 1

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Course Objectives

Chapter 2 - Names and Values

Course Objectives

Course objectives

- Make you R **programmers** rather than just R **users**, by working through most of the book "Advanced R" by Hadley Wickham: https://adv-r.hadley.nz/index.html.Solutions to the exercises in the textbook is also available online for free: https://advanced-r-solutions.rbind.io/
- Topics:
  - R objects: names and values
  - Basic data structures and programming.
    - vectors, subsetting, control flow, functions, environments
    - No tidyverse this time
  - R packages (based on the online text by Wickham and Bryan)
  - Object-oriented programming in R
  - Code performance: debugging, profiling, memory, calling Python, or C++ from R
  - Parallelizing R code (if time permits)

Courses Resources

- Lecture time: Tuesday, 12:30 - 2:20 PM at AQ3005.
- Textbook and Solutions
  - Textbook: **Advanced R, 2nd ed.** By Hadley Wickham. Available online for free at https://adv-r.hadley.nz/
  - Exercise Solutions: **The Advanced R Solutions, 2nd ed.**. Also available online for free at: https://advanced-r-solutions.rbind.io/
- Evaluations
  - In-class quizzes (50%): best 5 out of 6 quizzes.
  - Group course project (20%).
  - Closed-book final exam (30%).

Getting started with R, RStudio and git

- Follow the “getting started'' instructions on the class canvas page to get set up with R, RStudio and git.
  - R and RStudio will be familiar, but you may not have used git before, so leave some time for that.
- Please try to get R and RStudio installed and create an RStudio project linked to the class GitHub repository (or a forked copy) as soon as possible. A document shows you steps how to access lecture notes and etc. Here is the link: https://canvas.sfu.ca/courses/74856/files/20688259?wrap=1
- Those still having trouble after the lecture should ask our TA, Sidi Wu (wusidiw@sfu.ca), for help during the first lab sessions this week.
  - **Note: Lab starts from this week (week 2)**.

Reading

- Welcome, Preface and Chapters 1,2 of the text.

Chapter 2 - Names and Values

R objects

- In R, data structures and functions are all referred to as "objects".
- Objects are created with the assignment operator `<-` or =; e.g., `x <- c(1,2,3)`.
  - The objects a user creates from the R console are contained in the user's workspace, called the global environment.
  - Use 'ls()' to see a list of all objects in the workspace.
  - Use 'rm(x)' to remove object `x` from the workspace.

Digging deeper

- The above understanding is an over-simplification that is usually OK, but will sometimes lead to misunderstandings about memory usage and when R makes copies of objects
- Object copying is a **major** source of computational overhead in R, so it pays to understand what will trigger it.
- Reference: text, chapter 2

Binding names and to objects

- The R code `x <- c(1,2,3)` does two things:
    - (i) creates an object in computer memory that contains the values 1, 2, 3
    - (ii) "binds" that object to the "name" `x`.

```r
# install.packages("lobstr")
library(lobstr)
x <- c(1,2,3)
ls()
```

```
## [1] "x"
```

```r
obj_addr(x) # changes every time this code chunk is run
```

```
## [1] "0x7fc964f20a88"
```

Binding multiple names to the same object

- The following binds the name `y` to the same object that `x` is bound to.

```
y <- x
c(obj_addr(x), obj_addr(y))
```

```
## [1] "0x7fc964f20a88" "0x7fc964f20a88"
```

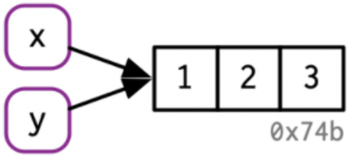


Figure 1: Bind two names to the same object

Aside: Syntactic *vs* non-syntactic

- Valid, or “syntactic” names in R can consist of letters, digits, . and _ but should start with a letter.
- Names that start with . are hidden from directory listing with `ls()`.
- Names that start with _ or a digit are non-syntactic and will cause an error.
- If you need to create or access a non-syntatic name, use backward single-quotes (“backticks”).

```r
x <- 1
.x <- 1
`_x` <- 1
ls()
```

```
## [1] "_x" "x"  "y"
```

Modifying causes copying

- Modifying a variable causes a copy to be made, with the modified variable name bound to the copy.

```r
x <- y <- c(1,2,3)
c(obj_addr(x),obj_addr(y))
```

```
## [1] "0x7fc925773098" "0x7fc925773098"
```

```r
y[[3]] <- 4 # Note: x[2] <- 10 has the same effect
c(obj_addr(x),obj_addr(y))
```

```
## [1] "0x7fc925773098" "0x7fc924b22468"
```

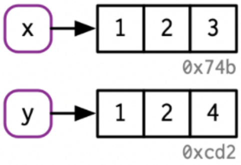


Figure 2: Bindings after copying

Tracing copying

- The `tracemem()` function marks an object so that a message is printed whenever a copy is made.

```
x <- c(1,2,3)
tracemem(x)
```

```
## [1] "<0x7fc924f20288>"
```

```
x[[2]] <- 10
```

```
## tracemem[0x7fc924f20288 -> 0x7fc964ac1c68]: eval eval eval_wi
```

```
untracemem(x)  # remove the trace
x[[1]] <- 10
```

More on `tracmem()`

- As the output of \textcolor{blue}{tracemem()`} suggests, the trace is on the object, not the name:

```
x <- c(1,2,3)
tracemem(x)
```

```
## [1] "<0x7fc945076068>"
```

```
y <- x
c(obj_addr(x),obj_addr(y))
```

```
## [1] "0x7fc945076068" "0x7fc945076068"
```

```
y[[2]] <- 10
```

```
## tracemem[0x7fc945076068 -> 0x7fc926042638]: eval eval eval_wi
```

```
c(obj_addr(x),obj_addr(y))
```

```
## [1] "0x7fc945076068" "0x7fc926042638"
```

Function calls

- R has a reputation for passing copies to functions, but in fact the **copy-on-modify** applies to functions too:

```r
f <- function(arg) { return(arg) }
x <- c(1,2,3)
y <- f(x) # no copy made, so x and y bound to same obj
c(obj_addr(x),obj_addr(y))
```

```
## [1] "0x7fc924f234e8" "0x7fc924f234e8"
```

```r
f <- function(arg) { arg <- 2*arg; return(arg) }
y <- f(x) # copy made
c(obj_addr(x),obj_addr(y))
```

```
## [1] "0x7fc924f234e8" "0x7fc924f20e18"
```

Lists

- List elements point to objects too:

```
l1 <- list(1, 2, 3)
rbind(obj_addr(l1),
      obj_addr(l1[[1]]),
      obj_addr(l1[[2]]),
      obj_addr(l1[[3]]))
```

```
##      [,1]
## [1,] "0x7fc925999ce8"
## [2,] "0x7fc964c44e30"
## [3,] "0x7fc964c44e68"
## [4,] "0x7fc964c31300"
```

```
# Note: ref(l1) will print a nicely formatted version of the above,
# but doesn't work with my slides
```

Copy-on-modify in lists

```r
l1 <- l2 <- list(1,2,3)
```

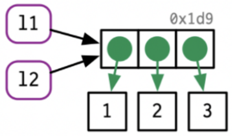


Figure 3: Bindings before

```r
l2[[3]] <- 4
```

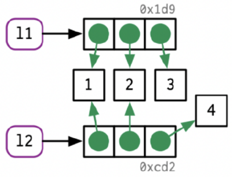


Figure 4: Bindings after modify

Copies of lists are said to be "shallow"

- As shown above, we copy the list itself and any list **elements** that are modified. This is called a "shallow" copy.
- By contrast, a "deep" copy would be a copy of all elements.

```
l1 <- list(1,2,3)
rbind(obj_addr(l1),obj_addr(l1[[1]]),
      obj_addr(l1[[2]]),obj_addr(l1[[3]]))
```

```
##      [,1]
## [1,] "0x7fc964b86478"
## [2,] "0x7fc9258d4db0"
## [3,] "0x7fc9258d4d78"
## [4,] "0x7fc9258d4d40"
```

```
l1[[3]] <- 4
rbind(obj_addr(l1),obj_addr(l1[[1]]),
      obj_addr(l1[[2]]),obj_addr(l1[[3]]))
```

```
##      [,1]
## [1,] "0x7fc924b21608"
## [2,] "0x7fc9258d4db0"
## [3,] "0x7fc9258d4d78"
## [4,] "0x7fc9258d4bb8"
```

Data frames are lists with columns as list items

```r
dd <- data.frame(x=1:3,y=4:6)
c(obj_addr(dd[[1]]),obj_addr(dd[[2]]))
```

```
## [1] "0x7fc964f93668" "0x7fc964f937b8"
```

```r
dd[,2] <- 7:9 # change a column
c(obj_addr(dd[[1]]),obj_addr(dd[[2]])) # only changes 2nd element
```

```
## [1] "0x7fc964f93668" "0x7fc945066240"
```

```r
dd[1,] <- c(11,22) # change a row
c(obj_addr(dd[[1]]),obj_addr(dd[[2]])) # changes to both elements
```

```
## [1] "0x7fc925999a68" "0x7fc925999a18"
```

```r
dd[1,1] <- 111 # change one element
c(obj_addr(dd[[1]]),obj_addr(dd[[2]])) # only changes 1st element
```

```
## [1] "0x7fc94504dbb8" "0x7fc925999a18"
```

Beware of data frame overhead

- Data frames are convenient, but the convenience comes at a cost.
  - For example, coercion to/from lists

```r
dd <- data.frame(x=rnorm(100)) # try yourself with rnorm(1e7)
tracemem(dd); tracemem(dd[[1]])
```

```
## [1] "<0x7fc9254cfb30>"
```

```
## [1] "<0x7fc954711240>"
```

```r
dmed <- lapply(dd,median) # makes a list copy of dd
```

```
## tracemem[0x7fc9254cfb30 -> 0x7fc9258f2568]: as.list.data.frame as.li
## tracemem[0x7fc954711240 -> 0x7fc95471aaa0]: sort.int sort.default so
```

```r
dd[[1]] <- dd[[1]] - dmed[[1]] #
```

```
## tracemem[0x7fc9254cfb30 -> 0x7fc925739318]: eval eval eval_with_user
## tracemem[0x7fc925739318 -> 0x7fc925619238]: [[<-.data.frame [[<- eva
```

- Fewer copies if we do the same with a list.

```r
ll <- list(x=rnorm(100))
tracemem(ll); tracemem(ll[[1]])
```

```
## [1] "<0x7fc964f15718>"
```

```
## [1] "<0x7fc954735a80>"
```

```r
lmed <- lapply(ll,median) # no need for a list copy
```

```
## tracemem[0x7fc954735a80 -> 0x7fc954735dd0]: sort.int sort.default so
```

```r
ll[[1]] <- ll[[1]] - dmed[[1]]
```

```
## tracemem[0x7fc964f15718 -> 0x7fc964ee56a0]: eval eval eval_with_user
```

Modify-in-place

- The text says there are two exceptions to the copy-on-modify:
  1. Modify an element of an object with one binding, or
  2. Modify an environment.

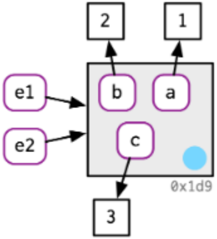
but in my experiments, only the second applies.

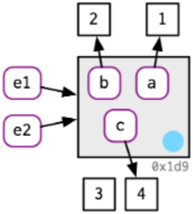
```
v <- c(1,2,3) # creates object (1,2,3) and binds v to it
tracemem(v)
```

```
## [1] "<0x7fc92615c6a8>"
```

```
v[[3]] <- 4 # for me, this triggers a copy
```

```
## tracemem[0x7fc92615c6a8 -> 0x7fc945147758]: eval eval eval_with_user
```





```r
e1 <- rlang::env(a = 1, b = 2, c = 3)
e2 <- e1
# note: can't use tracemem() on an environment
e1$c <- 4
e2$c
```

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

Object size

- Use `lobstr::obj_size()` to find the size of objects.

```
obj_size(dd)
```

```
## 1.53 kB
```

```
obj_size(ll)
```

```
## 1.13 kB
```

```
obj_size(e1)
```

```
## 840 B
```

```
obj_size(e2)
```

```
## 840 B
```

After lecture

- Read textbook Chapters 1 (introduction) and 2 (Names and values)
    - Link: https://adv-r.hadley.nz/names-values.html
- Try the corresponding exercise in chapter 1.
    - Solution can be found here: https://advanced-r-solutions.rbind.io/names-and-values.html
- Upcoming topic:
    - Vectors (Ch3)
    - Subsetting (Ch4)