

# 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. The solutions to exercises in the textbook is also available online for free.
- ▶ 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 (25%).
  - ▶ Closed-book final exam (25%).

## 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.

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

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

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

```
## [1] "0x7f98b272f688"
```

## 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] "0x7f98b272f688" "0x7f98b272f688"
```

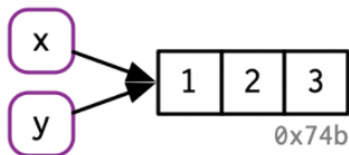


Figure 1: Bind two names to the same object

## 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-syntactic name, use backward single-quotes (“backticks”).

```
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.

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

```
## [1] "0x7f98b28ac698" "0x7f98b28ac698"
```

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

```
## [1] "0x7f98b28ac698" "0x7f98d1aa2c68"
```

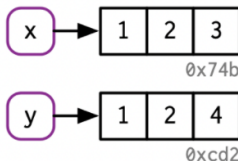


Figure 2: Bindings after copying

# 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] "<0x7f98b26b3288>"
```

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

```
## tracemem[0x7f98b26b3288 -> 0x7f98b34b4268]: eval eval eval_wi
```

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

## More on tracemem()

- ▶ 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] "<0x7f98b30d6c58>"
```

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

```
## [1] "0x7f98b30d6c58" "0x7f98b30d6c58"
```

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

```
## tracemem[0x7f98b30d6c58 -> 0x7f98d1d09be8]: eval eval eval_wi
c(obj_addr(x),obj_addr(y))
```

```
## [1] "0x7f98b30d6c58" "0x7f98d1d09be8"
```



# Function calls

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

```
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] "0x7f98b33f4e98" "0x7f98b33f4e98"
```

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

```
## [1] "0x7f98b33f4e98" "0x7f98b26b3dc8"
```

# 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,] "0x7f98d19ff8e8"
## [2,] "0x7f98d3519f00"
## [3,] "0x7f98d35036b8"
## [4,] "0x7f98d34ea0b0"
```

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

# Copy-on-modify in lists

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

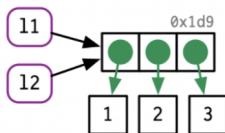


Figure 3: Bindings before

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

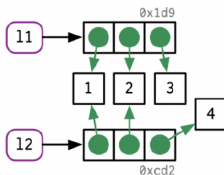


Figure 4: Bindings after modify

## 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,] "0x7f98d1aa1078"
## [2,] "0x7f98b325cd40"
## [3,] "0x7f98b325cd08"
## [4,] "0x7f98b325ccd0"
```

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

```
##      [,1]
## [1,] "0x7f98d1aa1e08"
## [2,] "0x7f98b325cd40"
## [3,] "0x7f98b325cd08"
## [4,] "0x7f98b325cb48"
```

# Data frames are lists with columns as list items

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

```
## [1] "0x7f98d1f3a5c0" "0x7f98d1f3a710"
```

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

```
## [1] "0x7f98d1f3a5c0" "0x7f98d3081198"
```

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

```
## [1] "0x7f98d19ff668" "0x7f98d19ff618"
```

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

```
## [1] "0x7f98b262e7b8" "0x7f98d19ff618"
```

# Beware of data frame overhead

- ▶ Data frames are convenient, but the convenience comes at a cost.

- ▶ For example, coercion to/from lists

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

```
## [1] "<0x7f98b2e57d68>"
```

```
## [1] "<0x7f98d2911750>"
```

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

```
## tracemem[0x7f98b2e57d68 -> 0x7f98b327a568]: as.list.data.frame as.li
```

```
## tracemem[0x7f98d2911750 -> 0x7f98d2955e20]: sort.int sort.default so
```

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

```
## tracemem[0x7f98b2e57d68 -> 0x7f98b38f2b50]: eval eval eval_with_user
```

```
## tracemem[0x7f98b38f2b50 -> 0x7f98b38f4a70]: [[<-data.frame [[<- eva
```

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

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

```
## [1] "<0x7f98b33fce70>"
```

```
## [1] "<0x7f98d29398a0>"
```

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

```
## tracemem[0x7f98d29398a0 -> 0x7f98d2939bf0]: sort.int sort.default so
```

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

```
## tracemem[0x7f98b33fce70 -> 0x7f98b2a35630]: 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.

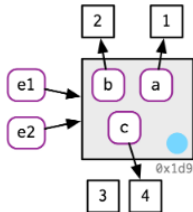
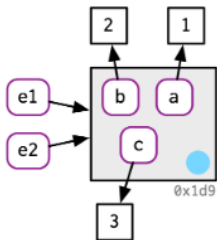
```
v <- c(1,2,3) # creates object (1,2,3) and binds v to it
tracemem(v)
```

```
## [1] "<0x7f98b34a46a8>"
```

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

```
## tracemem[0x7f98b34a46a8 -> 0x7f98b4840d58]: eval eval eval_with_user
```





```
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)