Computational Skills for Biostatistics I: Lecture 1

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September 28, 2017

Welcome!

- Biost 561 is an add-on to Biost 514
- 514 covers basic R commands, 561 covers more advanced R and other programming skills
- As a MS/PhD student in Biostats, you will do some serious programming!
- Good programming practices will help you with research, collaborating, your job search, and your long-term career... whichever path you choose!

Structure and expectations

- Weekly lectures
- Weekly homeworks
- Weekly office hours: HSB F-657. Tuesday 3-4?
- Office hours by appointment

Topics

Subject to change

- 9/28 Lecture 1: Advanced classes, methods, objects, debugging
- 10/5 Lecture 2: Efficient loops, functions
- 10/12 Lecture 3: Pipes
- 10/19 Lecture 4: ggplot
- 10/26 Lecture 5: latex *
- 11/2 Lecture 6: Markdown *
- 11/9 Lecture 7: unix, shell, UW cluster computing *
- 11/16 Lecture 8: version control, git, github, packages
- 11/23 no class; Thanksgiving
- 11/30 Lecture 9: Calling C/C++ in R *
- 12/7 Lecture 10: Python *

* indicates guest lecture by one of your classmates. A great opportunity to learn the latest and greatest!

Resources

- Available via github
  - Syllabus
  - Slides
  - Source code for slides
  - Examples
  - Homeworks
- Available via github classroom
  - Homework submission
- Available via email
  - Announcements

Expectations

What you should expect of me

- I will make your learning a priority
- I will give you timely feedback on your homeworks
- I will treat you as adults, I will treat you with respect
- I will talk slowly (tell me if I'm speaking too fast!)
- I will try to make class engaging and fun!

Expectations

What I will expect of you

- You make attending class a priority
- You submit your best work for homework: your own work, on time
- You engage in classroom discussion and quizzes!
- You learn from the class; you learn to teach yourself programming skills
- You treat me, guest lecturers, and each other with respect

Assessment

The only assessment in this course is homework.

- 10 or fewer homeworks
- You must submit a good attempt at every homework to receive credit for this course

I won't record attendance, but if you consistently do not show up you will not receive credit.

About me

[photo holding chickens]

[github page]

About you

Everyone is here with different backgrounds in programming and computing. Let's get statistical!

[Analyse survey here]

Class

There are many different *classes* of objects in R

```
x <- c(1, 2, 5)
y <- c("a", "b")
z <- as.factor(y)
c(class(x), class(y), class(z), class(c))
```

```
## [1] "numeric"   "character" "factor"    "function"
```

Others include `logical` (`TRUE`, `FALSE`), complex numbers…

Modes

R has different modes. The mode tells the way a variable is stored.

```r
mode(x)
```

```
## [1] "numeric"
```

```r
mode(y)
```

```
## [1] "character"
```

```r
mode(z) # factors are stored as numerics
```

```
## [1] "numeric"
```

```r
mode(c)
```

```
## [1] "function"
```

Modes

`is.[class]` asks about the class. Normally you will be interested in the class, not the mode.

```
is.numeric(x)
```

```
## [1] TRUE
```

```
is.factor(z)
```

```
## [1] TRUE
```

```
is.numeric(z) # we asked about class, not the mode
```

```
## [1] FALSE
```

Data structures

R can store data in various *objects*

- vector: one-dimensional, all data points have same mode
- matrix: two-dimensional, all data points have same mode
- data frame: two-dimensional, all data points in same column have same mode
- list: one-dimensional, data points can be of any type

Matrices

Matrices vs data frames: all elements have same mode in matrices

```r
cbind(c(1,2), c("a", "b"))
```

```
##      [,1] [,2]
## [1,] "1"  "a"
## [2,] "2"  "b"
```

Matrices

Be very careful with matrix operations!

```r
aa <- matrix(c(1, 2, 3, 5), nrow = 2, byrow = T)
bb <- c(0.5, 2)
aa
```

```
##      [,1] [,2]
## [1,]    1    2
## [2,]    3    5
```

```r
bb
```

```
## [1] 0.5 2.0
```

Matrices

```
aa %*% bb # matrix multiplication
```

```
##      [,1]
## [1,]  4.5
## [2,] 11.5
```

```
aa * bb # careful! pointwise
```

```
##      [,1] [,2]
## [1,]  0.5    1
## [2,]  6.0   10
```

Data frames

```
data.frame(c(1,2), c("a", "b"))
```

```
##   c.1..2. c..a....b..
## 1       1           a
## 2       2           b
```

```
dd <- data.frame("ID"=c(1,2), "name"=c("a", "b")) # better
dd
```

```
##   ID name
## 1  1    a
## 2  2    b
```

```
str(dd) # structure: compact info about frame & variables
```

```
## 'data.frame':    2 obs. of  2 variables:
##  $ ID  : num  1 2
##  $ name: Factor w/ 2 levels "a","b": 1 2
```

vectorisation

vectorisation: doing many calculations with a single command

```
x <- c(0.5, 2, 3, 6)
x^2
```

```
## [1]  0.25  4.00  9.00 36.00
```

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

```
## [1] 0.125 2.000 9.000 6.000
```

vectorisation

The slow way: with loops. Avoid where possible!

```
z <- rep(NA, 4)
for (i in 1:4) {
  z[i] <- x[i]^y[i]
}
z
```

Code is easier to read, and usually easier to debug, when vectorised

recycling

In many tasks, R recycles elements of one input until it has enough to match the other

```
aa
```

```
##      [,1] [,2]
## [1,]    1    2
## [2,]    3    5
```

```
bb
```

```
## [1] 0.5 2.0
```

```
aa + bb # vectors are treated as columns!
```

```
##      [,1] [,2]
## [1,]  1.5  2.5
## [2,]  5.0  7.0
```

```
cc <- c(1, 2, 3, 4)
aa + cc # the silent killer
```

Speed comparison

Vectorisation can cause major speed-ups, because task is optimised and precompiled in C/Fortran, not interpreted R.

```
dd <- matrix(rnorm(1e6), nrow = 1000)
cor(dd)

ee <- matrix(NA, 1000, 1000)
for (i in 1:1000) {
  for (j in 1:1000) {
    ee[i, j] <- cor(ee[, i], ee[, j])
  }
}
```

Speed up factor of vectorisation: 36!

Lists

Lists store information of many different types. Names are optional, but recommended!

```
amy <- list(office.num = 657, pets = TRUE,
            pets.names = c("Princess Jaws", "Friendly", "Mohawk",
                           "Canada", "USA", "Regina George"),
            is.cat = c(TRUE, rep(FALSE, 5)))
amy
```

```
## $office.num
## [1] 657
##
## $pets
## [1] TRUE
##
## $pets.names
## [1] "Princess Jaws" "Friendly"      "Mohawk"        "Canada"
## [5] "USA"           "Regina George"
##
## $is.cat
## [1]  TRUE FALSE FALSE FALSE FALSE FALSE
```

Lists

Double square brackets pull out individual elements. Single square brackets pull out subsets of the list. I recommend using names wherever possible!

```
amy[[3]] # subset third element
```

```
## [1] "Princess Jaws" "Friendly"      "Mohawk"        "Canada"
## [5] "USA"           "Regina George"
```

```
amy[3] # third element -- a list!
```

```
## $pets.names
## [1] "Princess Jaws" "Friendly"      "Mohawk"        "Canada"
## [5] "USA"           "Regina George"
```

Lists

```r
amy[2:3] # second and third elements -- a list!
```

```
## $pets
## [1] TRUE
##
## $pets.names
## [1] "Princess Jaws" "Friendly"      "Mohawk"        "Canada"
## [5] "USA"           "Regina George"
```

```r
amy$office # can also refer by name
```

```
## [1] 657
```

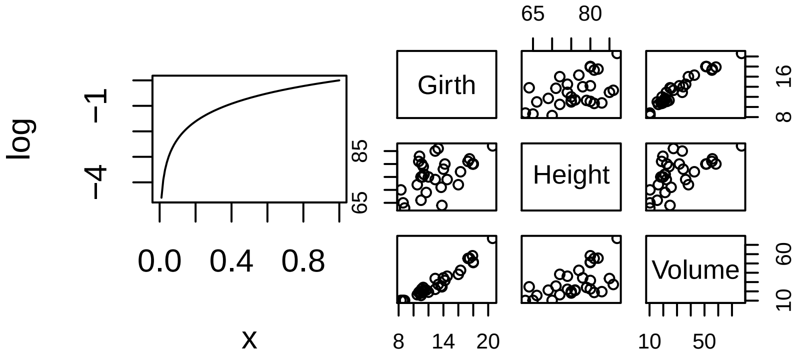
Generic functions

The same function can apply to objects of different classes. How does R know what to do?

```r
c(class(log), class(trees))
```

```
## [1] "function"   "data.frame"
```

```r
layout(t(1:2), widths = c(3,1)); plot(log); plot(trees)
```



Generic functions

plot is a *generic* function. Generic functions don't do anything themselves – they call *methods*, which are tailored to the class.

```
plot
```

```
## function (x, y, ...)
## UseMethod("plot")
## <bytecode: 0x7f9a75c14750>
## <environment: namespace:graphics>
```

```
methods("plot") # lists all types R knows how to plot
```

```
##  [1] plot.acf*           plot.data.frame*    plot.decomp
##  [4] plot.default        plot.dendrogram*    plot.densit
##  [7] plot.ecdf           plot.factor*        plot.formul
## [10] plot.function       plot.hclust*        plot.histog
## [13] plot.HoltWinters*   plot.isoreg*        plot.lm*
## [16] plot.medpolish*     plot.mlm*           plot.ppr*
```

Generic functions

To find the functions that apply to a class

```
methods(class = "lm")
```

```
##  [1] add1          alias          anova           case.r
##  [5] coerce        confint        cooks.distance  devian
##  [9] dfbeta        dfbetas        drop1           dummy.
## [13] effects       extractAIC     family          formul
## [17] hatvalues     influence      initialize      kappa
## [21] labels        logLik         model.frame     model.
## [25] nobs          plot           predict         print
## [29] proj          qr             residuals       rstand
## [33] rstudent      show           simulate        slotsF
## [37] summary       variable.names vcov
## see '?methods' for accessing help and source code
```

Generic functions

To see the code for a generic function, type `[function].[class]`

```
dimnames.data.frame
```

```
## function (x)
## list(row.names(x), names(x))
## <bytecode: 0x7f9a79d5ab10>
## <environment: namespace:base>
```

Help

There are many ways to get help with using functions or debugging code

1. The internet

[picture]

Help

2. `?fn` shows the documentation for `fn`... if it exists!

[picture]

Help

3. `help.search("topic")` searches help pages for "topic"

[picture]

Examples

The documentation pages often show examples (`example(plot)`) and have demos (`demo(plotmath)`). `vignette()` opens longer worked examples that are great for playing with new packages.

Keep in mind

- The user of a function assumes responsibility for giving arguments in the correct form
- arguments are ordered
  - Unnamed arguments are allocated as first arguments
  - Named arguments can be anywhere in ordering
- Not supplied arguments assume default value
  - Not supplying arguments without a default gives an error message

Don't get bogged down in reading *all* the documentation – experiment and learn from your mistakes instead!

Debugging

1. Stare at it until you identify the problem a.k.a. psychic debugging
2. Breakdown the components until you find the problem (bisection method converges linearly!)
3. `traceback()` – covered later in the course

Homework 1 and next week