

Programming with R



Educational Materials

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Data Structures

- R has a rich set of *self-describing* data structures.

```
> class(z)
```

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

```
> class(x)
```

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

```
> x[1:2, ]
```

```
  type      time
1 case -0.4791861
2 case -0.8718753
```

- There is no need to declare the types of the variables.

Data Structures (continued)

- `vector` - arrays of the same type
- `list` - can contain objects of different types
- `environment` - hashtable
- `data.frame` - table-like
- `factor` - categorical
- `Classes` - arbitrary record type
- `function`

Atomic Data Structures

- In R, vectors are the “base” type, not scalars.
- A vector contains an indexed set of values that are all of the same type:
 - *logical*
 - *numeric*
 - *complex*
 - *character*
- The numeric type can be further broken down into *integer*, *single*, and *double* types (but this is only important when making calls to foreign functions, eg. C or Fortran.)

Creating Vectors

There are two symbols that can be used for assignment: `<-` and `=`.

```
> v <- 1
```

```
> v
```

```
[1] 1
```

```
> v <- c(1, 2, 3)
```

```
> v
```

```
[1] 1 2 3
```

```
> s <- "a string"
```

```
> t <- TRUE
```

```
> length(letters)
```

```
[1] 26
```

```
> letters
```

```
[1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p"  
[17] "q" "r" "s" "t" "u" "v" "w" "x" "y" "z"
```

Creating Vectors with Functions

- `c` - concatenate
- `seq` (also `:`) and `rep` - patterns
- `vector` - new vector with default value.

```
> seq(1, 3)
```

```
[1] 1 2 3
```

```
> 1:3
```

```
[1] 1 2 3
```

```
> rep(c(1, 2), 3)
```

```
[1] 1 2 1 2 1 2
```

```
> vector(mode = "character", length = 5)
```

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

Matrices and Arrays

- Can be created using `matrix` and `array`.
- Are represented as a vector with a dimension attribute.
- R is column oriented for matrices.

Matrix Examples

```
> x <- matrix(1:10, nrow = 2)
```

```
> dim(x)
```

```
[1] 2 5
```

```
> x
```

```
      [,1] [,2] [,3] [,4] [,5]  
[1,]    1    3    5    7    9  
[2,]    2    4    6    8   10
```

```
> as.vector(x)
```

```
[1] 1 2 3 4 5 6 7 8 9 10
```


Naming

The elements of a vector can (and often should) be given names.

Names can be specified

- at creation time
- using `names`, `dimnames`, `rownames`, `colnames`

```
> x <- c(a = 0, b = 2)
```

```
> x
```

```
a b
```

```
0 2
```

```
> names(x) <- c("Australia", "Brazil")
```

```
> x
```

```
Australia    Brazil
```

```
0
```

```
2
```

Naming (continued)

```
> x <- matrix(c(4, 8, 5, 6), nrow = 2)
> dimnames(x) <- list(c("2005", "2006"), c("plane", "bus"))
> x
```

	plane	bus
2005	4	5
2006	8	6

Subsetting

- One of the most powerful features of R is its ability to manipulate subsets of vectors and arrays.
- Subsetting is indicated by `[,]`.
- Note that `[` is actually a function (try `get("[")`). The behavior can be customized for particular classes of objects.

Subsetting with Positive Indices

- A subscript consisting of a vector of positive integer values is taken to indicate a set of indices to be extracted.

```
> x <- 1:10
```

```
> x[2]
```

```
[1] 2
```

```
> x[1:3]
```

```
[1] 1 2 3
```

- A subscript which is larger than the length of the vector being subsetted produces an NA in the returned value.

```
> x[9:11]
```

```
[1] 9 10 NA
```

Subsetting with Positive Indices (continued)

- Subscripts which are zero are ignored and produce no corresponding values in the result.

```
> x[0:1]
```

```
[1] 1
```

```
> x[c(0, 0, 0)]
```

```
integer(0)
```

- Subscripts which are NA produce an NA in the result.

```
> x[c(10, 2, NA)]
```

```
[1] 10  2 NA
```

Assignments with Positive Indices

- Subset expressions can appear on the left side of an assignment. In this case the given subset is assigned the values on the right (recycling the values if necessary).

```
> x[2] <- 200
```

```
> x[8:10] <- 10
```

```
> x
```

```
[1] 1 200 3 4 5 6 7 10 10 10
```

- If a zero or NA occurs as a subscript in this situation, it is ignored.

Subsetting with Negative Indexes

- A subscript consisting of a vector of negative integer values is taken to indicate the indices which are not to be extracted.

```
> x[-(1:3)]
```

```
[1] 4 5 6 7 10 10 10
```

- Subscripts which are zero are ignored and produce no corresponding values in the result.
- NA subscripts are not allowed.
- Positive and negative subscripts cannot be mixed.

Assignments with Negative Indexes

- Negative subscripts can appear on the the left side of an assignment. In this case the given subset is assigned the values on the right (recycling the values if necessary).

```
> x = 1:10
```

```
> x[-(8:10)] = 10
```

```
> x
```

```
[1] 10 10 10 10 10 10 10 10 8 9 10
```

- Zero subscripts are ignored.
- NA subscripts are not permitted.

Subsetting by Logical Predicates

- Vector subsets can also be specified by a logical vector of TRUEs and FALSEs.

```
> x = 1:10
```

```
> x > 5
```

```
[1] FALSE FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE
```

```
> x[x > 5]
```

```
[1]  6  7  8  9 10
```

- NA values used as logical subscripts produce NA values in the output.
- The subscript vector can be shorter than the vector being subsetted. The subscripts are recycled in this case.
- The subscript vector can be longer than the vector being subsetted. Values selected beyond the end of the vector produce NAs.

Subsetting by Name

- If a vector has named elements, it is possible to extract subsets by specifying the names of the desired elements.

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

```
  c      a <NA>
  3      1   NA
```

- If several elements have the same name, only the first of them will be returned.
- Specifying a non-existent name produces an NA in the result.

Exercises

1. Determine (precisely) how R handles non-integer subscripts (e.g. `1.2`). How might this produce problems?

2. What value do the following expressions produce.

```
x = 1:10
```

```
x[-11]
```

3. How could you choose all elements of a vector which have odd subscripts? Even subscripts?

4. How are complex subscripts treated?

Subsetting matrices

- when subsetting a matrix, missing subscripts are treated as if all elements are named; so `x[1,]` corresponds to the first row and `x[,3]` to the third column.
- for arrays, the treatment is similar, for example `y[,1,]`.
- these can also be used for assignment, `x[1,]=20`

Subsetting Arrays

- Rectangular subsets of arrays obey similar rules to those which apply to vectors.
- One point to note is that arrays can be treated as either matrices or vectors. This can be quite useful.

```
> x = matrix(1:9, ncol = 3)
```

```
> x[x > 6]
```

```
[1] 7 8 9
```

```
> x[row(x) > col(x)] = 0
```

```
> x
```

```
      [,1] [,2] [,3]
[1,]    1    4    7
[2,]    0    5    8
[3,]    0    0    9
```

Custom Subsetting Example

```
> library("Biobase")  
> data(sample.ExpressionSet)  
  
> class(sample.ExpressionSet)
```

```
[1] "ExpressionSet"  
attr(,"package")  
[1] "Biobase"
```

```
> dim(sample.ExpressionSet)
```

```
Features  Samples  
      500      26
```

```
> slotNames(sample.ExpressionSet)
```

```
[1] "assayData"      "phenoData"      "featureData"  
[4] "experimentData" "annotation"     ".__classVersion__"
```

Custom Subsetting Example

```
> sample.ExpressionSet
```

```
ExpressionSet (storageMode: lockedEnvironment)
```

```
assayData: 500 features, 26 samples
```

```
  element names: exprs, se.exprs
```

```
phenoData
```

```
  sampleNames: A, B, ..., Z (26 total)
```

```
  varLabels and varMetadata:
```

```
    sex: Female/Male
```

```
    type: Case/Control
```

```
    score: Testing Score
```

```
featureData
```

```
  featureNames: AFFX-MurIL2_at, AFFX-MurIL10_at, ..., 31739_at (5
```

```
  varLabels and varMetadata: none
```

```
experimentData: use 'experimentData(object)'
```

```
Annotation [1] "hgu95av2"
```

Custom Subsetting Example

```
> sample.ExpressionSet[1:2, 2:5]
```

```
ExpressionSet (storageMode: lockedEnvironment)
```

```
assayData: 2 features, 4 samples
```

```
  element names: exprs, se.exprs
```

```
phenoData
```

```
  rowNames: B, C, D, E
```

```
  varLabels and varMetadata:
```

```
    sex: Female/Male
```

```
    type: Case/Control
```

```
    score: Testing Score
```

```
featureData
```

```
  rowNames: AFFX-MurIL2_at, AFFX-MurIL10_at
```

```
  varLabels and varMetadata: none
```

```
experimentData: use 'experimentData(object)'
```

```
Annotation [1] "hgu95av2"
```


Vectorized Arithmetic

- Most arithmetic operations in the R language are *vectorized*. That means that the operation is applied element-wise.

```
> 1:3 + 10:12
```

```
[1] 11 13 15
```

- In cases where one operand is shorter than the other the short operand is recycled, until it is the same length as the longer operand.

```
> 1 + 1:5
```

```
[1] 2 3 4 5 6
```

```
> paste(1:5, "A", sep = "")
```

```
[1] "1A" "2A" "3A" "4A" "5A"
```

- Many operations which need to have explicit loops in other languages do not need them with R. You should vectorize any functions you write.

Lists

- In addition to atomic vectors, R has a number of *recursive* data structures. Among the important members of this class are *lists* and *environments*.
- A list is a vector which can contain vectors and other lists (in fact arbitrary R objects) as elements. In contrast to atomic vectors, whose elements are homogeneous, lists and environments contain heterogeneous elements.

```
> lst = list(a = 1:3, b = "a list")
> lst

$a
[1] 1 2 3

$b
[1] "a list"
```

Environments

- One difference between lists and environments is that there is no concept of ordering in an environment. All objects are stored and retrieved by **name**.

```
> e1 = new.env(hash = TRUE)
> e1[["a"]] <- 1:3
> assign("b", "a list", e1)
> ls(e1)

[1] "a" "b"
```

- Another difference is that for lists partial matching of names is used, for environments it is **not**.

Subsetting and Lists

- Lists are useful as containers for grouping related things together (many R functions return lists as their values).
- Because lists are a recursive structure it is useful to have two ways of extracting subsets.
- The `[]` form of subsetting produces a sub-list of the list being subsetted.
- The `[[]]` form of subsetting can be used to extract a single element from a list.

List Subsetting Examples

- Using the [] operator to extract a sublist.

```
> lst[1]
```

```
$a
```

```
[1] 1 2 3
```

- Using the [[]] operator to extract a list element.

```
> lst[[1]]
```

```
[1] 1 2 3
```

- As with vectors, indexing using logical expressions and names are also possible.

List Subsetting by Name

- The dollar operator provides a short-hand way of accessing list elements by name. This operator is different from all other operators in R, it does not evaluate its second operand (the string).

```
> lst$a  
[1] 1 2 3  
> lst[["a"]]  
[1] 1 2 3
```

- For these accessors partial matching (!) is used.

Environment Accessing Elements

- Access to elements in environments can be through, `get`, `assign`, `mget`.
- You can also use the dollar operator and the `[[]]` operator, with character arguments only. No partial matching is done.

```
> e1$a
```

```
[1] 1 2 3
```

```
> e1[["b"]]
```

```
[1] "a list"
```

Assigning values in Lists and Environments

- Items in lists and environments can be replaced in much the same way as items in vectors are replaced.

```
> lst[[1]] = list(2, 3)
```

```
> lst[[1]]
```

```
[[1]]
```

```
[1] 2
```

```
[[2]]
```

```
[1] 3
```

```
> e1$b = 1:10
```

```
> e1$b
```

```
[1] 1 2 3 4 5 6 7 8 9 10
```


Data Frames

- Data frames are a special R structure used to hold a set of related variables. They are the R representation of a statistical *data matrix*. In a `data.frame`, the observations are the rows and the covariates are the columns.
- Data frames can be treated like matrices, and indexed with two subscripts. The first subscript refers to the observation, the second to the variable.
- Data frames are really lists, and list subsetting can also be used on them.

Data Frames (continued)

```
> df <- data.frame(type = rep(c("case", "control"), c(2,
+   3)), time = rexp(5))
> df
      type      time
1   case 0.24271208
2   case 0.17361331
3 control 0.02427679
4 control 3.51739205
5 control 0.22745696
> df$time
[1] 0.24271208 0.17361331 0.02427679 3.51739205 0.22745696
> names(df)
[1] "type" "time"
> rn <- paste("id", 1:5, sep = "")
> rownames(df) <- rn
> df[1:2, ]
      type      time
id1 case 0.2427121
id2 case 0.1736133
```

Classes

- A class consists of a set of *slots* each containing a specific type (character, numeric, etc.).
- *methods* can be defined for classes. A rectangle class that has slots for length and width could have an **area** method.
- Slots are accessed using @, but accessor methods are preferred.

Classes (example)

```
> setClass("Person", representation(name = "character",  
+   height = "numeric", country = "character"))
```

```
[1] "Person"
```

```
> p <- new("Person", name = "Alice", height = 5, country = "UK")  
> p
```

An object of class "Person"

Slot "name":

```
[1] "Alice"
```

Slot "height":

```
[1] 5
```

Slot "country":

```
[1] "UK"
```

```
> p@name
```

```
[1] "Alice"
```

Getting Help There are a number of ways of getting help:

- `help` and `?`: `help("data.frame")`
- `help.search`, `apropos`
- `RSiteSearch` (requires internet connection)
- `help.start`
- `sessionInfo`
- Online manuals
- Mailing lists (`sessionInfo`)

Packages

- In R one of primary mechanisms for distributing software is via *packages*
- CRAN is the major repository for getting packages.
- You can either download packages manually or use `install.packages` or `update.packages` to install and update packages.
- In addition, on Windows and in some other GUIs, there are menu items that facilitate package downloading and updating.
- It is important that you use the R package installation facilities. You cannot simply unpack the archive in some directory and expect it to work.

Packages - Bioconductor

- Bioconductor packages are hosted in CRAN-style repositories and are accessible using `install.packages`.
- The most reliable way to install Bioconductor packages (and their dependencies) is to use `biocLite`.
- Bioconductor has both a release branch and a development branch. Each Bioconductor release is compatible with a specific R release.
- Bioconductor packages all have vignettes.

Packages

- Having, and needing many more packages can cause some problems.
- When packages are loaded into R, they are essentially attached to the `search` list, see `search`.
- This greatly increases the probabilities of variable masking, that is one package provides a function that has the same name as a different function in another package.
- Name spaces were introduced in R 1.7.0 to provide tools that would help alleviate some of the problems.

Control-Flow R has a standard set of control flow functions:

- Looping: `for`, `while` and `repeat`.
- Conditional evaluation: `if` and `switch`.

Two Useful String Functions

1. Concatenate strings: `paste`
2. Search strings: `grep`

Example: `paste`

```
> s <- c("a", "b", "c")
> paste(s, "X", sep = "_")

[1] "a_X" "b_X" "c_X"

> paste(s, collapse = ", ")

[1] "a, b, c"
```

Example: `grep`

```
> library("ALL")
```

```
> data(ALL)
```

```
> class(ALL$mol.biol)
```

```
[1] "factor"
```

```
> negIdx <- grep("NEG", ALL$mol.biol)
```

```
> negIdx[1:10]
```

```
[1]  2  5  6  7  8  9 12 14 16 21
```

The apply Family

- A natural programming construct in R is to *apply* the same function to elements of a list, of a vector, rows of a matrix, or elements of an environment.
- The members of this family of functions are different with regard to the data structures they work on and how the answers are dealt with.
- Some examples, `apply`, `sapply`, `lapply`, `mapply`, `eapply`.

Using `apply`

- `apply` applies a function over the margins of an array.
- For example,
 - > `apply(x, 2, mean)`
computes the column means of a matrix `x`, while
 - > `apply(x, 1, median)`
computes the row medians.
- (`apply`) is implemented in a way which avoids the overhead associated with looping. (But it is still slow and you might use `rowSums` or `colSums`).

Writing Functions

- Writing R functions provides a means of adding new functionality to the language.
- Functions that a user writes have the same status as those which are provided with R.
- Reading the functions provided with the R system is a good way to learn how to write functions.
- If a user chooses she can make modifications to the system functions and use her modified ones, in preference to the system ones.

A Simple Function

- Here is a function that computes the square of its argument.

```
> square = function(x) x * x
```

```
> square(10)
```

```
[1] 100
```

- Because the underlying arithmetic is vectorized, so is this function.

```
> square(1:4)
```

```
[1]  1  4  9 16
```


Composition of Functions

- Once a function is defined, it is possible to call it from other functions.

```
> sumsq = function(x) sum(square(x))
```

```
> sumsq(1:10)
```

```
[1] 385
```

Returning Values

- Any single R object can be returned as the value of a function; including a function.
- If you want to return more than one object, you should put them in a list (usually with names), or an S4 object, and return that.
- The value returned by a function is either the value of the last statement executed, or the value of an explicit call to `return`.
- `return` takes a single argument, and can be called from anywhere in a function.
- `return` is lexically scoped, and can be passed out to other functions, to effect non-local returns.

Control of Evaluation

- In some cases you want to evaluate a function that may fail, but you do not want to exit from the middle of an evaluation.
- In these cases the function `try` can be used.
- `try(expr)` will either return the value of the expression `expr`, or an object of class *try-error*
- `tryCatch` provides a much more substantial mechanism for condition handling and error recovery.

Name Spaces

- Name spaces were introduced in R 1.7.0, see R News, Vol 3/1 for more details.
- They provide a mechanism that allows package writers to control what functions they import (and hence use) and export (and hence let others use).
- Related functions: `loadedNamespaces` and `::.`

Object Oriented Programming

- Object oriented programming is a style of programming where one attempts to have software reflections of real-world objects and to write functions (methods) that operate on these objects.
- The R language has two different object oriented paradigms, one S3 is older and should not be used for new projects. The second, S4 is newer and is currently under active development.
- These objects systems are more like OOP in Scheme, Lisp or Dylan than they are like OOP in Java or C++.

Classes

- In OOP there are two basic ingredients, objects and methods.
- An object is an instance of a class, and most OOP implementations have mechanisms to ensure that all objects of a particular class have some common characteristics.
- In most implementations there is some notion of inheritance or class extension. Class B is said to extend class A if a member of B has all the attributes that a member of A does, plus some other attributes.

Generic Functions

- A *generic function* is an interface, or a dispatcher, that examines the type or class of its arguments and invokes the most appropriate method.
- A method is registered with a generic function, by indicating its existence together with the number and types (classes) of its arguments.
- In the previous example, if a generic function is called with an instance of class B and there is no class B method, a class A method could be used.

S3

- S3 OOP has no real mechanism for defining classes or for creating objects from a specific class.
- One can make any object an instance of class *foo*, by assigning a class attribute, `class(x) = "foo"`.
- S3 handles inheritance by setting several different class attributes (but these are not always handled correctly).
- S3 is not suitable for the development of large scale complex systems.

S3 Generic Functions

- The relationship between a generic function and its methods is done by a naming convention. The generic function must have a call to `UseMethod` and the method must have a name that is the name of the generic function concatenated with the name of the class, with the two names separated by a dot.

```
> mean
```

```
function (x, ...)
```

```
UseMethod("mean")
```

```
<environment: namespace:base>
```

```
> methods("mean")
```

```
[1] mean.Date          mean.POSIXct      mean.POSIXlt     mean.data.frame
```

```
[5] mean.default      mean.difftime
```

References

- *The New S Language, Statistical models in S, Programming with Data*, by John Chambers and various co-authors.
- *Modern Applied Statistics, S Programming* by W. N. Venables and B. D. Ripley.
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- *Data Analysis and Graphics Using R* by J. Maindonald and J. Braun.