

Introduction to R

Nishant Gopalakrishnan, Martin Morgan

Fred Hutchinson Cancer Research Center

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Getting Started

Atomic Data structures

- Creating vectors

- Subsetting vectors

Factors

Matrices and arrays

Lists

- Subsetting a list

Environments

Data frames

Control flow

- apply

Functions

Visualizing data

Getting help in R

- ▶ `help` and `?`: `help("data.frame")` or `? data.frame`
- ▶ `help.search("slice"), apropos("mean")`
- ▶ `browseVignettes("Biobase")`
- ▶ `RSiteSearch` (requires internet connection)
- ▶ R/Bioconductor mailing lists (`sessionInfo()`)

Data structures in R

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

- ▶ vector - array of the same type
- ▶ factor - categorical
- ▶ list - can contain objects of different types
- ▶ data.frame - table-like
- ▶ matrix
- ▶ environment - hash table
- ▶ class - arbitrary record type
- ▶ function

Creating vectors

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

```
> v <- 123
```

```
[1] 123
```

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

```
[1] "a string"
```

```
> t <- TRUE
```

```
[1] TRUE
```

```
> letters          # 'letters' is a built-in variable
```

```
[1] "a" "b" "c" "d" "e" "f" "g" "h" "i"
```

```
[10] "j" "k" "l" "m" "n" "o" "p" "q" "r"
```

```
[19] "s" "t" "u" "v" "w" "x" "y" "z"
```

```
> length(letters)  # 'length' is a function
```

```
[1] 26
```

Functions for Creating vectors

- ▶ `c` - concatenate
- ▶ `:` - integer sequence, `seq` - general sequence
- ▶ `rep` - repetitive patterns
- ▶ `vector` - vector of given length with default value

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

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

```
> 1:3
```

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

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

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

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

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

Naming vectors

The elements of a vector can be named

- ▶ 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
```

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("[")`). `x[2, 3]` is equivalent to `"["(x, 2, 3)`. Its behavior can be customized for particular classes of objects.
- ▶ The number of indices supplied to `[` must be either the dimension of `x` or 1.

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 subset 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] 10
```

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

Subsetting with negative indices

- ▶ 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 indices

- ▶ Negative subscripts 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 = 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
```

```
[7]  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.

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
```

- ▶ When 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.

Factors

- ▶ A special type of vector with grouping information about its components
- ▶ A vector with its components grouped with distinct levels
- ▶

```
> col <- c("red", "green", "red", "yellow", "red")  
> factor(col)
```

```
[1] red    green  red    yellow red  
Levels: green red  yellow
```

Matrices and n -Dimensional Arrays

- ▶ Can be created using `matrix` and `array`.
- ▶ Are represented as a vector with a dimension attribute.
- ▶ left most index is fastest (like Fortran or Matlab) –

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 dimensions of matrix

```
> x <- matrix(c(4, 8, 5, 6, 4, 2, 1, 5, 7), nrow=3)
> dimnames(x) <- list(
+   year = c("2005", "2006", "2007"),
+   "mode of transport" = c("plane", "bus", "boat"))
> x
```

	mode of transport		
year	plane	bus	boat
2005	4	6	1
2006	8	4	5
2007	5	2	7

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 also be treated as 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

```
>
```

Lists

- ▶ A list is an ordered set of elements that can be arbitrary R objects (vectors, other lists, functions, ...). In contrast to atomic vectors, which are homogeneous, lists and environments can be heterogeneous.

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

```
> lst
```

```
$a
```

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

```
$b
```

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

```
$c
```

```
function (x) .Primitive("sqrt")
```

```
> lst$c(81)
```

```
[1] 9
```

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.

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Subsetting lists

- ▶ 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 is also possible.

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 \$ partial matching is used, for [[it is not by default, but can be turned on.

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()  
> e1[["a"]] <- 1:3  
> assign("b", "ciao", e1)  
> ls(e1)
```

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

- ▶ Names must match exactly (for lists, partial matching is used for the \$ operator).

Accessing elements in an environment

- ▶ Access to elements in environments can be through, `get`, `assign`, `mget`.

```
> mget(c("a", "b"), e1)
```

```
$a
```

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

```
$b
```

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

- ▶ 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] "ciao"
```

Assigning values to lists and environments

- Items in lists and environments can be (re)placed 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 spreadsheet like table. In a `data.frame`, the observations are the rows and the covariates are the columns.
- ▶ Data frames can be treated like matrices and be 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.

Create a data frame

```
> df <- data.frame(type=rep(c("case", "control"), c(2, 3)),  
+                   time=rexp(5))
```

```
> df
```

	type	time
1	case	0.2733713
2	case	0.6458722
3	control	1.2571422
4	control	0.6151090
5	control	0.7726357

```
> df$time
```

```
[1] 0.2733713 0.6458722 1.2571422  
[4] 0.6151090 0.7726357
```


Update row names

```
> names(df)
[1] "type" "time"

> rn <- paste("id", 1:5, sep="")
> rownames(df) <- rn
> df[1:2, ]

      type      time
id1 case 0.2733713
id2 case 0.6458722
```

Control Flow

R has a standard set of control flow functions:

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

apply family of functions

- ▶ 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`.

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

apply is usually not faster than a for loop. But it is more elegant.

```
> a = matrix(runif(1e6), ncol=10)
> ## 'apply'
> s1 = apply(a, 1, sum)
> ## 'for', pre-allocating for efficiency
> s2 = numeric(nrow(a))
> for(i in 1:nrow(a))
+   s2[i] = sum(a[i,])
> ## purpose-built function (much faster!)
> s3 = rowSums(a)
```

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.

Functions

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

```
> square = function(x){  
+           x*x  
+           }  
> square(10)
```

```
[1] 100
```

- ▶ Because the function body is vectorized, so is this new 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 (discussed later), 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.

Visualizing data in R

Basic plots

- ▶ plot: x-y plotting
- ▶ boxplot: box-whisker plot
- ▶ hist: histogram
- ▶ barplot: bar plot

Basic scatter plot

```
> df <- data.frame("y" = 1:10, "x" = rnorm(10))  
> plot(df$x, df$y, col = "red")
```

Trellis graphics

Lattice package

- ▶ `xyplot`: scatter plot
- ▶ `bwplot`: box-whisker plot
- ▶ `histogram`: histogram
- ▶ `densityplot`: kernel density plot

Lattice plots

```
> xyplot( y ~ x | c, data , groups = g)
```

- ▶ lattice function
- ▶ formula
 - ▶ primary variables
 - ▶ conditioning variable
- ▶ grouping variable
- ▶ data

Reading/writing data from/to files

- ▶ `read.delim("file"), read.table("file")`
- ▶ `write.table, write`
- ▶ `load, save`

Packages

- ▶ In R the primary mechanism for distributing software is via *packages*.
- ▶ The most reliable way to install Bioconductor packages (and their dependencies) is to use `biocLite`.
 - > `source("http://bioconductor.org/biocLite.R")`
 - > `biocLite("Biobase")`
- ▶ During an R session, use `library` to load a package in order to obtain access to its functionality.
 - > `library(Biobase)`

Selected references

- ▶ *Software for Data Analysis: Programming with R* by J. Chambers.
- ▶ *R Programming for Bioinformatics* by R. Gentleman.
- ▶ *Lattice: Multivariate Data Visualization with R* by D. Sarkar.
- ▶ *Introductory Statistics with R* by P. Dalgaard.
- ▶ *Modern Applied Statistics, S Programming* by W. N. Venables and B. D. Ripley.

Course resource

- ▶ *Bioconductor Case Studies* by F. Hahne, W. Huber, R. Gentleman, and S. Falcon.