Basic R tutorial
Data types and structures
Data Types

• A vector contains an indexed set of values that are all of the same type:
  – \textit{logical}
  – \textit{numeric}
  – \textit{complex}
  – \textit{character}

• The numeric type can be further broken down into \textit{integer}, \textit{single}, and \textit{double} types (but this is only important when making calls to foreign functions, eg. C or Fortran.)
Data Structures

- **vector** - arrays of the same type
- **factor** - categorical
- **list** - can contain objects of different types
- **matrix** - table of numbers
- **data.frame** - table of numbers and/or characters
- **environment** - hashtable
- **function**
Data Structures

```r
> x <- data.frame(type=rep(c("case", "control"),
+                     c(2, 3)), time=rnorm(5))
> y <- 10
> z <- "a string"
> class(z)
[1] "character"
> class(x)
[1] "data.frame"
```

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

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

> length(letters)
[1] 26
Functions for Creating Vectors

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

```r
> 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] "" "" "" "" ""
Vectorized Arithmetic

• Most arithmetic operations in the R language are \textit{vectorized}. That means that the operation is applied element-wise.

\begin{verbatim}
> 1:3 + 10:12
[1] 11 13 15
\end{verbatim}

• 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.

\begin{verbatim}
> 1 + 1:5
[1] 2 3 4 5 6
> paste(1:5, "A", sep="")
[1] "1A" "2A" "3A" "4A" "5A"
\end{verbatim}

• Many operations which need to have explicit loops in other languages do not need them with R. You should vectorize any functions you write.
Matrices and $n$-Dimensional Arrays

- Can be created using `matrix` and `array`.
- Are represented as a vector with a dimension attribute.

```r
> x <- matrix(1:10, nrow=2)
> dim(x)
[1] 2 5

> x
[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
```
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 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.

```r
> 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
```
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.

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

• Random access to large environment can be sped up by using hashing (see the manual page of `new.env`).

• Names must match exactly (for lists, partial matching is used for the `$` operator).
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.
## Data Frames (continued)

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

<table>
<thead>
<tr>
<th>type</th>
<th>time</th>
</tr>
</thead>
<tbody>
<tr>
<td>case</td>
<td>0.09374666</td>
</tr>
<tr>
<td>case</td>
<td>0.24307215</td>
</tr>
<tr>
<td>control</td>
<td>2.02119442</td>
</tr>
<tr>
<td>control</td>
<td>2.92433415</td>
</tr>
<tr>
<td>control</td>
<td>0.14771720</td>
</tr>
</tbody>
</table>

> df$time

[1] 0.09374666 0.24307215 2.02119442 2.92433415 0.14771720
```
Naming

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

- at creation time

- later by 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

```r
> 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
```
Data types for microarrays

- **ExpressionSet** - one channel data (package *Biobase*)
- **NChannelSet** - multiple channels data (package *Biobase*)
- **AffyBatch** - Affymetrix data (package *affy*)
- **BeadLevelList** and **lumiBatch** - Illumina data (package *beadarray* and *lumi* respectively)
ExpressionSet and Cie. structure

• **assayData** - expression values in identical sized matrices
• **phenoData** - sample annotation in AnnotatedDataFrame
• **featureData** - feature annotation in AnnotatedDataFrame
• **experimentData** - description of the experiment as a MIAME object
• **annotation** - type of chip as a character
• **protocolData** - scan dates as a character
ExpressionSet

> 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"    "protocolData"
[7] ".__classVersion__"
ExpressionSet

> sample.ExpressionSet

ExpressionSet (storageMode: lockedEnvironment)
assayData: 500 features, 26 samples
  element names: exprs, se.exprs
protocolData: none
phenoData
  sampleNames: A, B, ..., Z (26 total)
  varLabels and varMetadata description:
    sex: Female/Male
    type: Case/Control
    score: Testing Score
featureData: none
experimentData: use 'experimentData(object)'
Annotation: hgu95av2
Subsetting and assignments
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 subsetted produces an NA in the returned value.

  > x[9:11]
  [1] 9 10 NA
Subsetting with Positive Indices

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

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

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

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

```r
> 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).

```r
> 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 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.

```r
> 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.

```r
> 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.
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.

```r
> x = matrix(1:9, ncol=3)
> x[ x > 6 ]
[1] 7 8 9
> x[ x > 6 ] = 0
> x

[,1] [,2] [,3]
[1,]  1  4  0
[2,]  2  5  0
[3,]  3  6  0
```
Subsetting and Lists

• Lists are useful as containers for grouping related thing 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 is 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).

```r
> 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.
Accessing Elements in an Environment

- 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.

```r
> e1$a
[1] 1 2 3

> e1[['b']]  # [1] "ciao"
```


Assigning values in Lists and Environments

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

```r
> 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
```
Subsetting ExpressionSet

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

ExpressionSet (storageMode: lockedEnvironment)
assayData: 2 features, 4 samples
  element names: exprs, se.exprs
protocolData: none
phenoData
  sampleNames: B, C, D, E
  varLabels and varMetadata description:
    sex: Female/Male
    type: Case/Control
    score: Testing Score
featureData: none
experimentData: use 'experimentData(object)'
Annotation: hgu95av2
Packages
Packages

• In R the primary mechanism for distributing software is via packages.

• CRAN is the major repository for packages.

• You can either download packages manually or use `install.packages` or `update.packages` to install and update packages.

• In addition, on Windows and 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 its contemporary R release.

- Bioconductor packages have vignettes.
Useful Functions
Getting Help

There are a number of ways of getting help:

- `help.start` and the HTML help button in the Windows GUI
- `help` and `?: help("data.frame")`
- `help.search`, `apropos`
- `RSiteSearch` (requires internet connection)
- Online manuals
- Mailing lists
Get information about object

- class
- length - length of vectors or factors
- dim - dimensions of an object
- head and tail - first or last parts of an object
Reading/Writing files

- **read.table** - creates a `data.frame` from a table format file
- **write.table** - writes a table format file from a `data.frame`
- **save** - writes an external representation of R objects to a specified file
- **load** - reload datasets written with the function `save`
- **read.AnnotatedDataFrame** - creates a `AnnotatedDataFrame` from a table format file
Control-Flow

R has a standard set of control flow functions:

- Looping: \texttt{for}, \texttt{while} and \texttt{repeat}.
- Conditional evaluation: \texttt{if} and \texttt{switch}.
Two Useful String Functions

1. Concatenate strings: `paste`

2. Search strings: `grep`
Example: `paste`

```r
> s <- c("apple", "banana", "lychee")
> paste(s, "X", sep="_")

[1] "apple_X"  "banana_X"  "lychee_X"

> paste(s, collapse="", ")

[1] "apple, banana, lychee"
```
Example: `grep`

```r
> 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.
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)

> system.time({
+   s1 = apply(a, 1, sum)
+ })

user  system elapsed
 0.828   0.420   1.452

> system.time({
+   s2 = numeric(nrow(a))
+   for(i in 1:nrow(a))
+       s2[i] = sum(a[i,])
+ })

user  system elapsed
 0.508   0.036   0.694

See also: rowSums and colSums.
Writing Functions
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.
A Simple Function

• Here is a function that computes the square of its argument.
  
  ```r
  > square = function(x) x*x
  > square(10)
  [1] 100
  ```

• Because the function body is vectorized, so is this new function.
  
  ```r
  > 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.

```r
> 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.
Control of Evaluation

• In some cases you want to evaluate a function that may fail, but you do not want to get stuck with an error.

• 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 more configurable mechanism for condition handling and error recovery.