

Introduction to R

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Some Basics

- There are three types of data in R: numeric, character and logical.
- R supports vectors, matrices, lists and data frames.
- Objects can be assigned values using an equal sign (=) or the special <- operator.
- R is highly vectorized - almost all operations work equally well on scalars and arrays
- All the elements of a matrix or vector must be of the same type
- Lists provide a very general way to hold a collection of arbitrary R objects.
- A data frame is a cross between a matrix and a list – columns (variables) of a data frame can be of different types, but they all must be the same length.

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Using R

- Typing the name of any object will display a printed representation. Alternatively, the `print()` function can be used to display the entire object.
 - Element numbers are displayed in square brackets
 - Typing a function's name will display its argument list and definition, but sometimes it's not very enlightening.
- The `str()` function shows the structure of an object
- If you don't assign an expression to an R object, R will display the results, but they are also stored in the `.Last.value` object
- Function calls require parentheses, even if there are no arguments. For example, type `q()` to quit R.
- Square brackets (`[]`) are used for subscripting, and can be applied to any subscriptable value.

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Getting Data into R

- `c()` - allows direct entry of small vectors in programs.
- `scan()` - reads data from a file, a URL, or the keyboard into a vector.
 - Can be embedded in a call to `matrix()` or `array()`.
 - Use the `what=` argument to read character data.
- `read.table` - reads from a file or URL into a dataframe.
 - `sep=` allows a field separator other than white space.
 - `header=` specifies if the first line of the file contains variable names.
 - `as.is=` allows control over character to factor conversion
 - Specialized versions of `read.table()` include `read.csv()` (comma-separated values), `read.delim()` (tab-separated values), and `read.fwf` (fixed width formatted data).
- `data()` - reads preloaded data sets into the current environment.

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Where R stores your data

Each time you start R, it looks for a file called `.RData` in the current directory. If it doesn't exist it creates it. So managing multiple projects is easy - change to a different directory for each different project.

When you end an R session, you will be asked whether or not you want to save the data.

- You can use the `objects()` function to list what objects exist in your local database, and the `rm()` function to remove ones you don't want.
- You can start R with the `--save` or `--no-save` option to avoid being prompted each time you exit R.
- You can use the `save.image()` function to save your data whenever you want

Getting Help

To view the manual page for any R function, use the `help(functionname)` command, which can be abbreviated by following a question mark (?) by the function name.

The `help.search("topic")` command will often help you get started if you don't know the name of a function.

The command `help.start()` will open a browser pointing to a variety of (locally stored) information about R, including a search engine and access to more lengthy PDF documents. Once the browser is open, all help requests will be displayed in the browser.

Many functions have examples, available through the `example()` function; general demonstrations of R capabilities can be seen through the `demo()` function.

Libraries

Libraries in R provide routines for a large variety of data manipulation and analysis. If something seems to be missing from R, it is most likely available in a library.

You can see the libraries installed on your system with the command `library()` with no arguments. You can view a brief description of the library using `library(help=libraryname)`. Finally, you can load a library with the command `library(libraryname)`.

Many libraries are available through the CRAN (Comprehensive R Archive Network) at

<http://cran.r-project.org/src/contrib/PACKAGES.html> .

You can install libraries from CRAN with the `install.packages()` function, or through a menu item in Windows. Use the `lib.loc=` argument if you don't have administrative permissions.

Search Path

When you type a name into the R interpreter, it checks through several directories, known as the search path, to determine what object to use. You can view the search path with the command `search()`. To find the names of all the objects in a directory on the search path, type `objects(pos=num)`, where *num* is the numerical position of the directory on the search path.

You can add a database to the search path with the `attach()` function. To make objects from a previous session of R available, pass `attach()` the location of the appropriate `.RData` file. To refer to the elements of a data frame or list without having to retype the object name, pass the data frame or list to `attach()`. (You can temporarily avoid having to retype the object name by using the `with()` function.)

Sizes of Objects

The `nchar()` function returns the number of characters in a character string. When applied to numeric data, it returns the number of characters in the printed representation of the number.

The `length()` function returns the number of elements in its argument. Note that, for a matrix, `length()` will return the total number of elements in the matrix, while for a data frame it will return the number of columns in the data frame.

For arrays, the `dim()` function returns a list with the dimensions of its arguments. For a matrix, it returns a vector of length two with the number of rows and number of columns. For convenience, the `nrow()` and `ncol()` functions can be used to get either dimension of a matrix directly. For non-arrays `dim()` returns a `NULL` value.

Finding Objects

The `objects()` function, called with no arguments, prints the objects in your working database. This is where the objects you create will be stored.

The `pos=` argument allows you look in other elements of your search path. The `pat=` argument allows you to restrict the search to objects whose name matches a pattern. Setting the `all.names=` argument to `TRUE` will display object names which begin with a period, which would otherwise be suppressed.

The `apropos()` function accepts a regular expression, and returns the names of objects anywhere in your search path which match the expression.

get() and assign()

Sometimes you need to retrieve an object from a specific database, temporarily overriding R's search path. The `get()` function accepts a character string naming an object to be retrieved, and a `pos=` argument, specifying either a position on the search path or the name of the search path element. Suppose I have an object named `x` in a database stored in `rproject/.RData`. I can attach the database and get the object as follows:

```
> attach("rproject/.RData")
> search()
 [1] ".GlobalEnv"          "file:rproject/.RData" "package:methods"
 [4] "package:stats"      "package:graphics"    "package:grDevices"
 [7] "package:utils"      "package:datasets"    "Autoloads"
[10] "package:base"
> get("x",2)
```

The `assign()` function similarly lets you store an object in a non-default location.

Combining Objects

The `c()` function attempts to combine objects in the most general way. For example, if we combine a matrix and a vector, the result is a vector.

```
> c(matrix(1:4,ncol=2),1:3)
 [1] 1 2 3 4 1 2 3
```

Note that the `list()` function preserves the identity of each of its elements:

```
> list(matrix(1:4,ncol=2),1:3)
[[1]]
      [,1] [,2]
 [1,]    1    3
 [2,]    2    4

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

Combining Objects (cont'd)

When the `c()` function is applied to lists, it will return a list:

```
> c(list(matrix(1:4,ncol=2),1:3),list(1:5))
```

```
[[1]]
```

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

```
[1,]    1    3
```

```
[2,]    2    4
```

```
[[2]]
```

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

```
[[3]]
```

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

To break down anything into its individual components, use the `recursive=TRUE` argument of `c()`:

```
> c(list(matrix(1:4,ncol=2),1:3),recursive=TRUE)
```

```
[1] 1 2 3 4 1 2 3
```

The `unlist()` and `unclass()` functions may also be useful.

Subscripting

Subscripting in R provides one of the most effective ways to manipulate and select data from vectors, matrices, data frames and lists. R supports several types of subscripts:

- Empty subscripts - allow modification of an object while preserving its size and type.

`x = 1` creates a new scalar, `x`, with a value of 1, while

`x[] = 1` changes each value of `x` to 1.

Empty subscripts also allow referring to the *i*-th column of a data frame or matrix as `matrix[i,]` or the *j*-th row as `matrix[,j]`.

- Positive numeric subscripts - work like most computer languages

The sequence operator (`:`) can be used to refer to contiguous portions of an object on both the right- and left- hand side of assignments; arrays can be used to refer to non-contiguous portions.

Subscripts (cont'd)

- Negative numeric subscripts - allow exclusion of selected elements
- Zero subscripts - subscripts with a value of zero are ignored
- Character subscripts - used as an alternative to numeric subscripts

Elements of R objects can be named. Use `names()` for vectors or lists, `dimnames()`, `rownames()` or `colnames()` for data frames and matrices. For lists and data frames, the notation `object$name` can also be used.

- Logical subscripts - powerful tool for subsetting and modifying data

A vector of logical subscripts, with the same dimensions as the object being subscripted, will operate on those elements for which the subscript is `TRUE`.

Note: A matrix indexed with a single subscript is treated as a vector made by stacking the columns of the matrix.

Examples of Subscripting Operations

Suppose `x` is a 5×3 matrix, with column names defined by

```
dimnames(x) = list(NULL,c("one","two","three"))
```

`x[3,2]` is the element in the 3rd row and second column.

`x[,1]` is the first column.

`x[3,]` is the third row.

`x[3:5,c(1,3)]` is a 3×2 matrix derived from the last three rows, and columns 1 and 3 of `x`.

`x[-c(1,3,5),]` is a 2×3 matrix created by removing rows 1, 3 and 5.

`x[x[,1]>2,]` is a matrix containing the rows of `x` for which the first column of `x` is greater than 2.

`x[,c("one","three")]` is a 5×2 matrix with the first and third columns of `x`

More on Subscripts

By default, when you extract a single column from a matrix or data.frame, it becomes a simple vector, which may confuse some functions. Furthermore, if the column was named, the name will be lost. To prevent this from happening, you can pass the `drop=TRUE` argument to the subscript operator:

```
> mx = matrix(c(1:4,4:7,5:8),ncol=3,byrow=TRUE,
+ dimnames=list(NULL,c("one","two","three")))
> mx[,3]
[1] 3 5 5 8
> mx[,3,drop=FALSE]
      three
[1,]     3
[2,]     5
[3,]     5
[4,]     8
```

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[[Subscripting Operator

A general principle in R is that subscripted objects retain the mode of their parent. For vectors and arrays, this rarely causes a problem, but for lists (and data frames treated like lists), R will often have problems working directly with such objects.

```
> mylist = list(1:10,10:20,30:40)
> mean(mylist[1])
[1] NA
Warning message:
argument is not numeric or logical: returning NA in: mean.default(mylist[1])
```

For this purpose, R provides double brackets for subscripts, which extract the actual list element, not a list containing the element:

```
> mean(mylist[[1]])
[1] 5.5
```

For named lists, the problem can also be avoided using the `$` notation.

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Subscripting with Data Frames

Since a data frame is a cross between a matrix and a list, subscripting operations for data frames are slightly different than for either of those types.

- Double subscripts in a data frame behave exactly as with matrices.
- Single subscripts in a data frame refer to a data frame containing the appropriate columns. To extract the actual column(s), use double brackets or an empty first subscript.
- A dollar sign (\$) can be used to separate a data frame name from a column name to extract the actual column. If the column name has special characters, it must be surrounded by quotes.

`x[["name"]]`, `x[, "name"]` and `x$name` are all equivalent, but `x["name"]` is a data frame with one column.

`x[1, "name"]`, `x[1,]$name` or `x[1,]["name"]` all access name for the first observation.

Tables and Matrices

If a two column matrix is used as a subscript of a matrix, its rows are interpreted as row and column numbers, for both accessing and assigning values.

```
> a = matrix(c(1,1,1,2,2,3),ncol=2,byrow=TRUE)
```

```
> a
```

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

```
> x = matrix(0,nrow=4,ncol=3)
```

```
> x[a] = c(10,20,30)
```

```
> x
```

```
      [,1] [,2] [,3]
[1,]   10   20    0
[2,]    0    0   30
[3,]    0    0    0
[4,]    0    0    0
```

Type Conversion Functions

Occasionally it is necessary to treat an object as if it were of a different type. One of the most common cases is to treat a character value as if it were a number. The `as.numeric()` function takes care of this, and in general there are “`as.`” functions for most types of objects encountered in R. A complete list can be seen with `apropos('^as.')`; some common examples are `as.matrix()`, `as.integer()`, `as.data.frame()`, `as.list()`, `as.logical()`, and `as.vector()`.

These functions do not permanently change the type of their arguments.

Some functions related to type conversion include `round()` and `trunc()` for numeric values, and `paste()` for character values.

Some Functions for Vectors

- `c()` - combines values, vectors, and/or lists to create new objects.
- `unique()` - returns a vector containing one element for each unique value in the vector
- `duplicated()` - returns a logical vector which tells if elements of a vector are duplicated with regard to previous ones.
- `rev()` - reverse the order of elements in a vector
- `sort()` - sorts the elements in a vector.
- `append()` - append or insert elements in a vector.
- `sum()` - sum of the elements of a vector
- `min()` - minimum value in a vector
- `max()` - maximum value in a vector

Missing Values

In R, missing values are represented by the string `NA`. You can assign a missing value by setting a variable equal to `NA`, but you must use the `is.na()` function to test for a missing value.

Missing values are propagated in all calculations, so the presence of even a single missing value can result in a variety of problems.

Many statistical functions provide a `na.rm=` argument to remove missing values before computations. Alternatively, use logical subscripting to easily extract non-missing values:

```
> values = c(12,NA,19,15,12,17,14,NA,19)
> values[!is.na(values)]
[1] 12 19 15 12 17 14 19
> vv = matrix(values,ncol=3,byrow=TRUE)
> vv[!is.na(vv[,2]),,drop=FALSE]
      [,1] [,2] [,3]
[1,]   15   12   17
```

Reading R's Input from a File

The `source()` command accepts a file name or a URL, and executes the commands from the file or URL, just as if they were typed into the R interpreter.

If an error is encountered while `source` is processing a file, execution halts, and the remaining statements are not evaluated.

R's usual default of printing unassigned expressions is suppressed in `source()`, unless the `echo=TRUE` argument is used.

Note that `scan()` can read data into an R object, but the contents of the files accessed by `source()` are executed as R commands in the current R session. You can combine both capabilities by embedding a `scan` command inside of a file whose name will be passed to `source`.

Alternative Input: Connections

In addition to filenames, `scan()` and `read.table()` will accept a variety of connection functions, allowing data to be read from pipes, zipped files, URLs and sockets. (“`help(connections)`” provides complete information.) For example, the output of the UNIX `ps` command looks like this:

```
PID TTY          TIME CMD
26377 pts/1    00:00:00 tcsh
26392 pts/1    00:00:02 R
26647 pts/1    00:00:00 ps
```

The following commands read the output of the `ps` command into a data frame:

```
> read.table(pipe("ps"),header=TRUE)
  PID  TTY    TIME CMD
1 26377 pts/1 00:00:00 tcsh
2 26392 pts/1 00:00:02  R
3 26647 pts/1 00:00:00  ps
```

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Printing

The `print()` function can be used to print any R object, and is silently invoked when an expression is not assigned to a value. For lists and arrays, it will always include subscripting information.

```
> print(7)
[1] 7
> print(matrix(c(1,2,3,4),ncol=2))
  [,1] [,2]
[1,]  1   3
[2,]  2   4
```

The `cat()` function allows you to print the values of objects without any subscripting information. It accepts a variable number of (unnamed) input arguments and supports the following named arguments:

- `file=` filename or connection object to write to
- `sep=` character string to insert between objects
- `fill=` logical or numeric value determining automatic newlines
- `append=` should output be appended if `file=` was used

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Output Destinations

By default, the output from an interactive R session is sent to the screen. To divert this output to a file, use the `sink()` or `capture.output()` function. These provide an exact copy of the session's output.

To write the contents of a matrix or vector to a file, use the `write()` function. Remember that when writing a matrix, it will be written to the file by columns, so the transpose function (`t()`) may be useful. The `ncolumns=` argument can be used to specify the number of data values on each line; the `append=` argument can be used to avoid overwriting an existing file.

To write a data frame to a file, use the `write.table()` function; it is basically the mirror image of the `read.table()` function.

Recycling of Vectors

When a vector is involved in an operation that requires more elements than the vector contains, the values in the vector are recycled.

```
> x = matrix(1:3,nrow=2,ncol=6)
> x
      [,1] [,2] [,3] [,4] [,5] [,6]
[1,]    1    3    2    1    3    2
[2,]    2    1    3    2    1    3
```

A warning is printed if the desired length is not an even multiple of the original vector's length.

```
> matrix(1:4,nrow=2,ncol=5)
      [,1] [,2] [,3] [,4] [,5]
[1,]    1    3    1    3    1
[2,]    2    4    2    4    2
```

Warning message:

```
data length [4] is not a sub-multiple or multiple of the number of
columns [5] in matrix
```

Operators

All of the binary operators in R are vectorized, operating element by element on their arguments, recycling values as needed. These operators include:

<code>+</code>	addition	<code>-</code>	subtraction	<code>*</code>	multiplication
<code>/</code>	division	<code>^</code>	Exponentiation	<code>%%</code>	Modulus
		<code>%%/</code>	Integer Division		

Comparison operators will return the logical values `TRUE` or `FALSE`, or `NA` if any elements involved in a comparison are missing.

<code><</code>	less than	<code>></code>	greater than	<code><=</code>	l.t. or equal
<code>>=</code>	g.t. or equal	<code>==</code>	equality	<code>!=</code>	non-equality

Logical operators come in elementwise and pairwise forms.

<code>&</code>	elementwise and	<code>&&</code>	pairwise and	<code>!</code>	negation
<code> </code>	elementwise or	<code> </code>	pairwise or	<code>xor()</code>	exclusive or

The `%in%` operator can be used to test if a value is present in a vector or array.

Rounding Functions

The following functions are available for rounding numerical values:

- `round()` - uses IEEE standard to round up or down; optional `digits=` argument controls precision
- `signif()` - rounds numerical values to the specified `digits=` number of significant digits
- `trunc()` - rounds by removing non-integer part of number
- `floor()`, `ceiling()` - rounds to integers not greater or not less than their arguments, respectively
- `zapsmall()` - accepts a vector or array, and makes numbers close to zero (compared to others in the input) zero. `digits=` argument controls the rounding.

Non-vectorized functions

Although most functions in R are vectorized, returning objects which are the same size and shape as their input, some will always return a single logical value.

`any()` tests if any of the elements of its arguments meet a particular condition; `all()` tests if they all do.

```
> x = c(7,3,12,NA,13,8)
> any(is.na(x))
[1] TRUE
> all(x > 0)
[1] NA
> all(x > 0,na.rm=TRUE)
[1] TRUE
```

`identical()` tests if two objects are exactly the same. `all.equal()` allows for a `tolerance=` argument when dealing with numeric values, but returns a character string summarizing differences. You can test for numeric equality using a tolerance by combining the two:

```
> x = c(3.0001,4.0009,5.002)
> y = c(3,4,5)
> identical(all.equal(x,y,tolerance=.001),TRUE)
[1] TRUE
```

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Using Logical Expressions

We've seen that logical expressions can be effectively used to extract or modify subsets of data within vectors and arrays. Some other ways to use logical expressions include:

- Counting

The `sum()` function will automatically coerce `FALSE` to 0 and `TRUE` to 1, so taking the sum of a logical expression counts how many elements are `TRUE`.

- Locations

The `which()` function will return the positions within an array or vector for which a logical expression is `TRUE`. By default it treats arrays as column-wise vectors; the `arr.ind=TRUE` argument can be used to return array indices instead.

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Categorical Variables

Categorical variables in R are known as **factors**, and are stored as integer codes along with a set of labels. The `cut()` function creates factors from continuous variables.

```
> x = c(17,19,22,43,14,8,12,19,20,51,8,12,27,31,44)
> cut(x,3)
 [1] (7.96,22.3] (7.96,22.3] (7.96,22.3] (36.7,51] (7.96,22.3] (7.96,22.3]
 [7] (7.96,22.3] (7.96,22.3] (7.96,22.3] (36.7,51] (7.96,22.3] (7.96,22.3]
[13] (22.3,36.7] (22.3,36.7] (36.7,51]
Levels: (7.96,22.3] (22.3,36.7] (36.7,51]
> cut(x,3,labels=c("low","medium","high"))
 [1] low  low  low  high low  low  low  low  low  high
[11] low  low  medium medium high
Levels: low medium high
```

To return the codes in an ordinary (non-factor) variable, use the `labels=FALSE` argument.

To convert a factor to its integer codes, use the `unclass()` function; to convert to ordinary character values use `as.character()`.

Categorical Variables (cont'd)

You can control where `cut()` divides up your data using the `breaks=` argument. Given an integer, `cut()` breaks up the data at equal intervals; using a vector of values breaks up the data at those values. For example, to create quartiles, the breaks can be specified as the output from the `quantile()` function:

```
> cut(x,breaks=quantile(x,c(0,.25,.50,.75,1)),
+ labels=c("Q1","Q2","Q3","Q4"),include.lowest=TRUE)
 [1] Q2 Q2 Q3 Q4 Q2 Q1 Q1 Q2 Q3 Q4 Q1 Q1 Q3 Q4 Q4
Levels: Q1 Q2 Q3 Q4
```

Note the use of `include.lowest=TRUE` to insure that the minimum value is not set to missing.

The `rep()` function

The `rep()` function generates repetitions of values. The first argument to `rep()` is a vector containing the values to be repeated. If the second argument is a scalar, the entire first argument is repeated that many times; if it's a vector of the same length as the first argument, each element of the first list is repeated as many times as the corresponding element in the second list.

```
> rep(1:3,3)
[1] 1 2 3 1 2 3 1 2 3
> rep(1:3,c(5,2,1))
[1] 1 1 1 1 1 2 2 3
```

For the special case of generating levels for designed experiments, the `gl()` function provides a convenient wrapper.

Tabulation

The `table()` function is the main tool for tabulating data in R. Given a vector, it produces a frequency table:

```
> x = c(7,12,19,7,19,21,12,14,17,12,19,21)
> table(x)
x
 7 12 14 17 19 21
 2  3  1  1  3  2
```

Notice that the output is named based on the data values. To use them as numbers, they must be passed to the `as.numeric()` function:

```
> sum(table(x) * as.numeric(names(table(x))))
[1] 180
```

Cross-tabulation

If several equal length vectors are passed to `table()`, it will output an array with the counts of the vector's cross-tabulation:

```
> x1 = c(1,2,3,2,1,3,2,3,1)
> x2 = c(2,1,2,3,1,3,2,2,3)
> x3 = c(1,2,3,3,2,1,2,1,2)
> table(x1,x2)
  x2
x1 1 2 3
 1 1 1 1
 2 1 1 1
 3 0 2 1
```

For higher-dimensioned tables (producing higher-dimensioned arrays), the default output may not be very easy to use. The `ftable()` function can be used to "flatten" such a table.

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ftable()

```
> tbl = table(x1,x2,x3)
> tbl
, , x3 = 1
  x2
x1 1 2 3
 1 0 1 0
 2 0 0 0
 3 0 1 1
, , x3 = 2
  x2
x1 1 2 3
 1 1 0 1
 2 1 1 0
 3 0 0 0
, , x3 = 3
  x2
x1 1 2 3
 1 0 0 0
 2 0 0 1
 3 0 1 0
```

```
> ftable(tbl)
      x3 1 2 3
x1 x2
 1  1    0 1 0
   2    1 0 0
   3    0 1 0
 2  1    0 1 0
   2    0 1 0
   3    0 0 1
 3  1    0 0 0
   2    1 0 1
   3    1 0 0
```

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Date Values

The `as.Date()` function converts a variety of character date formats into R dates, stored as the number of days since January 1, 1970. The `format=` argument is a string composed of codes such as `%Y` for full year, `%y` for 2-digit year, `%m` for month number, and `%d` for day number.

Once converted to dates, the following functions will return information about dates: `weekdays()`, `months()`, `quarters()` and `julian()`.

In addition, the `cut()` function allows the following choices for the `breaks=` argument: `"day"`, `"week"`, `"month"`, or `"year"`.

Note: Alternative date and time formats are available through the `chron` and `POSIXct` libraries.

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Date Values: Examples

The `format=` argument allows a variety of formats:

```
> d1 = as.Date("20041201",format="%Y%m%d")
> d2 = as.Date("12/5/03",format="%m/%d/%y")
> d3 = as.Date("7-8-2001",format="%d-%m-%Y")
```

Many operators and functions will recognize dates.

```
> d1 - d2
Time difference of 362 days
> d1 - d2 > 360
[1] TRUE
> mean(c(d1,d2,d3))
[1] "2003-06-25"
> d1 > d2
[1] TRUE
```

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The `chron` library

The `chron` library provides an alternative representation for date values. In addition to dates, `chron` objects can also store times. The `chron()` function accepts separate arguments for `dates=` and `times=`. Similarly, the `format=` argument can be a vector or list with named `dates` and/or `times` elements. Formats for dates can be composed of `m`, `d`, `y`, `month`, `day`, or `year`; times can be composed of `h`, `m`, and `s`.

If the `date=` argument to `chron()` is numeric, it is interpreted as a Julian date; the `origin=` argument accepts a array of length 3 specifying a month, day and year for an alternative to the default January 1, 1970 origin.

The functions `as.Date()` and `as.chron()` can be used to convert between the two representations of dates.

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`chron` library: Examples

When using `chron`'s default formats (`m/d/y` and `h:m:s`), the `formats=` argument is not needed.

```
> d1 = chron('12/25/2004', '0:0:0') # default formats
```

The `origin=` argument is useful with Julian dates:

```
> d2 = chron(10, origin=c(12, 31, 2004))
```

```
> d2
```

```
[1] 01/10/05
```

Operations and functions which work with `Date` objects will usually work with `chron` objects:

```
> d3 = chron('7-6-2005', '6:00:00', format=c(dates='m-d-y', times='h:m:s'))
```

```
> d3 - d1
```

```
Time in days:
```

```
[1] 193.25
```

```
> weekdays(d3)
```

```
[1] Wed
```

```
Levels: Sun < Mon < Tue < Wed < Thu < Fri < Sat
```

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File System Interface

R provides a variety of functions to query and manipulate the file system.

- `file.info()` - accepts a character vector of filenames, and returns a data frame with information about the files.
- `file.access()` - provides information about read, write and execute access of files
- `list.files()` - returns a list of files from a given directory
- `file.choose()` - interactive file chooser, varies by operating system

The following functions are also available:

```
file.create()   file.exists()   file.remove()
file.rename()   file.append()   file.copy()
file.symlink()  dir.create()    file.show()
```

Operating System Interface

In addition to pipes, R provides the following functions to access and execute operating system commands

- `system` - executes an operating system command; with `intern=TRUE` returns the command's output, otherwise the system return code.
- `system.time()` - accepts and executes an R expression, and returns the execution time
- `proc.time()` - returns user, system and total time for the current R process and its children
- `Sys.info()` - information about the operating system
- `Sys.time()` - returns the current time from the operating system

Assignment Functions

Many functions in R can be used on the left hand side of an assignment operator, allowing various properties of objects to be modified conveniently. Some examples include `names()`, `diag()`, `dimnames()`, `length()`, `dim()` and `substr()`.

For example, one way to reshape a matrix would be to assign a value to the `dim()` function:

```
> m = matrix(1:12,4,3)          > dim(m) <- c(6,2)
> m                             > m
  [,1] [,2] [,3]                [,1] [,2]
[1,]   1   5   9                [1,]   1   7
[2,]   2   6  10                [2,]   2   8
[3,]   3   7  11                [3,]   3   9
[4,]   4   8  12                [4,]   4  10
                                [5,]   5  11
                                [6,]   6  12
```

Functions such as these have names which end in “<-”.

Writing Functions: Introduction

- Function definitions begin with the word `function`, followed by a parenthetic list of arguments.
- Writing functions in R is easy because the syntax is identical to ordinary R syntax.
- Variables which are modified in a function are local to the function, but all variables in the calling environment are available (read only). (You can override this using the `<<-` operator.)
- You can specify a return value through the `return()` function; otherwise, a function’s return value is the value of the last evaluated expression. (Use the `invisible()` function to suppress the return value from being automatically displayed)

A Simple Function Example

Suppose we wish to write a function that will subtract the median from a vector of numbers, and then optionally divide each number by the range. We will use one argument for the input vector, and create a `divide=` argument to decide if division is performed or not.

```
mSCALE = function(x,divide=TRUE)
{
  newx = x - median(x)
  if(divide){
    newx = newx / diff(range(x))
  }
  newx
}
```

1. Use `arg=value` for default values.
2. `newx` exists only within the function environment.
3. The final line insures that `newx` is properly returned.

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Functions for Working with Matrices

Note: Many of these functions will also work with data frames.

- `%*%` - binary operator for matrix multiplication
- `t()` - returns matrix transpose
- `matrix()` - creates a matrix from a vector
 - `byrows=` reads matrices by rows instead of columns.
 - `ncol=` and `nrow=` determine the size and shape
- `rbind()` and `cbind()` - return new matrix with added rows or columns.
- `solve()` - solve systems of linear equations
 - `x = solve(a,b)` solves $ax = b$
 - `solve(a)` returns the inverse of `a`
- `diag()` - extract or set the diagonal of a matrix
 - when passed an integer, returns an identity matrix.
- `row()` and `col()` - return matrices of same dimensions with row or column numbers for each element

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Generating Sequences

The colon (`:`) operator creates simple integer sequences. While it is often used as a subscript to “slice” an array, it can also be used on its own

```
> letters[10:15]
[1] "j" "k" "l" "m" "n" "o"
> x = 1:100
> mean(x)
[1] 50.5
```

The `seq()` function provides more control over the generated sequence. The first two arguments to `seq()` give the starting and ending values. Additional arguments include `by=` to specify an increment other than 1, or, alternatively `length=` to specify the number of elements in the generated sequence.

To generate a sequence for use in looping over an object, the `along=` argument can be used.

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sample()

The `sample()` function returns random samples or permutations of a vector. Passed an integer, `n`, it returns a random permutation of the integers from 1 to `n`.

The `size=` argument specifies the size of the returned vector.

The `prob=` argument provides a vector of probabilities for sampling.

By default, sampling is done without replacement; the `replace=TRUE` option will result in a random sample from the specified input.

```
> sample(10)
[1] 7 6 1 2 8 9 3 4 10 5
> sample(c("a","b","c","d","e"),size=10,replace=TRUE)
[1] "d" "c" "b" "b" "c" "a" "a" "e" "b" "a"
> sample(c("a","b","c"),size=10,prob=c(.5,.25,.25),replace=TRUE)
[1] "c" "b" "a" "a" "a" "a" "a" "c" "c" "a"
```

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Options

R has a number of global options which affect the way it behaves. The `options()` function, called with no arguments, will display the value of all options. Options can be set with `options()` by passing `optionname=value` pairs. Some common options include:

- `prompt` - controls `prompt`(default: ">")
- `width` - number of columns in output
- `digits` - number of digits displayed
- `height` - number of lines per page
- `browser` - used in `help.start()`
- `papersize` - for Postscript plots (default: "A4")

Functional Programming

R provides a number of tools that map or apply a function to various parts of a matrix, data frame, vector or list. These are often more useful than traditional programming constructs because they automatically determine the size of the object that they return, and any names assigned to the objects being manipulated are preserved.

These functions include

- `apply()` - operate on selected dimensions of arrays
- `lapply()`, `sapply()` - operate on each element of a vector or list
- `tapply()` - operate on elements based on a grouping variable
- `mapply()` - multivariate extension of `sapply`

In addition, some functions (for example `by()`, `sweep()`, and `aggregate()`) wrap these functions in a more convenient form.

apply()

`apply()` will execute a function on every row or every column of a matrix. Suppose the data frame `finance` contains the variables `Name`, `Price`, `Volume` and `Cap`, and we want the mean of each of the numerical variables.

```
> apply(finance[-1],2,mean)
      Price      Volume      Cap
21.46800 51584.51840      NA
```

The "2" passed as the second argument to `apply` means "columns". Note that the variable names were retained.

If additional arguments need to be passed to the function, they can simply be passed to `apply`:

```
> apply(finance[-1],2,mean,na.rm=TRUE)
      Price      Volume      Cap
21.46800 51584.51840 123.22597
```

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`lapply()` and `sapply()`

These functions apply a function to each element of a list or vector. `lapply()` always returns a list; `sapply()` will return a vector or array if appropriate.

One important use of these functions is to correctly process the columns of a data frame. Since `apply()` is designed for matrices, it can't retain the mode of individual data frame columns. Thus, commands like the following don't work:

```
> apply(finance,2,is.numeric)
names Price Volume  Cap
FALSE  FALSE  FALSE  FALSE
```

Using `sapply()` solves the problem:

```
> sapply(finance,is.numeric)
names Price Volume  Cap
FALSE  TRUE  TRUE  TRUE
```

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tapply()

`tapply()` allows you to map a function to a vector, broken up into groups defined by a second vector or list of vectors. Generally the vectors will all be from the same matrix or data frame, but they need not be.

Suppose we have a data frame called `banks` with columns `name`, `state` and `interest.rate`, and we wish to find the maximum interest rate for banks in each of the states.

```
with(banks,tapply(interest.rate,state,max,na.rm=TRUE))
```

Note the use of the `with()` function to avoid retyping the data frame name (`banks`) when referring to its columns.

The by() function

`tapply()` is simple to use when the variable being analyzed is a vector, but it becomes difficult to use when we wish to perform an analysis involving more than one variable. For example, suppose we have a data frame named `df` with four variables: `group`, `x`, `y`, and `z`, and we wish to calculate the correlation matrix of the last three variables for each level of `group`. To use `tapply` we would have to manipulate the indices of the data frame, but the `by()` function takes care of this automatically. The statement

```
by(df,df$group,cor)
```

returns a list with as many correlation matrices as there were levels of the variable `group`.

aggregate()

The `aggregate()` function presents a summary of a scalar valued statistic, broken down by one or more groups. While similar operations can be performed using `tapply()`, `aggregate()` presents the results in a data frame instead of a table.

```
> testdata = data.frame(one=c(1,1,1,2,2,2),two=c(1,2,3,1,2,3),
+                       three=rnorm(6))
> aggregate(testdata$three,list(testdata$one,testdata$two),mean)
  Group.1 Group.2      x
1      1      1 -0.62116475
2      2      1 -0.68367887
3      1      2  0.53058202
4      2      2 -0.61788020
5      1      3  0.02823623
6      2      3 -1.01561697
> tapply(testdata$three,list(testdata$one,testdata$two),mean)
      1      2      3
1 -0.6211648  0.5305820  0.02823623
2 -0.6836789 -0.6178802 -1.01561697
```

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aggregate() (cont'd)

If the first argument to `aggregate()` is a matrix or multicolumn data frame, the statistic will be calculated separately for each column.

```
> testdata = cbind(sample(1:5,size=100,replace=TRUE),
+                  matrix(rnorm(500),100,5))
> dimnames(testdata) = list(NULL,c("grp","A","B","C","D","E"))
> aggregate(testdata[,-1],list(grp=testdata[,1]),min)
  grp      A      B      C      D      E
1   1 -2.362126 -2.777772 -1.8970320 -2.152187 -1.966436
2   2 -1.690446 -2.202395 -1.6244721 -1.637200 -1.036338
3   3 -2.078137 -1.571017 -2.0555413 -1.401563 -1.881126
4   4 -1.325673 -1.660392 -0.8933617 -2.205563 -1.749313
5   5 -1.644125 -1.518352 -2.4064893 -1.664716 -1.994624
```

Note that the data frame returned by `aggregate()` has the appropriate column names, and that grouping variable names can be supplied with the list of grouping variables.

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split()

While `by()` and `aggregate()` simplify many tasks which arise in data manipulation, R provides the `split()` function which takes a data frame, and creates a list of data frames by breaking up the original data frame based on the value of a vector. In addition to being useful in its own right, the returned list can be passed to `lapply()` or `sapply()` as an alternative way of doing repetitive analyses on subsets of data.

```
> data(Orange)
> trees = split(Orange,Orange$Tree)
> sapply(trees,function(x)coef(lm(circumference~age,data=x)))
              3          1          5          2          4
(Intercept) 19.20353638 24.43784664 8.7583446 19.9609034 14.6376202
age          0.08111158 0.08147716 0.1110289 0.1250618 0.1351722
```

A similar result could be achieved by using

```
> by(Orange,Orange$Tree,function(x)coef(lm(circumference~age,data=x)))
```

The if/else statement

Like most programming languages, R provides an if/else construct. The basic form is

```
if (condition) expression
else other_expression
```

where the `else` clause is optional. Note that the condition must be a scalar; if not, only the first value of the condition is used. In all cases, `expressions` must be surrounded by curly braces if they consists of more than one line, and the

R also provides the `ifelse()` function, which takes three arguments: an object containing logical values, the value to return for true elements, and the value to return for false elements. It returns an object the same size as its first argument.

```
> z = c(7,10,-3,4,12,-5)
> ifelse(z>0,z,0)
[1] 7 10 0 4 12 0
```

Loops in R

R provides three types of loops, although they are not used as often as most other programming languages.

- for loop
 `for(var in sequence) expression`
- while loop
 `while(condition) expression`
- repeat loop
 `repeat expression`

In all cases, the **expressions** must be surrounded by curly braces if they are more than one line long.

Unassigned objects are not automatically printed inside of loops – you must explicitly use the `print()` or `cat()` functions.

To terminate loops at any time, use the `break` statement; to continue to the next iteration use the `next` statement.

Sorting

The `sort()` function will return a sorted version of a vector.

```
> x = c(19,25,31,15,12,43,82,22)
> sort(x)
[1] 12 15 19 22 25 31 43 82
```

The function `order()` returns a permutation vector which will reorder a vector so that it becomes sorted. This is especially useful if you wish to sort a matrix by the values in one of its rows:

```
> mat = matrix(c(12,3,7,9,10,11),ncol=2)
> mat
      [,1] [,2]
[1,]  12   9
[2,]   3  10
[3,]   7  11
> mat[order(mat[,1]),]
      [,1] [,2]
[1,]   3  10
[2,]   7  11
[3,]  12   9
```

Character Strings: `paste()`

The `paste()` function converts its arguments into character strings, and concatenates them. To specify a separator between the strings, use the `sep=` argument. Like most R functions, `paste` is vectorized:

```
> paste("x",1:5,sep="")
[1] "x1" "x2" "x3" "x4" "x5"
```

To create a result that is a single string, use the `collapse=` argument.

```
> paste("x",1:5,collapse="|",sep="*")
[1] "x*1|x*2|x*3|x*4|x*5"
```

One use of `paste` is to convert numeric values to character values:

```
> x = c("10"=110,"7"=107,"12"=112)
> x[paste(3 + 7)]
 10
110
```

Character Strings: `substring()`

The `substring()` function extracts substrings from character strings. The `first=` and `last=` arguments specify the size of the desired substring. Like most R functions, it is vectorized:

```
> animals = c("dog","cat","chicken","goat","sheep")
> substring(animals,2,4)
[1] "og" "at" "hic" "oat" "hee"
```

By default, the `last=` argument is set to a large number, so if you omit `last=`, `substring()` simply extracts until the end of the string.

An assignment form of `substring()` is also available, although it will not allow the resulting string to shrink or grow:

```
> pet = "Rover"
> substring(pet,2,3) = 'abcd'
> pet
[1] "Raber"
```

Note that only 2 characters were replaced in `pet`.

Splitting Character Strings

Many times a character string consists of several “words” which need to be separated. The `strsplit()` function accepts a character string and a regular expressions to split the character string, and returns a vector with the split pieces of the string. If the regular expression is of length 0, the string is split into individual characters.

The function is fully vectorized, and when the first argument is a vector of character strings, `strsplit()` will always return a list.

```
> strs = c("the razor toothed piranhas","of the genera Serrasalmus")
> strsplit(strs,c(" ",""))
[[1]]
[1] "the"      "razor"    "toothed"  "piranhas"

[[2]]
[1] "o" "f" " " "t" "h" "e" " " "g" "e" "n" "e" "r" "a" " " "S" "e" "r" "a"
[20] "s" "a" "l" "m" "u" "s"
```

Character Strings: Searching for Patterns

The `grep()` function searches for regular expressions in vectors of character strings. The first argument to `grep()` is the pattern to be searched for, and the second argument is the vector of strings to be searched. `grep` returns the indices of those elements in the vector which matched the pattern; with the `value=TRUE` argument, it returns the actual matches.

To find the locations of the patterns within the strings, the `regexpr()` function can be used with the same two required arguments as `grep`. It returns a vector of positions where the pattern was found, or -1 if the pattern was not found; in addition the returned value has an attribute containing the length of the match.

The argument `perl=TRUE` can be passed to either function to use perl-style regular expressions.

Searching for Patterns (cont'd)

The following simple example shows the returned values from `grep()` and `regexpr()`. The regular expression `a[lm]` means an "a" followed by either an "l" or an "m".

```
> states = c("Alabama","Alaska","California","michigan")
> grep("a[lm]",states,ignore.case=TRUE)
[1] 1 2 3
> regexpr("a[lm]",states)
[1] 5 -1 2 -1
attr(,"match.length")
[1] 2 -1 2 -1
```

You can retrieve attributes of stored objects with the `attr()` function.

Text Substitution

The functions `sub()` and `gsub()` can be used to create new character strings by replacing regular expressions (first argument) with replacement strings (second argument) in an existing string(third argument). The `ignore.case=TRUE` argument can be provided to ignore the case of the regular expression.

The only difference between the two functions is that `sub()` will only replace the first occurrence of a regular expression within elements of its third argument, while `gsub` replaces all such occurrences.

```
> vars = c("date98","size98","x98weight98")
> sub('98','04',vars)
[1] "date04"      "size04"      "x04weight98"
> gsub('98','04',vars)
[1] "date04"      "size04"      "x04weight04"
```

match() and pmatch()

The `match()` function accepts two vector arguments, and returns a vector of the same length as the first argument, containing the indices in the second argument that matched elements of the first argument. The `nomatch=` argument, which defaults to `NA`, specifies what is returned when no match occurs.

```
> match(1:10,c(7,2,5,4,3),nomatch=0)
[1] 0 2 5 4 3 0 1 0 0 0
```

For character values, `pmatch()` allows for partial matching, meaning that extra characters at the end are ignored when comparing strings of different length.

To get a logical vector instead of positions, use the `%in%` operator.

Merging Matrices and Dataframes

Many times two matrices or data frames need to be combined by matching values in a column in one to values in a column of the other. Consider the following two data frames:

```
> one                > two
  a b                a y
1 1 12              1 9 108
2 7 18              2 3 209
3 9 24              3 2 107
4 3 19              4 7 114
                    5 8 103
```

We wish to combine observations with common values of `a` in the two data frames. The `merge()` function makes this simple:

```
> merge(one,two,by="a")
  a b y
1 3 19 209
2 7 18 114
3 9 24 108
```

Merging Matrices and Dataframes (cont'd)

By default, only the rows that matched are included in the output. Using the `all=TRUE` argument will display all the rows, adding NAs where appropriate.

```
> merge(one,two,by="a",all=TRUE)
  a  b  y
1 1 12 NA
2 2 NA 107
3 3 19 209
4 7 18 114
5 8 NA 103
6 9 24 108
```

To prevent sorting of the `by=` variable, use `sort=FALSE`.

A vector of names or column numbers can be given for the `by=` argument to perform a merge on multiple columns.

If the matrices to be merged need to be treated differently, the arguments `by.x=`, `by.y=`, `all.x=` and `all.y=` can be used.

reshape()

Suppose we have a data frame named `firmdata`, with several observations of a variable `x` recorded at each of several `times`, for each of several `firms`, and we wish to create one observation per firm, with new variables for each of the values of `x` contained in that observation. In R terminology, the original format is called "long", and the desired format is called "wide".

Our original data set would look like this:

```
firm time  x
   7    1  7
   7    2 19
   7    3 12
  12    1 13
  12    2 18
  12    3  9
  19    1 21
  19    2 15
  19    3  7
```

reshape(), cont'd

The following arguments to `reshape` explain the role that the variables play in the transformation. Each argument is a character string or vector of strings.

- `timevar`= the variable which specifies which new variable will be created from a given observation
- `idvar`= the variable which identifies the unique observations in the new data set. There will be one observation for each level of this variable.
- `v.names`= the variables of interest which were recorded multiple times
- `direction`= "long" or "wide" to described the desired result
- `varying`= when converting to "long" format, the variables which will be broken up to create the new (`v.names`) variable.

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reshape(), cont'd

The following R statements perform the desired transformation:

```
> newdata = reshape(firmdata,timevar="time",idvar="firm",
+                   v.names="x",direction="wide")
> newdata
  firm x.1 x.2 x.3
1    7   7  19  12
4   12  13  18   9
7   19  21  15   7
```

Once converted, a call to `reshape()` in the opposite direction needs no other arguments, because the reshaping information is stored with the data.

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expand.grid()

The `expand.grid()` function accepts vectors or lists of vectors, and creates a data frame with one row for each combination of values from the vectors. Combined with `apply()`, it can easily perform a grid search over a specified range of values.

```
> values = expand.grid(x=seq(-3,3,length=10),
  y=seq(-3,3,length=10))
> result = cbind(values,
  result=apply(values,1,function(z)sin(z[1])*cos(z[2])))
> dim(result)
[1] 100  3
> result[which(result[,3] == max(result[,3])),]
      x y      result
3 -1.666667 -3 0.9854464
93 -1.666667  3 0.9854464
```

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Probability Distributions and Random Numbers

R provides four types of functions for dealing with distributions. Each type begins with a letter designating its purpose, followed by a name specifying the distribution.

- **q** - quantile function (argument is probability - returns deviate)
- **p** - probability (argument is deviate, returns probability)
- **d** - density (argument is deviate, returns density value)
- **r** - random numbers (argument is n, returns vector of random numbers)

Among the possible distributions are:

<code>norm</code>	Normal	<code>exp</code>	Exponential	<code>gamma</code>	Gamma
<code>pois</code>	Poisson	<code>binom</code>	Binomial	<code>chisq</code>	Chi-square
<code>t</code>	Student's t	<code>f</code>	F	<code>unif</code>	Uniform

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Descriptive Statistics

Among the functions for descriptive, univariate statistics are

```
mean()  median()  range()  kurtosis()*  skewness()*  
var()   mad()     sd()     IQR()       weighted.mean()
```

* - in `e1071` library

All of these functions accept an argument `na.rm=TRUE` to ignore missing values.

The `stem()` function produces a (ASCII) stem-and-leaf diagram; the `boxplot()` function produces a high-quality representation.

The `cor()` function computes correlations among multiple variables. (Specify cases to use with the `use=` argument, with choices "all.obs" (default), "complete.obs", or "pairwise.complete.obs".)

The `summary()` function provides minimum, mean, maximum and quartiles in a single call.

The `quantile()` function returns the values of any desired quantiles (percentiles).

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Hypothesis Tests

R provides a number of functions for simple hypothesis testing. They each have a `alternative=` argument (with choices `two.sided`, `less`, and `greater`), and a `conf.level=` argument for prespecifying a confidence level.

Among the available functions are:

<code>prop.test</code>	Equality of proportions	<code>wilcox.test</code>	Wilcoxon test
<code>binom.test</code>	One sample binomial	<code>chisq.test</code>	Contingency tables
<code>t.test</code>	Student's t-test	<code>var.test</code>	Equality of variances
<code>cor.test</code>	Correlation coefficient	<code>ks.test</code>	Goodness of fit

For example, the following code performs a t-test on two unequal sized groups of data:

```
> x = c(12,10,19,22,14,22,19,14,15,18,12)  
> y = c(18,13,12,13,21,14,12,10,11,9)  
> t.test(x,y,alt="two.sided",conf.level=.95)
```

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Results of `t.test()`

Welch Two Sample t-test

```
data: x and y
t = 1.6422, df = 18.99, p-value = 0.117
alternative hypothesis: true difference in means
is not equal to 0
95 percent confidence interval:
-0.766232  6.348050
sample estimates:
mean of x mean of y
16.09091  13.30000
```

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Statistical Models in R

R provides a number of functions for statistical modeling, along with a variety of functions that extract and display information about those models. Using object-oriented design principles, most modeling functions work in similar ways and use similar arguments, so changing a modeling strategy is usually very simple. Among the modeling functions available are:

<code>lm()</code>	Linear Models	<code>aov</code>	Analysis of Variance
<code>glm</code>	Generalized Linear Models	<code>gam</code> ¹	Generalized Additive Models
<code>tree</code>	Classification and Regression Trees	<code>cph</code> ²	Cox Proportional Hazards
<code>nls</code>	Non-linear Models	<code>loess</code>	Local Regression Models

Some of the functions which display information about models are `summary()`, `coef()`, `predict()`, `resid()` and `plot()`.

¹ - in `mgcv` library

² - in `Design` library

Formulas

R provides a notation to express the idea of a statistical model which is used in all the modeling functions, as well as some graphical functions. The dependent variable is listed on the left-hand side of a tilde (~), and the independent variables are listed on the right-hand side, joined by plus signs (+).

Most often, the variables in a formula come from a data frame, but this is not a requirement; in addition expressions involving variables can also be used in formulas

Inside of formulas, some symbols have special meanings, as shown below.

+	add terms	-	remove terms	:	interaction
*	crossing	%in%	nesting	^	limit crossing

To protect an arithmetic expression inside of a formula, use the I() function.

Example of Formulas

Additive Model

$$y \sim x1 + x2 + x3$$

Additive Model without Intercept

$$y \sim x1 + x2 + x3 - 1$$

Regress **response** versus all other variables in data frame

$$\text{response} \sim .$$

Fully Factorial ANOVA model (a, b, and c are factors)

$$y \sim a*b*c$$

Factorial ANOVA model limited to depth=2 interactions

$$y \sim (a*b*c)^2$$

Polynomial Regression

$$y \sim x + I(x^2) + I(x^3)$$

Common Arguments to Modeling Functions

The following arguments are available in all of the modeling functions:

- `formula=` first argument – specifies the model
- `data=` specify a data frame to attach for the duration of the model
- `subset=` logical expression to select data to be used
- `weights=` vector of weights to be applied to model
- `na.action=` function to preprocess data regarding missing values
 - `na.fail` prints error message
 - `na.omit` default, omit observations with missing values
 - `na.pass` do nothing

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Graphics in R

The graphics system in R consists of three components:

- High level functions - These functions produce entire plots with a single command. Examples include `barplot()`, `boxplot()`, `contour()`, `dotchart()`, `hist()`, `pairs()`, `persp()`, `pie()`, and `plot()`.
- Low level functions - These functions add to existing plots. Examples include `abline()`, `arrows()`, `axis()`, `frame()`, `legend()`, `lines()`, `points()`, `rug()`, `symbols()`, `text()`, and `title()`
- Graphics parameters - Accessed through either plotting commands or the `par()` function, these are arguments that change the layout or appearance of a plot. These parameters control things like margins, text size, tick marks, plotting style, and overall size of the plot.

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Device Drivers

. By default, a window will automatically be opened to display your graphics. Some other devices available include `postscript()`, `pdf()`, `bitmap()` and `jpeg()`. (See the help for `Devices` for a complete list.)

To use an alternative driver, either call the appropriate function before plotting, or use the `dev.copy()` function to specify a device to which to copy the current plot, always ending with a call to `dev.off()`.

For example, to create a PostScript plot, use statements like

```
postscript(file="myplot.ps")
... plotting commands go here ...
dev.off()
```

To create a jpeg image from the currently displayed plot, use

```
dev.copy(device=jpeg,file="picture.jpg")
dev.off()
```

Multiple Plots on a Page

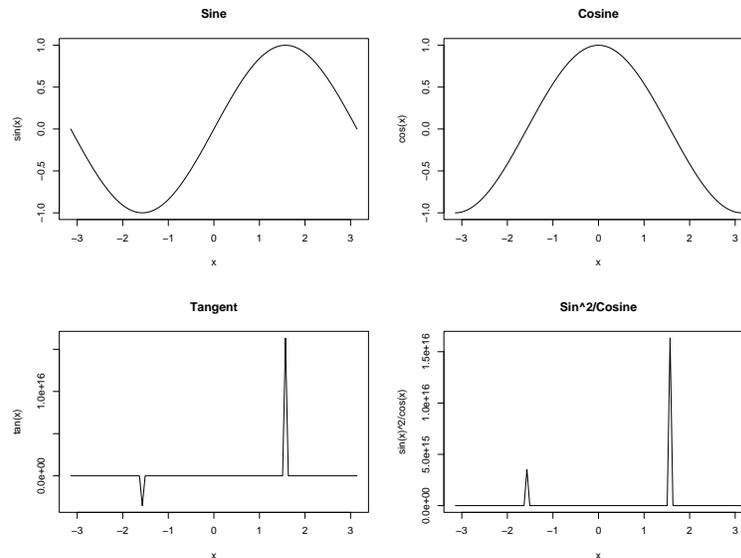
The graphics parameters `mfrow=c(nrow,ncol)` or `mfc1=c(nrow,ncol)` allow multiple plots of equal size to be placed on a page in an $nrow \times ncol$ array. When using `mfrow=`, plots are drawn by rows and with `mfc1=` they are drawn by column.

Since these parameters determine the layout of subsequent plots they can only be specified through the `par()` function, and they must be set before any plotting commands are entered.

Suppose we wish to create a 2×2 array of plots of various trigonometric functions, plotted in the range of $-\pi$ to π . The following code uses the `curve()` function to produce the plots:

```
par(mfrow=c(2,2))
curve(sin(x),from=-pi,to=pi,main="Sine")
curve(cos(x),from=-pi,to=pi,main="Cosine")
curve(tan(x),from=-pi,to=pi,main="Tangent")
curve(sin(x)^2/cos(x),from=-pi,to=pi,main="Sin^2/Cosine")
```

Multiple Plots on a Page



The margins can be reduced through the graphics parameters `mar=` or `mai=` for the inner margins, and `oma=` or `omi=` for the outer margins.

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Plot Types

The `plot()` function accepts a `type=` argument, which can be set to any of the following values: "p" for points, "l" for lines, "b" for both, "s" for stairstep, and "n" for none.

By setting `type="n"`, axes will be drawn, but no points will be displayed, allowing multiple lines to be plotted on the same set of axes. (The `matplot()` function is also useful in this setting.)

```
> data(USArrests)
> popgroup = cut(USArrests$UrbanPop,3,labels=c("Low","Medium","High"))
> plot(range(USArrests$Murder),range(USArrests$Rape),type="n",
+       xlab="Murder",ylab="Rape")
> points(USArrests$Murder[popgroup=="Low"],
+        USArrests$Rape[popgroup=="Low"],col="Red")
> points(USArrests$Murder[popgroup=="Medium"],
+        USArrests$Rape[popgroup=="Medium"],col="Green")
> points(USArrests$Murder[popgroup=="High"],
+        USArrests$Rape[popgroup=="High"],col="Blue")
```

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Legends

The `legend()` function can produce a legend on a plot, displaying points or lines with accompanying text. The function accepts `x=` and `y=` arguments to specify the location of the legend, and a `legend=` argument with the text to appear in the legend, as well as many graphics parameters, often in vector form to accommodate the multiple plots or points on a graph.

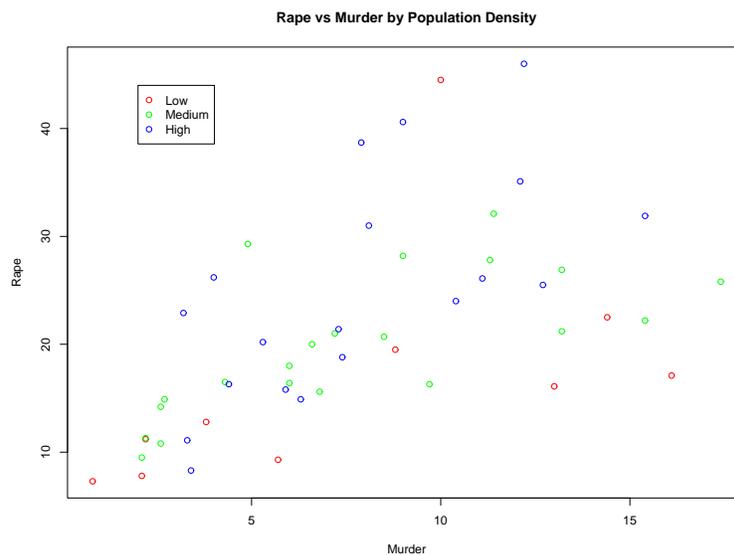
The following code could be used to place a legend on the previous plot; the `title()` function is also used to add a title.

```
legend(2,44,levels(popgroup),col=c("Red","Green","Blue"),
      pch=1)
title("Rape vs Murder by Population Density")
```

The `locator()` function can be used to interactively place the legend.

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Multiple Sets of Points on a Plot



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Some Useful Graphics Parameters

These parameters can be passed to the `par()` function, or directly to an individual plotting routine. They can also be queried using `par("parameter")`

- `cex`= character expansion (default=1)
- `pch`= plotting character (use character or integer)
- `usr`= vector of length 4 giving minimum and maximums of figure
- `col`= colors - use names from the `colors()` function
- `srt`= string rotation, in degrees clockwise
- `pin`= vector with width and height of plotting region
- `fin`= vector with width and height of figure region
- `lty`= integer specifying line type

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Plotting Limits

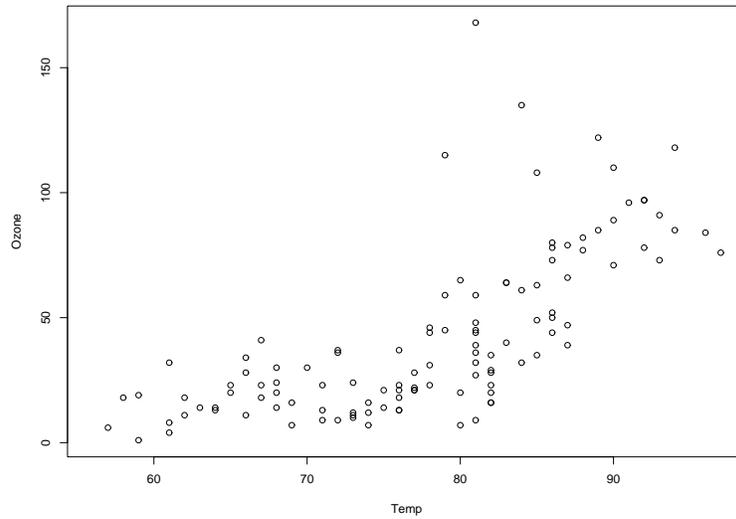
While R's default will usually produce an attractive plot, it is sometimes useful to restrict plotting to a reduced range of points, or to expand the range of points. Many plotting routines accept `xlim`= and `ylim`= arguments, which can be set to a vector of length 2 giving the range of points to be displayed.

For example, the `airquality` data set contains data on different measures of the air quality in New York City. We could plot the ozone level versus the temperature for the complete set of points with the following statements:

```
data(airquality)
with(airquality,plot(Temp,Ozone))
```

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Ozone vs. Temperature

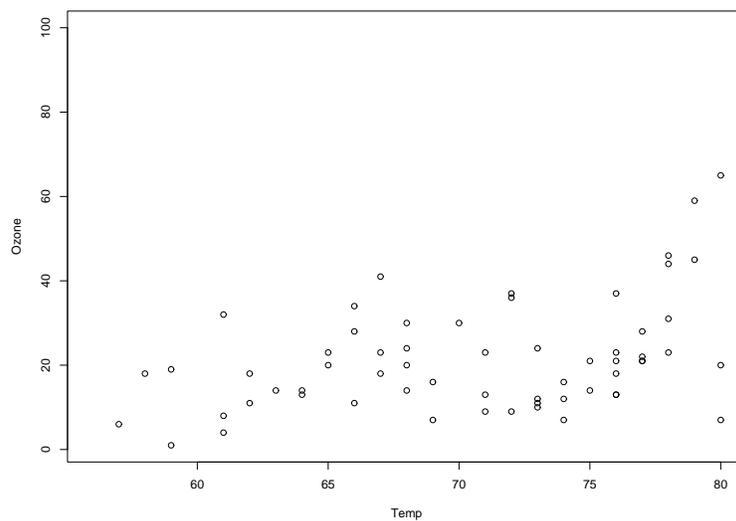


To display temperatures less than 80 and ozone less than 100, we could use

```
with(airquality,plot(Temp,Ozone,xlim=c(min(Temp,na.rm=TRUE),80),  
ylim=c(min(Ozone,na.rm=TRUE),100)))
```

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Limiting the Range in Plots



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Custom Axes

The `axis()` function allows creation of custom axes. Graphics parameters `xaxt=` and `yaxt=` can be set to "n" to suppress the default creation of axes when producing a plot.

Arguments to `axis()` include `side=` (1=bottom, 2=left, 3=top, and 4=right), `at=`, a vector of locations for tick marks and labels, and `labels=` to specify the labels.

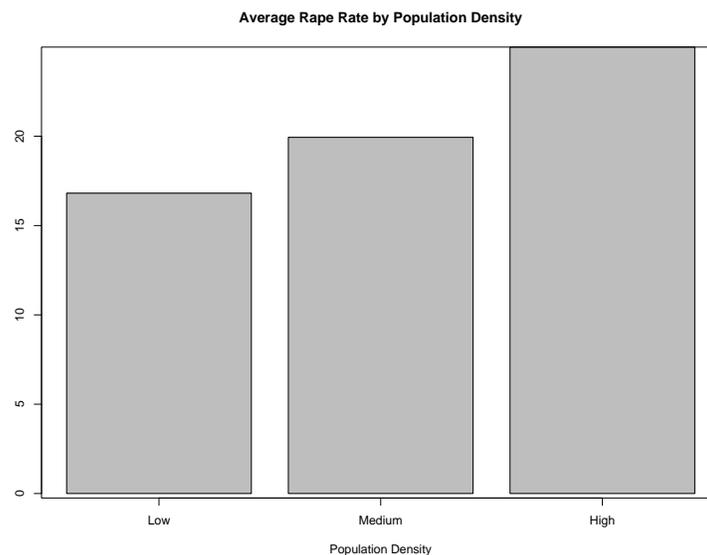
We can create a barplot showing mean Murder rates for states in the three population groups with the following code:

```
rmeans = with(USArrests, aggregate(Rape, list(popgroup), mean))
where = barplot(mmeans[,2], xlab="Population Density")
axis(1, at=where, labels=as.character(rmeans[,1]))
box()
title("Average Rape Rate by Population Density")
```

The return value from `barplot()` gives the centers of the bars; the `box()` function draws a box around the plot.

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Custom Axis on a Barplot



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The `lattice` library

The `lattice` library provides a complete set of functions for producing conditioning plots.

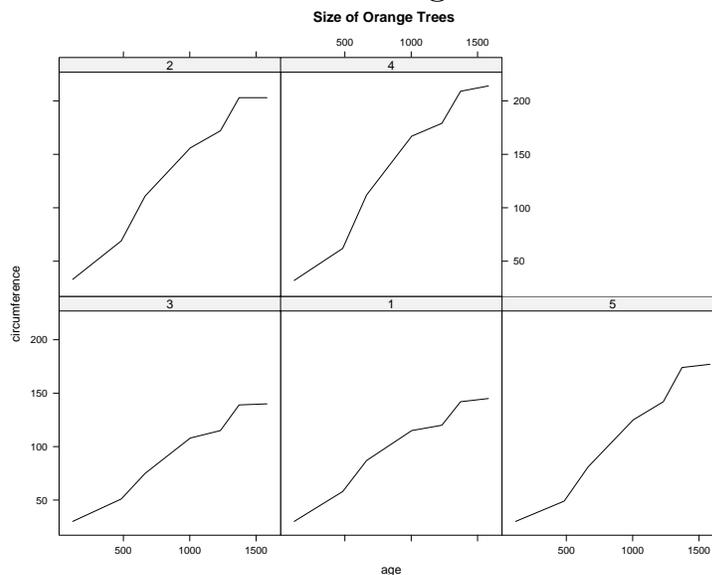
In a conditioning plot, a data set is broken up into several parts, and each part is plotted on identical axes. The `lattice` library uses the formula notation of statistical models to describe the desired plot, adding the vertical bar (`|`) to specify the conditioning variable.

For example, the `Orange` dataset contains information on the circumference and age on each of five orange trees. Assuming the `lattice` library is loaded, the following statements will produce a conditioned scatter plot:

```
xyplot(circumference~age|Tree,data=Orange,  
       main="Size of Orange Trees",type="l")
```

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Conditioning Plots



Note that all the scales are identical, and all margins between the plots have been eliminated, making it very easy to compare the graphs.

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Other Conditioning Plots

In addition to `xyplot()` for scatter plots, the `lattice` library provides the following functions:

<code>cloud()</code>	3D Scatter plots	<code>histogram()</code>	histogram
<code>qq()</code>	Quantile-Quantile plots	<code>barchart()</code>	Bar charts
<code>dotplot()</code>	Dot Plots	<code>countourplot()</code>	Contour plots
<code>wireframe()</code>	3D Surface plots	<code>spiom()</code>	Scatterplot matrices

The `panel=` argument to these functions determines what is plotted for each group. The default panel functions for each function are named `panel.function`, and can be used as a model to modify the function's behaviour. In addition, the low-level functions `panel.abline()`, `panel.arrows()`, `panel.lines()`, `panel.points()`, `panel.segments()`, and `panel.text()` are available as replacements for their basic plotting counterparts.

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Customizing Panel Functions

Suppose we wish to add a regression line to the conditioned scatterplot in the previous slide. We can create a function called `mypanel()`:

```
mypanel = function(x,y)
{
  panel.xyplot(x,y)
  panel.abline(lm(y~x))
}
```

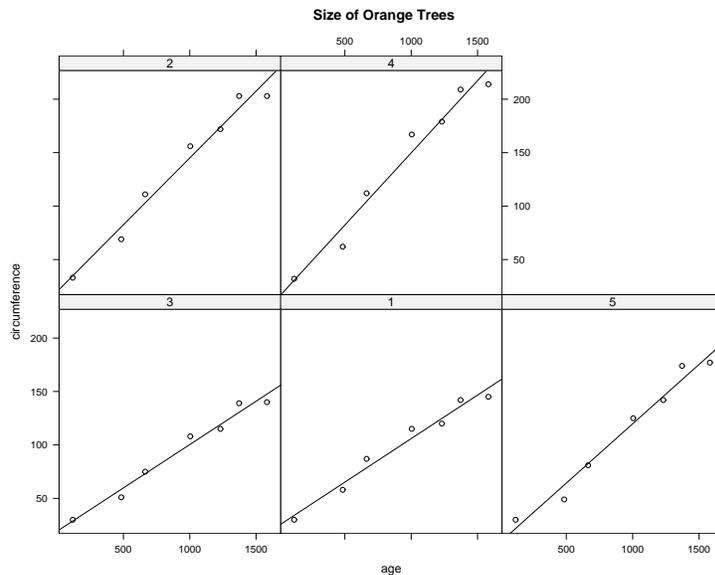
Now this function can be passed to `xyplot()` as the `panel=` argument:

```
xyplot(circumference~age|Tree,data=Orange,panel=mypanel,
  main="Size of Orange Trees")
```

Note that it's the function name that is passed to `xyplot()`, not an actual call to the function.

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Customizing Panel Functions(cont'd)



The linear nature of the relationships, as well as the relative magnitudes of the slopes is now more apparent.

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Other Options to Lattice Functions

Some arguments which are recognized by most lattice plotting routines:

- `layout=` a vector of length 2 or 3 giving the number of rows in the lattice display, the number of columns, and optionally the number of pages
- `as.table=` set to `TRUE`, prints panels in ascending order from left to right and top to bottom
- `subscripts=` set to `TRUE`, provides an argument called `subscripts` containing the subscripts of observations in the current panel. Can be used in a custom panel routine to display values of variables other than those being plotted
- `page=` function to be called after each page of a multipage display. Set to `readline` to imitate `par(ask=TRUE)`

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Trellis Objects

The trellis library optimizes its plots depending on the current device. This can lead to problems if `dev.copy()` is used, since it will be using settings from the current device. To avoid this problem, trellis plots can be stored in a device dependent way, and rendered for a particular device with the `print()` function.

For example, if the current device is `x11`, using `dev.copy()` will create a PostScript version of the `x11`-optimized lattice plot. Trellis objects avoid this problem:

```
obj = xyplot( ... )
print(obj)      # required to view the plot if stored as an object
postscript(file="out.ps")
print(obj)      # creates PostScript file
dev.off()
```

The file `out.ps` will now be optimized for PostScript.