R Data Import/Export


R Development Core Team
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# Table of Contents

Acknowledgements ........................................ 1

1 Introduction ............................................. 2
   1.1 Imports ............................................. 2
   1.2 Export to text files ................................ 3
   1.3 XML .................................................. 4

2 Spreadsheet-like data ................................. 5
   2.1 Variations on `read.table` ......................... 5
   2.2 Fixed-width-format files .......................... 7
   2.3 Using `scan` directly .............................. 7
   2.4 Re-shaping data .................................... 8
   2.5 Flat contingency tables ............................ 9

3 Importing from other statistical systems ... 10
   3.1 EpiInfo, Minitab, S-PLUS, SAS, SPSS, Stata .... 10
   3.2 Octave ................................................ 10

4 Relational databases ................................. 11
   4.1 Why use a database? ............................... 11
   4.2 Overview of RDBMSs ............................... 11
   4.2.1 SQL queries ..................................... 12
   4.2.2 Data types ...................................... 13
   4.3 R interface packages ............................... 13
   4.3.1 Packages DBI and RMySQL ...................... 14
   4.3.2 Package RODBC .................................. 15
   4.3.3 Package RPgSQL ................................. 16
   4.3.4 Package RmSQL ................................... 18

5 Binary files ........................................... 19
   5.1 Binary data formats ............................... 19

6 Connections ........................................... 20
   6.1 Types of connections ............................... 20
   6.2 Output to connections ............................. 21
   6.3 Input from connections ............................ 21
   6.3.1 Pushback ........................................ 22
   6.4 Listing and manipulating connections ............ 22
   6.5 Binary connections ................................. 23
   6.5.1 Special values ................................... 23
7 Network interfaces ......................... 25
  7.1 Reading from sockets ......................... 25
  7.2 Using download/file ......................... 25
  7.3 DCOM interface .......................... 25
  7.4 CORBA interface .......................... 25

Appendix A  References ..................... 27

Function and variable index ................... 28

Concept index ............................... 30
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1 Introduction

Reading data into a statistical system for analysis and exporting the results to some other system for report writing can be frustrating tasks that can take far more time than the statistical analysis itself, even though most readers will find the latter far more appealing.

This manual describes the import and export facilities available either in R itself or via packages which are available from CRAN. Some of the packages described are still under development but they already provide useful functionality.

Unless otherwise stated, everything described in this manual is available for both Unix/Linux and Windows versions of R.

In general, statistical systems like R are not particularly well suited to manipulations of large-scale data. Some other systems are better than R at this, and part of the thrust of this manual is to suggest that rather than duplicating functionality in R we can make the other system do the work! (For example Therneau & Grambsch (2000) comment that they prefer to do data manipulation in SAS and then use survival in S for the analysis.) Several recent packages allow functionality developed in languages such as Java, perl and python to be directly integrated with R code, making the use of facilities in these languages even more appropriate. (See the Java, RSPerl and RSPython packages.)

It is also worth remembering that R like S comes from the Unix tradition of small re-usable tools, and it can be rewarding to use tools such as awk and perl to manipulate data before import or after export. The case study in Becker, Chambers & Wilks (1988, Chapter 9) is an example of this, where Unix tools were used to check and manipulate the data before input to S. R itself takes that approach, using perl to manipulate its databases of help files rather than R itself, and the function read.fwf used a call to a perl script until it was decided not to require perl at run-time. The traditional Unix tools are now much more widely available, including on Windows.

1.1 Imports

The easiest form of data to import into R is a simple text file, and this will often be acceptable for problems of small or medium scale. The primary function to import from a text file is scan, and this underlies most of the more convenient functions discussed in Chapter 2 [Spreadsheet-like data], page 5.

However, all statistical consultants are familiar with being presented by a client with a floppy disc or CD-R of data in some proprietary binary format, for example ‘an Excel spreadsheet’ or ‘an SPSS file’. Often the simplest thing to do is to use the originating application to export the data as a text file (and statistical consultants will have copies of the commonest applications on their computers for that purpose). However, this is not always possible, and Chapter 3 [Importing from other statistical systems], page 10 discusses what facilities are available to access such files directly from R.

In a few cases, data have been stored in a binary form for compactness and speed of access. One application of this that we have seen several times is imaging data, which is normally stored as a stream of bytes as represented in memory, possibly preceded by a header. Such data formats are discussed in Chapter 5 [Binary files], page 19 and Section 6.5 [Binary connections], page 23.
For much larger databases it is common to handle the data using a database management system (DBMS). There is once again the option of using the DBMS to extract a plain file, but for many such DBMSs the extraction operation can be done directly from an R package: See Chapter 4 [Relational databases], page 11. Importing data via network connections is discussed in Chapter 7 [Network interfaces], page 25.

1.2 Export to text files

Exporting results from R is usually a less contentious task, but there are still a number of pitfalls. There will be a target application in mind, and normally a text file will be the most convenient interchange vehicle. (If a binary file is required, see Chapter 5 [Binary files], page 19.)

Function `cat` underlies the functions for exporting data. It takes a `file` argument, and the `append` argument allows a text file to be written via successive calls to `cat`.

The commonest task is to write a matrix or data frame to file as a rectangular grid of numbers, possibly with row and column labels. This can be done by the functions `write.table` and `write`. Function `write` just writes out a matrix or vector in a specified number of columns (and transposes a matrix). Function `write.table` is more convenient, and writes out a data frame (or an object that can be coerced to a data frame) with row and column labels.

There are a number of issues that need to be considered in writing out a data frame to a text file.

1. **Precision**
   
   These functions are based on `cat` not `print`, and the precision to which numbers are printed is governed by the current setting of `options(digits)`. It may be necessary to increase this to avoid losing precision. For more control, use `format` on a data frame, possibly column-by-column.

2. **Header line**
   
   R prefers the header line to have no entry for the row names, so the file looks like
   
   ```
   Greenmantle 2.5 650 16.083
   ...
   ```
   
   Some other systems require a (possibly empty) entry for the row names, which is what `write.table` will provide if argument `col.names = NA` is specified. Excel is one such system.

3. **Separator**
   
   A common field separator to use in the file is a comma, as that is unlikely to appear in any of the fields, in English-speaking countries. Such files are known as CSV (comma separated values) files. In some locales the comma is used as the decimal point (set this in `write.table` by `dec = ",",`) and there CSV files use the semicolon as the field separator.

   Using a semicolon or tab (`sep = "\t"`) are probably the safest options.

4. **Missing values**
   
   By default missing values are output as `NA`, but this may be changed by argument `na`. Note that `NaNs` are treated as `NA` by `write.table`, but not by `cat` nor `write`.
5. **Quoting strings**

By default strings are quoted (including the row and column names). Argument `quote` controls quoting of character and factor variables.

Some care is needed if the strings contain embedded quotes. Three useful forms are

```r
> df <- data.frame(a = I("a \" quote"))
> write.table(df)
"a"
"1" "a \" quote"
> write.table(df, qmethod = "double")
"a"
"1" "a " " quote"
> write.table(df, quote = FALSE, sep = ",")
a
1,a " quote
```

The second is the form of escape commonly used by spreadsheets.

Note that `write.table` is often not the best way to write out very large matrices, for which it can use excessively large amounts of memory. Function `write.matrix` in package `MASS` provides a specialized interface for writing matrices, with the option of writing them in blocks and thereby reducing memory usage.

It is possible to use `sink` to divert the standard R output to a file, and thereby capture the output of (possibly implicit) `print` statements. This is not usually the most efficient route, and the `options(width)` setting may need to be increased.

### 1.3 XML

When reading data from text files, it is the responsibility of the user to know and to specify the conventions used to create that file, e.g. the comment character, whether a header line is present, the value separator, the representation for missing values (and so on) described in Section 1.2 [Export to text files], page 3. A markup language which can be used to describe not only content but also the structure of the content can make a file self-describing, so that one need not provide these details to the software reading the data.

The eXtensible Markup Language – more commonly known simply as XML – can be used to provide such structure, not only for standard datasets but also more complex data structures. XML is becoming extremely popular and is emerging as a standard for general data markup and exchange. It is being used by different communities to describe geographical data such as maps, graphical displays, mathematics and so on.

The XML package provides general facilities for reading and writing XML documents within both R and S-PLUS in the hope that we can easily make use of this technology as it evolves. Several people are exploring how we can use XML for, amongst other things, representing datasets to be shared across different applications; storing R and S-PLUS objects so they can be shared by both systems; representing plots via SVG (Scalable Vector Graphics, a dialect of XML); representing function documentation; generating “live” analyses/reports that contain text, data and code.

A description of the facilities of the XML package is outside the scope of this document: see the package’s Web page at [http://www.omegahat.org/RSXML](http://www.omegahat.org/RSXML) for details and examples.
2 Spreadsheet-like data

In Section 1.2 [Export to text files], we saw a number of variations on the format of a spreadsheet-like text file, in which the data are presented in a rectangular grid, possibly with row and column labels. In this section we consider importing such files into R.

2.1 Variations on read.table

The function read.table is the most convenient way to read in a rectangular grid of data. Because of the many possibilities, there are several other functions that call read.table but change a group of default arguments.

Beware that read.table is an inefficient way to read in very large numerical matrices: see scan below.

Some of the issues to consider are:

1. Header line

   We recommend that you specify the header argument explicitly. Conventionally the header line has entries only for the columns and not for the row labels, so is one field shorter than the remaining lines. (If R sees this, it sets header = TRUE.) If presented with a file that has a (possibly empty) header field for the row labels, read it in by something like

   \[
   \text{read.table("file.dat", header = TRUE, row.names = 1)}\]

   Column names can be given explicitly via the col.names; explicit names override the header line (if present).

2. Separator

   Normally looking at the file will determine the field separator to be used, but with white-space separated files there may be a choice between the default sep = "" which uses any white space (spaces, tabs or newlines) as a separator, sep = " " and sep = "\t". Note that the choice of separator affects the input of quoted strings.

   If you have a tab-delimited file containing empty fields be sure to use sep = "\t".

3. Quoting

   By default character strings can be quoted by either ‘"’ or ‘’’, and in each case all the characters up to a matching quote are taken as part of the character string. The set of valid quoting characters (which might be none) is controlled by the quote argument. For sep = "\n" the default is changed to quote = "".

   If no separator character is specified, quotes can be escaped within quoted strings by immediately preceding them by ‘\’, C-style.

   If a separator character is specified, quotes can be escaped within quoted strings by doubling them as is conventional in spreadsheets. For example

   ‘One string isn’t two’,"one more"

   can be read by

   \[
   \text{read.table("testfile", sep = ",")}\]

   This does not work with the default separator.
4. **Missing values**
   By default the file is assumed to contain the character string `NA` to represent missing values, but this can be changed by the argument `na.strings`, which is a vector of one or more character representations of missing values.
   Empty fields in numeric columns are also regarded as missing values.

5. **Unfilled lines**
   It is quite common for a file exported from a spreadsheet to have all trailing empty fields (and their separators) omitted. To read such files set `fill = TRUE`.

6. **White space in character fields**
   If a separator is specified, leading and trailing white space in character fields is regarded as part of the field. To strip the space, use argument `strip.white = TRUE`.

7. **Blank lines**
   By default, `read.table` ignores empty lines. This can be changed by setting `blank.lines.skip = FALSE`, which will only be useful in conjunction with `fill = TRUE`, perhaps to indicate missing data in a regular layout.

8. **Classes for the variables**
   Unless you take any special action, `read.table` tries to select a suitable class for each variable in the data frame. It tries in turn `logical`, `integer`, `numeric` and `complex`, moving on if any entry is not missing and cannot be converted.\(^1\) If all of these fail, the variable is converted to a factor.

   Arguments `colClasses` and `as.is` provide greater control. `as.is` suppresses conversion of character vectors to factors (only). Using `colClasses` allows the desired class to be set for each column in the input.

   Note that `colClasses` and `as.is` are specified per column, not per variable, and so include the column of row names (if any).

9. **Comments**
   By default, `read.table` uses `#` as a comment character, and if this is encountered (except in quoted strings) the rest of the line is ignored. Lines containing only white space and a comment are treated as blank lines.

   If it is known that there will be no comments in the data file, it is safer (and may be faster) to use `comment.char = ""`.

   Convenience functions `read.csv` and `read.delim` provide arguments to `read.table` appropriate for CSV and tab-delimited files exported from spreadsheets in English-speaking locales. The variations `read.csv2` and `read.delim2` are appropriate for use in countries where the comma is used for the decimal point.

   If the options to `read.table` are specified incorrectly, the error message will usually be of the form

   ```
   Error in scan(file = file, what = what, sep = sep, :  
   line 1 did not have 5 elements
   ```

   or

\(^1\) This is normally fast as looking at the first entry rules out most of the possibilities.
Chapter 2: Spreadsheet-like data

Error in read.table("files.dat", header = TRUE) :
  more columns than column names

This may give enough information to find the problem, but the auxiliary function `count.fields` can be useful to investigate further.

Efficiency can be important when reading large data grids. It will help to specify `colClasses` as one of the atomic vector types (logical, integer, numeric, complex or character) for each column, and to give `nrows`, the number of rows to be read (and a mild over-estimate is better than not specifying this at all).

### 2.2 Fixed-width-format files

Sometimes data files have no field delimiters but have fields in pre-specified columns. This was very common in the days of punched cards, and is still sometimes used to save file space.

Function `read.fwf` provides a simple way to read such files, specifying a vector of field widths. The function reads the file into memory as whole lines, splits the resulting character strings, writes out a temporary tab-separated file and then calls `read.table`. This is adequate for small files, but for anything more complicated we recommend using the facilities of a language like `perl` to pre-process the file.

### 2.3 Using `scan` directly

Both `read.table` and `read.fwf` use `scan` to read the file, and then process the results of `scan`. They are very convenient, but sometimes it is better to use `scan` directly.

Function `scan` has many arguments, most of which we have already covered under `read.table`. The most crucial argument is `what`, which specifies a list of modes of variables to be read from the file. If the list is named, the names are used for the components of the returned list. Modes can be numeric, character or complex, and are usually specified by an example, e.g. 0, "" or 0i. For example

```r
cat("2 3 5 7", "11 13 17 19", file="ex.dat", sep="\n")
scan(file="ex.dat", what=list(x=0, y="", z=0), flush=TRUE)
```

returns a list with three components and discards the fourth column in the file.

There is a function `readLines` which will be more convenient if all you want is to read whole lines into R for further processing.

One common use of `scan` is to read in a large numeric matrix. Suppose file `"matrix.dat"` just contains the numbers for a 200 x 2000 matrix. Then we can use

```r
A <- matrix(scan("matrix.dat", n = 200*2000), 200, 2000, byrow = TRUE)
```

On one test this took 2 seconds whereas

```r
A <- as.matrix(read.table("matrix.dat"))
```

took 32 seconds (and a lot more memory). (Using `comment.char = ""` saved 3 seconds.)
2.4 Re-shaping data

Sometimes spreadsheet data is in a compact format that gives the covariates for each subject followed by all the observations on that subject. R’s modelling functions need observations in a single column. Consider the following sample of data from repeated MRI brain measurements:

<table>
<thead>
<tr>
<th>Status</th>
<th>Age</th>
<th>V1</th>
<th>V2</th>
<th>V3</th>
<th>V4</th>
</tr>
</thead>
<tbody>
<tr>
<td>P</td>
<td>23646</td>
<td>45190</td>
<td>50333</td>
<td>55166</td>
<td>56271</td>
</tr>
<tr>
<td>CC</td>
<td>26174</td>
<td>35535</td>
<td>38227</td>
<td>37911</td>
<td>41184</td>
</tr>
<tr>
<td>CC</td>
<td>27723</td>
<td>25691</td>
<td>25712</td>
<td>26144</td>
<td>26398</td>
</tr>
<tr>
<td>CC</td>
<td>27193</td>
<td>30949</td>
<td>29693</td>
<td>29754</td>
<td>30772</td>
</tr>
<tr>
<td>CC</td>
<td>24370</td>
<td>50542</td>
<td>51966</td>
<td>54341</td>
<td>54273</td>
</tr>
<tr>
<td>CC</td>
<td>28359</td>
<td>58591</td>
<td>58803</td>
<td>59435</td>
<td>61292</td>
</tr>
<tr>
<td>CC</td>
<td>25136</td>
<td>45801</td>
<td>45389</td>
<td>47197</td>
<td>47126</td>
</tr>
</tbody>
</table>

There are two covariates and up to four measurements on each subject. The data were exported from Excel as a file ‘mr.csv’.

We can use `stack` to help manipulate these data to give a single response.

```r
zz <- read.csv("mr.csv", strip.white = TRUE)
zzz <- cbind(zz[,1:2], stack(zz[,3:6]))
```

with result:

<table>
<thead>
<tr>
<th>Status</th>
<th>Age</th>
<th>values ind</th>
</tr>
</thead>
<tbody>
<tr>
<td>X1</td>
<td>23646</td>
<td>45190 V1</td>
</tr>
<tr>
<td>X2</td>
<td>CC</td>
<td>26174 35535 V1</td>
</tr>
<tr>
<td>X3</td>
<td>CC</td>
<td>27723 25691 V1</td>
</tr>
<tr>
<td>X4</td>
<td>CC</td>
<td>27193 30949 V1</td>
</tr>
<tr>
<td>X5</td>
<td>CC</td>
<td>24370 50542 V1</td>
</tr>
<tr>
<td>X6</td>
<td>CC</td>
<td>28359 58591 V1</td>
</tr>
<tr>
<td>X7</td>
<td>CC</td>
<td>25136 45801 V1</td>
</tr>
<tr>
<td>X11</td>
<td>P</td>
<td>23646 50333 V2</td>
</tr>
</tbody>
</table>

Function `unstack` goes in the opposite direction, and may be useful for exporting data. Another way to do this is to use the function `reshape`, by

```r
> reshape(zz, idvar="id", timevar="var",
          varying=list(c("V1","V2","V3","V4")), direction="long")
```

with result:

<table>
<thead>
<tr>
<th>Status</th>
<th>Age</th>
<th>var</th>
<th>V1</th>
<th>id</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.1</td>
<td>P</td>
<td>1</td>
<td>45190</td>
<td>1</td>
</tr>
<tr>
<td>2.1</td>
<td>CC</td>
<td>1</td>
<td>35535</td>
<td>2</td>
</tr>
<tr>
<td>3.1</td>
<td>CC</td>
<td>1</td>
<td>25691</td>
<td>3</td>
</tr>
<tr>
<td>4.1</td>
<td>CC</td>
<td>1</td>
<td>30949</td>
<td>4</td>
</tr>
<tr>
<td>5.1</td>
<td>CC</td>
<td>1</td>
<td>50542</td>
<td>5</td>
</tr>
<tr>
<td>6.1</td>
<td>CC</td>
<td>1</td>
<td>58591</td>
<td>6</td>
</tr>
<tr>
<td>7.1</td>
<td>CC</td>
<td>1</td>
<td>45801</td>
<td>7</td>
</tr>
<tr>
<td>1.2</td>
<td>P</td>
<td>2</td>
<td>50333</td>
<td>1</td>
</tr>
<tr>
<td>2.2</td>
<td>CC</td>
<td>2</td>
<td>38227</td>
<td>2</td>
</tr>
</tbody>
</table>

The `reshape` has a more complicated syntax than `stack` but can be used for data where the ‘long’ form has more than the one column in this example. With `direction="wide`, `reshape` can also perform the opposite transformation.
2.5 Flat contingency tables

Displaying higher-dimensional contingency tables in array form typically is rather inconvenient. In categorical data analysis, such information is often represented in the form of bordered two-dimensional arrays with leading rows and columns specifying the combination of factor levels corresponding to the cell counts. These rows and columns are typically “ragged” in the sense that labels are only displayed when they change, with the obvious convention that rows are read from top to bottom and columns are read from left to right. In R, such “flat” contingency tables can be created using `ftable`, which creates objects of class "ftable" with an appropriate print method.

As a simple example, consider the R standard data set `UCBAdmissions` which is a 3-dimensional contingency table resulting from classifying applicants to graduate school at UC Berkeley for the six largest departments in 1973 classified by admission and sex.

```r
> data(UCBAdmissions)
> ftable(UCBAdmissions)

<table>
<thead>
<tr>
<th>Dept</th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Admit</td>
<td>Gender</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Admitted</td>
<td>Male</td>
<td>512</td>
<td>353</td>
<td>120</td>
<td>138</td>
<td>53</td>
</tr>
<tr>
<td>Female</td>
<td>89</td>
<td>17</td>
<td>202</td>
<td>131</td>
<td>94</td>
<td>24</td>
</tr>
<tr>
<td>Rejected</td>
<td>Male</td>
<td>313</td>
<td>207</td>
<td>205</td>
<td>279</td>
<td>138</td>
</tr>
<tr>
<td>Female</td>
<td>19</td>
<td>8</td>
<td>391</td>
<td>244</td>
<td>299</td>
<td>317</td>
</tr>
</tbody>
</table>
```

The printed representation is clearly more useful than displaying the data as a 3-dimensional array.

There is also a function `read.ftable` for reading in flat-like contingency tables from files. This has additional arguments for dealing with variants on how exactly the information on row and column variables names and levels is represented. The help page for `read.ftable` has some useful examples. The flat tables can be converted to standard contingency tables in array form using `as.table`.

Note that flat tables are characterized by their “ragged” display of row (and maybe also column) labels. If the full grid of levels of the row variables is given, one should instead use `read.table` to read in the data, and create the contingency table from this using `xtabs`.
Chapter 3: Importing from other statistical systems

3 Importing from other statistical systems

In this chapter we consider the problem of reading a binary data file written by another statistical system. This is often best avoided, but may be unavoidable if the originating system is not available.

3.1 EpiInfo, Minitab, S-PLUS, SAS, SPSS, Stata

The recommended package foreign provides import facilities for files produced by these statistical systems, and for export to Stata. In some cases these function may require substantially less memory than read.table would.

Stata ’.dta’ files are a binary file format. Files from versions 5.0, 6.0 and 7.0 of Stata can be read and written by functions read.dta and write.dta. Stata variables with value labels are optionally converted to (and from) R factor.

EpiInfo versions 5 and 6 stored data in a self-describing fixed-width text format. read.epiinfo will read these .REC files into an R data frame.

Function read.mtp imports a ‘Minitab Portable Worksheet’. This returns the components of the worksheet as an R list.

Function read.xport reads a file in SAS Transport (XPORT) format and return a list of data frames. If SAS is available on your system, function read.ssd can be used to create and run a SAS script that saves a SAS permanent dataset (.ssd or .sas7bdat) in Transport format. It then calls read.xport to read the resulting file.

Function read.spss can read files created by the ‘save’ and ‘export’ commands in SPSS. It returns a list with one component for each variable in the saved data set. SPSS variables with value labels are optionally converted to R factors.

Function read.S which can read binary objects produced by S-PLUS 3.x, 4.x or 2000 on (32-bit) Unix or Windows (and can read them on a different OS). This is able to read many but not all S objects: in particular it can read vectors, matrices and data frames and lists containing those.

Function data.restore reads S-PLUS data dumps (created by data.dump) with the same restrictions (except that dumps from the Alpha platform can also be read). It should be possible to read data dumps from S-PLUS 5.x and 6.x written with data.dump(oldStyle=T).

If you have access to S-PLUS, it is usually more reliable to dump the object(s) in S-PLUS and source the dumpfile in R. For S-PLUS 5.x and 6.x you may need to use dump(., oldStyle=T), and to read in very large objects it may be preferable to use the dumpfile as a batch script rather than source.

3.2 Octave

Octave is a numerical linear algebra system, and function read.octave in package e1071 can read the first vector or matrix from an Octave ASCII data file created using the Octave command save -ascii.
4 Relational databases

4.1 Why use a database?

There are limitations on the types of data that R handles well. Since all data being manipulated by R are resident in memory, and several copies of the data can be created during execution of a function, R is not well suited to extremely large data sets. Data objects that are more than a few (tens of) megabytes in size can cause R to run out of memory.

R does not easily support concurrent access to data. That is, if more than one user is accessing, and perhaps updating, the same data, the changes made by one user will not be visible to the others.

R does support persistence of data, in that you can save a data object or an entire worksheet from one session and restore it at the subsequent session, but the format of the stored data is specific to R and not easily manipulated by other systems.

Database management systems (DBMSs) and, in particular, relational DBMSs (RDBMSs) are designed to do all of these things well. Their strengths are
1. To provide fast access to selected parts of large databases.
2. Powerful ways to summarize and cross-tabulate columns in databases.
3. Store data in more organized ways than the rectangular grid model of spreadsheets and R data frames.
4. Concurrent access from multiple clients running on multiple hosts while enforcing security constraints on access to the data.
5. Ability to act as a server to a wide range of clients.

The sort of statistical applications for which DBMS might be used are to extract a 10% sample of the data, to cross-tabulate data to produce a multi-dimensional contingency table, and to extract data group by group from a database for separate analysis.

4.2 Overview of RDBMSs

Traditionally there have been large (and expensive) commercial RDBMSs (Informix; Oracle; Sybase; IBM’s DB/2; Microsoft SQL Server on Windows) and academic and small-system databases (such as MySQL, PostgreSQL, Microsoft Access, ...), the former marked out by much greater emphasis on data security features. The line is blurring, with the Open Source PostgreSQL having more and more high-end features, and ‘free’ versions of Informix, Oracle and Sysbase being made available on Linux.

There are other commonly used data sources, including spreadsheets, non-relational databases and even text files (possibly compressed). Open Database Connectivity (ODBC) is a standard to use all of these data sources. It originated on Windows (see http://www.microsoft.com/data/odbc/) but is also implemented on Linux.

All of the packages described later in this chapter provide clients to client/server databases. The database can reside on the same machine or (more often) remotely. There is an ISO standard (in fact several: SQL92 is ISO/IEC 9075, also known as ANSI X3.135-1992,
and SQL99 is coming into use) for an interface language called SQL (Structured Query Language, sometimes pronounced ‘sequel’; see Bowman et al. 1996 and Kline and Kline 2001) which these DBMSs support to varying degrees.

4.2.1 SQL queries

The more comprehensive R interfaces generate SQL behind the scenes for common operations, but direct use of SQL is needed for complex operations in all. Conventionally SQL is written in upper case, but many users will find it more convenient to use lower case in the R interface functions.

A relational DBMS stores data as a database of tables (or relations) which are rather similar to R data frames, in that they are made up of columns or fields of one type (numeric, character, date, currency, . . .) and rows or records containing the observations for one entity.

SQL ‘queries’ are quite general operations on a relational database. The classical query is a SELECT statement of the type

\[
\text{SELECT State, Murder FROM USArrests WHERE rape > 30 ORDER BY Murder}
\]

\[
\text{SELECT t.sch, c.meanses, t.sex, t.achieve FROM student as t, school as c WHERE t.sch = c.id}
\]

\[
\text{SELECT sex, COUNT(*) FROM student GROUP BY sex}
\]

\[
\text{SELECT sch, AVG(seстат) FROM student GROUP BY sch LIMIT 10}
\]

The first of these selects two columns from the R data frame USArrests that has been copied across to a database table, subsets on a third column and asks the results be sorted. The second performs a database join on two tables student and school and returns four columns. The third and fourth queries do some cross-tabulation and return counts or averages. (The five aggregation functions are COUNT(*) and SUM, MAX, MIN and AVG, each applied to a single column.)

SELECT queries use FROM to select the table, WHERE to specify a condition for inclusion (or more than one condition separated by AND or OR), and ORDER BY to sort the result. Unlike data frames, rows in RDBMS tables are best thought of as unordered, and without an ORDER BY statement the ordering is indeterminate. You can sort (in lexicographical order) on more than one column by separating them by commas. Placing DESC after an ORDER BY puts the sort in descending order.

SELECT DISTINCT queries will only return one copy of each distinct row in the selected table.

The GROUP BY clause selects subgroups of the rows according to the criterion. If more than one column is specified (separated by commas) then multi-way cross-classifications can be summarized by one of the five aggregation functions. A HAVING clause allows the select to include or exclude groups depending on the aggregated value.

If the SELECT statement contains an ORDER BY statement that produces a unique ordering, a LIMIT clause can be added to select (by number) a contiguous block of output rows. This can be useful to retrieve rows a block at a time. (It may not be reliable unless the ordering is unique, as the LIMIT clause can be used to optimize the query.)
There are queries to create a table (CREATE TABLE, but usually one copies a data frame to the database in these interfaces), INSERT or DELETE or UPDATE data. A table is destroyed by a DROP TABLE ‘query’.

Kline and Kline (2001) discuss the details of the implementation of SQL in SQL Server 2000, Oracle, MySQL and PostgreSQL.

### 4.2.2 Data types

Data can be stored in a database in various data types. The range of data types is DBMS-specific, but the SQL standard defines many types, including the following that are widely implemented (often not by the SQL name).

- **float**(p)  Real number, with optional precision. Often called **real** or **double** or **double precision**.
- **integer**  32-bit integer. Often called **int**.
- **smallint** 16-bit integer
- **character**(n)  fixed-length character string. Often called **char**.
- **character varying**(n)  variable-length character string. Often called **varchar**.
- **boolean**  true or false. Sometimes called **bool**.
- **date**  calendar date
- **time**  time of day
- **timestamp**  date and time

There are variants on **time** and **timestamp**, with **timezone**.

The more comprehensive of the R interface packages hide the type conversion issues from the user.

### 4.3 R interface packages

There are several packages available on CRAN to help R communicate with DBMSs. They provide different levels of abstraction. Some provide means to copy whole data frames to and from databases. All have functions to select data within the database via SQL queries, and (except RmSQL) to retrieve the result as a whole as a data frame or in pieces (usually as groups of rows, but RPgSQL can retrieve columns).

All except RODBC are tied to one DBMS, but work is in progress towards a unified ‘front-end’ package DBI ([http://developer.r-project.org/db](http://developer.r-project.org/db)) in conjunction with a ‘back-end’, the most developed of which is RMySQL. Also on CRAN are the back-ends ROracle and RSQLite (which works with the included DBMS SQLite, [http://www.hwaci.com/sw/sqlite](http://www.hwaci.com/sw/sqlite)).
4.3.1 Packages DBI and RMySQL

Package RMySQL on CRAN provides an interface to the MySQL database system (see http://www.mysql.com and Dubois, 2000.). The description here applies to version 0.5-0: earlier versions had a substantially different interface. The current version requires the DBI package, and this description will apply with minor changes to all the other back-ends to DBI.

MySQL exists on Unix/Linux and Windows: as from version 3.23.x (Jan 2001) it is released under GPL. MySQL is a ‘light and lean’ database. (It preserves the case of names where the operating file system is case-sensitive, so not on Windows.) Package RMySQL has been used on both Linux and Windows.

The call dbDriver("MySQL") returns a database connection manager object, and then a call to dbConnect opens a database connection which can subsequently be closed by a call to the generic function dbDisconnect. Use dbDriver("Oracle") or dbDriver("SQLite") with those DBMSs and ROracle or RSQLite respectively.

SQL queries can be sent by either dbSendQuery or dbGetQuery. dbGetQuery sends the query and retrieves the results as a data frame. dbSendQuery sends the query and returns an object of class inheriting from "DBIResult" which can be used to retrieve the results, and subsequently used in a call to dbClearResult to remove the result.

Function fetch is used to retrieve some or all of the rows in the query result, as a list. The function dbHasCompleted indicates if all the rows have been fetched, and dbGetRowCount returns the number of rows in the result.

These are convenient interfaces to read/write/test/delete tables in the database. dbReadTable and dbWriteTable copy to and from an R data frame, mapping the row names of the data frame to the field row_names in the MySQL table.

```r
> library(RMySQL) # will load DBI as well
## open a connection to a MySQL database
> con <- dbConnect(dbDriver("MySQL"), dbname = "test")
## list the tables in the database
> dbListTables(con)
## load a data frame into the database, deleting any existing copy
> data(USArrests)
> dbWriteTable(con, "arrests", USArrests, overwrite = TRUE)
TRUE
> dbListTables(con)
[1] "arrests"
## get the whole table
> dbReadTable(con, "arrests")

<table>
<thead>
<tr>
<th>Murder</th>
<th>Assault</th>
<th>UrbanPop</th>
<th>Rape</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alabama</td>
<td>13.2</td>
<td>236</td>
<td>58</td>
</tr>
<tr>
<td>Alaska</td>
<td>10.0</td>
<td>263</td>
<td>48</td>
</tr>
<tr>
<td>Arizona</td>
<td>8.1</td>
<td>294</td>
<td>80</td>
</tr>
<tr>
<td>Arkansas</td>
<td>8.8</td>
<td>190</td>
<td>50</td>
</tr>
</tbody>
</table>

## Select from the loaded table: all on one line
> dbGetQuery(con, "select row_names, Murder from arrests
where Rape > 30 order by Murder")

row_names Murder
1 Colorado 7.9
2 Arizona 8.1
```
4.3.2 Package RODBC

Package RODBC on CRAN provides an interface to database sources supporting an ODBC interface. This is very widely available, and allows the same R code to access different database systems. RODBC runs on both Linux and Windows, and many database systems provide support for ODBC, including most of those on Windows (such as Microsoft Access), and MySQL, Oracle and PostgreSQL on Unix/Linux.

On Windows ODBC support is normally installed, and current versions are available from [http://www.microsoft.com/data/odbc/](http://www.microsoft.com/data/odbc/) as part of MDAC. On Unix/Linux you will need an ODBC Driver Manager such as unixODBC ([http://www.unixODBC.org](http://www.unixODBC.org)) or iOBD (http://www.iOBD.org) and an installed driver for your database system. The FreeODBC project ([http://www.jepstone.net/FreeODBC/](http://www.jepstone.net/FreeODBC/)) is a repository of information related to ODBC.

Two groups of interface functions are provided. The odbc* group provide a low-level interface to the basic ODBC functions: see the help page (?RODBC) for details. The sql* group provide an interface between R data frames and SQL tables.

Up to 16 simultaneous connections are possible. A connection is opened by a call to odbcConnect or odbcDriverConnect (which on Windows allows a database to be selected via dialog boxes) which returns a handle used for subsequent access to the database. A connection is closed by close or odbcClose. Details of the tables on a connection can be found using sqlTables.

Function sqlSave copies an R data frame to a table in the database, and sqlFetch copies a table in the database to an R data frame.

An SQL query can be sent to the database by a call to sqlQuery. This returns the result in an R data frame. (sqlCopy sends a query to the database and saves the result as a table in the database.) A finer level of control is attained by first calling odbcQuery and then sqlGetResults to fetch the results. The latter can be used within a loop to retrieve a limited number of rows at a time.

Here is an example using PostgreSQL, for which the ODBC driver maps column and data frame names to lower case. We use a database testdb we created earlier, and had the DSN (data source name) set up in ‘~/odbc.ini’ under unixODBC. Exactly the same code worked using MyODBC to access a MySQL database under Linux or Windows (where MySQL also maps names to lowercase). Under Windows, DSNs are set up in the ODBC applet in the Control Panel (‘Data Sources (ODBC)’ in the ‘Administrative Tools’ section on 2000/XP).

```r
library(RODBC)
## tell it to map names to l/case
> channel <- odbcConnect("testdb", uid="ripley", case="tolower")
```
## load a data frame into the database
```r
> data(USArrests)
> sqlSave(channel, USArrests, rownames = "state")
> rm(USArrests)
```

## list the tables in the database
```r
> sqlTables(channel)
```

<table>
<thead>
<tr>
<th>TABLE_QUALIFIER</th>
<th>TABLE_OWNER</th>
<th>TABLE_NAME</th>
<th>TABLE_TYPE</th>
<th>REMARKS</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>usarrests</td>
<td>TABLE</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

## list it
```r
> sqlFetch(channel, "USArrests", rownames = "state")
```

```r
murder assault urbanpop rape
Alabama 13.2 236 58 21.2
Alaska 10.0 263 48 44.5
```

## an SQL query, originally on one line
```r
> sqlQuery(channel, "select state, murder from USArrests
where rape > 30 order by murder")
```

```r
state murder
1 Colorado 7.9
2 Arizona 8.1
3 California 9.0
4 Alaska 10.0
5 New Mexico 11.4
6 Michigan 12.1
7 Nevada 12.2
8 Florida 15.4
```

## remove the table
```r
> sqlDrop(channel, "USArrests")
```

## close the connection
```r
> odbcClose(channel)
```

As a simple example of using ODBC under Windows with a Excel spreadsheet, suppose that an DSN for spreadsheet ‘bdr.xls’ has been set up in the Control Panel. Then we can read from the spreadsheet by
```r
> library(RODBC)
> channel <- odbcConnect("bdr.xls")
```

## list the spreadsheets
```r
> sqlTables(channel)
```

<table>
<thead>
<tr>
<th>TABLE_CAT</th>
<th>TABLE_SCHEM</th>
<th>TABLE_NAME</th>
<th>TABLE_TYPE</th>
<th>REMARKS</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 C:\bdr</td>
<td>NA</td>
<td>Sheet1$</td>
<td>SYSTEM TABLE</td>
<td>NA</td>
</tr>
<tr>
<td>2 C:\bdr</td>
<td>NA</td>
<td>Sheet2$</td>
<td>SYSTEM TABLE</td>
<td>NA</td>
</tr>
<tr>
<td>3 C:\bdr</td>
<td>NA</td>
<td>Sheet3$</td>
<td>SYSTEM TABLE</td>
<td>NA</td>
</tr>
<tr>
<td>4 C:\bdr</td>
<td>NA Sheet1$Print_Area</td>
<td>TABLE</td>
<td>NA</td>
<td></td>
</tr>
</tbody>
</table>

## retrieve the contents of sheet 1, by either of
```r
> sh1 <- sqlFetch(channel, "Sheet1")
> sh1 <- sqlQuery(channel, "select * from [Sheet1$]"
```

Notice that the specification of the table is different from the name returned by `sqlTables`: as from version 0.9-1 `sqlFetch` is able to map the differences.

The ODBC interface to Excel spreadsheets is read-only; you cannot alter the spreadsheet data.

### 4.3.3 Package RPgSQL

Package RPgSQL at http://rpgsql.sourceforge.net/ and in the Devel area on CRAN provides an interface to PostgreSQL. Development appears to have ceased.
PostgreSQL is described by its developers as ‘the most advanced open source database server’ (Momjian, 2000). It would appear to be buildable for most Unix-alike OSes and Windows (under Cygwin or U/Win). PostgreSQL has most of the features of the commercial RDBMSs.

To make use of RPgSQL, first open a connection to a database using \texttt{db.connect}. (Currently only one connection can be open at a time.) Once a connection is open an R data frame can be copied to a PostgreSQL table by \texttt{db.write.table}, whereas \texttt{db.read.table} copies a PostgreSQL table to an R data frame.

RPgSQL has the interesting concept of a proxy data frame. A data frame proxy is an R object that inherits from the “\texttt{data.frame}” class, but contains no data. All accesses to the proxy data frame generate the appropriate SQL query and retrieve the resulting data from the database. A proxy data frame is set up by a call to \texttt{bind.db.proxy}. To remove the proxy, just remove the object which \texttt{bind.db.proxy} created.

A finer level of control is available via sending SQL queries to the PostgreSQL server via \texttt{db.execute}. This leaves a result in PostgreSQL’s result cache, unless flushed by \texttt{clear = TRUE} (the default). Once a result is in the cache, \texttt{db.fetch.result} can be used to fetch the whole result as a data frame. Functions such as \texttt{db.result.columns} and \texttt{db.result.rows} will report the number of columns and rows in the cached table, and \texttt{db.read.column} will fetch a single column (as a vector). An individual cell in the result can be read by \texttt{db.result.get.value}. \texttt{db.clear.result} will clear the result cache.

One disadvantage is that PostgreSQL maps all table and column names to lower case, so for maximal flexibility, only use lower case in R names. Functions \texttt{sql.insert} and \texttt{sql.select} provide convenience wrappers for the INSERT and SELECT queries.

We can explore these functions in a simple example. The database ‘testdb’ had already been set up, and as PostgreSQL was running on a standalone machine no further authentication was required to connect.

```r
> library(RPgSQL)
> db.connect(dbname="testdb")  # add authentication as needed
 Connected to database "testdb" on ""
> data(USArrests)
> usarrests <- USArrests
> names(umarrests) <- tolower(names(USArrests))
> db.write.table(USArrests, write.row.names = TRUE)
> db.write.table(umarrests, write.row.names = TRUE)
> rm(USArrests, usarrests)
## db.ls lists tables in the database.
> db.ls()
[1] "USArrests"  "umarrests"
> db.read.table("USArrests")
Murder Assault UrbanPop Rape
Alabama 13.2 236 58 21.2
Alaska 10.0 263 48 44.5
...  
## set up a proxy data frame. Remember USArrests has been removed
> bind.db.proxy("USArrests")
## USArrests is now a proxy, so all accesses are to the database
> USArrests[, "Rape"]
        Rape
1  21.2
2  44.5
...  
```
Chapter 4: Relational databases

> rm(USArrests) # remove proxy
> db.execute("SELECT rpgsql_row_names, murder FROM usarrests",
    "WHERE rape > 30 ORDER BY murder", clear=FALSE)
> db.fetch.result()
murder
Colorado 7.9
Arizona 8.1
California 9.0
Alaska 10.0
New Mexico 11.4
Michigan 12.1
Nevada 12.2
Florida 15.4
> db.rm("USArrests", "usarrests") # use ask=FALSE to skip confirmation
Destroy table USArrests? y
Destroy table usarrests? y
> db.ls()
character(0)
> db.disconnect()

Notice how the row names are mapped if write.row.names = TRUE to a field rpgsql_row_names in the database table and transparently restored provided we preserve that field in the query.

RPgSQL provides means to extend its mapping between R classes within a data frame and PostgreSQL types.

4.3.4 Package RmSQL

Package RmSQL on CRAN provides an interface to the Mini SQL database system (also known as mSQL, http://www.hughes.com.au, Yarger et al., 1999). The package documentation describes mSQL as

Note that mSQL is NOT GPL licenced but free of charge for universities and noncommercial organisations.

RmSQL provides the most basic interface of those in this chapter, a wrapper to the C-API of mSQL with no additional functionality.

A database connection is opened by first selecting a host with msqlConnect and then a database by msqlSelect. The connection is closed by a call to msqlClose. Then an SQL query is sent by a call to msqlQuery, and the results stored by a call to msqlStoreResult. When a query is finished with, the result can be freed by msqlFreeResult.

Once the result of a query has been stored, the values can be retrieved row by row using msqlFetchRow. This fetches the rows in order unless the position is reset by a call to msqlDataSeek. A call to msqlNumRows gives the total number of rows in the result.

No example is given here as the basic interface makes any example lengthy, but there is one in the 'Example' directory of the package.
5 Binary files

Binary connections (Chapter 6 [Connections], page 20) are now the preferred way to handle binary files.

5.1 Binary data formats

Packages **hdf5** and **netCDF** on CRAN provide experimental interfaces to NASA’s HDF5 (Hierarchical Data Format, see [http://hdf.ncsa.uiuc.edu/HDF5/](http://hdf.ncsa.uiuc.edu/HDF5/)) and to UCAR’s netCDF data files (network Common Data Form, see [http://www.unidata.ucar.edu/packages/netcdf/](http://www.unidata.ucar.edu/packages/netcdf/)), respectively.

Both of these are systems to store scientific data in array-oriented ways, including descriptions, labels, formats, units, . . . . HDF5 also allows groups of arrays, and the R interface maps lists to HDF5 groups, and can write numeric and character vectors and matrices.

The R interface can only read netCDF, not write it (yet).
Chapter 6: Connections

6 Connections

Connections are used in R in the sense of Chambers (1998), a set of functions to replace the use of file names by a flexible interface to file-like objects.

6.1 Types of connections

The most familiar type of connection will be a file, and file connections are created by function file. File connections can (if the OS will allow it for the particular file) be opened for reading or writing or appending, in text or binary mode. In fact, files can be opened for both reading and writing, and R keeps a separate file position for reading and writing.

Note that by default a connection is not opened when it is created. The rule is that a function using a connection should open a connection (needed) if the connection is not already open, and close a connection after use if it opened it. In brief, leave the connection in the state you found it in. There are generic functions open and close with methods to explicitly open and close connections.

Files compressed via the algorithm used by gzip can be used as connections created by the function gzfile, whereas files compressed by bzip2 can be used via bzfile.

Unix programmers are used to dealing with special files stdin, stdout and stderr. These exist as terminal connections in R. They may be normal files, but they might also refer to input from and output to a GUI console. (Even with the standard Unix R interface, stdin refers to the lines submitted from readline rather than a file.)

The three terminal connections are always open, and cannot be opened or closed. stdout and stderr are conventionally used for normal output and error messages respectively. They may normally go to the same place, but whereas normal output can be re-directed by a call to sink, error output is sent to stderr unless re-directed by sink, type="message"). Note carefully the language used here: the connections cannot be re-directed, but output can be sent to other connections.

Text connections are another source of input. They allow R character vectors to be read as if the lines were being read from a text file. A text connection is created and opened by a call to textConnection, which copies the current contents of the character vector to an internal buffer at the time of creation.

Text connections can also be used to capture R output to a character vector. textConnection can be asked to create a new character object or append to an existing one, in both cases in the user’s workspace. The connection is opened by the call to textConnection, and at all times the complete lines output to the connection are available in the R object. Closing the connection writes any remaining output to a final element of the character vector.

Pipes are a special form of file that connects to another process, and pipe connections are created by the function pipe (currently implemented on Unix and Rterm only). Opening a pipe connection for writing (it makes no sense to append to a pipe) runs an OS command, and connects its standard input to whatever R then writes to that connection. Conversely, opening a pipe connection for input runs an OS command and makes its standard output available for R input from that connection.
URLs of types http://, ftp:// and file:// can be read from using the function url. For convenience, file will also accept these as the file specification and call url.

Sockets can also be used as connections via function socketConnection on platforms which support Berkeley-like sockets (most Unix systems, Linux and Windows). Sockets can be written to or read from, and both client and server sockets can be used.

6.2 Output to connections

We have described functions cat, write, write.table and sink as writing to a file, possibly appending to a file if argument append = TRUE, and this is what they did prior to R version 1.2.0.

The current behaviour is equivalent, but what actually happens is that when the file argument is a character string, a file connection is opened (for writing or appending) and closed again at the end of the function call. If we want to repeatedly write to the same file, it is more efficient to explicitly declare and open the connection, and pass the connection object to each call to an output function. This also makes it possible to write to pipes, which was implemented earlier in a limited way via the syntax file = "|cmd" (which can still be used).

There is a function writeLines to write complete text lines to a connection.

Some simple examples are

```r
zz <- file("ex.data", "w")  # open an output file connection
cat("TITLE extra line", "2 3 5 7", "", "11 13 17",
    file = zz, sep = "\n")
cat("One more line\n", file = zz)
close(zz)
```

```
## convert decimal point to comma in output, using a pipe (Unix)
## both R strings and (probably) the shell need \ doubled
zz <- pipe(paste("sed s/\\./,/ >", "outfile"), "w")
cat(format(round(rnorm(100), 4)), sep = "\n", file = zz)
close(zz)
```

```
## now look at the output file:
file.show("outfile", delete.file = TRUE)
```

```
## capture R output: use examples from help(lm)
zz <- textConnection("ex.lm.out", "w")
sink(zz)
example(lm, prompt.echo = "> ")
sink()
close(zz)
```

```
## now 'ex.lm.out' contains the output for further processing.
## Look at it by, e.g.,
cat(ex.lm.out, sep = "\n")
```

6.3 Input from connections

The basic functions to read from connections are scan and readLines. These take a character string argument and open a file connection for the duration of the function call, but explicitly opening a file connection allows a file to be read sequentially in different formats.
Other functions that call \texttt{scan} can also make use of connections, in particular \texttt{read.table}. As from R version 1.3.0, \texttt{read.table} reads the data in a single pass and so works better with non-file connections.

Some simple examples are

```r
## read in file created in last examples
readLines("ex.data")
unlink("ex.data")

## read listing of current directory (Unix)
readLines(pipe("ls -1"))

# remove trailing commas from an input file.
# Suppose we are given a file `data` containing
# 450, 390, 467, 654, 30, 542, 334, 432, 421,
# 357, 497, 493, 550, 549, 467, 575, 578, 342,
# 446, 547, 534, 495, 979, 479
# Then read this by
scan(pipe("sed -e s/,$// data"), sep=",")
```

For convenience, if the \texttt{file} argument specifies a FTP or HTTP URL, the URL is opened for reading via \texttt{url}. Specifying files via \texttt{file://foo.bar} is also allowed.

### 6.3.1 Pushback

C programmers may be familiar with the \texttt{ungetc} function to push back a character onto a text input stream. R connections have the same idea in a more powerful way, in that an (essentially) arbitrary number of lines of text can be pushed back onto a connection via a call to \texttt{pushBack}.

Pushbacks operate as a stack, so a read request first uses each line from the most recently pushbacked text, then those from earlier pushbacks and finally reads from the connection itself. Once a pushbacked line is read completely, it is cleared. The number of pending lines pushed back can be found via a call to \texttt{pushBackLength}.

A simple example will show the idea.

```r
> zz <- textConnection(LETTERS)
> readLines(zz, 2)
[1] "A" "B"
> scan(zz, ",", 4)
Read 4 items
[1] "C" "D" "E" "F"
> pushBack(c("aa", "bb"), zz)
> scan(zz, ",", 4)
Read 4 items
[1] "aa" "bb" "G" "H"
> close(zz)
```

Pushback is only available for connections opened for input in text mode.

### 6.4 Listing and manipulating connections

A summary of all the connections currently opened by the user can be found by \texttt{showConnections()}, and a summary of all connections, including closed and terminal connections, by \texttt{showConnections(all = TRUE)}
The generic function \texttt{seek} can be used to read and (on some connections) reset the current position for reading or writing. Unfortunately it depends on OS facilities which may be unreliable (e.g. with text files under Windows). Function \texttt{isSeekable} reports if \texttt{seek} can change the position on the connection given by its argument.

The function \texttt{truncate} can be used to truncate a file opened for writing at its current position. It works only for file connections, and is not implemented on all platforms.

### 6.5 Binary connections

Functions \texttt{readBin} and \texttt{writeBin} read to and write from binary connections. A connection is opened in binary mode by appending "b" to the mode specification, that is using mode "rb" for reading, and mode "wb" or "ab" (where appropriate) for writing. The functions have arguments

\begin{verbatim}
readBin(con, what, n = 1, size = NA, endian = .Platform$endian)
writeBin(object, con, size = NA, endian = .Platform$endian)
\end{verbatim}

In each case \texttt{con} is a connection which will be opened if necessary for the duration of the call, and if a character string is given it is assumed to specify a file name.

It is slightly simpler to describe writing, so we will do that first. \texttt{object} should be an atomic vector object, that is a vector of mode \texttt{numeric}, \texttt{integer}, \texttt{logical}, \texttt{character} or \texttt{complex}, without attributes. By default this is written to the file as a stream of bytes exactly as it is represented in memory.

\texttt{readBin} reads a stream of bytes from the file and interprets them as a vector of mode given by \texttt{what}. This can be either an object of the appropriate mode (e.g. \texttt{what=integer()} or a character string describing the mode (one of the five given in the previous paragraph or "double" or "int"). Argument \texttt{n} specifies the maximum number of vector elements to read from the connection: if fewer are available a shorter vector will be returned. Argument \texttt{signed} allows 1-byte and 2-byte integers to be read as signed (the default) or unsigned integers.

The remaining two arguments are used to write or read data for interchange with another program or another platform. By default binary data is transferred directly from memory to the connection or \textit{vice versa}. This will not suffice if the file is to be transferred to a machine with a different architecture, but between almost all R platforms the only change needed is that of byte-order. Intel \texttt{ix86}-based machines, Compaq Alpha and Vaxen are \texttt{little-endian}, whereas Sun Sparc, mc680x0 series, IBM R6000, SGI and most others are \texttt{big-endian}. (Network byte-order (as used by XDR, eXternal Data Representation) is big-endian.) To transfer to or from other programs we may need to do more, for example to read 16-bit integers or write single-precision real numbers. This can be done using the \texttt{size} argument, which (usually) allows sizes 1, 2, 4, 8 for integers and logicals, and sizes 4, 8 and perhaps 12 or 16 for reals. Transferring at different sizes can lose precision, and should not be attempted for vectors containing \texttt{NA}'s.

Character strings are read and written in C format, that is as a string of bytes terminated by a zero byte. Functions \texttt{readChar} and \texttt{writeChar} provide greater flexibility.
6.5.1 Special values

Functions \texttt{readBin} and \texttt{writeBin} will pass missing and special values, although this should not be attempted if a size change is involved.

The missing value for R logical and integer types is \texttt{INT\_MIN}, the smallest representable \texttt{int} defined in the C header ‘\texttt{limits.h}’, normally corresponding to the bit pattern \texttt{0xffffffff}.

The representation of the special values for R numeric and complex types is machine-dependent, and possibly also compiler-dependent. The simplest way to make use of them is to link an external application against the standalone \texttt{Rmath} library which exports double constants \texttt{NA\_REAL}, \texttt{R\_PosInf} and \texttt{R\_NegInf}, and include the header ‘\texttt{Rmath.h}’ which defines the macros \texttt{ISNAN} and \texttt{R\_FINITE}.

If that is not possible, on all common platforms IEC 60559 (aka IEEE 754) arithmetic is used, so standard C facilities can be used to test for or set \texttt{Inf}, \texttt{-Inf} and \texttt{NaN} values. On such platforms \texttt{NA} is represented by the \texttt{NaN} value with low-word \texttt{0x7a2} (1954 in decimal).
Chapter 7: Network interfaces

Some limited facilities are available to exchange data at a lower level across network connections.

7.1 Reading from sockets

Base R comes with some facilities to communicate via BSD sockets on systems that support them (including the common Linux, Unix and Windows ports of R). One potential problem with using sockets is that these facilities are often blocked for security reasons or to force the use of Web caches, so these functions may be more useful on an intranet than externally. For new projects it is suggested that socket connections are used instead.

The earlier low-level interface is given by functions make.socket, read.socket, write.socket and close.socket.

7.2 Using download.file

Function download.file is provided to read a file from a Web resource via FTP or HTTP and write it to a file. Often this can be avoided, as functions such as read.table and scan can read directly from a URL, either by explicitly using url to open a connection, or implicitly using it by giving a URL as the file argument.

7.3 DCOM interface

DCOM is a Windows protocol for communicating between different programs, possibly on different machines. Thomas Baier’s StatConnector program available from CRAN under Software->Other->Non-standard provides an interface to the proxy DLL which ships with the Windows version of R and makes an DCOM server. This can be used to pass simple objects (vectors and matrices) to and from R and to submit commands to R.

The program comes with a Visual Basic demonstration, and there is an Excel plug-in by Erich Neuwirth available in the same area on CRAN. This interface is in the other direction to most of those considered here in that it is another application (Excel, or written in Visual Basic) that is the client and R is the server.

7.4 CORBA interface

CORBA (Common Object Request Broker Architecture) is similar to DCOM, allowing applications to call methods, or operations, in server objects running in other applications, potentially programmed in different languages and running on different machines. There is a CORBA package available from the Omegahat Project (at http://www.omegahat.org/RSCORBA/), currently for Unix but a Windows version looks to be possible.

This package allows R commands to be used to locate available CORBA servers, query the methods they provide, and dynamically invoke methods on these objects. R values given
as arguments in these calls are exported in the call and made available to that operation invocation. Primitive data types (vectors and lists) are exported by default, while more complex objects are exported by reference. Examples of using this include communicating with the Gnumeric (http://www.gnumeric.org) spreadsheet, and also interacting with the data visualization system ggobi.

One can also create CORBA servers within R, allowing other applications to call these methods. For example, one might offer access to a particular dataset or to some of R's modelling software. This is done dynamically by combining R data objects and functions. This allows one to explicitly export data and functionality from R.

One can also use the CORBA package to achieve distributed, parallel computing in R. One R session acts as a manager and dispatches tasks to different servers running in other R worker sessions. This uses the ability to invoke asynchronous or background CORBA calls in R. More information is available from the Omegahat Project, at http://www.omegahat.org/RSCORBA/.
Appendix A References


### Function and variable index

<table>
<thead>
<tr>
<th>B</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>bind.db.proxy</td>
<td>17</td>
</tr>
<tr>
<td>bzfile</td>
<td>20</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>C</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>cat</td>
<td>3, 21</td>
</tr>
<tr>
<td>close</td>
<td>15, 20</td>
</tr>
<tr>
<td>close.socket</td>
<td>25</td>
</tr>
<tr>
<td>count.fields</td>
<td>7</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>D</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>data.restore</td>
<td>10</td>
</tr>
<tr>
<td>db.clear.result</td>
<td>17</td>
</tr>
<tr>
<td>db.connect</td>
<td>17</td>
</tr>
<tr>
<td>db.execute</td>
<td>17</td>
</tr>
<tr>
<td>db.fetch.result</td>
<td>17</td>
</tr>
<tr>
<td>db.read.column</td>
<td>17</td>
</tr>
<tr>
<td>db.read.table</td>
<td>17</td>
</tr>
<tr>
<td>db.result.columns</td>
<td>17</td>
</tr>
<tr>
<td>db.result.get.value</td>
<td>17</td>
</tr>
<tr>
<td>db.result.rows</td>
<td>17</td>
</tr>
<tr>
<td>db.write.table</td>
<td>17</td>
</tr>
<tr>
<td>dbClearResult</td>
<td>14</td>
</tr>
<tr>
<td>dbConnect</td>
<td>14</td>
</tr>
<tr>
<td>dbDisconnect</td>
<td>14</td>
</tr>
<tr>
<td>dbDriver</td>
<td>14</td>
</tr>
<tr>
<td>dbExistsTable</td>
<td>14</td>
</tr>
<tr>
<td>dbGetQuery</td>
<td>14</td>
</tr>
<tr>
<td>dbReadTable</td>
<td>14</td>
</tr>
<tr>
<td>dbRemoveTable</td>
<td>14</td>
</tr>
<tr>
<td>dbSendQuery</td>
<td>14</td>
</tr>
<tr>
<td>dbWriteQuery</td>
<td>14</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>F</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>fetch</td>
<td>14</td>
</tr>
<tr>
<td>file</td>
<td>20</td>
</tr>
<tr>
<td>format</td>
<td>3</td>
</tr>
<tr>
<td>ftable</td>
<td>9</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>G</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>gzfile</td>
<td>20</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>H</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>hdf5</td>
<td>19</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>I</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>isSeekable</td>
<td>22</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>M</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>make.socket</td>
<td>25</td>
</tr>
<tr>
<td>msqlClose</td>
<td>18</td>
</tr>
<tr>
<td>msqlConnect</td>
<td>18</td>
</tr>
<tr>
<td>msqlDataSeek</td>
<td>18</td>
</tr>
<tr>
<td>msqlFetchRow</td>
<td>18</td>
</tr>
<tr>
<td>msqlFreeResult</td>
<td>18</td>
</tr>
<tr>
<td>msqlNumRows</td>
<td>18</td>
</tr>
<tr>
<td>msqlQuery</td>
<td>18</td>
</tr>
<tr>
<td>msqlSelect</td>
<td>18</td>
</tr>
<tr>
<td>msqlStoreResult</td>
<td>18</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>N</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>netCDF</td>
<td>19</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>O</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>odbcClose</td>
<td>15</td>
</tr>
<tr>
<td>odbcConnect</td>
<td>15</td>
</tr>
<tr>
<td>odbcDriverConnect</td>
<td>15</td>
</tr>
<tr>
<td>odbcFetchRows</td>
<td>15</td>
</tr>
<tr>
<td>odbcQuery</td>
<td>15</td>
</tr>
<tr>
<td>open</td>
<td>20</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>P</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>pipe</td>
<td>20</td>
</tr>
<tr>
<td>pushBack</td>
<td>22</td>
</tr>
<tr>
<td>pushBackLength</td>
<td>22</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>R</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>read.csv</td>
<td>6</td>
</tr>
<tr>
<td>read.csv2</td>
<td>6</td>
</tr>
<tr>
<td>read.delim</td>
<td>6</td>
</tr>
<tr>
<td>read.delim2</td>
<td>6</td>
</tr>
<tr>
<td>read.dta</td>
<td>10</td>
</tr>
<tr>
<td>read.epiinfo</td>
<td>10</td>
</tr>
<tr>
<td>read.ftable</td>
<td>9</td>
</tr>
<tr>
<td>read.fwf</td>
<td>7</td>
</tr>
<tr>
<td>read.mtp</td>
<td>10</td>
</tr>
<tr>
<td>read.octave</td>
<td>10</td>
</tr>
<tr>
<td>read.S</td>
<td>10</td>
</tr>
<tr>
<td>read.socket</td>
<td>25</td>
</tr>
<tr>
<td>read.spss</td>
<td>10</td>
</tr>
<tr>
<td>read.table</td>
<td>5, 21</td>
</tr>
<tr>
<td>read.xport</td>
<td>10</td>
</tr>
<tr>
<td>readBin</td>
<td>23</td>
</tr>
<tr>
<td>readChar</td>
<td>23</td>
</tr>
<tr>
<td>readLines</td>
<td>7, 21</td>
</tr>
<tr>
<td>reshape</td>
<td>8</td>
</tr>
<tr>
<td>S</td>
<td>T</td>
</tr>
<tr>
<td>---------</td>
<td>---------</td>
</tr>
<tr>
<td>scan</td>
<td>textConnection</td>
</tr>
<tr>
<td>seek</td>
<td>truncate</td>
</tr>
<tr>
<td>showConnections</td>
<td></td>
</tr>
<tr>
<td>sink</td>
<td></td>
</tr>
<tr>
<td>socketConnection</td>
<td></td>
</tr>
<tr>
<td>sql.insert</td>
<td></td>
</tr>
<tr>
<td>sql.select</td>
<td></td>
</tr>
<tr>
<td>sqlCopy</td>
<td></td>
</tr>
<tr>
<td>sqlFetch</td>
<td></td>
</tr>
<tr>
<td>sqlGetResults</td>
<td></td>
</tr>
<tr>
<td>sqlQuery</td>
<td></td>
</tr>
<tr>
<td>sqlSave</td>
<td></td>
</tr>
<tr>
<td>sqlTables</td>
<td></td>
</tr>
<tr>
<td>stack</td>
<td></td>
</tr>
<tr>
<td>stderr</td>
<td></td>
</tr>
<tr>
<td>stdin</td>
<td></td>
</tr>
<tr>
<td>stdout</td>
<td></td>
</tr>
<tr>
<td>T</td>
<td>U</td>
</tr>
<tr>
<td>textConnection</td>
<td>unstack</td>
</tr>
<tr>
<td>truncate</td>
<td>url</td>
</tr>
<tr>
<td>W</td>
<td></td>
</tr>
<tr>
<td>write</td>
<td></td>
</tr>
<tr>
<td>write.dta</td>
<td></td>
</tr>
<tr>
<td>write.matrix</td>
<td></td>
</tr>
<tr>
<td>write.socket</td>
<td></td>
</tr>
<tr>
<td>write.table</td>
<td></td>
</tr>
<tr>
<td>writeSin</td>
<td></td>
</tr>
<tr>
<td>writeChar</td>
<td></td>
</tr>
<tr>
<td>writeLines</td>
<td></td>
</tr>
</tbody>
</table>
# Concept index

## A

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>AWK</td>
<td>2</td>
</tr>
</tbody>
</table>

## B

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Binary files</td>
<td>19, 23</td>
</tr>
</tbody>
</table>

## C

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>comma separated values</td>
<td>3</td>
</tr>
<tr>
<td>Compressed files</td>
<td>20</td>
</tr>
<tr>
<td>Connections</td>
<td>20, 21, 22</td>
</tr>
<tr>
<td>CORBA</td>
<td>25</td>
</tr>
<tr>
<td>CSV files</td>
<td>3, 6</td>
</tr>
</tbody>
</table>

## D

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>DBMS</td>
<td>11</td>
</tr>
<tr>
<td>DCOM</td>
<td>25</td>
</tr>
</tbody>
</table>

## E

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>EpiInfo</td>
<td>10</td>
</tr>
<tr>
<td>Exporting to a text file</td>
<td>3</td>
</tr>
</tbody>
</table>

## F

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>File connections</td>
<td>20</td>
</tr>
<tr>
<td>Fixed-width-format files</td>
<td>7</td>
</tr>
<tr>
<td>Flat contingency tables</td>
<td>9</td>
</tr>
</tbody>
</table>

## H

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hierarchical Data Format</td>
<td>19</td>
</tr>
</tbody>
</table>

## I

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Importing from other statistical systems</td>
<td>10</td>
</tr>
</tbody>
</table>

## M

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mini SQL database system</td>
<td>18</td>
</tr>
<tr>
<td>Minitab</td>
<td>10</td>
</tr>
<tr>
<td>Missing values</td>
<td>3, 6</td>
</tr>
<tr>
<td>MySQL database system</td>
<td>14, 15</td>
</tr>
</tbody>
</table>

## N

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>network Common Data Form</td>
<td>19</td>
</tr>
</tbody>
</table>

## O

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Octave</td>
<td>10</td>
</tr>
<tr>
<td>ODBC</td>
<td>11, 15</td>
</tr>
<tr>
<td>Open Database Connectivity</td>
<td>11, 15</td>
</tr>
</tbody>
</table>

## P

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>perl</td>
<td>2, 7</td>
</tr>
<tr>
<td>Pipe connections</td>
<td>20</td>
</tr>
<tr>
<td>PostgreSQL database system</td>
<td>15, 16</td>
</tr>
<tr>
<td>proxy data frame</td>
<td>17</td>
</tr>
<tr>
<td>Pushback on a connection</td>
<td>22</td>
</tr>
</tbody>
</table>

## Q

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Quoting strings</td>
<td>4, 5</td>
</tr>
</tbody>
</table>

## R

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Re-shaping data</td>
<td>8</td>
</tr>
<tr>
<td>Relational databases</td>
<td>11</td>
</tr>
</tbody>
</table>

## S

<table>
<thead>
<tr>
<th>Concept</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>S-PLUS</td>
<td>10</td>
</tr>
<tr>
<td>SAS</td>
<td>10</td>
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