Foundational and Applied Statistics for Biologists using R

Electronic Appendix (Introduction to R)

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INTRODUCTION TO R

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Contents

I believe that **R** currently represents the best medium for quality software in support of data analysis.

John Chambers, a developer of S

R is a real demonstration of the power of collaboration, and I don't think you could construct something like this any other way.

Ross Ihaka, original co-developer of **R**

1 Introduction to R

R is a computer language and an open source setting for statistics, data management, computation, and graphics. The outward mien of the **R-**environment is minimalistic, with only low-level interactive facilities. This is in contrast to conventional statistical software consisting of extensive, high-level, often inflexible tools. The simplicity of **R** allows one to easily evaluate, edit, and build procedures for data analysis.

R is useful to biologists for two major reasons. First, it provides access to a large number of existing statistical, graphical, and organizational procedures, many of which have been designed specifically for biological research. Second, it allows one to "get under the hood", look at the code, and check to see what algorithms are doing. If, after examining an **R-**algorithm we are unsatisfied, we can generally modify its code or create new code to meet our specific needs.

1.1 A very brief history

R was created in the early 1990s by Australian computational statisticians Ross Ihaka and Robert Gentleman to address scoping and memory use deficiencies in the language S (Ihaka and Gentleman 1996). At the insistence of Swiss statistician Martin Maechler, Ihaka and Gentleman made the **R** source code available via the internet in 1995. Because of its relatively easy-to-learn language, **R** was quickly extended with code and packages developed by its users (§ 7). The rapid growth of **R** gave rise to the need for a group to guide its progress. This led, in 1997, to the establishment of the **R-development core team**, an international panel that modifies, troubleshoots, and manages source code.

Because of its freeware status, the overall number of **R-**users is difficult to determine. Nonetheless, experts in the computer industry estimated that between 1 and 2 million individuals were actively using **R** in 2009[1]. This number has undoubtedly increased as the number of **R-**packages has continued to increase exponentially (Fox 2009). Other reports indicate that the internet traffic for **R** topics exceeds discussions for all other types of statistical software[2]. In addition, recent searches using Google scholar® (http://scholar.google.com/) show that the number of citations of **R** and its packages in scientific articles has increased dramatically since 2005 while citations for software giants SAS® and SPPS® have declined[3,4]. **R** is currently the 5th most popular programming language in the world among data scientists (Python, SQL, Java and Amazon ML are 1- 4), is the "least hated" programming language[5], and is ranked 7th in world by the Institute of Electrical and Electronics Engineers

[1]http://bits.blogs.nytimes.com/2009/01/08/r-you-ready-for-r/ accessed 8/23/2021

[2]http://r4stats.com/articles/popularity/ accessed 8/23/2021.

[3]http://www.r-bloggers.com/rs-continued-growth-in-academia/ accessed 8/23/2021

[4]For additional information on the historical and technical development of **R** see Hornick (2009) and Venebles et al. (2008).

[5] http://blog.revolutionanalytics.com/popularity/accessed 8/23/2021

(IEEE) for general programming use.

Recent developments
According to Thieme (2018), a growing component of the current **R** culture include individuals who are ``Less interested in the mechanics of **R** than in what R allowed them to do." This group has been well represented by Hadley Wickham, creator of the *ggplot2* and *dplyr* R packages. The collection of packages championed by Wickham is often called the *tidyverse*.

The future of **R** will be determined by its community who have donated years of their lives to its development, without monetary compensation, to see **R** flourish. Like most coding and software companies, **R** has been male dominated. The has been changing since 2012 with the founding of the first chapter of the **R** Ladies group (https://rladies.org/) by Gabriela de Queiroz. Today there are chapters in 122 cities and 28,000 members worldwide.

1.2 The R language

The **R** language is based on the older languages S, developed at Bell Laboratories (Becker and Chambers 1978, Becker and Chambers 1981, Becker et al. 1988), Scheme, developed initially at MIT (Sussman and Steele 1975, Steele 1978), and Lisp, also developed at MIT (McCarthy et al. 1960). Ihaka and Gentleman (1996) used the name **R** both to acknowledge the influence of S (because R and S are juxtaposed in the alphabet), and to celebrate their personal efforts (because R was the first letter of their first names). S has since been adapted to run the commercial software S-Plus® which as of 2021 morphed to include TIBCO connected intelligence software, with some **R** open source applications. The **R** and S languages remain very similar, and code written for S can generally be run unaltered in **R**. The method of function implementation in R, however, remains more similar to Scheme.

R differs from S in two important ways (Ihaka and Gentelmen 1996). First, the **R**-environment is given a fixed amount of memory at startup. This is in contrast to S-engines which adjust available memory to session needs. Among other things, this difference means more available pre-reserved computer memory, and fewer **virtual pagination**[6] problems in **R** (Ihaka and Gentelmen 1996). It also makes **R** faster than S-Plus for many applications (Hornik 2009). Second, **R** variable locations are **lexically scoped.** In computer science, **variables** are storage areas with identifiers, and **scope** defines the context in which a variable name is recognized. So-called **global variables** are accessible in every scope (for instance, both inside and outside functions). In contrast, **local variables** exist only within the scope of a function. Formal parameters defined in **R** functions, including arguments, are (generally) local variables, whereas variables created outside of functions are global variables. Lexical scoping allows functions in **R** access to variables that were in effect when the function was defined in a session. S, however, does not allow such free variables. The characteristics of **R** functions and details concerning lexical scoping are further addressed in § 21.

1.3 R copyrights and licenses

R is free, and as a result there are no warranties on its environment or packages. As its copyright framework **R** uses the **GNU** (a recursive acronym for GNU is not Unix) General Public License (GPL). This allows users to share and change **R** and its functions. The associated legalese can read by typing `RShowDoc("COPYING")` in the **R**-console. Because its functions can be legally (and easily) recycled and altered we should always give credit to developers, package maintainers, or whoever wrote the **R** functions we are using.

[6] Virtual pagination is a memory management scheme that allows a computer to store and retrieve data from secondary storage for use in main memory.

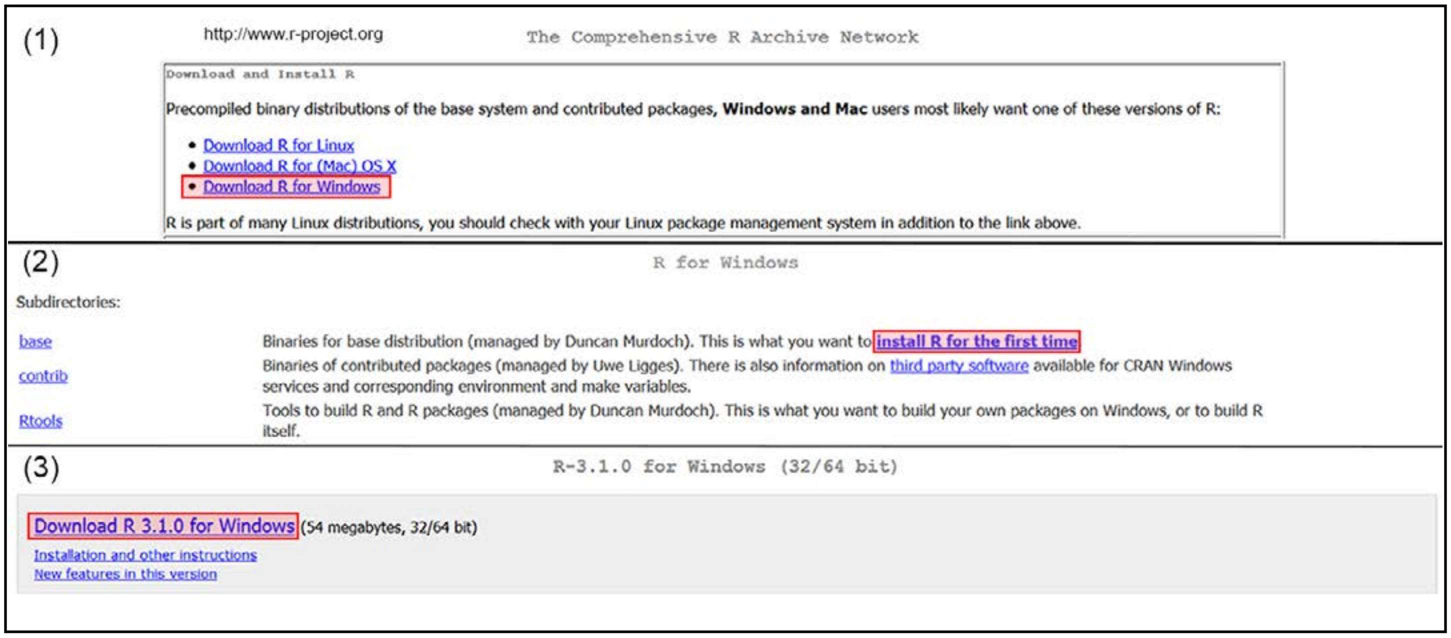
1.4 R and reliability

The lack of an **R** warranty has frightened away some scientists. But be assured, with few exceptions **R** works as well or better than "top of the line" analytical commercial software. Indeed, SAS® and SPSS® have recently made **R** applications accessible from within their products (Fox 2009). For specialized or advanced statistical techniques **R** often outperforms other alternatives because of its diverse array of continually updated applications.

The computing engine and packages that come with a conventional **R** download (see § 1.5) meet or exceed U.S. federal analytical standards for clinical trial research (**R** Foundation for Statistical Computing 2008). In addition, core algorithms used in **R** are based on seminal and trusted functions. For instance, **R** random number generators include some of the most venerated and thoroughly tested functions in computer history (Chambers 2008). Similarly, the **LAPACK** algorithms (Anderson et al. 1999), used by **R** for linear algebra, are among the world's most stable and best-tested software (Chambers 2008).

1.5 Installation

To install **R**, first go to the website http://www.r-project.org/. On this page specify which platform you are using (Figure 1, step 1). **R** can currently be used on Unix-like, Windows and Mac operating systems. This appendix has been created specifically for Windows users of **R**. In almost every case, however, it will also be applicable to other platforms. Once an operating system has been selected one can click on the "base" link to download the precompiled base binaries if **R** currently exists on your computer. If **R** has not been previously installed on your computer click on "Install **R** for the first time" (Figure 1, step 2). You will delivered to a window containing a link to download the most recent version of **R**. Click on the "Download" link (Figure 1, step 3).


(1) http://www.r-project.org The Comprehensive R Archive Network

Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- Download R for Linux
- Download R for (Mac) OS X
- Download R for Windows

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

(2) R for Windows

Subdirectories:

base	Binaries for base distribution (managed by Duncan Murdoch). This is what you want to install R for the first time
contrib	Binaries of contributed packages (managed by Uwe Ligges). There is also information on third party software available for CRAN Windows services and corresponding environment and make variables.
Rtools	Tools to build R and R packages (managed by Duncan Murdoch). This is what you want to build your own packages on Windows, or to build R itself.

(3) R-3.1.0 for Windows (32/64 bit)

Download R 3.1.0 for Windows (54 megabytes, 32/64 bit)
Installation and other instructions
New features in this version

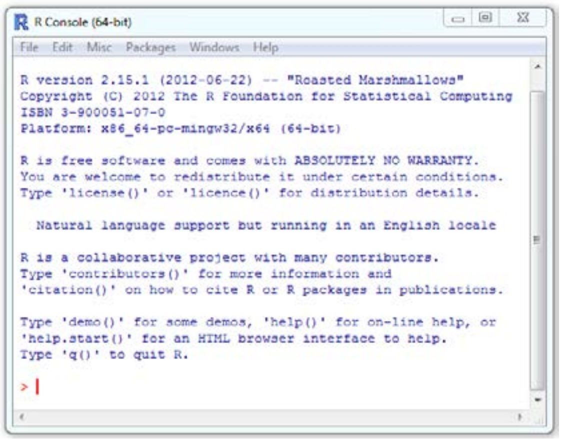
Figure 1 Method for installing **R** for the 1st time.

Two new versions of **R** are generally released each year, one in April and one in October. New packages (§ 7), and newer versions of older packages are released on a continual basis at the discretion of their developers. Archived versions of **R** and its packages are also available from http://www.r-project.org/.

2 Basics

Upon opening **R** two things that will appear in the **console** of the **Graphical User Interface** (**R-**GUI). These are the license disclaimer and the **command line prompt**, i.e., > (Figure 2). The prompt indicates that **R** is ready for a command. All commands must begin at >. **R** user commands are colored red, and output, including errors and warnings are colored blue.

We can exit **R** at any time by typing `q()` in the console, closing the GUI window (non-Unix only), or by selecting "exit" from the pulldown File menu (non-Unix only).



```
R version 2.15.1 (2012-06-22) -- "Roasted Marshmallows"
Copyright (C) 2012 The R Foundation for Statistical Computing
ISBN 3-900051-07-0
Platform: x86_64-pc-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> 
```

Figure 2 The **R** console. **R** version 2.15.1, "Roasted Marshmallows"

2.1 First operations

As an introduction we can use **R** as a calculator. Type `2 + 2` and press Enter.

```
2 + 2
[1] 4
>
```

The `[1]` means, "this is the first requested element". In this case there is just one requested element, 4, the solution to 2 + 2. If the output elements cannot be held on a single console line, then **R** would begin the second line of output with the element number comprising the first element of the new line. For instance, the command `rnorm(20)` will take 20 random samples from a standard normal distribution (see Ch. 3 in the **Foundational and Applied Statistics** text). We have:

```
rnorm(20)
[1]  0.73704627  0.06572694 -0.19401659  1.55767302 -0.66656940 -0.63375586
[7] -0.38926816  0.46596203 -0.35382023  0.72729659  0.42944759 -0.50559415
[13]  0.95743654  0.49844963  0.01833043 -0.29257820 -0.56753070  0.25374833
[19] -0.27808670 -0.83199069
>
```

The reappearance of the command line prompt indicates that **R** is ready for another command.

Multiple commands can be entered on a single line, separated by semicolons. Note, however, that this is considered poor programming style, as it may make your code more difficult to understand by a third party.

```
2 + 2; 3 + 2
[1] 4
[1] 5
>
```

R commands are generally insensitive to spaces. This allows the use of spaces to make code more legible. The command `2 + 2` is simply easier to read and debug than `2+2`.

2.2 Use your scroll keys

As with many other command line environments, the scroll keys (Figure 3) provide an important shortcut in **R**. Instead of editing a line of code by tediously mouse-searching for an earlier command to copy, paste and then modify it, you can simply scroll back through your earlier work using the upper scroll key, i.e., ↑. Accordingly, scrolling down using ↓ will allow you to move forward through earlier commands.

Figure 3 Direction keys on a keyboard.

2.3 Note to self:

R will not recognize commands preceded by `#`. As a result this is a good way for us to leave messages to ourselves.

```
# Note at beginning of line
2 + 2
[1] 4
2 +  # Note in middle of line
+ 2
[1] 4
```

In the "best" code writing style it is recommended that one place a space after `#` before beginning a comment, and to insert two spaces following code before placing `#` in the middle of a line. This convention is followed above.

2.4 Unfinished commands

R will be unable to move on to a new task when a command line is unfinished. For example, type

```
2 +
```

and press Enter. We note that a **continuation prompt**, by default `+` , is now in the place the command prompt should be. **R** is telling us the command is unfinished. We can get back to the command prompt by finishing the function, clicking **Misc>Stop current computation** or **Misc>Stop all computations** (non-Unix only), typing Ctrl-C (Unix only), or by hitting the Esc key (Windows only). Other related shortcuts include Ctrl + c, which kills a process, and Ctrl + z, which suspends a process.

2.5 Basic options

To enhance our experience, we can adjust the appearance of the **R-**console and customize **options** that affect function output. These include the characteristics of the graphics devices, the width of print output in the **R-**console, and the number of print lines and print digits. Changes to some of these parameters can be made by going to **Edit>GUI Preferences** in the **R** toolbar. Many other parameters can be changed using the `options` function. To see all alterable options one can type:

```
options()
```

To change default `options` one would simply define the desired change within parenthesis following the `options` function name. For instance, to see the default number of digits in **R** output I would type:

```
options("digits")
$digits
[1] 7
```

To change the default number of digits in output from 7 to 5, in the current session I would type:

```
options(digits = 5)
```

To establish user defaults for all future sessions one will need to change the **R-**console file located (currently) in the **etc** directory of the version of **R** you are using. This can either be done manually, or by using **Edit>GUI Preferences>Save** in the **R** toolbar

By default the **R working directory** is set to be the home directory of the workstation. The command `getwd()` shows the current file path for the working directory.

```
getwd()
[1] "C:/Users/User/Documents"
```

The working directory can be changed with the command `setwd(filepath)`, where `filepath` is the location of the directory, or by using pulldown menus, i.e., **File>Change dir** (non-Unix only).

An `.Rprofile` file exists in your Windows **R**/**R**-version/etc directory. **R** will silently run commands in the file upon opening. By customizing the `.Rprofile` file one can set options, install frequently loaded non-default packages (§ 7), define your favorite package repository, and create aliases and defaults for frequently used functions.

Here is the content of my current `.Rprofile` file.

```
options(repos = structure(c("http://ftp.osuosl.org/pub/cran/")))

.First <- function(){
 library(asbio)
 cat("\nWelcome to R Ken! ", date(), "\n")
}

.Last <- function(){
 cat("\nGoodbye Ken", date(), "\n")
}
```

The `options(repos = structure(c("http://ftp.osuosl.org/pub/cran/")))` command defines my favorite **R**-repository. The function `.First( )` will be run at the start of the **R** session and `.Last( )` will be run at the end of the session. As we go through this primer it will become clear that these functions force **R** to say hello and to load my package *asbio* when it opens, and to say goodbye when it closes (although the farewell will only be seen when running **R** from a command line interface).

The `.Rprofile` file in the /etc directory is the so-called `.Rprofile.site` file. Additional `.Rprofile` files can be placed in the working and user directories. **R** will check for these and run them after running the `.Rprofile.site` file.

One can create `.Rprofile` files, or any type of **R** extension file using the function `file.create`. For instance, the code:

```
file.create("defaults.Rprofile")
```

places an empty, editable, `.Rprofile` file called `defaults` in the working directory.

2.6 Saving and loading your work

As noted earlier, an **R** session is allocated with a fixed amount of memory that is managed in an on-the-fly manner. An unfortunate consequence of this is that if **R** crashes all unsaved information from the work session will be lost. Thus, session work should be saved often. Note that **R** will not give a warning if you are writing over another file from the **R** console with the same name! The old file will simply be replaced.

Saving the R History

To view the **history** (i.e., the **commands** that have been used in a session) one can use `history(n)` where `n` is

```
history(3)
```

To save the session history in Windows one can use **File>Save History** (non-Unix only) or the function `savehistory`. For instance, to save the session history to the working directory under the name `history1` I could type:

```
savehistory(file = "history1.Rhistroy")
```

We can view the code in this file from any text editor[7].

To load the history from a previous session one can use **File>Load History** (non-Unix only) or the function `loadhistroy`. For instance, to load `history1` I would type:

```
loadhistory(file = "history1.Rhistroy")
```

To save the history at the end of (almost) every interactive Windows or Unix-alke R session, one can alter the `.Rprofile` file `.Last` function to include:

```
.Last <- function() if(interactive()) try(savehistory("~/.Rhistory"))
```

Saving R Objects
To save all of the **objects** (see § 4) available in the current **R**-session one can use **File>Save Workspace** (non-Unix only), or simply type:

```
save.image()
```

This procedure saves session objects (see § 4) to the working directory as a nameless file with an `.RData` extension. The file will be opened, silently, with the inception of the next **R**-session, and cause objects used or created in the previous session to be available. Indeed, **R** will automatically execute all `.RData` files in the working directory for use in a session. `.RData` files can also be loaded using **File>Load Workspace** (non-Unix only). One can also save the `.RData` objects to a specific directory location and use a specific file name using **File>Save Workspace,** or with the `file` argument in `save.image`, or with the flexible function `save` (see § 2.6).

R data file formats, including `.rda`, and `.RData`, (extensions for **R** data files), and `.R` (the format for **R** scripts), can be read into **R** using the function `load`. Users new to a command line environment will be reassured by typing:

[7] Importantly, the functions `savehistory()`, `loadhistory()` and `history()` are not currently supported for Mac OS X. There are ways around this. For instance, in RStudio (§ 21) the Mac OS X command history can be obtained by clicking the History icon history that appears on the tool bar at the top of the console window. As an additional issue, Windows and Unix-alike.plaforms have different implementations for `savehistory()` and `loadhistory()`. Get the help pages for these particular functions within your platform for particulars.

```
load(file.choose())
```

This will allow one to browse interactively for files using dialog boxes.

Detailed procedures for importing and exporting (saving) data with a row and column format, and an explicit delimiter (e.g. .csv files) are described in § 12 and 13, respectively.

Saving R Scripts
To save **R** code as executable source file, one can save the code in the **R**-script editor (go to **File>New script**, or simply type `fix()`) or within some other **R**-compatible text editor (e.g., ESS, TinnR, etc.) as an .R extension file. **R** scripts can be called and executed using the function `source`. For instance to go looking interactively for source code to execute I could type:

```
source(file.choose())
```

or go to **File>Source R code**.

3 Getting help in R

There is no single perfect source for information/documentation for all aspects of **R**. Detailed information concerning base operations and package development are described at the **R** website http://www.r-project.org/, but is generally intended for those familiar with both Unix/Linux systems, and command based formats. They may not be especially helpful to new **R** users used to point-and-click formats, and no programming history.

3.1 `help`

A comprehensive help system is built into **R**. The system can be accessed question mark (`?`) and `help` functions. For instance, if I wanted to know more about the `plot` function I could type:

```
?plot
```

or

```
help(plot)
```

Documentation for functions will include a list of arguments for functions, and a description of variables for datasets, and other pertinent information. Quality of documentation will generally be excellent for functions from packages in the default **R** download (see § 7), but will vary from package to package otherwise.

A list of arguments for a function, and their default values, can (often) be obtained using the function `formals`.

```

formals(plot)
$x

$y

$...
```

For help and information regarding programming metacharacters used in **R** (for instance `$`, `?`, `[[`, `&`, or `^`), one would enclose the metacharacters with quotes. For example, to find out more information about the logical operator `&` I could type `help("&")` or `?"&"`.

Placing two question marks in front of a word or function will cause **R** to search for help files concerning with respect to all packages in a workstation. For instance type:

```
??lm
```

or, alternatively

```
help.search(lm)
```

for a huge number of help files on linear model functions identified through **fuzzy matching**. Help for particular **R**-questions can often be found online using the search engine at http://search.r-project.org/. This link is provided in the **Help** pulldown menu in the **R** console (non-Unix only).

The function `demo` allows one access to examples developers have worked out (complete with **R** code) for a particular function or topic. For instance, type:

```
demo(graphics)
```

for a brief demonstration of **R** graphics or `demo(persp)` for a demonstration of 3D perspective plots. Typing:

```
demo(Hershey)
```

will provide a demonstration of available of modifiable symbols from the Hershey family of fonts (see Hershey 1967; 9.6). Typing:

```
demo()
```

lists all of the demos available in the loaded libraries for a particular workstation. The function `example` usually provides less involved demonstrations from the **man** directories (short for user manual) in packages, along with code requirements. For instance, type:

```
example(plotmath)
```

for a demonstration of mathematical graphics complete with code.

R packages often contain **vignettes**. These are short documents that generally describe the theory underlying algorithms and guidance on how to correctly use package functions. Vignettes can be accessed with the function `vignette`. To view all available vignettes for packages attached for a current work session type:

```
vignette(all = FALSE)
```

To view all vignettes for all installed packages type:

```
vignette(all = TRUE)
```

To view all vignettes for the installed package *asbio*:

```
vignette(package = "asbio")
```

To see the vignette `simpson` in package *asbio* I would load *asbio*, then type:

```
vignette(simpson)
```

The function `browseVignettes()` provides an HTML-browser that allows interactive vignette searches.

3.2 Manuals and additional information

Because the **Foundational and Applied Statistics for Biologists using R** textbook is primarily about statistics and not **R**, this appendix is not intended to be an exhaustive operators manual. General guidance for **R**-programming can be found in Chambers (2008), or more recently Matloff (2011). In addition to **Foundational and Applied Statistics**, good resources for **R** in an applied statistical context include Venables and Ripley (2002), Crawley (2007), Adler (2010) and Fox (2011). The **R** website http://www.r-project.org/ provides access to the **R journal**, and a large number of helpful (and free) vignettes and manuals. **R** also has an a large and engaged electronic community that actively considers user programming questions, see: www.stackoverflow.com/questions/tagged/r, or http://statsexchange.com/questions/tagged/r, or even www.twitter.com/search/rstats.

4 Expressions and assignments

All entries in **R** are either expressions or assignments. If a command is an **expression** it will be evaluated, printed and discarded. Examples include: `2 + 2`. Conversely, an **assignment** evaluates an expression, and assigns the output to an **R**-object (§ 5), but does not automatically print the results.

To convert an expression to an assignment we use the **assignment operator**, `<-`, which represents an arrow. The assignment operator can go on either side of an object. For instance, if I type:

```
x <- 2 + 2
```

or

```
2 + 2 <- x
```

then the sum 2 + 2 will be assigned to the object `x`. To **print** the result (to see `x`) I simply type:

```
x
[1] 4
```

or

```
print(x)
[1] 4
```

Note that we could have also typed `x = 2 + 2` with the same assignment results. However in this document we will continue to use the arrow operator for assignments, and save = for specifying arguments in functions.

4.1 Naming objects

When assigning names to **R-**objects we should try to keep the names simple, and avoid names that already represent important definitions and functions. These include: `TRUE`, `FALSE`, `NULL`, `NA`, `NaN`, and `Inf`. In addition, we cannot have names:

- beginning with a numeric value
- containing spaces, colons, and semicolons
- containing mathematical operators (e.g., `*`, `+`, `-`, `^`, `/`, `=`)
- containing important **R** metacharacters (e.g., `@`, `#`, `?`, `!`, `%`, `&`, `|`).

Names should also be self explanatory. Thus, for a object containing 20 random observations from a normal distribution, the name `rN20` is far superior to the, albeit easily-typed, name `a`. Finally, with assignment commands we should also remember that, like most software developed under Unix/Linux, **R** is **case sensitive**. That is, each of the following 2^4 combinations will be recognized as distinct:

`name`, `Name`, `nAme`, `naMe`, `namE`, `NAme`, `nAMe`, `naME`, `NaMe`, `nAmE`, `NamE`, `naME`, `NAMe`, `nAME`, `NaME`, `NAmE`, `NAME`.

4.2 Combining objects with `c`

To define a collection of numbers (or other data, or objects) as a single entity, one can use the important **R** function `c`, which means "combine." For instance, to define the numbers 23, 34, and 10 as the object `x`, I would type:

```
x <- c(23, 34, 10)
```

We could then do something like:

```
x + 7
[1] 30 41 17
```

5 R objects and R classes

Before proceeding further it is important to make two observations.

- First, everything created or loaded in **R** is an **object.** This means, in the sense of **object oriented programming (OOP)**, that they possess certain traits that describe them[8].
- Second, every **R**-object belongs to at least one **class**. This requirement means that **R**-objects can be classified in a way that allows them to be recognized and used correctly by both users and other objects. Object classes allow for custom utility functions, e.g., `plot`, `print`, `summary`, to be created for particular classes. These can be called by simply using generic function names e.g., `plot`, `print`, `summary` (Section 21.11). Among other things, this means fewer function names to memorize.

For the object `x` below:

```
x <- 2 + 2
```

we have the following class:

```
class(x)
[1] "numeric"
```

Thus, the object `x` belongs to class `numeric`. Objects in class `numeric` can be evaluated mathematically.

Objects can also be distinguished by their storage mode or **type** (the way **R** caches them in its primary memory). For `x` we have:

```
typeof(x)
[1] "double"
```

This means that `x` is stored with **64 bit floating point double precision**: a computer number format usually occupying 64 bits in computer memory. This topic is readdressed in § 20. Object type names and class names are often identical.

Many **R**-objects will also have **attributes** (characteristics particular to the object or object class). Typing:

```
attributes(x)
NULL
```

indicates that `x` does not have additional attributes. However, using coercion (§ 18) we can define `x` as an object of class **matrix** (a collection of data in a row and column format):

```
x <- as.matrix(x)
```

[8] OOP languages include R, C#, C++, Objective-C, Smalltalk, Java, Perl, Python and PHP. C is not considered an OOP language.

Now x has the attribute dim (i.e., dimension).

```
attributes(x)
$dim
[1] 1 1
```

Now x is a one-celled matrix. It has one row and one column.

Amazingly, classes and attributes allow **R** to simultaneously store and distinguish objects with the same name[9]. For instance:

```
mean <- mean(c(1, 2, 3))
mean
[1] 2
mean(c(1, 2, 3))
[1] 2
```

In general it is not advisable to name objects after frequently used functions. Nonetheless, the function mean is distinguishable from the new user-created object mean because these objects have different identifiable characteristics.

The function str attempts display the internal **structure** of an **R** object. It is extremely useful for succinctly displaying the contents of lists (§ 10).

```
str(x)
num [1, 1] 4
```

Thus, x is a 1 × 1 matrix structure containing the number 4.

5.1 Listing objects

By typing:

```
ls()
```

or

```
objects()
```

one can see a list of the available **R**-objects in a particular **R** session. Currently, we have:

[9]Note, however, naming conflicts with global variables often causes issues with package development. The code: `mean <- NA; rm(mean)` will remove the offending user-created object mean above, leaving behind the global variable

```
ls()
[1] "mean" "x"
```

6 Mathematical operations

6.1 Mathematical operators and functions

Usual (and unusual) mathematical operators and functions are easily specified in **R**. In applications below, `x` represents either a user-specified scalar (single number) or a vector (collection of numbers).

`+`	addition
`-`	subtraction
`*`	multiplication
`/`	division
`^`	exponentiation
`%%`	modulo (find the remainder in division)
`Inf`	∞
`-Inf`	$-\infty$
`pi`	$\pi = 3.141593\ldots$
`exp(1)`	$e = 2.718282\ldots$
`exp(x)`	e^x
`sqrt(x)`	$\sqrt{x}$
`log(x)`	$\log_e(x)$
`log(x, 10)`	$\log_{10}(x)$
`factorial(x)`	$x!$
`choose(n, x)`	$\binom{n}{x}$
`gamma(x)`	$\Gamma(x)$
`cos(x)`	cosine (x)
`sin(x)`	sin(x)
`tan(x)`	tangent(x)
`acos(x)`	arccosin(x)
`asin(x)`	arcsin(x)
`atan(x)`	arctan(x)
`abs(x)`	absolute value of x
`round(x, digits)`	rounds x to the digits given in `digits`
`ceiling(x)`	rounds x up to closest whole number
`floor(x)`	rounds x down to closest whole number
`D(expression(y), x)`	$\frac{dy}{dx}$ or $\frac{\delta y}{\delta x}$
`integrate(function(x), a, b)`	$\int_b^a f(x)dx$

`min(x)`	minimum value in x
`max(x)`	maximum value in x
`sum(x)`	$\sum_{i=1}^{n} x_i$
`prod(x)`	$\prod_{i=1}^{n} x_i$
`cumsum(x)`	cumulative sum of elements in x
`cumprod(x)`	cumulative product of elements in x

As with functions from all programming languages **R** functions generally require a user to specify **arguments** (in parentheses) following the function name.

For instance, `sqrt` and `factorial` each require one argument, a call to data. Thus, to solve $1/\sqrt{22!}$, I type:

```
1/sqrt(factorial(22))
[1] 2.982749e-11
```

and to solve $\Gamma\left(\sqrt[3]{23\pi}\right)$, I type:

```
gamma((23 * pi)^(1/3))
[1] 7.410959
```

The `log` function can also compute logarithms to a particular base by specifying the base in an optional second argument called `base`. For instance, to solve the operation: $\log_{10}(3)+\log_{3}(5)$, one would simply type:

```
log(3, 10) + log(5, 3)
[1] 1.942095
```

By default the function `log` computes natural logarithms, i.e.,

```
log(exp(1))
[1] 1
```

That is, by default `base` = Euler's constant = e = 2.718282... .

Arguments can be specified by the order that they occur in the list of arguments in the function code, or by calling the argument by name. In the code above I know that the first argument in `log` is a call to data, and the second argument is the base. I may not, however, remember the argument order in a function, or may wish to only change certain arguments from a large allotment. In this case it is better to specify the argument by calling its name and defining its value with an equals sign.

```
log(x = 3, base = 10) + log(x = 5, base = 3)
[1] 1.942095
```

Trigonometry

R assumes that the inputs for the trigonometric functions are in radians. Of course degrees can be obtained from radians using $Deg = Rad \times 180/\pi$, or conversely $Rad = Deg \times \pi/180$. Thus, to find cos(45º) I type:

```
cos(45 * pi/180)
[1] 0.7071068
```

This is correct because cos(45º) = $\sqrt{2}/2 = 0.7071068$.

```
sqrt(2)/2
[1] 0.7071068
```

Derivatives

The function `D` finds symbolic and numerical derivatives of simple expressions. It requires two arguments, a mathematical function specified as an `expression` [i.e., a list (§ 10) that can be evaluated with the function `eval`], and the denominator in the difference quotient. Here is an example of how `expression` and `eval` are used:

```
eval(expression(2 + 2))
[1] 4
```

Of course we wouldn't bother to use `expression` and `eval` in this simple application.

|| Example 1

To demonstrate `expression` and `D` (the latter calls `eval`) we will evaluate the following derivatives:

$$\frac{d}{dx}0.5x^4,$$
$$\frac{d}{dx}\log(x), \text{ and}$$
$$\frac{d}{dx}\cos(2x).$$

```
D(expression(0.5 * x^4), "x")
0.5 * (4 * x^3)
```

```
D(expression(log(x)),"x")
1/x
```

```
D(expression(cos(2 * x)),"x")
-(sin(2 * x) * 2)
```

Symbolic solutions to partial derivatives are also possible. For instance, consider

$$\frac{\delta}{\delta x} 3x^2 + 4xy.$$

We have:

```
D(expression(3 * x^2 + (4 * x * y)), "x")
3 * (2 * x) + 4 * y
```

Integration

Integration requires specifying an integrand in the form of a **function**. Recursively speaking, a function is defined by a function named `function`. Arguments will be contained in a set of parentheses following the call to `function`. The function contents follow, generally delineated by curly brackets. Thus, we have the following form for a function called "example" with *n* arguments:

```
example <- function(argument_1, argument_2,...., argument_n){function contents}
```

Recall that `<-` is the assignment operator (see § 4). Functions are explained in detail in § 21.

The **R** function for integration, `integrate`, requires, as its 1st argument, a user-defined function describing the integrand. The 2nd and 3rd arguments for `integrate` will be the lower and upper bounds for definite integration. The integrand function, in turn, must have as its 1st argument the name of the variable to be integrated.

|| Example 2

To solve for:

$$\int_2^3 3x^2 dx$$

we can use the following code:

```
f <- function(x){3 * x^2}

integrate(f, 2, 3)
19 with absolute error < 2.1e-13
```

A large number of advanced mathematical operations can be handled by **R** including multivariate integration (package *cubature*, Exercise 3), solving systems of differential equations (package *deSolve*, `||` Example 22, Exercise 16), linear algebra (Exercise 4), and solving systems of linear equations (function `solve`). Linear algebra and associated **R** functions are discussed in the Appendix for mathematics review in the **Foundational and Applied Statistics for Biologists** textbook.

Some mathematical operators will ordinarily be used with a collection of data, i.e., a vector, not a single datum. These include `min`, `max`, `sum` and `prod`, along with most statistical operators.

```
x <- c(23, 34, 10)
```

```
prod(x)
[1] 7820
```

A summary of additional mathematical applications and packages are listed at https://cran.rstudio.com/web/views/NumericalMathematics.html.

6.2 Statistical operators

R, of course, contains a huge number of functions for statistical point and interval estimates. Below is an extremely abbreviated list of statistical functions and their meaning. Some of the listed functions require the package *asbio*. The object `x` in the list below represents a user-specified numeric vector (collection of numbers).

`mean(x)`	Arithmetic mean of x
`mean(x, trim = 0.2)`	Arithmetic mean of x with 20% trimming
`G.mean(x)`	Geometric mean of x
`H.mean(x)`	Harmonic mean of x
`median(x)`	Median of x
`HL.mean(x)`	Pseudomedian of x
`huber.mu(x)`	Huber M-estimator of location for x
`Mode(x)`	Mode(s) of x
`var(x)`	Variance of x
`sd(x)`	Standard deviation of x
`IQR(x)`	Interquartile range of x
`mad(x)`	Median absolute deviation of x

`quantile(x)`	Quantiles of x at the 0th, 25th, 50th, 75th and 100th percentiles
`quantile(x, probs = 0.75)`	Quantile of x at the 75th percentile
`skew(x)`	Skewness of x
`kurt(x)`	Kurtosis of x
`range(x)`	Range of x
`length(x)`	Number of observations in x
`length(x[is.na(x)])`	Number of missing observations in x
`ci.mu.z(x, conf = 0.95)`	95% confidence interval for μ, σ^2 known
`ci.mu.t(x, conf = 0.95)`	95% confidence interval for μ, σ^2 unknown
`ci.median(x, conf = 0.95)`	95% confidence interval for the true median
`ci.sigma(x, conf = 0.95)`	95% confidence interval for σ^2
`ci.p(x, conf = 0.95)`	95% confidence interval for the binomial parameter π
`cov(x, y)`	Covariance of x and y
`cor(x, y)`	Pearson correlation of x and y

For instance, consider the dataset `x` below:

```
x <- c(1, 2, 3, 2, 1)
```

The mean is

```
mean(x)
[1] 1.8
```

and the median is:

```
median(x)
[1] 2
```

The formulae and underlying theory for point estimators such the mean, variance, and median are dealt with in Chapter 4 in the **Foundational and Applied Statistics** text. Interval estimators are addressed in Ch. 5.

7 R packages

An **R** package contains a set of related functions, documentation, and data files that have been bundled together. As of 6/2016 packages provided in the basic **R** distribution are those shown in Table 1. **R** distribution packages are directly controlled by the **R** core team and are extremely well-vetted and trustworthy.

Table 1 R "distributed" core packages.

Package	Maintainer	Topic(s) addressed by package:	Current Citation/Author
base	**R** Core Team	Base **R** functions	**R** Core Team (2017)
compiler	**R** Core Team	**R** byte code compiler	**R** Core Team (2017)
datasets	**R** Core Team	Base **R** datasets	**R** Core Team (2017)
grDevices	**R** Core Team	Graphics devices for base and grid graphics	**R** Core Team (2017)
graphics	**R** Core Team	**R** functions for base graphics	**R** Core Team (2017)
grid	**R** Core Team	Grid graphics layout capabilities	**R** Core Team (2017)
methods	**R** Core Team	Formally defined methods and classes for **R** objects	**R** Core Team (2017)
parallel	**R** Core Team	Support for parallel computation	**R** Core Team (2017)
splines	**R** Core Team	Regression spline functions and classes	**R** Core Team (2017)
stats	**R** Core Team	**R** statistical functions	**R** Core Team (2017)
stats4	**R** Core Team	Statistical functions with S4 classes	**R** Core Team (2017)
tcltk	**R** Core Team	Interface and language bindings to Tcl/Tk GUI elements	**R** Core Team (2017)
tools	**R** Core Team	Tools for package development and administration	**R** Core Team (2017)
utils	**R** Core Team	**R** utility functions	**R** Core Team (2017)

Packages in Table 2 constitute *recommended* packages. These are not necessarily controlled by the **R** core team, but are also extremely useful, well-tested, and stable. Like **R** distribution packages (Table 1), recommended **R** packages are included in conventional downloads of **R**.

Aside from distributed and recommended packages, there are a large number of user-defined contributed packages that are useful to biologists and biometrists (> 10000 as of 9/5/2017). Table 3 lists a few. Contributed **R** packages can be downloaded from **CRAN** (the Comprehensive **R** Archive Network). To do this, one can go to **Packages>Install package(s)** on the **R-GUI** toolbar, and choose a nearby CRAN mirror site to minimize download time (non-Unix only). Once a mirror site is selected, the packages available at the site will appear. One can simply click on the desired packages to install them. Packages can also be downloaded directly from the command line. To install the package *vegan* (Table 3), I would simply type:

```
install.packages("vegan")
```

Of course, both of these approaches require that your computer has web access. If local web access is not available, libraries can be saved from the CRAN website or some other source as compressed (.zip, .tar) files which can then be placed manually on a workstation by inserting the package files into the "library" folder within the top level **R** directory, or into a path-defined **R** library folder in a user directory. This package can then be loaded for a particular session.

Once a package is installed it never needs to be re-installed. However, for use in an R session one will need load the package using the `load` function. For instance, to load the vegan package I would type.

```
load(vegan)
```

Or one could go to **Packages>Load package(s)** on the **R-GUI** toolbar (non-Unix only) Notwithstanding user modification, none of packages in Table 1 require loading, as they will be loaded automatically upon opening **R**. Typing `search()` lets one see all the attached (loaded) packages (and other attached objects) currently available in a work session.

Table 2 "Recommended" **R** packages.

Package	**Maintainer**	**Topic(s) addressed by package:**	**Current Citation/Author**
KernSmooth	B. Ripley	Functions for kernel smoothing (and density estimation)	Wand (2015)
MASS	B. Ripley	Wide variety of important statistical methods.	Venables and Ripley (2002)
Matrix	M. Maechler	Classes and methods and operations for matrices using 'LAPACK' and 'SuiteSparse'	Bates and Maechler (2016)
boot	B. Ripley	Bootstrapping and analytical extensions	Canty and Ripley (2016), Davison and Hinkley (1997)
class	B. Ripley	Functions for classification	Venables and Ripley (2002)
cluster	M. Maechler	Functions for cluster analysis	Maechler et al. (2016)
codetools	S. Wood	Code analysis tools	Tierney (2016)
foreign	**R** core team	Functions for reading and writing data stored by non-**R** statistical software, e.g. SAS	**R** Core Team (2016)
lattice	D. Sarkar	Lattice graphics, an implementation of Trellis graphics functions	Sarkar (2008)
mgcv	S. Wood	Generalized Additive Models (GAMS)	Wood (2011)
nlme	**R** core team	Linear and non-linear mixed effect models	Pinheiro et al. (2016)
nnet	B. Ripley	Software for “feed-forward neural networks”	Venables and Ripley (2002)
rpart	B. Ripley	Recursive PARTitioning and regression trees	Venables and Ripley (2002)
spatial	B. Ripley	Functions for kriging and point pattern analysis	Venables and Ripley (2002)
survival	T. M. Therneau	Functions for survival analysis, including penalized likelihood	Therneau (2015)

As noted in § 3, once a package is installed information its functions can be accessed using `help`. For example, information about the *vegan* package can be accessed by typing `help(package= "vegan").`

Given web access, newer (updated) versions of packages can be obtained using the command:

```
update.packages()
```

Note, however, that this will only give you the latest possible package applicable to the version of **R** that you are running. Acquiring the “very latest” version of a package may require downloading the latest version of **R**

To remove *vegan* (and its functions) from a particular session I would type:

```
detach(package:vegan)
```

Aside from CRAN, there are currently two large repositories of **R** packages. First, the **bioconductor** project (http://www.bioconductor.org/packages/release/Software/html) contains a large number of packages for genomic analysis (1,383 as of Sept 2017) that are not found at CRAN. Packages can be downloaded from bioconductor using an **R** script called `biocLite`. To download the package *rRytoscape* from biocondctor I would type:

```
source("http://bioconductor.org/biocLite.R")
biocLite("RCytoscape")
```

Second, **R-forge** (http://r-forge.r-project.org/) contains alpha releases of packages that have not yet been implemented into CRAN, and other miscellaneous code. Either of these sources can be specified from **Packages>Select Repositories** in the **R**-GUI (non-Unix only)[10].

Table 3 Additional, contributed **R** packages that may be useful to biologists and biometricians.

Package	**Maintainer**	**Topic(s) addressed by package:**	**Current Citation/Author**
akima	A. Gebhardt	Interpolation of irregularly spaced data	Akima (2012)
asbio	K. Aho	Statistical pedagogy and applied statistics for biologists	Aho (2017)
car	J. Fox	A companion package to the book “An **R** and S Companion to Applied Regression”	Fox (2011)
coin	T. Hothorn	Advanced applications of non-parametric analysis	Hothorn et al. (2006, 2008)
ggplot2	H. Wickham	Data visualizations using the "grammar of graphics"	Wickham et al. (2009)
lmodel2	Jari Oksanen	Model II regression	Legendre (2013)
lme4	B. Bolker	Linear mixed-effects models using eigen and S4	Bates et al. (2015)
plotrix	J. Lemon et al.	Helpful graphical ideas	Lemon (2006)
spdep	R. Bivand	Spatial analysis	Bivand et al. (2013), Bivand and Piras (2015)
vegan	J. Oksanen	Multivariate analysis and ecological analysis	Oksanen et al. (2016)

7.1 Datasets in packages

At this point it would be helpful to have a dataset to play with. The command: `data(package = "base")` lets us see all of the datasets available in the **R** `base` package while the command: `data()` lets us see all the datasets available within all the packages loaded onto a particular computer workstation. We will learn how to enter our own data into **R** shortly.

[10] I do not encourage downloading all of the **R** packages that have been developed for analysis of biological data, much less trying out all of their functions. It is remarkable, however, to consider the range of topics these packages encompass. There are **R** packages for bioinformatics including packages devoted only to phylogenetics (e.g. packages *ouch, picante, apTreeshape*) or compiling amino acid sequences (package: *seqinr*). There are libraries that allow interpolation with geographic information system software (e.g. *GRASS*), packages specifically created for animal tracking data (*adehabitat*), functions for finding spatial patterns in cells (applications in package *spatstat*), and even algorithms for quantifying the existence of indicator species using count data from benthic environments (package *bio.infer*), or discerning the effect of fishing methods (package *fishingmethods*).

|| Example 3 -- A brief R session

The dataset `Loblolly` in the `base` package describes the height and age of loblolly pine trees (*Pinus taeda*), a commercially important species in the southeastern United States. To make the dataset available, we type:

```
data(Loblolly)
```

We can then type: `Loblolly` to look at the entire dataset.

```
Loblolly
   height age  Seed
1    4.51   3  301
15  10.89   5  301
29  28.72  10  301
43  41.74  15  301
57  52.70  20  301
71  60.92  25  301
...............................................
70  49.12  20  331
84  59.49  25  331
```

We can type `head(Loblolly)` To view just the first few lines of data:

```
head(Loblolly)
   height age  Seed
1    4.51   3  301
15  10.89   5  301
29  28.72  10  301
43  41.74  15  301
57  52.70  20  301
71  60.92  25  301
```

Because the name `Loblolly` is rather difficult to type, we can use the assignment operator to call the dataset something else. To assign `Loblolly` the name `lp` I simply type:

```
lp <- Loblolly
```

Note that `Loblolly` still exists, `lp` is just a copy.

Typing:

```
summary(lp)
```

provides a simple statistical summary of `lp`, i.e. the minimum response, 1st quartile, median (or 2nd quartile), mean, 3rd quartile and maximum response. These statistics (excluding the mean) are known as the 5 number summary.

```
summary(lp)
     height            age             Seed
 Min.   : 3.46   Min.   : 3.0   329    : 6
 1st Qu.:10.47   1st Qu.: 5.0   327    : 6
 Median :34.00   Median :12.5   325    : 6
 Mean   :32.36   Mean   :13.0   307    : 6
 3rd Qu.:51.36   3rd Qu.:20.0   331    : 6
 Max.   :64.10   Max.   :25.0   311    : 6
                                (Other):48
```

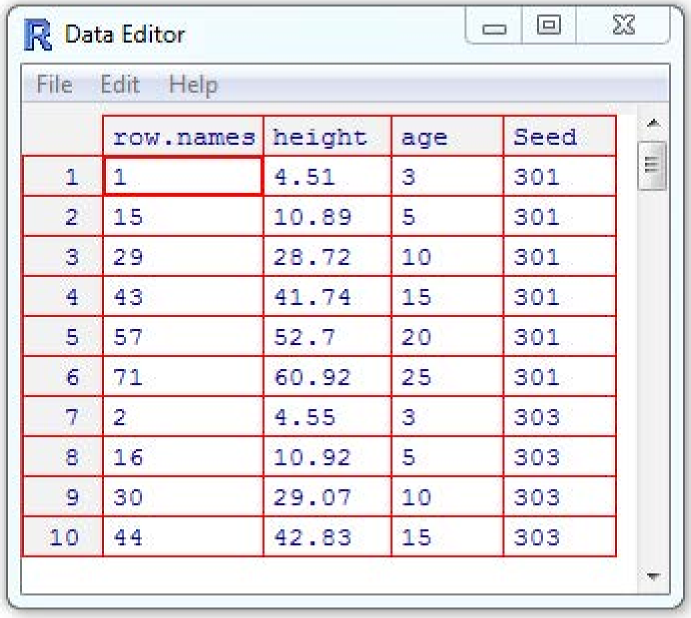
Notice that the third column "Seed" has a different sort of summary. **R** recognizes this column (correctly) as containing categorical data; i.e., six seed type categories and an "other" category (that includes still other seed types). The sixes are counts of experimental units within a particular seed type.

8 R and spreadsheets

A data editor is provided by typing `fix(x)` or `View(x)`, when `x` is a dataframe or matrix (see § 10 for information on these object classes). For instance, the command `fix(lp)` will open the Loblolly pine dataset in the **R** data editor (Figure 4). When `x` is a function or character string, then `fix(x)` opens a script editor containing `x`.

The data editor has limited flexibility compared to software whose interface is a worksheet, and whose primary purpose is data entry and manipulation, e.g., Microsoft Excel®. However, it is possible to access **R** from Excel® (and vice versa) through use of the **RExcel** package (see Heiberger and Nuewirth 2009).

Changes made to an object using `fix` will only be maintained for the current work session. They will not permanently alter objects brought in remotely to a session.



	row.names	height	age	Seed
1	1	4.51	3	301
2	15	10.89	5	301
3	29	28.72	10	301
4	43	41.74	15	301
5	57	52.7	20	301
6	71	60.92	25	301
7	2	4.55	3	303
8	16	10.92	5	303
9	30	29.07	10	303
10	44	42.83	15	303

Figure 4 The first ten observations from the Lobolly dataset in an editable spreadsheet.

8.1 `attach` and `detach`

The function `attach` will let **R** recognize the column names of a dataframe (more on what a dataframe is later). For instance, typing:

```
attach(lp)
```

will let **R** recognize the individual columns in `lp` (a dataframe) by name. The function `detach` is the programming inverse of `attach`. For instance, typing:

```
detach(Loblolly)
```

does not remove `Loblolly`, but will prevent **R** from recognizing the variables in `Loblolly` by name.

8.2 `with`

A safer alternative to `attach` is the function `with`. Using `with` eliminates concerns about multiple variables with the same name becoming mixed up in functions. This is because the variable names for a dataframe specified in `with` will not be permanently attached in an **R**-session. For instance, try:

```
detatch(lp)
with(lp, age + height)
```

8.3 `remove` and `rm`

Typing:

```
remove(Loblolly)
```

or

```
rm(Loblolly)
```

will remove `Loblolly` completely from a work session. Happily, the object Loblolly (a dataset in the package *datasets*) cannot actually be destroyed/deleted using `rm` or `remove` (or any other commands) at the **R-**console.

8.4 Cleaning up

By now we can see that the **R**-console can quickly become cluttered and confusing. To remove clutter on the console (without actually getting rid of any of the objects in a session) press **Ctrl+L** or using the Edit pulldown menu to click on "Clear console"[11] (non-Unix only). To remove all objects in the current session, including saved objects brought in from the working directory, one can type:

```
rm(list = ls(all = TRUE))
```

Of course, one should never include this or other equivalent lines of code in a distributed function, since it would cause users to delete their work.

[11] Many other keyboard shortcuts for **R** are available including **Ctrl+U** which deletes all the text from the current line, and **Ctrl+K** which deletes text from the current character to the end of the line. Conventional shortcuts are also valid, e.g. **Ctrl+C** = copy and **Ctrl+V** = paste. For guidance go to **Help>Console** (non-Linux ony).

9 R graphics

A strong feature of **R** is its capacity to create publication-quality graphs with tremendous user flexibility. The conventional workhorse of **R**-graphics is the function `plot`. These examples in this section present just a few **R** graphical ideas. An extensive discussion of **R** graphics is given in Murrell (2005). For additional demonstrations go to my personal webpage https://sites.google.com/a/isu.edu/aho/ or the book website http://www2.cose.isu.edu/~ahoken/book/.

9.1 `plot`

The function `plot` allows representation of objects defined with respect to Cartesian coordinates. It has only two required arguments.

- `x` defines the x-coordinate values.
- `y` defines the y-coordinate values.

Important optional arguments include the following:

- `pch` specifies the symbol type(s), i.e., the plotting character(s) to be used.
- `col` defines the color(s) to be used with the symbols.
- `cex` defines the size (character expansion) of the plot symbols and text.
- `xlab` and `ylab` allow the user to specify the x and y-axis labels.
- `type` allows the user to define the type of graph to be drawn. Possible types are `"p"` for points (the default), `"l"` for lines, `"b"` for both, `"c"` for the lines part alone of `"b"`, `"o"` for overplotted, `"h"` for 'histogram' like vertical lines, `"s"` for stair steps, and `"n"` for no plotting. Note that the command `box()` will also place a box around the plotting region.

We can see some symbol and color alternatives for **R**-plots in Figure 5.

```
plot(1:20, 1:20, pch = 1:20, col = 1:20, ylab ="Symbol number", xlab =
"Color number", cex = 1.5)
```

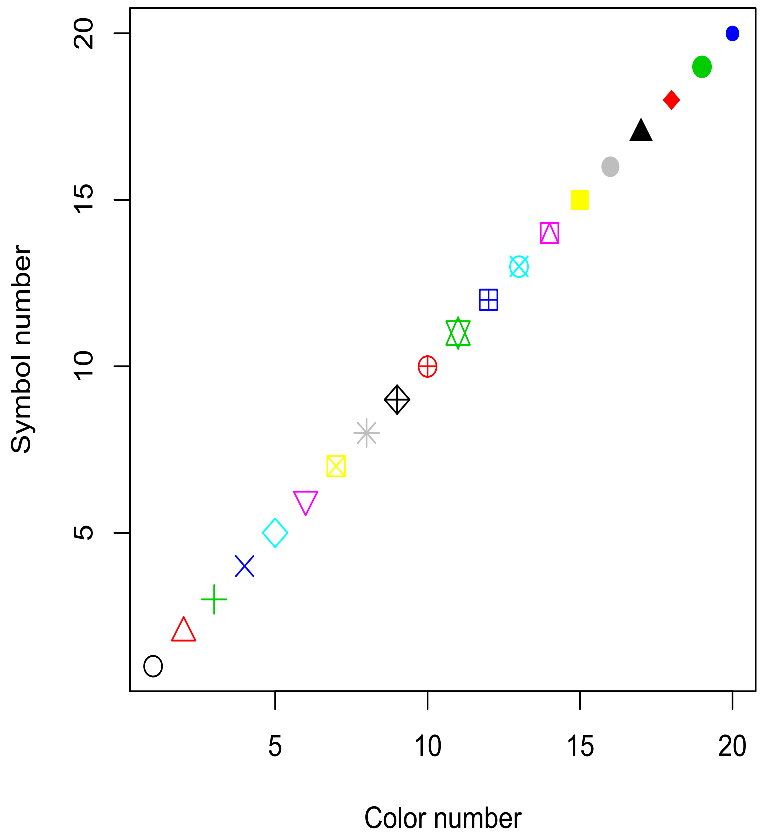


Figure 5 Some symbol and color plotting possibilities.

In the code above the x and y coordinates are both sequences of numbers from 1 to 20 obtained from the command `1:20`. I varied symbol colors and plotting characters (`col` and `pch` respectively) using `1:20` as well. The combination `col = 1` and `pch = 1` results in a black open circle, whereas the combination `col = 20`, `pch = 20` results in a blue filled circle. Note that we need to enclose the axis names in quotations for **R** to recognize them as text. Symbol numbers 21-26 allow background color specification using the argument `bg`. Many other symbol types are also possible including thousands of unicode options.

An enormous number of color choices for plots are possible and these can be specified in at least six different ways. First, we can specify colors with integers as I did in Figure 5. Additional varieties can be obtained by drawing numbers `colors()[number]` (Figure 6).

```
e <- expand.grid(1:20, 1:32)
plot(e[,1], e[,2], bg = colors()[1:640], pch = 22, cex = 2.5, xaxt = "n", yaxt =
"n", xlab = "", ylab = "")
text(e[,1], e[,2], 1:640, cex = .4)
```

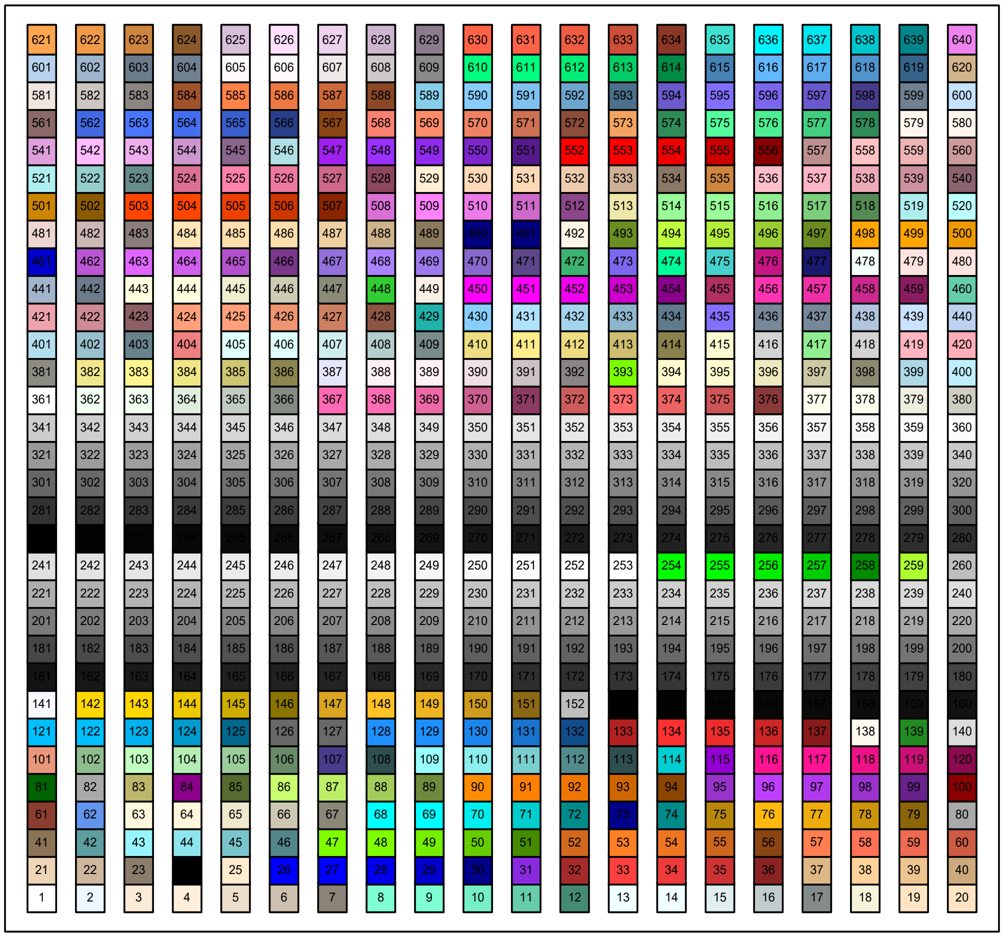


Figure 6 Color choices from `colors()`.

Second, we can specify colors using actual color names, e.g. `"white"`, `"red"`, `"yellow"`. For a visual display of essentially all the available named colors in **R** type: `example(colors)`.

Third, we can define colors by requesting red green and blue color intensities with the function `rgb`. Usable light intensities can be made to vary individually from 0 to 255 (i.e., within an 8 bit format). Fourth, we can specify colors using the function `hcl` which controls hues, chroma, and luminescence and transparency. Fifth, we can define colors using **hexadecimal codes**[12], e.g., blue = #0000FF. Finally we can specify colors using entirely different palettes. Figure 7 shows six pie plots. Each pie plot uses a different color palette. Each pie slice from each pie represents a distinct segment of the palette.

```
Fig.7()   # See Appendix code
```

[12]A data coding system that uses 16 symbols: the numbers 1-9, and the letters A-F. Hexadecimals are primarily used to provide a more intuitive representation of binary-coded values (see §20).

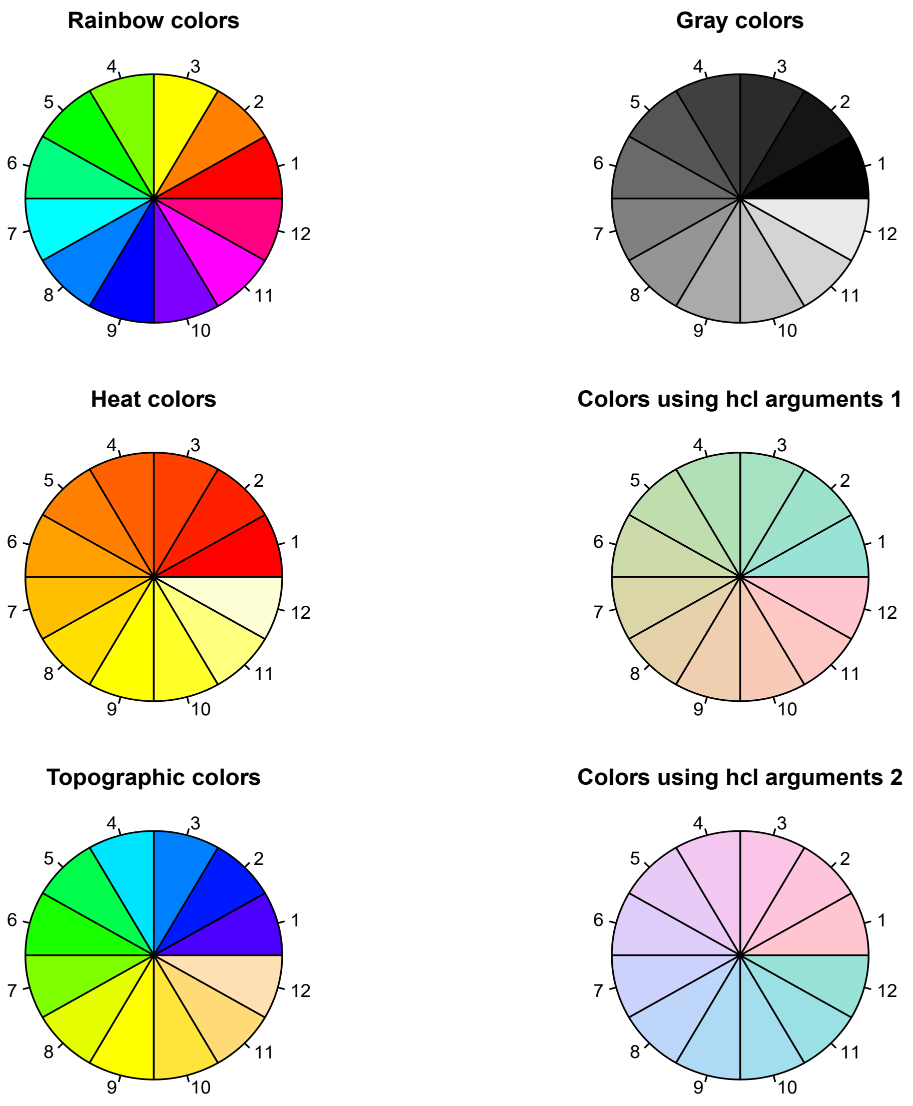


Figure 7 Use of color palettes in **R**. Note that the numbers do not correspond to actual color type designations.

A large number of additional palettes (including color-blind-safe palettes) can be obtained using the **R**-package *RColorBrewer*.

```
display.brewer.all(n = 7, colorblindFriendly = T)
```

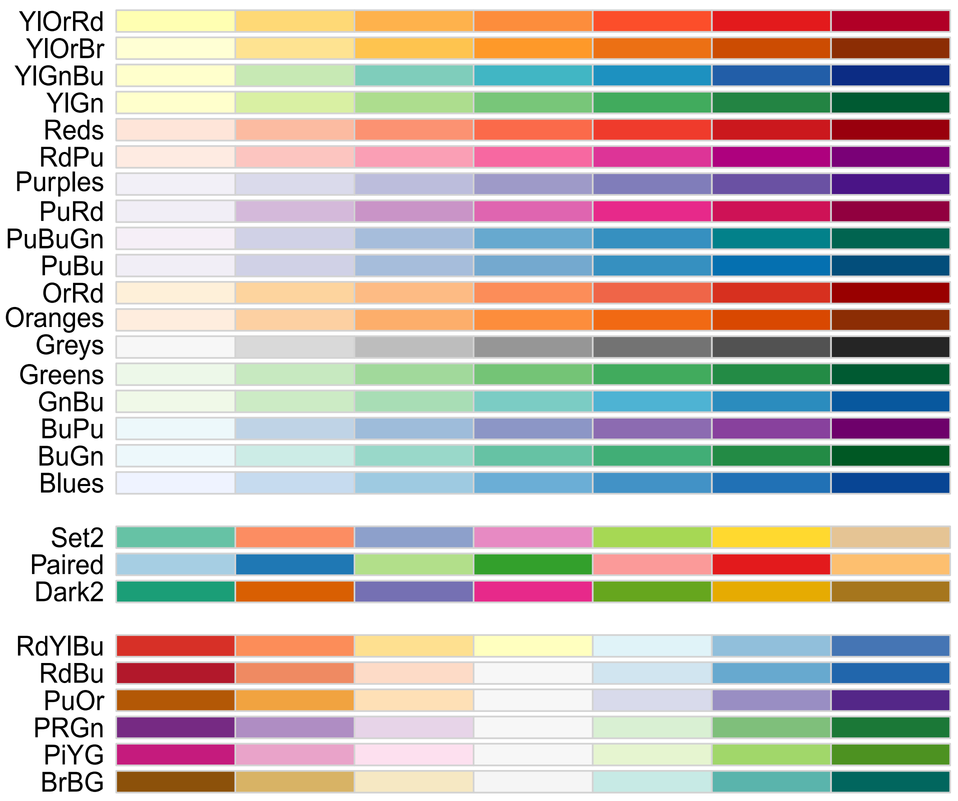


Figure 8 *RColorBrewer* color-blind-safe seven category palettes. Top palettes are so-called "sequential" palettes, middle palettes are "qualitative", and bottom palettes are "divergent".

Here are the hexadecimal names for the "Set2" palette chunks in Figure 8.

```
brewer.pal(7,"Set2")
[1] "#66C2A5" "#FC8D62" "#8DA0CB" "#E78AC3" "#A6D854" "#FFD92F" "#E5C494"
```

9.2 Scatterplots

The most common type of graph projects points at the intersection of paired observations describing two quantitative variables. The result is a **scatterplot.** Scatterplots are often presented in conjunction with **regression analyses** in which one models the behavior of one variable (the response) as a function of a second variable (the predictor.

|| Example 4 – Further Exploration of the `Loblolly` Dataset.

Let's visualize the relationship of the age and height of Loblolly pines using a scatterplot (Figure 9).

```
with(lp, plot(age, height))
```

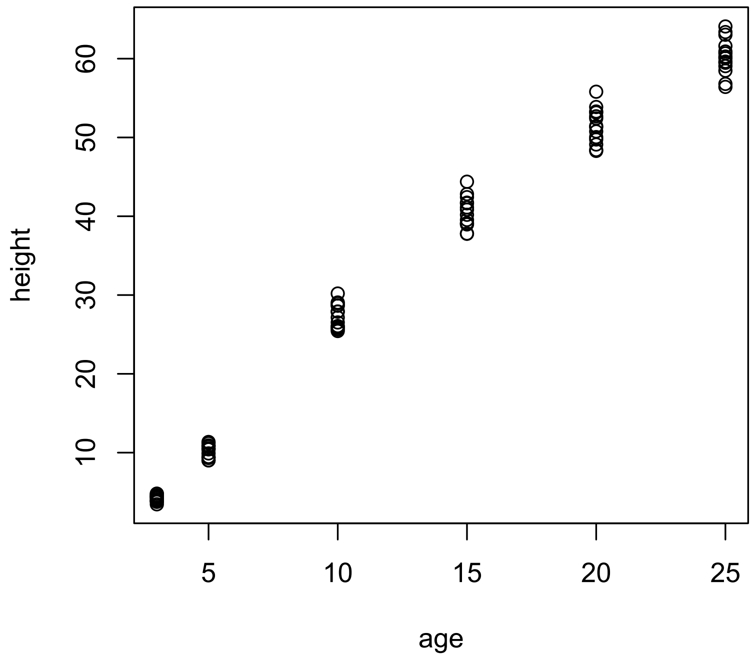


Figure 9 Scatterplot of height and age from the loblolly pine dataset.

Not surprisingly, there appears to be a strong positive correlation between these variables.

Now let's fit a simple linear regression for loblolly pine height as a function of age. A regression line will show the best possible linear fit for a response variable as a function of an quantitative explanatory variable. The **R** function for a linear model is `lm`. It encompasses and allows a huge number of statistical procedures, including regression (see Chs. 9, 10, and 11 in the **Foundational and Applied Statistics** text). We have:

```
ha.lm <- lm(height ~ age, data = lp)
```

The tilde lets **R** know that I want height to be a function of age. We note that the function `lm` has a built-in version of `with` which is specified with the argument `data`. Objects of class `lm` have their own summary function. This can be called (in this case) by simply typing:

```
summary(ha.lm)
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.31240    0.62183  -2.111   0.0379 *
age          2.59052    0.04094  63.272   <2e-16 ***
```

The output shows us the Y-intercept, -1.31240, and slope, 2.59052, of the regression line.

The `abline` function allows the plotting of a line over an existing plot. The first two arguments for `abline` are the Y-intercept and slope (Figure 10).

```
with(lp, plot(age,height, pch=2, col=3))
abline(-1.312396, 2.590523)
```

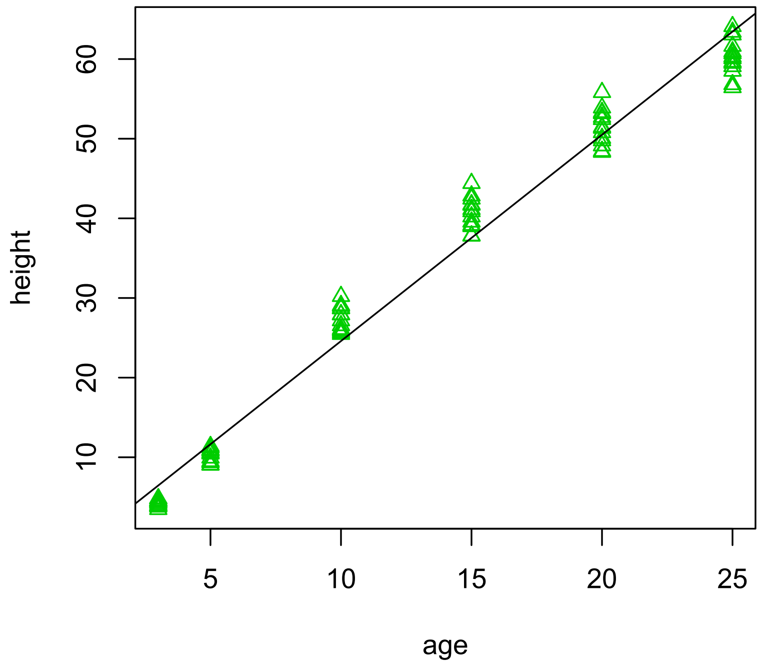


Figure 10 Scatterplot of height and age with a regression line overlaid.

9.3 Graphical devices

Graphics in **R** are created within **graphics devices** that vary with respect to storage modes, display modes, available typefaces and other characteristics. In the current **R**-windows download, six graphics devices will be available including `windows`, `pdf`, `postscript`, and `X11`. The `X11` device is a windows graphics system for bitmap displays, and is commonly used in Unix-alike operating systems. Six other devices will also exist, although they may return a warning if **R** was not compiled to use them upon installation. These are `cairo_pdf`, `svg`, `png`, `jpeg`, `bmp`, and `tiff`.

Multiple devices (currently up to 63) may exist simultaneously in an **R** work session, although there will only be one active device. To find the current (active) graphics device's flavor we can type `dev.cur()`. I get:

```
dev.cur()
windows
      2
```

R tells me there are two devices open. The current device is a `windows` device. The second device is the so-called "null device". The null device is always open but only serves as a placeholder. Any attempt to use it will open a new device in **R**. Occasionally, on purpose or by accident, all graphics devices (except the null device) may become turned off. A new active graphics device can be created at any time by typing:

```
dev.new()
```

The active device can be changed using the function `dev.set()`.

9.4 `par`

Parameters for a graphics device (which may contain several plots) can be accessed and modified using the function `par`. Below are important arguments for `par`. Some of these can also be specified as arguments in `plot`, with different results.

- `bg` gives the background color for the graphical device. When used in `plot` it gives the background color of plotting symbols.
- `bty` is the box-type to be drawn around the plots. If `bty` is one of `"o"` (the default), `"l"`, `"7"`, `"c"`, `"u"`, or `"]"` the resulting box resembles the corresponding upper case letter. The value `"n"` suppresses the box.
- `fg` gives the foreground color.
- `font` is an integer that specifies the font typeface. `1` corresponds to regular text (the default), `2` to bold face, `3` to italic and `4` to bold italic
- `las` is the style of axis labels: `0` always parallel to the axis (default), `1` always horizontal, `2` always perpendicular to the axis, `3` always vertical.
- `mar` will have the form `c(bottom, left, top, right)` and gives the number of lines of margin to be specified on the four sides of the plot. The default is `c(5, 4, 4, 2) + 0.1`.
- `mfrow` will have the form `c(number of rows, number of columns)` that indicates the number and position of plots in a graphical layout.
- `oma` specifies the outer margins of a graphical device, given multiple plots, using a vector using a matrix of the form: `c(bottom, left, top, right`.
- `usr` will have the form `c(x1, x2, y1, y2)` giving the extremes of the user coordinates of the plotting region.

When setting graphical parameters, it is good practice to revert back to the original parameter values. Assume that I want to background of the graphics device to be black. To set this I would type:

```
old.par <- par(no.readonly = TRUE) # save default, for resetting...
par(bg = "black") # change background parameter
```

To return to the default settings for background I would type:

```
par(old.par)
```

Defaults will also be reset by closing the graphics device containing the customized parameters, or by opening a new device. For instance, using `dev.new()`.

Other fundamental properties of the default graphics device, such as device `height`, `width` and `pointsize`, can be adjusted using the `dev.new` function. For instance, to create a graphical device 9 inches wide, and 4 inches high, I would type:

```
dev.new(width = 9, height = 4)
```

9.5 Exporting graphics

To export **R** graphics, one can often copy snapshots to a Windows clipboard using pull down menus on the `windows` graphical device. These can then be pasted into Windows programs (e.g., word processors) as **bitmaps** (a spatially mapped array of bits) or **metafiles**, a generic term for a file format that can store multiple types of (generally graphical) data. To create the best possible graphs, however, one should save device output using **postcript** (**ps**), **portable document format** (**pdf**), or other universal high resolution graphical formats. This can be done directly by:

- Using pulldown menus on a `windows` or `X11` graphics device itself (currently only metafile and postscript saves are available).
- Clicking on the extent of a `windows` or `X11` graphics device and then going to **File>Save as** on the **R**-GUI pulldown menus (obviously, non-Linux only).
- Using save-associated arguments included in graphical device functions, i.e., `pdf`, `tiff`, `jpeg`, `bmp`, `tiff`, `postscript`, and `win.metafile` (= metafile).

The third alternative allows fine scale control with respect to resolution (dpi), figure size, and other characteristics. For instance, to save a graphics device image as a pdf under the file name example.pdf in the working directory I would type:

```
pdf(file ="example.pdf")
```

I would then make the plot, for instance

```
plot(1:10)
```

The plot will not be shown because the graphical device is engaged with `pdf`. As a final step I close the device.

```
dev.off()
```

The graphics file will now be contained in your working directory. If the file argument is unspecified `pdf` will save a file called `Rlot.pdf`.

Creating high resolution images in R:

By default, the **raster graphics formats** BMP, JPEG, PNG and TIFF have a width and height of 480 pixels, and a "large" point size (1/72 inch) in R. This results in a rather coarse (72 ppi) image resolution. However, changing the `res` (resolution) argument in a graphical device function without changing the `pointsize`, or `height` and `width` arguments will generally result in unusable figures.

Because 500 ≈ 72 x 6, one can generate a > 400 ppi TIFF called fig1.tiff by typing:

```
tiff("fig1.tiff", res = 72 * 6, height = 480 * 6, width = 480 * 6)
plot(1:10)
dev.off()
```

With respect to graphical formats, documentation in the *grDevices* package states:

> "The PNG format is **lossless** (data compression without loss of information) and is best for line diagrams and blocks of color. The JPEG format is **lossy** (data compression in which unnecessary information is discarded), but may be useful for image plots, for example. The BMP format is standard on Windows, and supported by most viewers elsewhere. TIFF is a meta-format: the default format written by the function `tiff(compression = none)` is lossless and stores RGB values uncompressed—such files are widely accepted, which is their main virtue over PNG."

So-called **scalar vector graphics** (SVGs) can be created with the functions `pdf`, `svg`, `cairo_pdf` and `cairo_ps`. All three scripts apply the **cairographics** application programming interface (API). This device will recognize a large number of symbols and fonts not available for document and image generation in the default setting of the `windows postscript` and `pdf` devices.

9.6 Typeface families

Font typefaces can be changed using a number of graphical functions, including `par`, via the argument `family`. The general typeface families: `"serif"`, `"mono"`, and `"sans"`, and the Hershey family of fonts (type `?Hershey` for more information) are transferable across all graphics devices employed in **R**. To change the font in a graphical device from the default sans serif (similar to Arial) to serif (similar to Times New Roman) one could type `par(family = "serif")`. To use a Courier-type **monospace** font one would use `par(family = "mono")`.

Many other typeface families are possible, although they may not be transportable to all graphical devices and graphical storage formats. In the code below I bring in a large number of conventional font families using a function from the book website. These typefaces (and many others) will typically be available on Windows platform machines, although not all will be supported by non-`windows` graphics devices. The result can be seen in Figure 11.

```
source(url("http://www2.cose.isu.edu/~ahoken/book/win_fonts.R"))

tiff(file = "fonts.tiff", res = 600,  width = 7.7, height = 7.7, units = "in")

x <- rep(c(2.8, 6.4, 9.6), each = 33)
y <- rep(seq(10, 0.25, by = -.2965), 3)
font.type <- paste(rep("f", length(fonts)), 1:length(fonts), sep = "")

par(mar = c(0.1,0.1,0.1,0.1), cex = 1.1)
plot(0:10,type="n", xaxt= "n", yaxt = "n", xlab = "", ylab = "")
for(i in 1:length(fonts)){
text(x[i],y[i], labels=fonts[i] , family = font.type[i])
}
dev.off()
```

The figure displays examples of text from ninety-nine Windows typefaces. To save myself from typing an inordinate amount of code, I use a for loop to place the fonts one at a time in the graphics device (see Section 21.6). Note that I use the function `tiff` to create a high resolution .tiff graphical file. Running the entirety of the preceding code chunk will create the image file fonts.tiff in your working directory.

Importantly, the typefaces imported from the first line of code in the chunk will now be available for graphics functions using the `windows` graphical device. To see the available `windows` fonts one can type:

```
windowsFonts()
```

Similarly, one can see the available fonts for `postscript` and `pdf` graphics devices using:

```
names(pdfFonts())
```

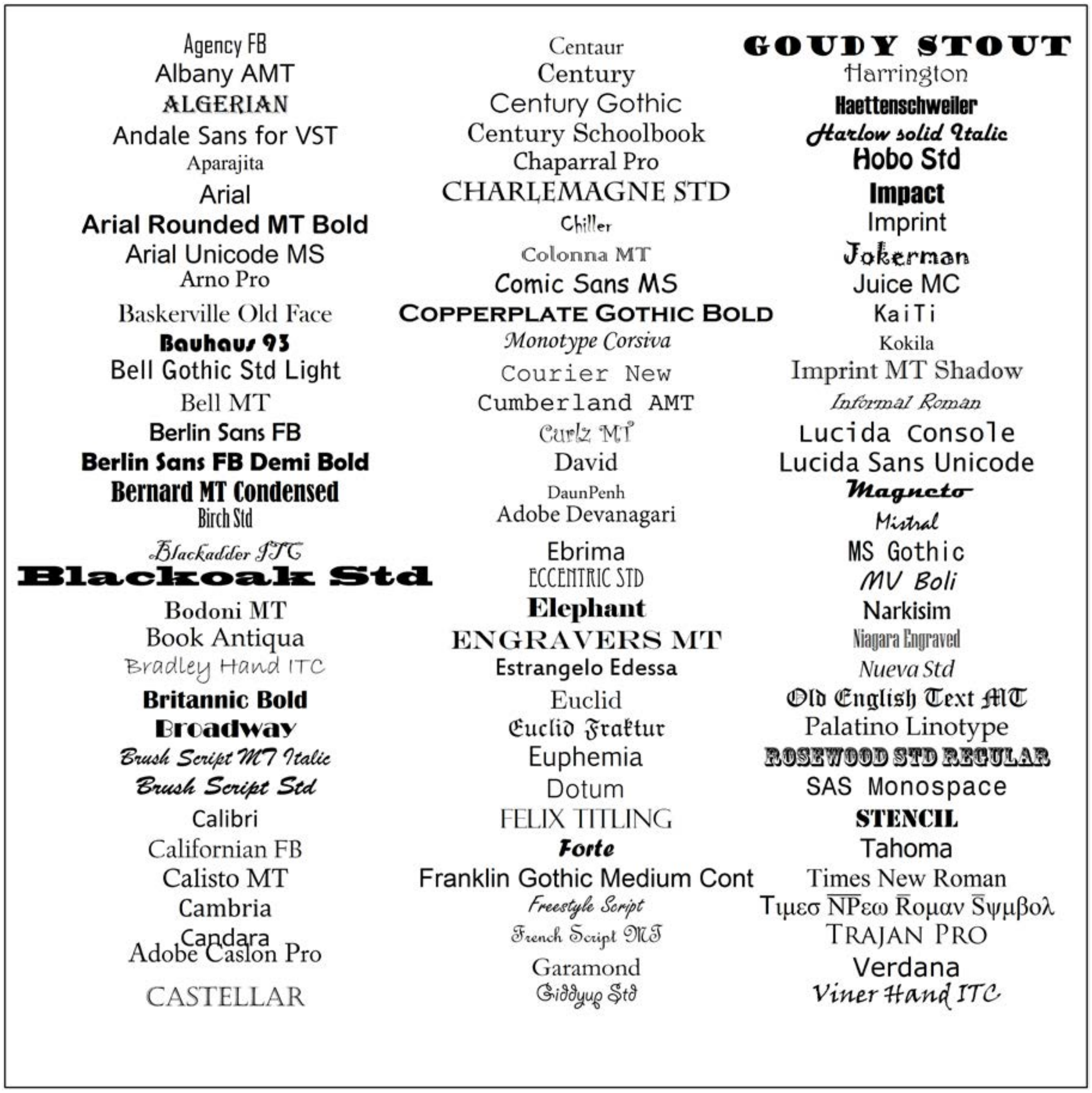


Figure 11 Examples of font families that can be used in **R** graphics.

9.7 `text, lines, points, paste`

The functions `text`, `lines` and `points` can be used to place text, lines and points in a plot, respectively. As with `plot()` the first two arguments of these functions are the x and y coordinates for the plotted items. Other arguments concern characteristics of the plotted items. For instance, to plot the text "example" at plot coordinates $x = 0$, $y = 1$, with a character expansion that was two times the default, I would type:

```
text(x = 0, y = 1, "example", cex = 2)
```

The function `paste` can be used to concatenate elements from text strings in plots or output. For instance, try:

```
a <- c("a", "b", "c")
b <- c("d", "e", "f")
paste(a, b)
[1] "a d" "b e" "c f"
```

To plot a dashed line between the points (0, 2) and (1, 3), I would type:

```
lines(x = c(0, 1), y = c(2, 3), lty = 2)
```

or

```
points(x = c(0, 1), y = c(2, 3), lty = 2, type = "l")
```

To place a red inverted triangle at the point (0, 1), I would type:

```
points(x = 0, y = 1, pch = 6, col = 2)
```

Geometric shapes can be drawn using a number of functions including `rect` (which draws rectangles) and `polygon` (which draws shapes based on user-supplied vertices).

9.8 `plotmath`

R has useful functions for the plotting of mathematical expressions. These include the Greek letters, mathematical operators, italicization, and sub- and super-scripts. These are generally called as an `expression` in the text argument in the functions `text` or `mtext`. For example, to paste the formula for the sample variance

$$\frac{\sum_{i=1}^{n}(x_i - \bar{x})^2}{n-1},$$

into a plot at coordinates (0, 1) I would type:

```
varexp <- expression(over(sum(paste("(",italic(x[i] - bar(x)),")"^2),
italic(i)==1, italic(n)),(italic(n) - 1)))

text(0, 1, varexp)
```

Complete coverage of `plotmath` mathematical expressions would be unwieldy to summarize here. For more information type `?plotmath`.

9.9 `axis`

The function `axis` can be used to create new axes on a plot or to customize axis characteristics. Its first argument (`side`) specifies the side of the plot that the new axis will occupy `1=bottom, 2=left, 3=top, 4=right`. Other arguments include a vector of axis labels (argument `labels`), and the locations of labels (argument `at`).

For instance, to create a right hand axis I would type:

```
axis(4)
```

9.10 `mtext`

To place text in the margin of a plot we can use the function `mtext`. For its first argument the function requires the character string to be written into the plot. The 2nd argument defines the plot margin to be written on: `1=bottom, 2=left, 3=top, 4=right`.

For instance, to place the text "Axis 2" on the right hand axis I would type:

```
mtext("Axis 2", 4)
```

|| Example 5 --A complex multiplot example

Consider a rather comprehensive `par` example. The object `C.isotope` in the library *asbio* is a dataset describing variations in the quantity $\delta\,^{14}C$ over time in La Jolla California. $\delta\,^{14}C$ is the ratio of carbon 14 to carbon 12 (^{14}C is unstable, while ^{12}C is a stable isotope of carbon) compared to a standard ratio. We will create a figure with four subplots (Figure 12).

- It will have dimensions 8" x 7".
- The outer margins (in number of lines) will be bottom = 0.1, left = 0.1, top = 0, right = 0.
- The inner margins (for each plot) will be bottom = 4, left = 4.4, top = 2, right = 2. The plot margins will be light gray. We can specify gray gradations with the function `gray`. We will use `gray(0.97)`.
- The first plot will show $\delta\,^{14}C$ as a function of date. The plotting area will be dark gray, i.e., `colors()[181]`. Points will be white circles with a black border.
- The second plot will be a line plot of atmospheric carbon as a function of date. It will have a light green plotting area: `colors()[363]`.
- The third plot will be a scatterplot of $\delta\,^{14}C$ as a function of atmospheric carbon. Points will be yellow circles with a black border. The plotting area will be light red: `colors()[580]`.
- The fourth plot will show the sample variance of atmospheric carbon in the time series. It will have a custom (albeit meaningless) axis with the labels: a, b, c, and d. It will also have a horizontal axis label inserted with `mtext`.

```
library(asbio) # loads the library asbio
data(C.isotope) # dataset in asbio
dev.new(height = 8, width = 7)
op <- par(mfrow = c(2, 2), oma = c(0.1, 0.1, 0, 0), mar = c(4, 4.4, 2, 2),
bg = gray(.97))
```

```
#-------------------------------- plot 1 -------------------------------#
with(C.isotope, plot(Decimal.date, D14C, xlab = "Date", ylab =
expression(paste(delta^14,"C (per mille)")), type = "n"))
rect(par("usr")[1], par("usr")[3], par("usr")[2], par("usr")[4], col =
colors()[181])
with(C.isotope, points(Decimal.date, D14C, pch = 21, bg = "white"))
```

```
#-------------------------------- plot 2 -------------------------------#
with(C.isotope, plot(Decimal.date, CO2, xlab = "Date", ylab =
expression(paste(CO[2]," (ppm)")), type = "n"))

rect(par("usr")[1], par("usr")[3], par("usr")[2], par("usr")[4], col =
colors()[363])
with(C.isotope, points(Decimal.date, CO2, type = "l"))
```

```
#-------------------------------- plot 3 -------------------------------#
with(C.isotope, plot(CO2, D14C, xlab = expression(paste(CO[2], "(ppm)")),
ylab = expression(paste(delta^14,"C (per mille)")), type = "n"))

rect(par("usr")[1], par("usr")[3], par("usr")[2], par("usr")[4], col =
colors()[580])
with(C.isotope, points(CO2, D14C, pch = 21, bg = "yellow"))
```

```
#-------------------------------- plot 4 -------------------------------#
plot(1:10, 1:10, xlab = "", ylab = "", xaxt = "n", yaxt = "n", type = "n")
rect(par("usr")[1], par("usr")[3], par("usr")[2], par("usr")[4], col =
"white")
text(5.5, 5.5, expression(paste(over(sum(paste("(",italic(x[i] -
bar(x)),")"^2), italic(i)==1, italic(n)),(italic(n) - 1)), " = 78.4")), cex
= 1.5)
axis(side = 1, at = c(2, 4, 6, 8), labels = c("a", "b", "c", "d"))
mtext(side = 1, expression(paste("Variance of ", CO[2], " concentration")),
line = 3)
par(op)
```

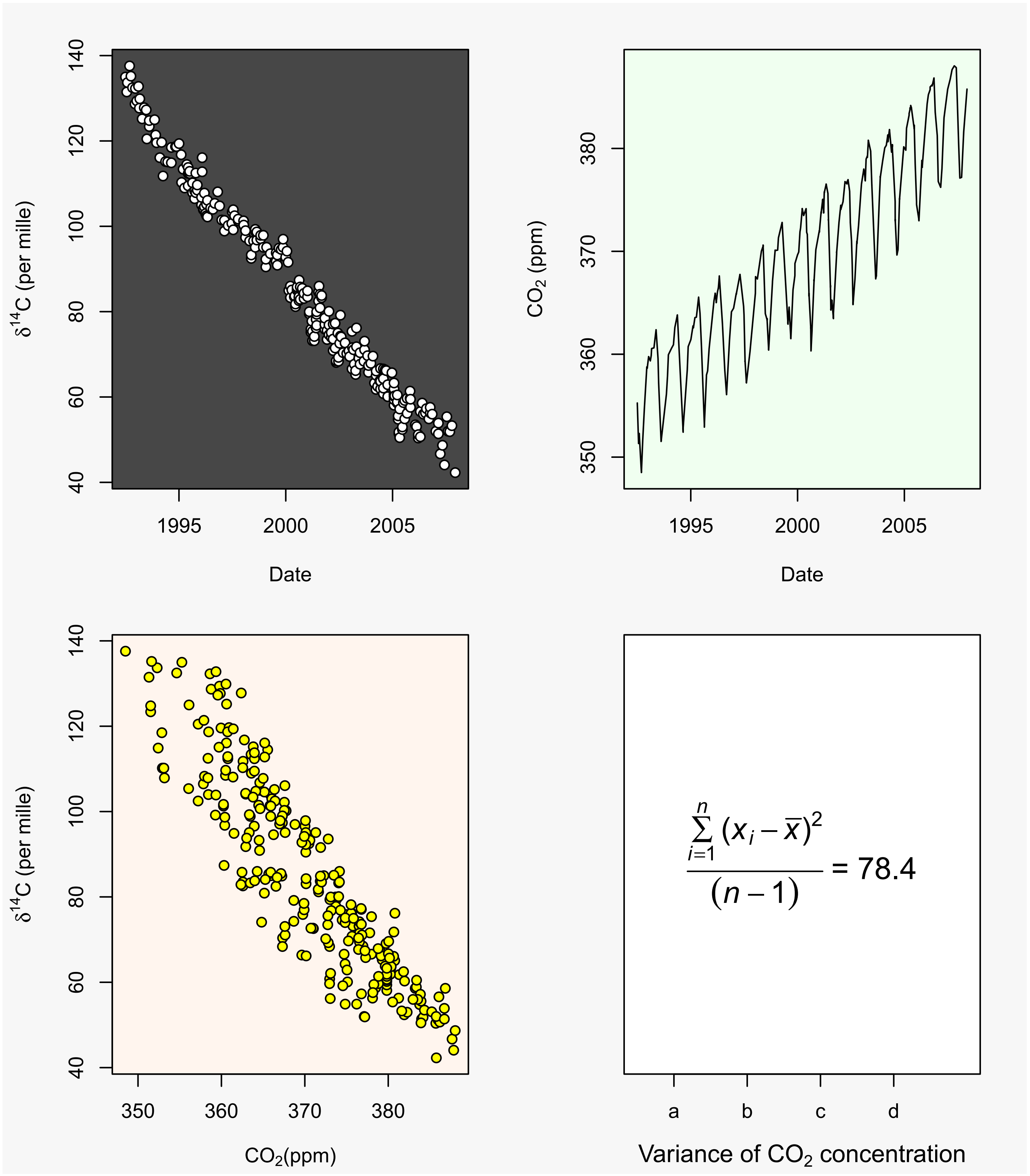


Figure 12 Figure resulting from code in ⌊⌋ Example 5

9.11 Histograms

Histograms are vital for considering the distributional characteristics of data. They consist of rectangles whose area is proportional or equivalent to the frequency of particular numeric intervals (bins) describing that variable.

|| Example 6 – Exploration of Data from Bryce Canyon National Park

The `brycesite` dataset from library *labdsv* consists of environmental variables recorded at, or calculated for, each of 160 plots in Bryce Canyon National Park in Southern Utah.

```
install.packages("labdsv")
library(labdsv)
data(brycesite)
```

Here are the names of the site environmental variables (columns) in the `brycesite` dataset:

```
names(brycesite)
 [1] "annrad" "asp"    "av"     "depth"  "east"   "elev"   "grorad" "north"
 [9] "pos"    "quad"   "slope"
```

Let's look at the distribution of the `slope` variable (Figure 13). This variable describes slope (in degrees) of sites in the dataset.

```
with(brycesite, hist(slope, xlab = "Slope (Degrees)", ylab = "Frequency of
observations", main = ""))
```

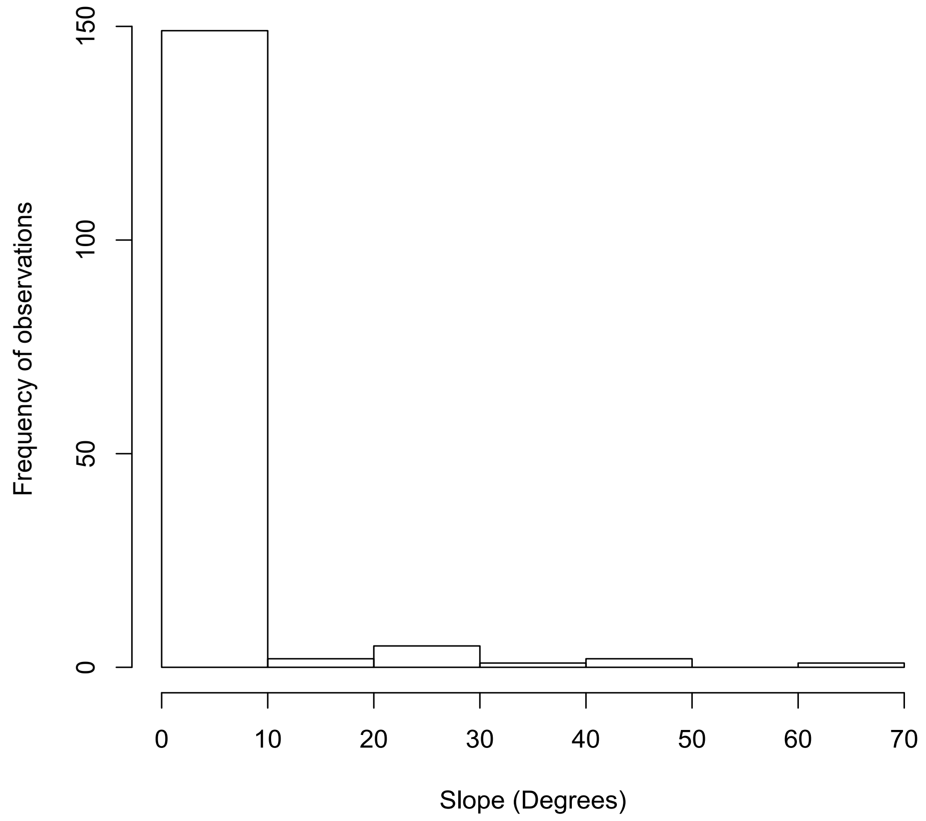


Figure 13 Histogram of slope observations in the `brycesite` dataset.

The distribution of slope is strongly right skewed (i.e. most slopes are gradual, and only few are extremely steep).

Consideration of raw aspect values in analyses is problematic because the measurements are circular. As a result the values 1 and 360 are numerically 359 units apart, although they in fact only differ by one degree. One solution is to use the transformation [1 - cos(aspect° - 45)]/2. This index will have highest values on southwest slopes (at 225 degrees), and lowest values on northeast facing slopes (at 45 degrees). This acknowledges the fact that highest temperatures in the Northern Hemisphere occur on Southwest facing slopes because they receive ambient warming during the morning, coupled with late afternoon direct radiation. We have:

```
asp.val <- (1 - cos(((brycesite$asp - 45) * pi)/180))/2
```

The distribution of aspect values in the Bryce Canyon dataset is shown in Figure 14.

```
hist(asp.val, ylab = "Frequency of observations", xlab = "Aspect value", main
= "")
```

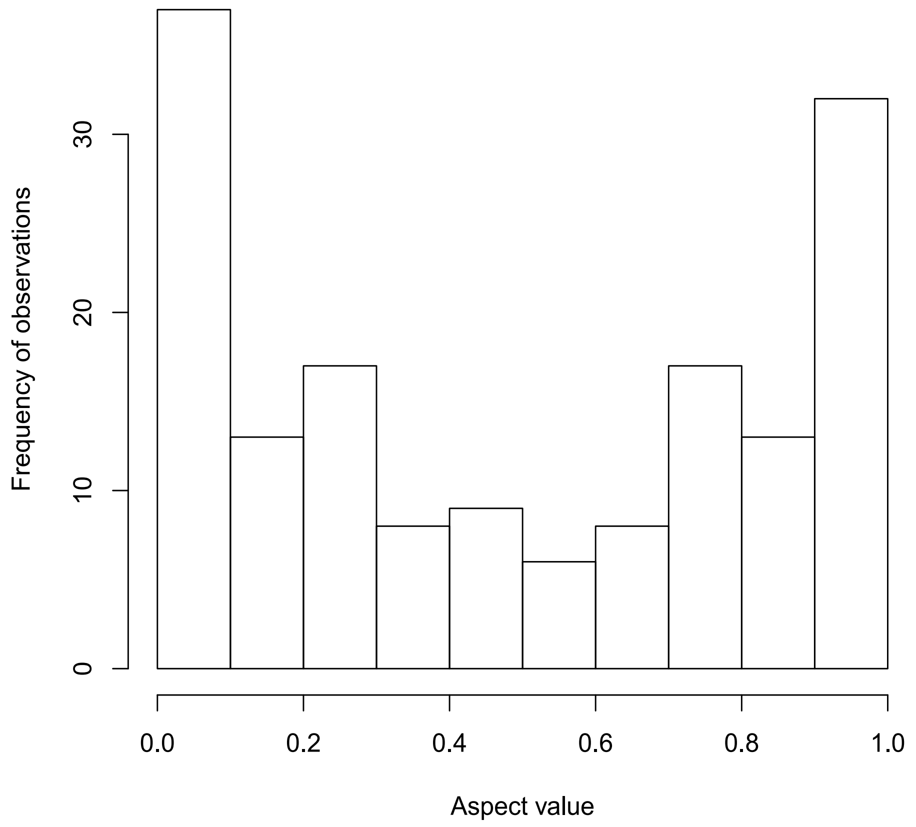


Figure 14 Histogram of observed aspect values from the `brycesite` dataset.

We have a bimodal distribution. Specifically, there are a lot of northeast-facing and southwest-facing sites, and fewer northwest and southeast-facing sites.

9.12 Subsetting scatterplot arguments using a categorical variable

It is often useful to distinguish points in scatterplots with respect to a categorical variable.

| | Example 7

The plot below shows `brycesite` radiation (in Langleys) as a function of aspect value. A **Langley** (Ly) is a measure of energy per unit area, per unit time. To be precise, one Ly = 1calorie m^{-2} min^{-1}. In SI units 1Ly = 41840.00 J m^{-2}. The plot also distinguishes five topographic positions using both point color and shape. For clarity I also create a legend. We see that ridgetop sites have mostly northeastern aspect, and hence have lower radiation inputs (Figure 15).

```
with(brycesite, plot(asp.val, annrad, xlab = "Aspect value", ylab
= "Annual radiation (Langleys)", col = as.numeric(pos), pch =
as.numeric(pos)))

legend("bottomright",legend = levels(brycesite$pos), pch = 1:5, col =
1:5)
```

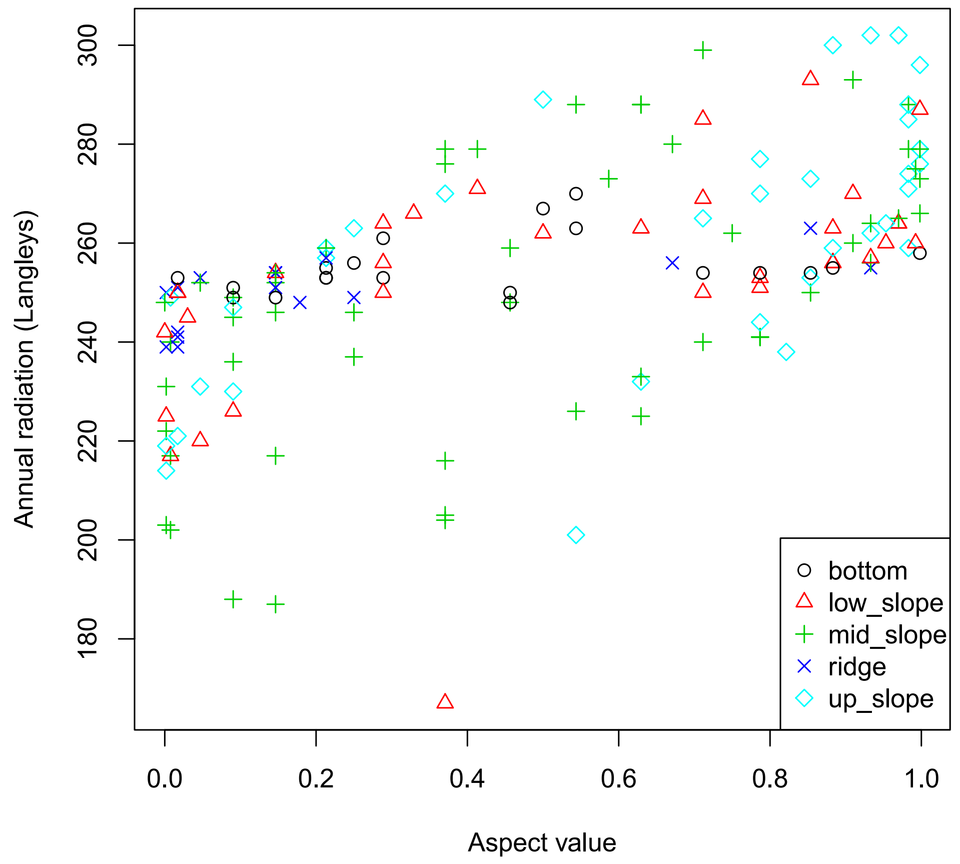


Figure 15 Scatterplot of aspect value versus annual radiation with topographic positions indicated

To assign colors and plotting characters appropriately, I coerce the categorical topographic position vector, `pos`, to be numeric with `as.numeric`. The result is:

```
as.numeric(brycesite$pos)
  [1] 4 3 3 4 5 3 3 5 3 3 2 2 3 4 3 3 3 1 2 2 2 5 4 4 3 5 4 3 5 3 5 3 2 5 5 4 1
 [38] 1 2 4 4 3 3 3 3 4 3 5 3 3 3 2 5 3 5 3 3 5 5 4 3 3 5 2 3 3 5 2 2 5 2 2 3 3
 [75] 3 2 2 3 3 2 4 3 4 2 5 3 3 2 2 3 5 5 3 5 5 3 3 3 3 5 5 3 3 3 3 5 1 2 4 1 2
[112] 1 2 3 5 1 5 3 3 3 3 1 3 2 2 5 2 1 2 2 1 2 1 1 1 1 1 1 2 1 1 4 5 5 5 4 5 2
[149] 2 4 1 5 5 5 3 2 2 1 5 4
```

Ones correspond to the first alphanumeric level in `pos`, `bottom`, whereas fives correspond to the last alphanumeric level, `up_slope`. The color and symbols assignments are made within the plot using:

```
col = as.numeric(brycesite$pos)
pch = as.numeric(brycesite$pos)
```

Legends in **R** can be created using the function `legend`. The first argument(s) will be a specific *X*,*Y* position for the legend, or one of: `"bottomright"`, `"bottom"`, `"bottomleft"`, `"left"`, `"topleft"`, `"top"`, `"topright"`, `"right"` or `"center"`. The legend argument names the categories to be depicted. The function `levels` used in this argument lists the categories in a categorical variable alphanumerically.

9.13 Plotting variables using additional axes

It may be necessary to add additional axes in order to plot additional variables. In **R** this will involve laying one plot on top of another, by specifying `par(new = TRUE)`, and defining `axes = FALSE`, `xlab = FALSE`, and `ylab = ""` in the arguments of the second plot.

|| Example 8

Consider Figure 16 in which both `brycesite` annual radiation and annual growing season radiation are plotted as a function of aspect value.

```
op <- par(mar = c(5,4.5,1,4.5), cex = 1.1)
with(brycesite, plot(asp.val, annrad, xlab = "Aspect value", ylab = "Annual
radiation (Langleys)"))
par(new = TRUE)
with(brycesite, plot(asp.val, grorad, pch = 19, axes = FALSE, xlab = "",
ylab = ""))
axis(4)
mtext(side=4,"Growing season radiation (Langleys)",line = 3, cex=1.1)
legend("bottomright", pch=c(1,19), legend=c("Annual radiation", "Growing sea-
son radiation"),bty = "n")
par(op)
```

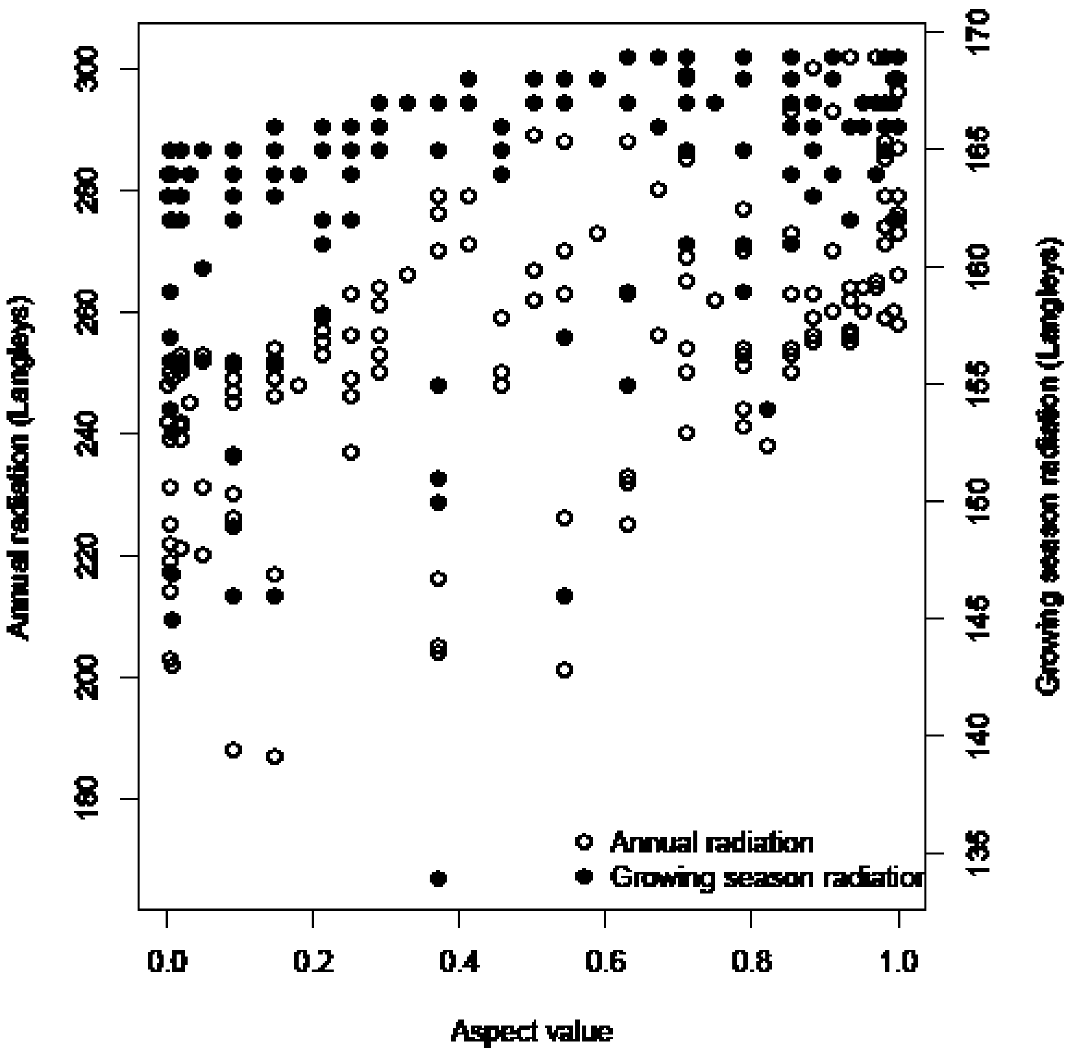


Figure 16 Plot of the relationships of annual radiation, growing season radiation, and aspect value.

The line `par(new = TRUE)` tells **R** to not clean the graphical device before drawing a new plot. The argument `axes = FALSE` in the second plot, suppresses default plot plotting of axis units on the left and bottom axes.

9.14 Barplots

Barplots are frequently used to compare single number summaries (e.g., sum, median, mean, etc.) of categorical levels.

|| Example 9 -- Greenhouse gas emissions

Of great concern to both citizens and scientists are rising global levels of atmospheric greenhouse gasses. Atmospheric CO_2 concentrations have increased approximately 40% since the start of the industrial revolution while more potent greenhouse gasses like CH_4 and NO_2 have increased 150% and 23% respectively (Mann and Kump 2009). We will take a detailed look at recent global patterns of CO_2 emissions and human population numbers in this exercise.

The US department of energy has data since 1980 detailing total CO_2 emissions from the consumption and flaring of fossil fuels. In addition, midyear population data can be obtained, by country, from the US census bureau. CO_2 and population data are available as `world.co2` and `world.pop` respectively in *asbio*.

We will first import these data.

```
library(asbio); data(world.co2); data(world.pop)
```

To make them easier to call, we will give the datasets shorter names.

```
co2 <- world.co2
wp <- world.pop
```

The CO_2 data has two additional countries (columns) compared to the world population data: Belgium and Ghana. We will get rid of these columns and the "year" column in the CO_2 dataset.

```
co2.1 <- co2[,-c(1, 3, 8)]
```

We will also want to look at the 2006 CO_2 data by itself. It is in row 27.

```
co2.2006 <- co2.1[27,]
```

The names of some of the counties are too long to fit on the *X*-axis for the barplot we wish to create (Figure 17). We can deal with this in at least four ways. First, we can increase the bottom margin (e.g. `par(mar = c(6, 4, 2, 2))`. Second, we can decrease the font-size of the names using the `cex.names` argument (the default for `barplot` names is `cex.names = 1`). Third, we can make the country names perpendicular to the *X*-axis instead of parallel using the `las` argument. Lastly, we can simply make the country names shorter by changing the column names in the dataframe or matrix. For instance we could use some variant on:

```
colnames(co2.1) <- c("Afgan.", "Brazil", "Canada", "China", "Finland",
"Italy", "Japan", "Kenya", "Mexico", "S. Arabia", "UAE", "US", "Total")
```

We use the column names from `co2.1` as the column names for `co2.2006`

```
colnames(co2.2006) <- colnames(co2.1)
barplot(as.matrix(co2.2006),las = 3,ylab = expression(paste("2006 ", CO[2], "
Emissions (metric tons x ", 10^6, ")")))
```

We add a horizontal grid to make levels among countries more discernible.

```
grid(ny = 20, nx = 0)
```

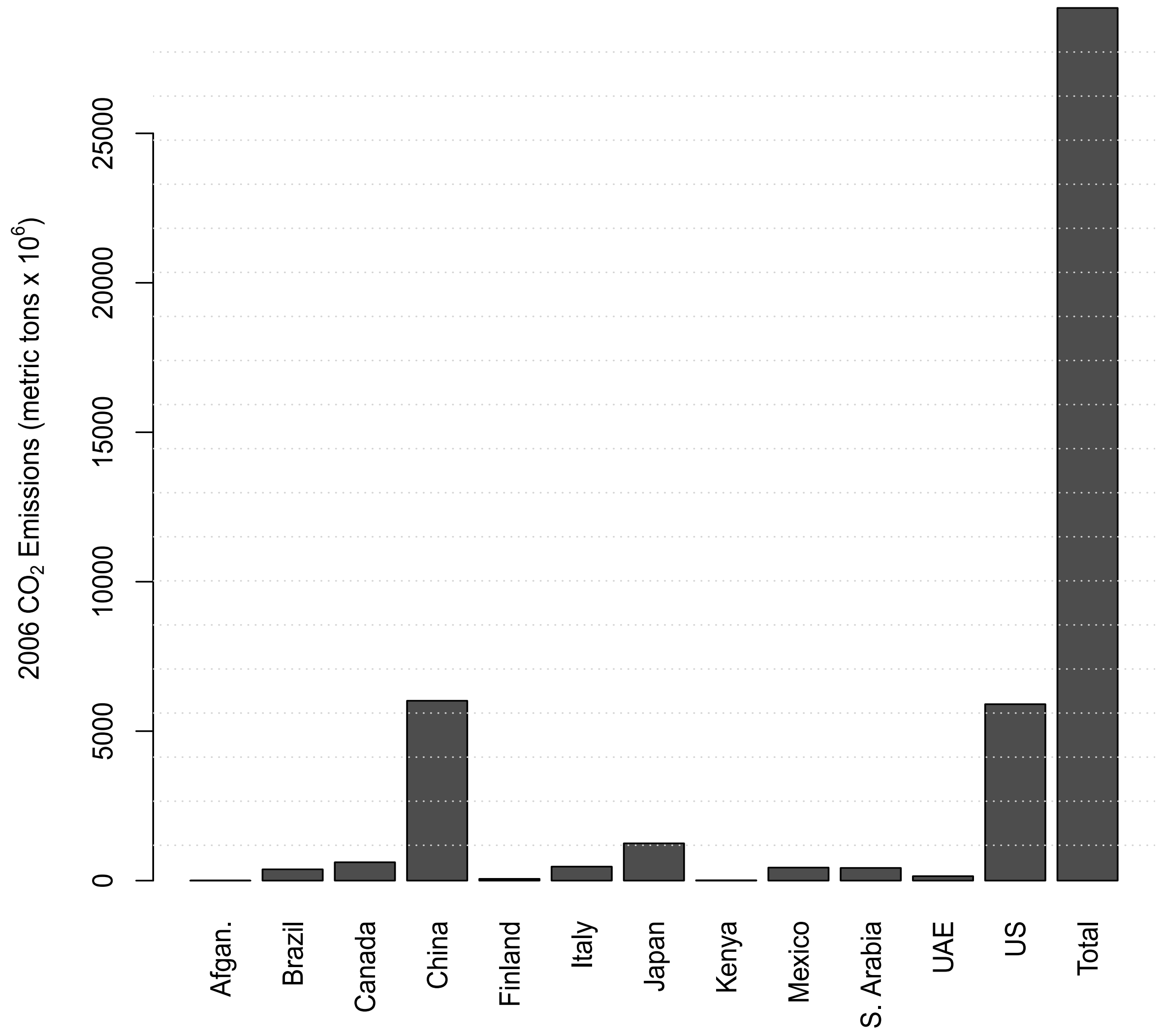


Figure 17 2006 CO_2 emissions, by country.

Next we will create a stacked bar graph of carbon emissions from 1980-2006, with countries as bars, and each bar stacked by year (Figure 18). We will leave out world totals to make patterns among countries easier to discern. By default **R** will impose its own coloring scheme for the stacked bars. We will create a twenty-seven step grayscale coloring scheme of our own by using the argument `col = gray(seq(0:26)/27)`. Type `?gray` for more information. We will also include a legend to describe the stacked bars. Type `?legend` for more information.

```
barplot(as.matrix(co2.1[,1:12]), las = 3, ylab = expression(paste(CO[2],
" Emissions (metric tons x ",  10^6, ")")), col = gray(seq(0:26)/27))
legend("topleft", fill = gray(seq(0,26,1)/27), legend = seq(1980, 2006, 1),
cex = .5)
```

Figure 18 Stacked bars of the CO2 emissions data.

By default `barplot` builds stacked bar plots. To create side-by-side barplots one would use the arguments `beside = TRUE`. I will make the figure wider to make it easier to view the large number of side-by-side bars (Figure 19).

```
dev.new(height=5,width=8); op <- par(mar=c(5,4.5,2,1))
barplot(as.matrix(co2.1[,1:12]), las = 3, ylab = expression(paste(CO[2], "
Emissions (metric tons x ",  10^6, ")")), col = gray(seq(0:26)/27), beside =
T)
legend("topleft", fill = gray(seq(0,26,1)/27), legend = seq(1980, 2006, 1),
cex = .5)
par(op)
```

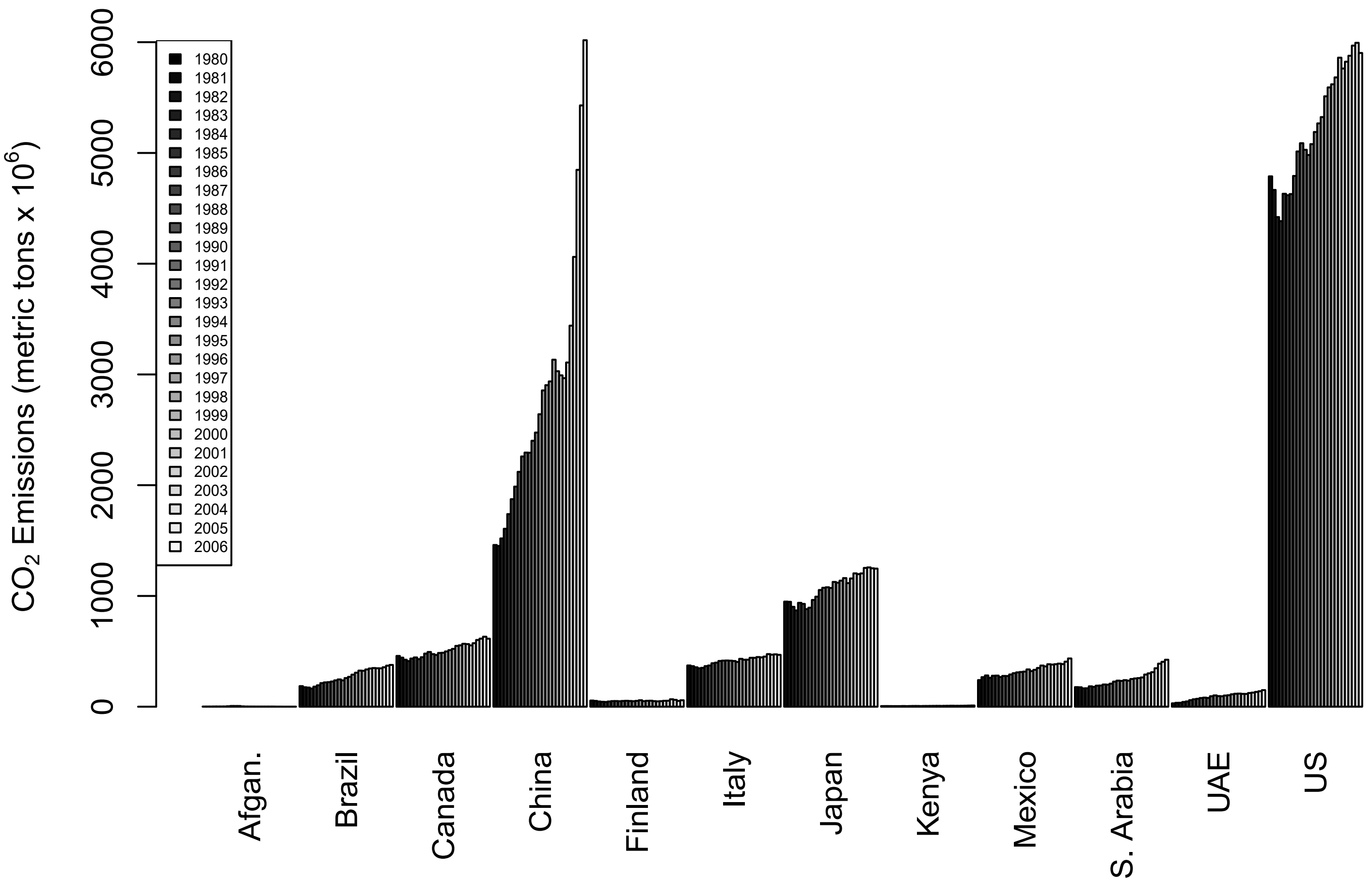


Figure 19 Side by side bars of the CO2 emissions data.

9.15 Multivariate line and scatterplots

As noted in § 9.1, line plots can be generated by specifying `type = "l"` in `plot()`. Lines can also be added to a plot one at a time using `points()` or `lines()` (see § 9.7). A more efficient method, however, uses the function `matplot()`.

|| Example 10

To illustrate, we will create a line plot with 13 lines (one for each country, and one for world totals) showing the carbon emission variability from 1980 to 2006 (Figure 20). We will make the lines in the plot of different types. We will also include a legend to describe the lines.

```
matplot(1980:2006, co2.1, ylab = expression(paste(CO[2], " Emissions (metric
tons x ", 10^6,")")),type  = "l", xlab = "Year", col = c(gray(0:11/15),1),
lwd = c(rep(1,12),2), lty = c(seq(1:6),seq(1:6),1), ylim = c(1,200000),log =
"y")
```

```
legend("topleft", col = c(gray(0:11/15),1), lty = c(rep(1:6, 2),1), lwd =
c(rep(1,12), 2), legend = colnames(co2.1), cex = .7, ncol = 4, bty = "n")
```

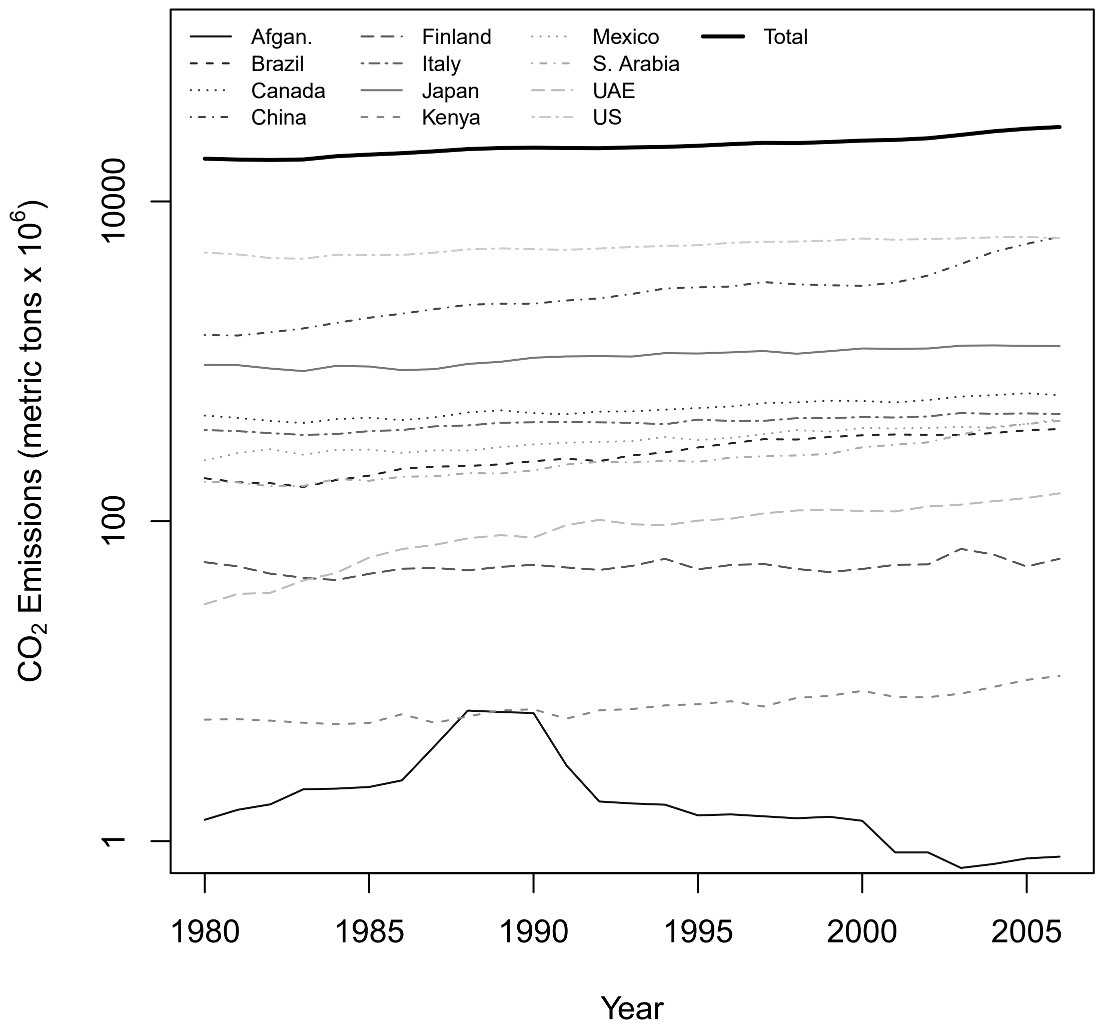


Figure 20 Line plot of world CO_2 emissions.

We see that the US and China have the highest emissions, and that China's emissions are increasing rapidly. Of additional interest, Afghanistan's CO_2 emissions peaked in the late 80's, then collapsed as a result of war and political strife.

Note that we log transform the *Y*-axis to allow better discrimination among low CO_2 emitting countries. Finally, we utilize the census data to create a line plot of per capita emissions by country (Figure 21)

```
wp.1 <- wp[,-c(1)]#get rid of the year column
per.cap <- (10^6) * co2.1/wp.1
```

```
matplot(seq(1980,2006,1), per.cap, type = "l", col = gray(seq(0 : 13)/15),
xlab = "Year", ylab = "Per capita emissions (metric tons)", lty = seq(1:6))

legend("topleft", col = gray(seq(0 : 13)/15), lty = seq(1:6), legend =
colnames(co2.1)[-13],cex = .8, bg = "white")
```

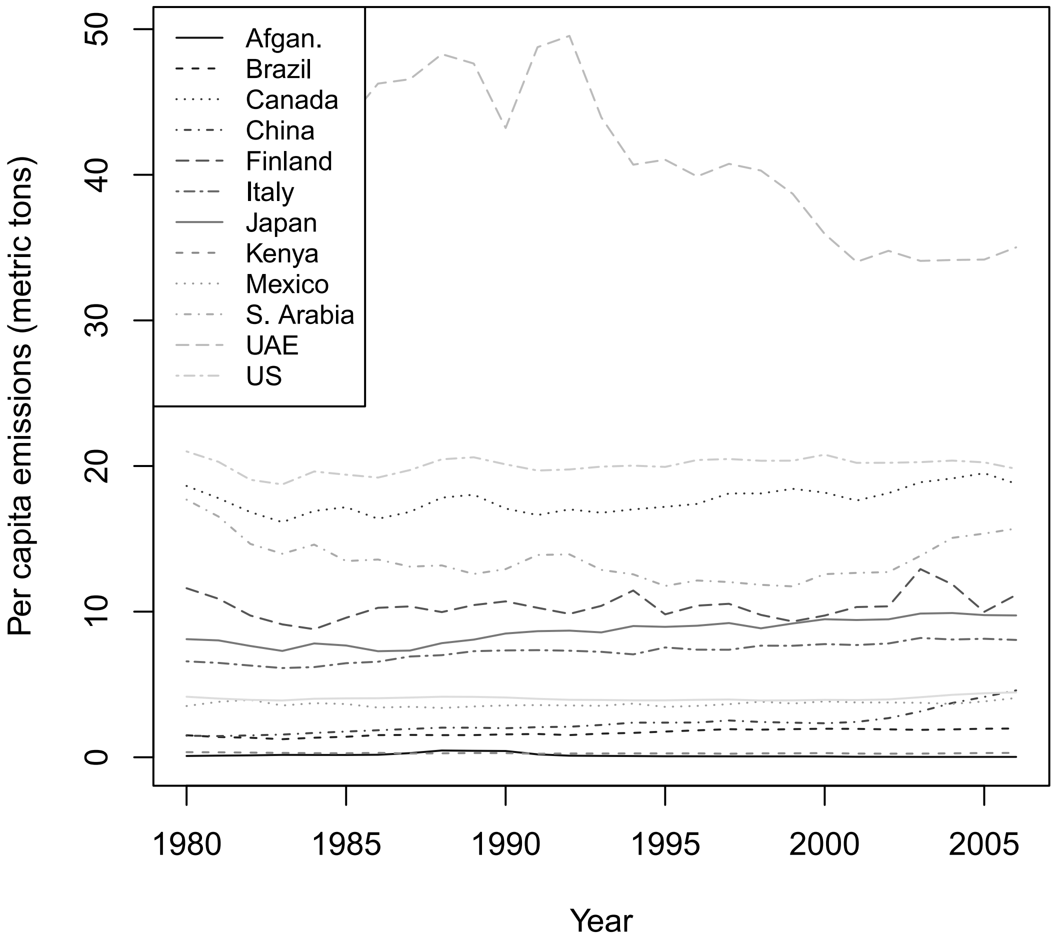


Figure 21 Per capita CO_2 emissions by country.

The United Arab Emirates has, by far, the highest levels of per capita CO_2 emissions.

9.16 Boxplots

Boxplots or **box and whisker plots** and their variants are an excellent way to quickly summarize and compare the distributions of levels in a categorical variable with respect to a quantitative variable. The function `boxplot` does this by graphically providing **a five number summary** for factor levels. Specifically, the upper and lower hinges of boxes from `boxplot` show the 1st and 3rd quartiles. The black stripe in the middle of each box shows the median. The whiskers extend to the most extreme data point which is no more than `coef` times the length of the box away from a hinge (by default `coef = 1.5`). Circle symbols are outlying observations (outside the whiskers).

|| Example 11

We can easily create a boxplot of the `slope` variable with respect to shallow or topographic position categories (Figure 17). The data appear to be positively skewed for most topographic categories.

```
with(brycesite, plot(slope ~ pos, ylab = "Slope (Degrees)", xlab =
"Topographic position"))
```

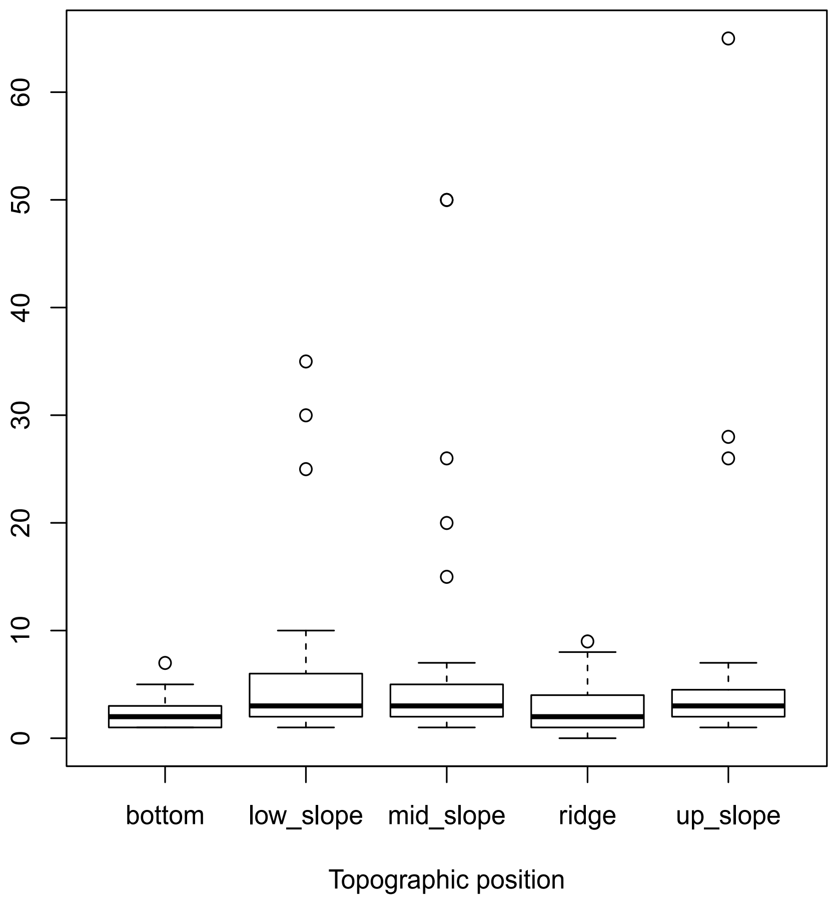


Figure 22 Slope versus topographic position for the `brycesite` dataset.

9.17 Interval plots

The function `bplot` from *asbio* is a wrapper for `barplot` that creates bars whose heights show location measures (e.g. means, medians, etc.), along with error bars representing, for each factor level, measures of dispersion. Error bar options include standard error (the default), standard deviation, confidence interval, interquartile range, median absolute deviation, or user defined errors. Thus, the function provides a conventional graphical complement to statistical procedures that compare location values of factor levels. Overlaying confidence intervals (the confidence levels in `bplot` are controlled with the argument `conf`) results in a frequently misinterpreted graphical summary called an **interval plot**.

|| Example 12

In Figure 23 is an interval plot of the `brycesite` slope variable with respect to topographic position categories. To better distinguish topographies, a gray color gradient is created using: `bar.col = gray(1:5/5)`.

```
library(asbio)

with(brycesite, bplot(slope, pos, ylab = "Slope (Degrees)", xlab =
"Topographic position", bar.col = gray(1:5/5)))
```

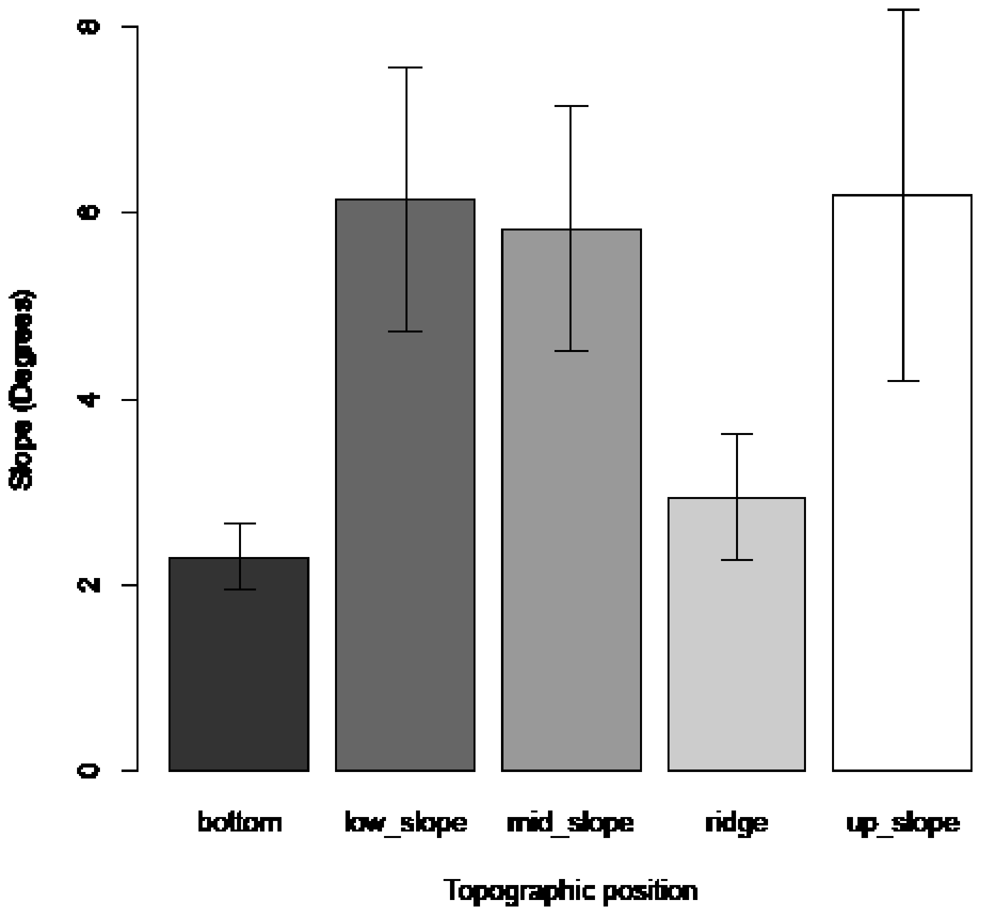


Figure 23 Slope means and standard errors for topographic levels from the `brycesite` dataset.

9.18 Three dimensional plots

When considering two quantitative variables as the function of a third quantitative variable, three dimensional plotting approaches are often useful.

|| Example 13 –Taiga/tundra vegetation in Scandinavia

To consider three dimensional plotting we will use two datasets from the library *vegan* describing Scandinavian taiga/tundra. Vegetation data are contained in the dataset `varespec` while soil chemistry data for the same sites are contained in the dataset `varechem`.

```
data(varespec)
data(varechem)
```

Let's look at the distribution of the heath plant *Vaccinium vitis-idaea* (a common species in boreal forest understories) with respect to both pH and % soil nitrogen (Figure 24). Note that we allow symbol sizes to change with the cover of *V. vitis-idaea.*

```
with(varechem, plot(N, pH, xlab = "% soil N", pch = 16, cex = varespec$Vac.
vit/100 * 15))
```

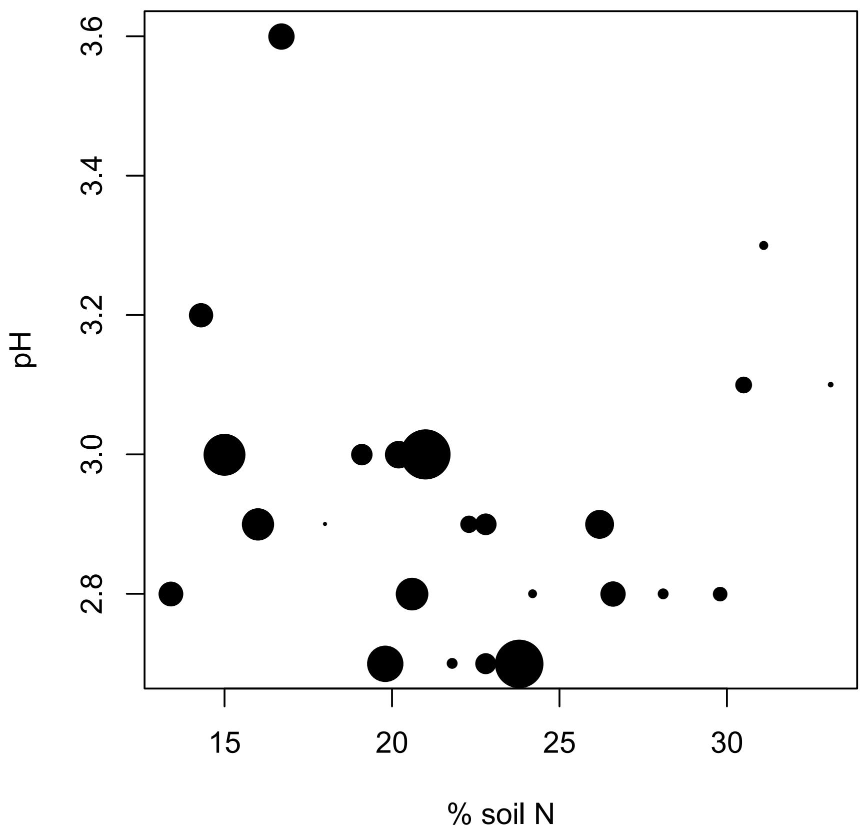


Figure 24 Cover of *Vaccinium vitis-idaea* with respect to pH and % soil nitrogen. Larger symbols indicate higher percent plant cover.

Vaccinium vitis-idaea appears to prefer intermediate to low levels of soil N, and acidic soils. The somewhat negative association between soil N and pH is probably due to soil leaching, because H^+ (and Al^{3+}) cations are more strongly adsorbed by soil colloids than bases in poorly drained soils.

A 3D plot of the same associations can be created using the **scatterplot3d** library (Figure 25).

```
install.packages("scatterplot3d"); library(scatterplot3d)
Fig <- function(angle = 55){
s3d <- scatterplot3d(cbind(varechem$N, varechem$pH, varespec$Vaccviti),
type="h", highlight.3d = TRUE,
angle = angle, scale = .7, pch = 16, xlab = "N", ylab = "pH", zlab = express
ion(paste(italic(Vaccinium), " ", italic(vitis-idaea), " % cover")))
lm1 <-lm(varespec$Vaccviti ~ varechem$N + varechem$pH)
s3d$plane3d(lm1)
}
Fig()
```

I define the figure to be a function (named `Fig`) to allow the angle of rotation for the 3D scatterplot to be easily changed using the `angle` argument in `Fig`. By stipulating `highlight.3d = TRUE` objects that are closer to us in the *X* plane are given warmer colors. A regression "plane" is also overlaid on the graph. The fitted plane is produced from a linear model (the command `lm`).

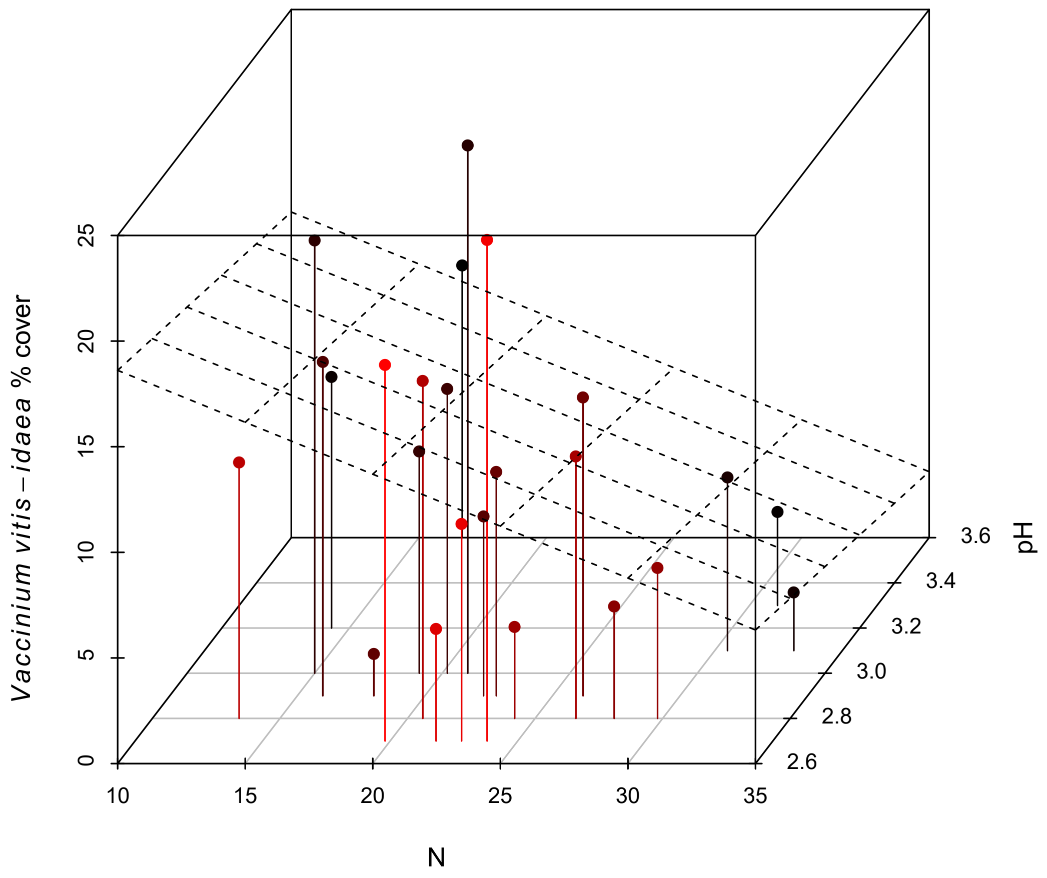


Figure 25 Cover of Vaccinium vitis-idaea in a 3D plot with respect to pH and % soil nitrogen.

9.19 Auxiliary graphics packages

There are a large number auxiliary packages in **R** specifically for graphics. Several of these, including the popular package *lattice* (Sarkar 2008) depend on the **Trellis graphical system**, so-called because it often utilizes a rectangular array of plots, resembling a garden trellis. The *lattice* package is implemented by *grid* low-level graphics (Murrel 2005; 2017) whose approach and arguments are non-analogous to **R**-base functions like `plot()`, discussed so far. Despite these differences, auxiliary graphics packages generally utilize the base graphics devices described in § 9.3, although see Murrell (2005).

|| Example 14

Figure 26 provides an example of graphics generation using the *lattice* package. The functions `levelplot()`, `contourplot()`, and `wireframe()` are *lattice* approaches for making three dimensional scatterplots and surfaces. The functions are most easily used when data are in a spatial grid format with row and column numbers defining evenly spaced intervals from some reference point, and cell responses themselves constituting "heights" for the *Z* (vertical) axis.

The popular `volcano` dataset, used here, describes the topography of Maungawhau / Mount Eden, a scoria cone in the Mount Eden suburb of Auckland, New Zealand. In this case, rows and columns represent 10m Cartesian intervals. The first row contains elevations (in meters above sea level) for Northernmost points, whereas the first column contains elevations of Westernmost points.

The argument `split` is a vector of 4 integers, `c(x,y,nx,ny)` used to position plots in a *lattice* multiple plot presentation.

```
library(lattice)
plot(levelplot(volcano, col.regions = heat.colors, xlab = "x", ylab =
"y"), split = c(1, 1, 1, 3), more = TRUE, panel.width = list(x = 6,units =
"inches"))

plot(contourplot(volcano, cuts = 20, label = FALSE, xlab = "x", ylab = "y",
col = "green"), split = c(1, 2, 1, 3), more = TRUE, panel.width = list(x =
6,units = "inches"))

plot(wireframe(volcano, panel.aspect = 0.7, zoom = 1, lwd = 0.01, xlab =
"x", ylab = "y", zlab = "z"), split = c(1, 3, 1, 3), more = FALSE, panel.
width = list(x = 6,units = "inches"))
```

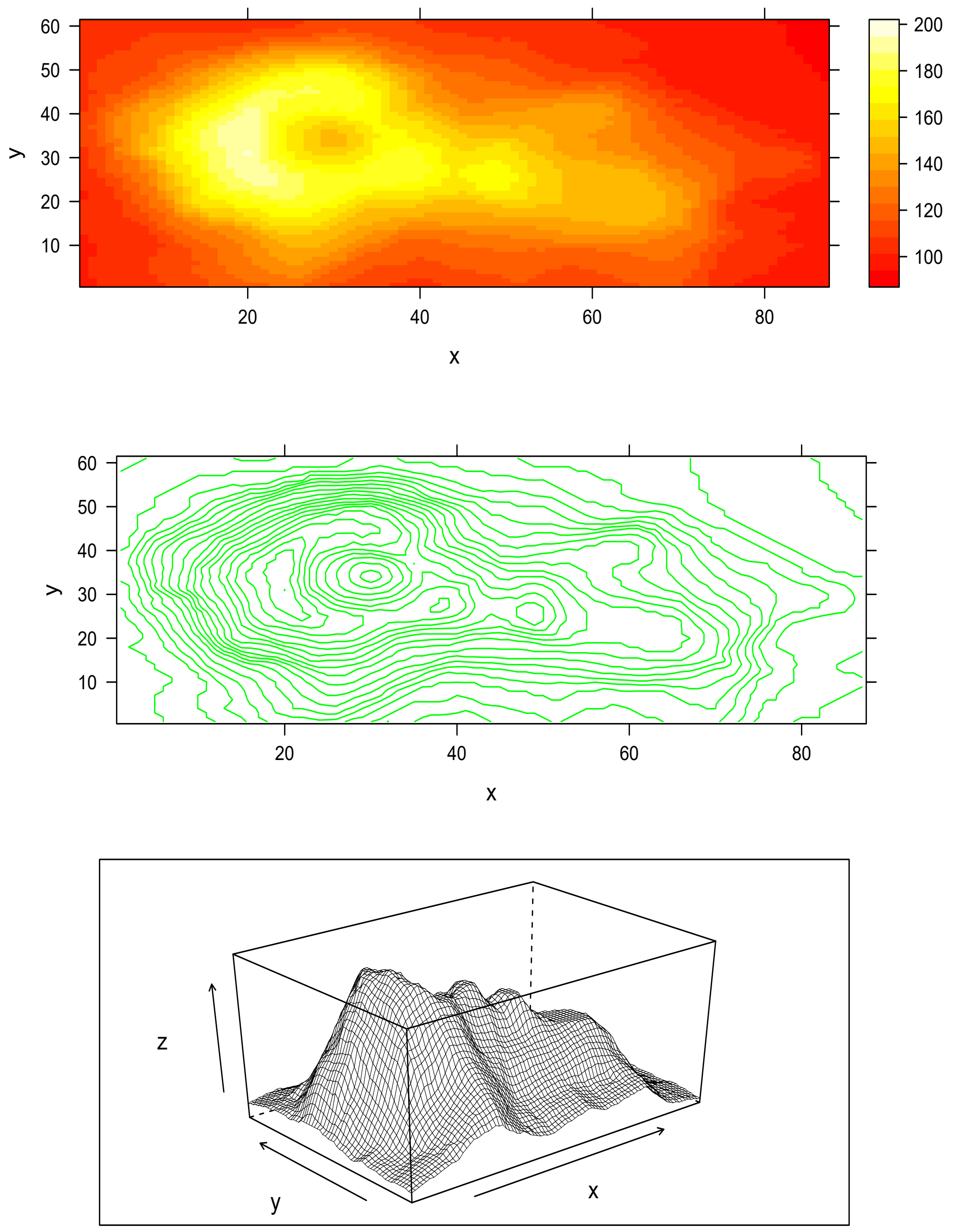


Figure 26 Maungawhau (Mt Eden), a volcano in the Auckland, New Zealand volcanic field.

ggplot2

A great deal of excitement has been generated by the *grid*-based graphics package *ggplot2* (formerly *ggplot*). Philosophically, *ggplot2* emulates Wilkinson's (2005) "grammar of graphics", which describes features that underlie all statistical graphics. According to its developer: "*ggplot2* ... tries to take the good parts of *base* and *lattice* graphics and none of the bad." A detailed description of *ggplot2* attributes can be found in Wickham (2009), and in the *ggplot2* manual (https://cran.r-project.org/web/packages/ggplot2/ggplot2.pdf).

Probably the easiest to use function in *ggplot2* is `qplot()` (for "quick plot"). The function was intended to be similar to `plot()` in some respects, and thus acts as a bridge from *base* R graphics. For instance, both `plot` and `qplot` call Cartesian coordinates in initial arguments for creation of scatterplots. The `qplot` function, however, can implement a wider array of plot types, and facilitate the creation overlays with the argument `geom`, short for geometric object.

Examples include, for bivariate relationships:

- Scatterplots → `geom = "point",` the default graphic if both `x` and `y` coordinates are supplied.
- Smoothers → `geom = "smooth",` fits a smoother and standard errors to quantitative bivariate data.
- Boxplots → `geom = "boxplot",` produces a box-and-whisker plot if `x` is categorical and `y` is quantitative.
- Line plot → `geom = "line",` Joins points with a line, from left to right.

For univariate displays (in which only x is supplied) useful geoms include:

- Histograms → `geom = "histogram",` fits a histogram
- Density plot → `geom = "density",` fits relative frequency curves that are constrained, like a probability density function, to have an area of one beneath the curve.

Other geoms can be layered atop a *ggplot2* graphic.

|| Example 15

Figure 27 applies three distinct geoms (`"smooth"`, `"line"`, and `"point"`) to the `varchem` variables representing soil pH and %N. A curvilinear association between pH and %N is shown by the smoother that was not apparent in a simple scatterplot, i.e., Figure 25.

```
library(ggplot2)

with(varechem, qplot(N, pH, xlab = "% soil N", geom = c("point", "smooth",
"line")))
```

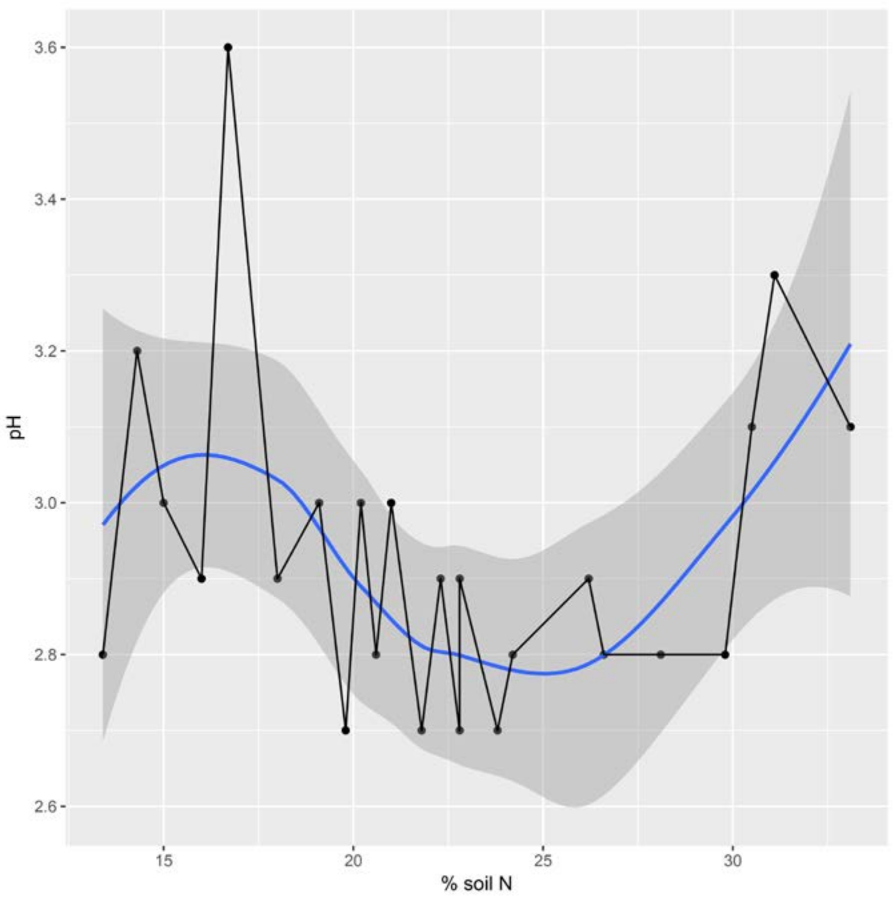


Figure 27 Plot of pH and % soil nitrogen from the `varechem` dataset. The shaded envelope shows standard errors of the smoother fit. The smooth is generated by the function `loess()`.

`qplot()` assumes that if defined with a vector, point colors (`qplot` argument `colours`) and point shapes (`qplot` argument `shape`), represent a categorical variable, causing the function to print a legend.

|| Example 16

Consider , which ostensibly remakes Figure 15 using `qplot()`.

```
Position <- brycesite$pos
with(brycesite, qplot(asp.val, annrad, xlab = "Aspect value", ylab = "An-
nual radiation (Langleys)", colour = Position, shape = Position))
```

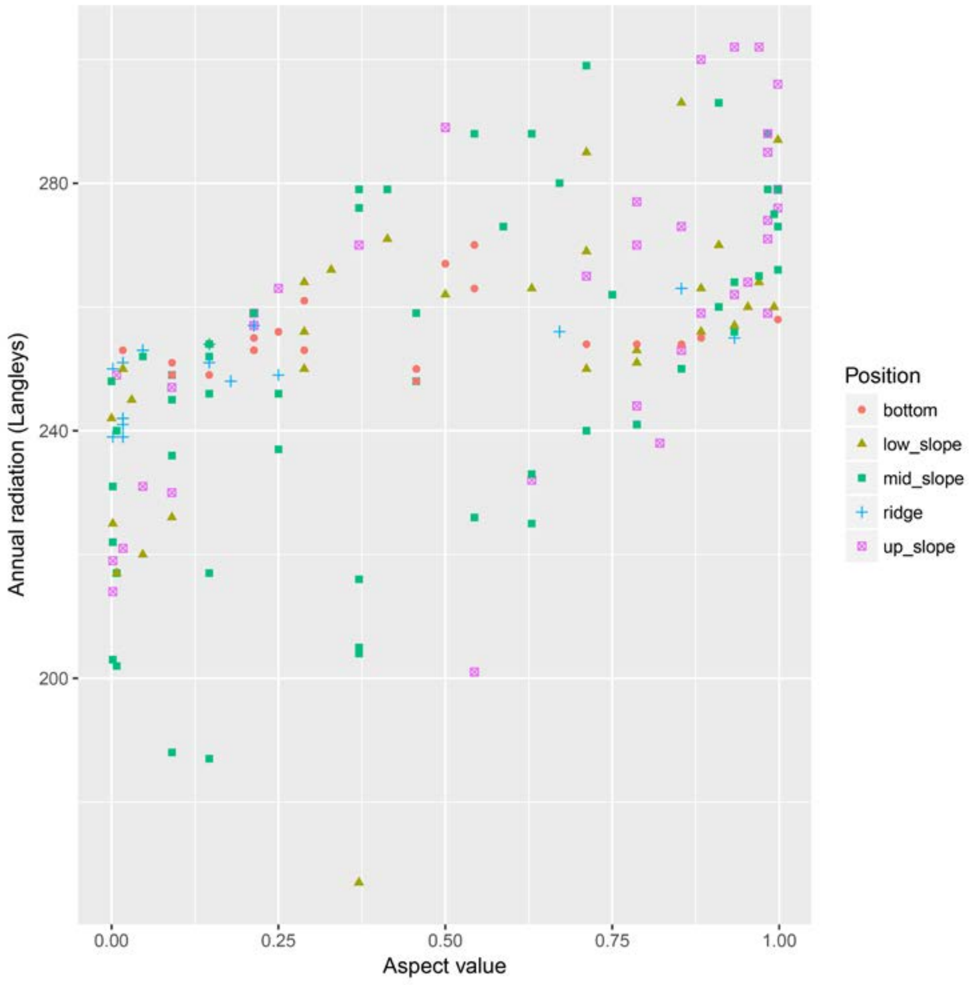


Figure 28 A remake of Figure 15 using `qplot()`.

One can modify characteristics of *ggplot2* graphics additively using the function `theme()`.

For instance, upon considering Fig , I find, along with other issues, that the margins are too narrow and the axis title and text are too small. Smoothers might be nice as well for each topographic type. Thus, I change the theme in the following ways:

```
p <- with(brycesite, qplot(asp.val, annrad, xlab = "Aspect value", ylab =
"Annual radiation (Langleys)",
colour = Position, shape = Position) +
## increase symbol size in plot and legend , disable SEs in smooths
geom_point(size=3) + geom_smooth(se = F))
## change margins
p <- p + theme(plot.margin = unit(c(1,1,1.25,1), "cm"))
## Increase y-axis label size
p <- p + theme(axis.title.y = element_text(size=13, hjust = 0.5, vjust =
7))
```

```
## Increase y-axis text size
p <- p + theme(axis.text.y = element_text(size=13))
## Increase x-axis label size
p <- p + theme(axis.title.x = element_text(size=13, vjust = -5))
## Increase y-axis text size
p <- p + theme(axis.text.x = element_text(size=13))
## Get rid of background grid
p <- p + theme(panel.background = element_rect(fill = "white"))
## Get rid of grey grid behind key
p <- p + theme(legend.key = element_rect(fill = "white"))
## Put in black border
p <- p + theme(panel.border = element_rect(fill = NA, color = "black"))
## Define legend position
p <- p + theme(legend.position = c(0.9, .15))
## print graph
p
```

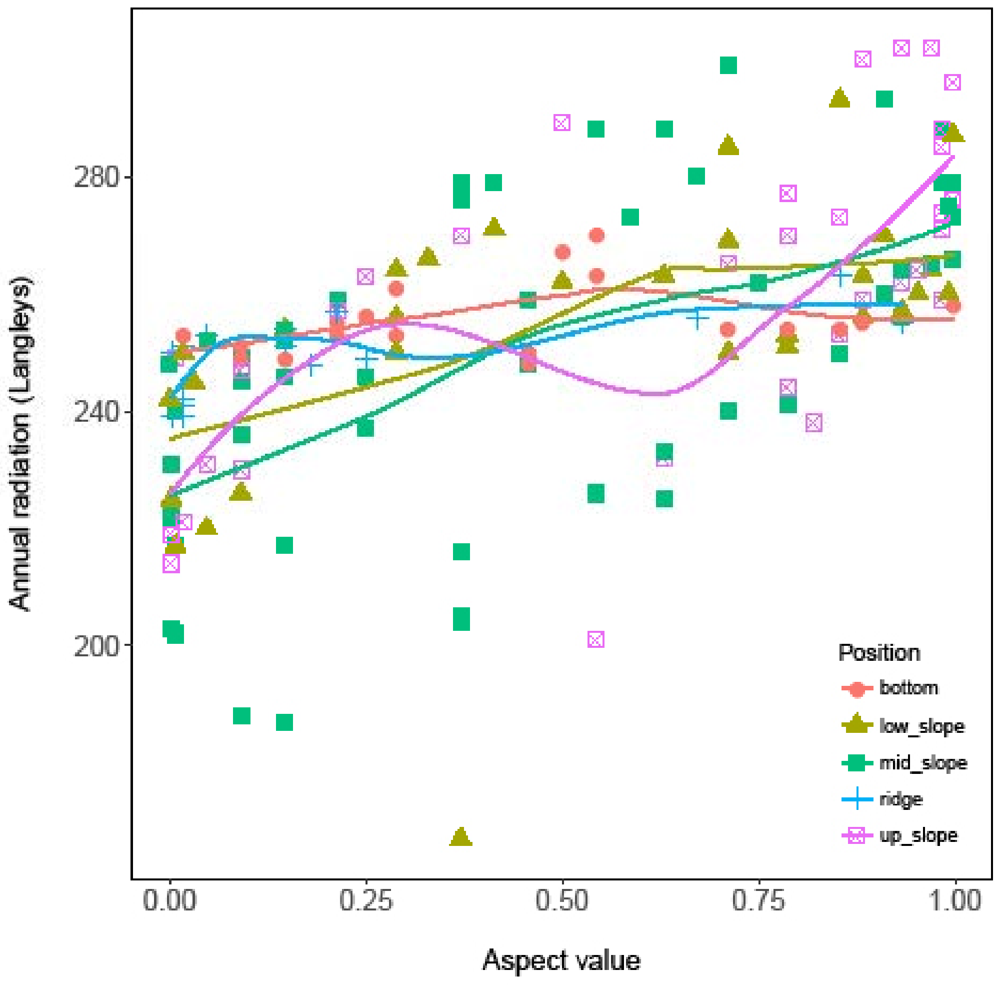


Figure 29 Result following `theme` edits to Figure 28.

10 Data structures

There are five primary data structures in **R**. We will use each of them repeatedly.

10.1 Vectors

In **R** a **vector** is collection of data with order and length, but no dimension. This is very different than the matrix algebra definition of a vector. In this case a **row vector** with *n* elements has dimension 1 x *n* (1 row and *n* columns), whereas a **column vector** has dimension *n* x 1. We can create vectors with the function `c`. Recall that `c` means combine.

```
x <- c(1, 2, 3)

is.vector(x)
[1] TRUE

length(x)
[1] 3

dim(x)
NULL

dim(as.matrix(x))
[1] 3 1
```

The function `as.matrix` coerces the vector `x` to have a matrix structure with dimension 3 x 1. Thus, in **R** a matrix (see below) has dimensions, but a vector does not. Elements in vectors must have a single data storage mode: e.g.,`"integer"`, `"double"`, `"complex"`, `"character"` . That is, a vector cannot contain both numeric and categorical data.

When an operation is simultaneously applied to two unequal length vectors, **R** will generate a warning and automatically **recycle** elements of the shorter vector, beginning with its first element, until it is has the same length as the longer one. For instance:

```
c(1, 2, 3) + c(1, 0, 4, 5, 13)
[1]  2  2  7  6 15
Warning message:
In c(1, 2, 3) + c(1, 0, 4, 5, 13) :
longer object length is not a multiple of shorter object length
```

In this case the result of the addition of the two vectors is 1 + 1, 2 + 0, 3 + 4, 1 + 5, and 3 + 13. This is because the first two elements in the first object are recycled in the addition. **R** users should obviously be aware of default presence of recycling and its potentially detrimental effects to analyses.

10.2 Matrices

Matrices are two-dimensional (row and column) data structures whose elements are all comprised of a single type of data: quantitative, categorical, or ordinal. The function `matrix` can be used to create matrices.

```
a <- c(1, 2, 3, 2, 3, 4)
matrix(ncol = 2, nrow = 3, data = a)
   [,1] [,2]
[1,]    1    2
[2,]    2    3
[3,]    3    4
```

10.3 Arrays

Arrays are one, two (matrix), or three or more dimensional data structures whose elements contain a single type of data. The function `array` can be used to create arrays. Below we create a 2 x 2 x 2 array using data using the object `a` from above.

```
a <- c(1, 2, 3, 4, 5, 6, 7, 8)
array(a, c(2, 2, 2))
, , 1

     [,1] [,2]
[1,]    1    3
[2,]    2    4

, , 2

     [,1] [,2]
[1,]    5    7
[2,]    6    8
```

The first argument in `array` defines the data, while the second argument is a vector that defines both the number of dimensions (this will be the length of the vector) and the number of levels in each dimension (numbers in dimension elements). The function above took the first half of observations in the object `a` and put them in the first level of component 1. It put the other four observations in the second level of component 1. The four elements in each component are arranged into 2 x 2 matrices.

Arrays are useful for containing results made up of multiple matrices or dataframes (see below). For instance, a Markov Chain Monte Carlo (MCMC) analysis of the dataset `cuckoo` requires six parameters, each of which will be described with multiple Markov chains. Below I specify the creation of two chains, each comprised of three steps. The output is an array.

```
data(cuckoo); mcmc.norm.hier(cuckoo, 3, 2)
, , Chain# 1

    theta1   theta2   theta3       mu      s.sq    tau.sq
1 23.25000 23.85000 23.85000 23.65000 1.7612736 0.0551980
2 23.71469 23.29092 23.33157 23.33031 1.3925030 2.8243915
3 23.37465 22.92141 22.55939 22.73779 0.8880371 3.9218969

, , Chain# 2
    theta1   theta2   theta3       mu      s.sq    tau.sq
1 23.85000 23.05000 23.05000 23.31667 0.7906798  1.473440
2 23.13697 23.26426 22.78453 24.19186 0.8380785  4.067955
3 23.17203 23.25774 22.59440 22.41249 0.5772941 46.341983
```

10.4 Dataframes

Dataframes are two-dimensional data structures whose columns can contain different types of data, e.g. quantitative or categorical. Note that all data in a single column must be of the same class, e.g. `numeric`, `factor`, etc. Each column and row in a dataframe may be given an identifying label. Labels can be assigned in a number of ways, including within the `data.frame` function (see example below). Confusingly, dataframe columns can be named with the function `names`, whereas a parallel approach with a matrix object requires the function `colnames`. The function `rownames` works for assigning row names in both dataframes and matrices. Columns can be called by name in a dataframe using the functions `attach` or `with`, or the operator `$`.

Here we apply the function `data.frame` to create a dataframe called `data`.

```
data <- data.frame(numeric = c(1, 2, 3), non.numeric = c("a", "b", "c"))
data
  numeric non.numeric
1       1           a
2       2           b
3       3           c
```

Here we access the column in `data` called `non.numeric`.

```
data$non.numeric
[1] a b c
Levels: a b c
```

10.5 Lists

Lists are often used to contain miscellaneous associated objects. Like dataframes, lists need not contain a single type of data (e.g. categorical or quantitative). Unlike dataframes, however, lists can simultaneously include objects with different data classes including **strings** (i.e. units of character variables), matrices, dataframes and even other lists. Thus, lists do not require a row-column structure, and list components need not be the same length. Recall that the **R**-object we produced earlier, `ha.lm`, from the creation of a linear model, was a list. Like dataframes, objects in lists can be called using the expression `$`. The function `list` can be used to create lists.

```
data <- list(a = c(1, 2, 3), b = "this.is.a.list")
data
$a
     [,1]
[1,]    1
[2,]    2
[3,]    3

$b
[1] "this.is.a.list"
```

List elements can also be identified using double square brackets. Below is the first list component of the list `data`.

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

|| Example 17 -- Downs syndrome data

Let's create a dataframe with three numeric columns using data in Table 4. Note that this is part of a dataset for Down's syndrome collected in British Columbia by the British Columbia Health Surveillance Registry (Geyer 1991).

Table 4 British Columbia Down's syndrome data.

Mothers age	Number of births	Number of Down's syndrome cases
17	13555	16
20.5	22005	22
21.5	23896	16
29.5	15685	9
30.5	13954	12
38.5	4834	15
39.5	3961	30
40.5	2952	31
44.5	596	22
45.5	327	11
47	249	7

We will give this data subset the name `Downs`.

```
Downs <- data.frame(Age = c(17, 20.5, 21.5, 29.5, 30.5, 38.5, 39.5, 40.5,
44.5, 45.5, 47), Births = c(13555, 22005, 23896, 15685, 13954, 4834, 3961,
2952, 596, 327, 249), Cases = c(16, 22, 16, 9, 12, 15, 30, 31, 22, 11, 7))
```

```
Downs
    Age Births Cases
1  17.0  13555    16
2  20.5  22005    22
3  21.5  23896    16
4  29.5  15685     9
5  30.5  13954    12
6  38.5   4834    15
7  39.5   3961    30
8  40.5   2952    31
9  44.5    596    22
10 45.5    327    11
11 47.0    249     7
```

Columns in `Downs` can be called without attaching the dataframe by using the `$` expression.

```
Downs$Age
[1] 17.0 20.5 21.5 29.5 30.5 38.5 39.5 40.5 44.5 45.5 47.0
```

We can also assemble items from `Downs` into a list. For instance:

```
Dlist <- list(age = Downs$Age, births = Downs$Births, message = "Data from the
British Columbia health surveillance registry")
```

```
Dlist
$age
[1] 17.0 20.5 21.5 29.5 30.5 38.5 39.5 40.5 44.5 45.5 47.0

$births
[1] 13555 22005 23896 15685 13954  4834  3961  2952   596   327   249

$message
[1] "Data from the British Columbia health surveillance registry"
```

11 Data entry at the command line

A question of obvious importance is: "how do I get my data into **R**?" The answer is: "two ways." First, one can enter data "by hand" at the command line. Second, one can read in data files. We concentrate on command line entry in this section. Data import is described in § 12.

11.1 `scan`, `cbind`, `rbind`

As we know data can be combined into a single entity with the function `c`.

```
a <- c(1, 2, 3); b <- c(2, 3, 4)
```

To create an **R**-object containing character strings, e.g., a categorical variable, we will need to place quotation marks around entries.

```
x <- c("low", "med", "high")
x
[1] "low"  "med"  "high"
```

Command line data entry is made easier with the function `scan` (which can also be used for file import) because a prompt is given for each data point, and separators are created by the function itself. For instance:

```
a <- scan()
1: 1 2 3
4:
Read 3 items
```

The function will be terminated by a blank line or an **end of file** (**EOF**) signal. These will be Ctrl+D in Unix and Ctrl+Z in Windows.

We can use `cbind` to combine columns,

```
cbind(a, b)
     a b
[1,] 1 2
[2,] 2 3
[3,] 3 4
```

while `rbind` lets us combine rows.

```
rbind(a, b)
  [,1] [,2] [,3]
a    1    2    3
b    2    3    4
```

We see that the objects `a` and `b` can be interpreted either as columns or rows.

11.2 Facilitating command line entry: `seq` and `rep`

R has a number of functions that can speed up command line data entry. For instance, what if I want to create a sequence from 1990 to 2008? I would type: `seq(1990, 1998)`, or `seq(1990 : 1998)`, or simply

```
1990 : 2008
[1] 1990 1991 1992 1993 1994 1995 1996 1997 1998
```

The first two arguments in `seq` are the start and end of the sequence (unless a sequence is specified in the first argument). The third argument specifies the increment between items in the sequence. For example, if I wanted the vector 1990, 1992, 1994, 1996, 1998, I could simply type:

```
seq(1990, 1998, 2)
[1] 1990 1992 1994 1996 1998
```

One can easily create a vector with repeated values using the function `rep`. For example, to repeat the sequence 1991, 1992, 1993, 1994 ten times. I could type:

```
rep(c(1991, 1992, 1993, 1994), 10)
 [1] 1991 1992 1993 1994 1991 1992 1993 1994 1991 1992 1993 1994 1991 1992 1993
[16] 1994 1991 1992 1993 1994 1991 1992 1993 1994 1991 1992 1993 1994 1991 1992
[31] 1993 1994 1991 1992 1993 1994 1991 1992 1993 1994
```

The first argument, `c(1991, 1992, 1993, 1994)`, defines the thing we want to repeat. The second argument, `10`, specifies the number of repetitions.

Using these foundations we can create extremely complex sequences. For instance, to compose a sequence in which 1991, 1992, and 1993 were each repeated twice, and then to repeat that sequence three times we have:

```
rep(1991 : 1993, each = 2, times = 3)
[1] 1991 1991 1992 1992 1993 1993 1991 1991 1992 1992 1993 1993 1991 1991 1992
[16] 1992 1993 1993
```

12 Importing data into R

While it is possible to enter data into **R** at the command line (§ 11) this will normally be inadvisable except for small datasets. In general it will be much easier to import data.

R can import data from many different kinds of formats including .txt, and .csv (comma separated) files, and files with space, tab, and carriage return datum separators. I generally organize my datasets using Excel or some other spreadsheet program (although **R** can handle much larger datasets than these platforms; § 12.5), then save them as .csv files. I then import the .csv files into **R** using the `read.table`, `read.csv`, or `scan` functions. The function `load` can be used to import data files in rda data formats, or other **R** objects. The program R studio (§ 21.12) allows menu-driven import of file types from a number of spreadsheet and statistical packages including Excel®, SPSS®, SAS®, and Stata®, making the sections below largely unnecessary.

12.1 `read.table`

In the code below I use `read.table` to import a data file called veg.csv which is located within a series of nested directories in my C drive. Missing data in the file are indicated with periods.

```
read.table("C:/Users/User/Documents/veg.csv", sep = ",", header = TRUE, row.names
= 1, na.strings = ".")
```

The first three arguments from `read.table` are very important.

- The first argument, `file`, refers to the location and name of the file. Above, I specify: `file = "C:/Users/User/Documents/veg.csv"`.
- The second argument, `header`, refers to the dataset column names. If we specify `header = TRUE` this indicates that the first row of dataset are column names. By default `header = FALSE`, and the function gives column names as `"V"` (for variable) followed by the column number.
- The third argument, `sep`, refers to the type of data separator used. Comma separated files use commas to distinguish data entries. Thus I specify `sep = ","` above. Other common separators include tabs, specified as `"\t"` and spaces, specified as `" "`.

Other useful `read.table` arguments include `row.names` and `na.strings`:

- By specifying `row.names = 1` I indicate that the first column of data contains row names.
- The argument `na.strings = "."` indicates that missing values in the imported dataset are designated with periods. **R** uses the term `NA` to indicate "not available". Blank fields are considered by **R** to be missing values and are given `NA` entries upon import.

Note that **R** locates files using forward slashes rather than backslashes. To use backslashes one must double them; a legacy of **R**'s development under Unix/Linux. Consider the file above described above

```
read.table("C:\\R.data\\veg.csv", sep = ",", header = T, row.names = 1, na.strings
= ".")
```

Data can also be read directly from the working directory. For instance:

```
read.table("veg.csv", sep = ",", row.names = 1, header = T)
```

12.2 `read.csv`

The function `read.csv` has the same arguments as `read.table` with the exception that data separators are assumed to be commas, precluding the necessity of the `sep` argument. Thus, for the example above we would have:

```
read.csv("veg.csv", header = TRUE, row.names = 1, na.strings = ".")
```

12.3 `scan`

The function `scan` can read in data from an essentially unlimited number of formats, and is extremely flexible with respect to character fields and storage modes of numeric data

In addition to arguments used by `read.table`, `scan` has the arguments:

- `what` which describes the storage mode of data e.g., `logical`, `integer`, etc., or if `what` is a list, components of variables including column names (see below), and
- `dec` which describes the decimal point character (European scientists and journals often use commas).

Assume that veg.csv has column of species names, called `species`, that will serve as row names, and 3 columns of numeric data, named `site1`, `site2`, and `site3`. We would read the data in with `scan` using:

```
scan("veg.csv", what = list(species = "", site1 = 0, site2 = 0, site3 = 0),
na.strings = ".")
```

The empty string `species = ""` in the list comprising the argument `what`, indicates that `species` contains character data. Stating that the remaining variables equal 0, or any other number, indicates that they contain numeric data.

12.4 Easy imports: use of `file.choose()`

Possibly the easiest way to import data is to use `read.csv`, `read.table`, or `scan` with `file.choose` function as the `file` argument. For instance, by typing:

```
read.csv(file.choose())
```

we can now browse for .csv files to open.

Other arguments (e.g., `header`, `row.names`) will need to be used, when appropriate, to import the file correctly.

12.5 Additional comments

It is generally recommended that datasets imported and used by **R** be smaller than 25% of the physical memory of the computer. For instance, they should use less than 3GB on a 32-bit operating system. Note that this still equates to a roughly 13,700 x 8000 element data array. **R** can handle **extremely** large datasets, i.e. > 10GB, and > 1.2 x 10^{10} rows. In this case specific **R** packages can be used to aid in efficient data handling. Parallel "cluster" computing and workstation modifications may allow even greater efficiency. The actual upper physical limit for an **R** dataframe is 2 x 10^{31}-1 elements. Note that this exceeds the latest limits for Excel worksheets by 21 orders of magnitude (Excel 2010 worksheets can handle approximately 1.7 x 10^{10} cell elements).

R allows interfacing with a number relational database storage platforms. These include open source entities that express queries in **SQL** (**Structured Query Language**). For more information see Chambers (2008, pg. 178) and Adler (2010, pg. 157).

13 Exporting data from R

It is easy to export data from **R**.

The functions `write.table` and `write.csv` let one write output for a large number of formats. For example, the commands below will write the matrix `test` to the working directory as a .csv file.

```
test <- matrix(nrow = 2, ncol = 2, data = c(2, 1, 3, 4))
write.csv(test, "test.csv", sep = ",")
```

- The first argument in `write.table` is the object I wish to export, i.e. `test`.
- The second argument tells **R** where to export the object, and the storage name of the object.
- The third argument, `sep`, tells **R** what kind of separator to use to distinguish data entries. The function `write.csv` facilitates the creation of .csv spreadsheets and assumes `sep = ","`.

Several other optional arguments in `write.table` are important.

- `col.names = TRUE` indicates that the first row of data are column names.
- `row.names = 1` indicates that the first column of data are row names.
- `na = "NA"` indicates that missing values are specified in the data matrix with `"NA"`.

We can also use the `write.table` command to "copy" data to a **clipboard**. For instance:

```
write.table(test, "clipboard", sep = "\t", col.names = NA)
```

Now we can go to Excel® or Word® or some other program and paste the information using toolbars or Crtl+V.

One can save a function, dataframe, or data matrix as a binary `.rda` or `.RData` file using the `save` function. For instance:

```
save(test,file = "test.RData")
```

saves `test.RData` to the working directory.

14 Subsetting matrix, dataframe and array components

R allows us to easily specify particular subsets of dataframe, matrix or array using subset brackets, i.e. `[ ]`. Gaining skills with subsets will greatly enhance one's ability to manipulate datasets in **R**.

A dataframe or matrix name followed by brackets with a comma preceding a number inside the brackets, indicates a column number, i.e. `[,column number]`. For instance, the command `Downs[,1]` specifies column 1 in the dataframe `Downs` defined on page 74.

```
Downs[,1]
[1] 17.0 20.5 21.5 29.5 30.5 38.5 39.5 40.5 44.5 45.5 47.0
```

A dataframe or matrix name followed by brackets with a comma following a number inside the brackets, indicates a row number, i.e., `[row number,]`. For instance, the command `Downs[1,]` specifies row 1 in `Downs`.

```
Downs[1,]
    Age Births Cases
1  17  13555    16
```

Brackets without commas can be used to subset individual elements in a data matrix. It should be noted that by default **R** reads datasets by column. For instance, the command `Downs[16]` indicates the sixteenth element in the `Downs` dataset, which also happens to be fifth element in column 2.

```
Downs <- as.matrix(Downs)
Downs[16]
[1] 13954
```

Note that in the operation above I convert the `Downs` dataframe to a matrix. This will force the subset (element 16) to work correctly. For more information on coercing **R**-objects see § 18.

The command `Downs[1, 1]` or `Downs[c(1, 1)]` specifies element 1 in column 1.

```
Downs[1, 1]
Age
 17
```

The command `Downs[c(5:8),]` specifies rows 5 through 8 in `Downs`.

```
Downs[c(5:8),]
   Age Births Cases
5 30.5  13954    12
6 38.5   4834    15
7 39.5   3961    30
8 40.5   2952    31
```

The command `Downs[-c(5:8),]` specifies `Downs` without rows 5 through 8

```
Downs[-c(5:8),]
    Age Births Cases
1  17.0  13555    16
2  20.5  22005    22
3  21.5  23896    16
4  29.5  15685     9
9  44.5    596    22
10 45.5    327    11
11 47.0    249     7
```

Rows, columns, and layers from arrays can also be accessed using subset brackets. For instance, to obtain all the row and columns from the second layer of the array `obj` I would type:

```
obj[, , 2]
```

Note: when a subset results in zero observations for a level in a categorical variable, then it will be useful to use `droplevels()` to remove the empty levels. This is because **R** will consider these levels to still be an implicit part of the subset data, potentially complicating or preventing analyses.

Dataframe columns can also be accessed by name when using square brackets.

```
Downs["Age"]
    Age
1  17.0
2  20.5
3  21.5
4  29.5
5  30.5
6  38.5
7  39.5
8  40.5
9  44.5
10 45.5
11 47.0
```

15 Operations on matrices and dataframes

Operators can be applied individually to every row or column of a matrix using a number of time saving methods. Actual **R**-applications for linear algebra (e.g. matrix multiplication, matrix inverses, eigenanalysis and matrix decompositions) are described in the mathematical Appendix in the **Foundational and Applied Statistics** textbook.

|| Example 18

As a simple example we will plot Down's syndrome cases per live birth from the `Downs` dataset. To do this I would simply divide the `Cases` column by the `Births` column and plot the result as a function of `Age` (Figure 30). To accomplish this using variable (column) names we first coerce (§ 18) `Downs` back into a dataframe.

```
Downs <- as.data.frame(Downs) #coerce back to dataframe
with(Downs, plot(Age, Cases/Births))
```

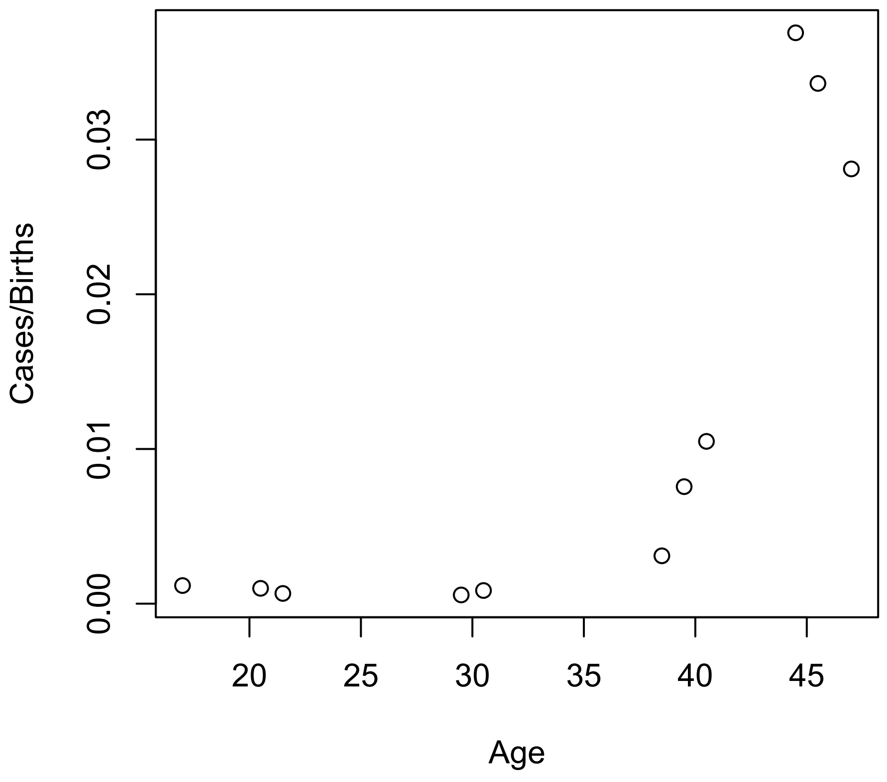


Figure 30 The rate of Down's syndrome births as a function of mother's age.

Converting back to a data frame allows the column names in `Downs` to be recognizable. We can see that the rate of Down's syndrome increases dramatically in older mothers.

15.1 `apply`

Operations can be performed quickly on matrices with the function `apply`. The function requires three arguments.

- In the first argument, `X`, we specify a matrix, array, or dataframe to be analyzed.
- In the second argument, `MARGIN`, we specify whether rows or columns are to be analyzed (`1` indicates rows, `2` indicates columns, while `c(1, 2)` indicates rows and columns).
- In the third argument, `FUN`, we specify a function to be applied to the margins of the object in the first argument.

```
max.val <- apply(Downs, 2, max)
max.val
   Age Births  Cases
    47  23896     31
```

In the operation above I created an object called `max.val` that contains the maximum value from each column of `Downs`. Similarly the command below creates a vector made up of the minimum responses at each row.

```
min.val <- apply(Downs, 1, min)
min.val
[1] 16.0 20.5 16.0  9.0 12.0 15.0 30.0 31.0 22.0 11.0  7.0
```

We can use the `apply` command to apply any statistical function (i.e. `mean, sd, median` etc.) to all the rows and/or columns of a matrix.

```
means <- apply(Downs, 2, mean)
means
       Age     Births      Cases
  34.04545 9274.00000   17.36364
```

Several summary statistical functions exist for matrices that can be used in the place of `apply`. These include `rowMeans` and `colMeans` which give the sample means of specified rows and columns, respectively, and `rowSums` and `colSums` which give the sums of specified rows and columns, respectively. For instance:

```
colMeans(Downs)
      Age     Births      Cases
  34.04545 9274.00000   17.36364
```

15.2 **`tapply`**

Imagine that we have a categorical variable in the `Downs` dataset with two factor levels (categories). The first factor level is associated with the first 6 experimental units, while the second level is associated with the last 5 experimental units. That is,

```
Categories <- factor(c(rep(1, 6), rep(2, 5)))
cbind(Downs, Categories)
    Age Births Cases Categories
1  17.0  13555    16          1
2  20.5  22005    22          1
3  21.5  23896    16          1
4  29.5  15685     9          1
5  30.5  13954    12          1
6  38.5   4834    15          1
7  39.5   3961    30          2
8  40.5   2952    31          2
9  44.5    596    22          2
10 45.5    327    11          2
11 47.0    249     7          2
```

The mixture of categorical and quantitative variables is allowed because `Downs` is a dataframe.

We can easily summarize our data with respect to the categories in `Categories` by using the function `tapply`. Like `apply`, `tapply` requires three arguments.

- The first argument, `X`, specifies which vector to evaluate.
- The second argument, `INDEX`, will be vector of categories that can be used to subset `X`.
- The third argument, `FUN`, describes the function to be applied to `X` for each level in `INDEX`.

```
 tapply(X = Downs[,2], INDEX = Categories, FUN = mean)
       1        2
15654.83  1617.00
```

15.3 **`outer`**

Another important function for matrix operations is the function `outer`. The function lets us create an array that contains all possible combinations of two vectors or arrays with respect to a particular function. For example, suppose I wished to find the mean of all possible pairs of observations from a vector. I would type the following commands:

```
 x <- c(1, 2, 3, 5, 4)
o <- outer(x, x, "+")/2
o
[,1] [,2] [,3] [,4] [,5]
[1,]  1.0  1.5  2.0  3.0  2.5
[2,]  1.5  2.0  2.5  3.5  3.0
[3,]  2.0  2.5  3.0  4.0  3.5
[4,]  3.0  3.5  4.0  5.0  4.5
[5,]  2.5  3.0  3.5  4.5  4.0
```

The upper and lower triangles of the matrix `o` contain the pairwise means while the diagonal contains the means of the objects with themselves. That is, the diagonal contains the original data in `x`.

15.4 `lower.tri`, `upper.tri` and `diag`

We can use the commands `lower.tri`, `upper.tri` and `diag` to examine the upper triangle, lower triangle, and diagonal parts of a matrix. For instance,

```
 o[upper.tri(o)]
[1] 1.5 2.0 2.5 3.0 3.5 4.0 2.5 3.0 3.5 4.5
o[lower.tri(o)]
[1] 1.5 2.0 3.0 2.5 2.5 3.5 3.0 4.0 3.5 4.5
diag(o)
[1] 1 2 3 5 4
```

Note that I use square brackets to subset the data in `o`.

15.5 `stack` and `unstack`

When manipulating matrices and dataframes it is often useful to stack and unstack columns. These operations are handled with the functions `stack` and `unstack`. Consider the 4 x 4 dataframe below.

```
s <- data.frame(matrix(nrow=4, ncol=4, rnorm(16)))
s
            [,1]       [,2]       [,3]       [,4]
[1,] -0.08879353  0.5075496  0.8077366  0.6685438
[2,] -0.84689275 -1.1091304 -0.1530534 -1.7209322
[3,]  2.33278611  1.1339444 -0.3599148  0.2705621
[4,]  0.06433390  0.2264004  0.2190580  0.3001240
```

The command `rnorm(16)` generates 16 random values from a standard normal distribution (Ch. 3). Say that we wish to assign distinct treatments to the columns and stack them. Applying `stack` we have:

```
st <- stack(s)
st
        values ind
1  -0.04941294  X1
2  -1.37260663  X1
3   2.21704986  X1
4   0.89460072  X1
5   0.25489102  X2
6   0.81068275  X2
7   1.04691132  X2
8  -0.83447166  X2
9   2.72308681  X3
10  0.48653472  X3
11  0.12804772  X3
12  0.89494172  X3
13 -0.54162277  X4
14 -1.11219031  X4
15 -1.60632784  X4
16  0.32180719  X4
```

Unstacking we have:

```
unstack(st)
           X1         X2        X3         X4
1 -0.04941294  0.2548910 2.7230868 -0.5416228
2 -1.37260663  0.8106827 0.4865347 -1.1121903
3  2.21704986  1.0469113 0.1280477 -1.6063278
4  0.89460072 -0.8344717 0.8949417  0.3218072
```

16 Logical commands

Computer languages like **R** that can dichotomously classify true and false statements are called logical or **Boolean**. **R** uses the following logical operators:

- `>` "greater than"
- `>=` "greater than or equal to"
- `<` "less than"
- `<=` "less than or equal to"
- `==` "equal to"
- `!=` "not equal to"
- `&` "and"
- `|` "or"

In **R** logical queries, comparisons, or commands will return the Boolean categories `TRUE` and `FALSE`.

|| Example 19

We will demonstrate the use of logical commands with the `Downs` dataset.

```
attach(Downs)
Age >= 30
 [1] FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
Age != 30.5
 [1]  TRUE  TRUE  TRUE  TRUE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
Age != 30.5&Age < 40
 [1]  TRUE  TRUE  TRUE  TRUE FALSE  TRUE  TRUE FALSE FALSE FALSE FALSE
Age < 30.5|Age == 47
[1]  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE
```

We can subset data with logical commands by using square brackets. For instance the following code requests age data in the `Downs` dataset less than 30.5, or equal to 47.

```
Age[Age < 30.5|Age == 47]
[1] 17.0 20.5 21.5 29.5 47.0
```

Using the function `subset` we have:

```
subset(Age, Age < 30.5|Age == 47)
[1] 17.0 20.5 21.5 29.5 47.0
```

R allows users to use `T` and `F` in the place of `TRUE` and `FALSE`, although this may result in problems if you have variables named `T` or `F`.

16.1 `ifelse`

A number of functions can be used in combination with a logical argument to evaluate a vector and provide outcomes if the argument is true or false. One example is the `ifelse` function. It requires three arguments

- The first argument, `test`, gives the logical test to be evaluated.
- The second argument, `yes`, provides the output if the test is true.
- The third argument, `no`, provides the output if the test is false. For instance:

```
ifelse(Age < 25, "Young", "Not so young")
 [1] "Young"        "Young"        "Young"        "Not so young" "Not so young"
 [6] "Not so young" "Not so young" "Not so young" "Not so young" "Not so young"
[11] "Not so young"
```

16.2 `if`, `else`, `any`, and `all`

A more generalized approach to providing a condition and then defining the consequences uses the functions `if` and `else`. For instance:

```
if(any(Age < 25))"Young" else "Not so Young"
[1] "Young"
```

The `any` function looks through the vector Age to see if *any* of the elements meet the specified criterion. Conversely, the function `all` will look through a vector or vectors to see if *all* of the specified elements meet the specified criterion.

```
if(all(Age < 25))"Young" else "Not so Young"
[1] "Not so Young"
```

17 Simple functions for data management

An attractive attribute of **R** is its capacity to efficiently manage large, complex datasets. In this section I list a few functions and approaches useful for data management.

17.1 `replace`

We can replace elements in a vector with the function `replace`. The function requires three arguments.

- The first argument, `x`, specifies the vector to be analyzed.
- The second argument, `list`, tells **R** which elements need to be replaced. A logical argument can be used here as a replacement index.
- The third argument, `values`, tells **R** what these elements need to be replaced with.

For instance:

```
replace(Age, Age < 25, "R is Cool")
[1] "R is Cool" "R is Cool" "R is Cool" "29.5"      "30.5"      "38.5"
[7] "39.5"      "40.5"      "44.5"      "45.5"      "47"
```

Recall that a vector is not allowed to contain both quantitative and categorical data. As a result **R** made all of the output from `replace` categorical.

17.2 `which`

The function `which` can be used with logical commands to subset data. For instance:

```
which(Age > 30)
[1]  5  6  7  8  9 10 11
```

The result tells us which elements in `Age` were in agreement with the logical argument `Age>30`.

To find which element in `Age` is closest to 32 I type:

```
which(abs(Age - 32) == min(abs(Age - 32)))
[1] 5
```

According to **R,** the 5th element in the `Age` is closest to 32. We can see that this is true.

```
abs(Age - 32)
[1] 15.0 11.5 10.5  2.5  1.5  6.5  7.5  8.5 12.5 13.5 15.0
```

Three other functions related to `which` are `sort`, `rank`, and `match`.

17.3 `sort`

The function `sort` sorts alphanumeric data from a vector into an ascending order.

```
sort(Age)
[1] 17.0 20.5 21.5 29.5 30.5 38.5 39.5 40.5 44.5 45.5 47.0

sort(c("a", "d", "c", "Inf"))
[1] "a"   "c"   "d"   "Inf"
```

Data can be sorted in a descending order by specifying `decreasing = T`.

```
sort(Age, decreasing = T)
[1] 47.0 45.5 44.5 40.5 39.5 38.5 30.5 29.5 21.5 20.5 17.0
```

17.4 `rank`

The function `rank` gives the ascending alphanumeric rank of elements in a vector. Ties are given the average of their ranks. This operation is important to rank-based permutation analyses (see Ch. 6 in the **Foundational and Applied Statistics** text).

```
x <- c(1, 2, 3, 4, 4, 3)
rank(x)
[1] 1.0 2.0 3.5 5.5 5.5 3.5
```

17.5 `order`

The function `order` is more difficult to understand than `sort` and `rank`. It alphanumerically sorts a vector and returns the original element order overlaid on the sorted vector. This allows us to sort a vector, matrix or dataframe into an ascending or descending order, based on one or several vectors. For instance:

```
x <- c(1, 3, 2, 4, 0.5)
o <- order(x)
o
[1] 5 1 3 2 4
```

The 5th element in `x` has the smallest value, thus the number five is placed first in vector `o`. The 1st element in `x` has the next smallest value, thus the number one is placed second in `o`. The 3rd element is the next smallest, and so on.

We see here how we would utilize the vector `o`.

```
x[o]
[1] 0.5 1.0 2.0 3.0 4.0
```

Of course we get the same answer as if we were to use `sort(x)`.

```
sort(x)
[1] 0.5 1.0 2.0 3.0 4.0
```

However, the uses of `order` extend beyond sorting single vectors. Consider the following dataset describing the percent cover of plant species, in which species are signified with four letter (**ge**nus, **sp**ecies) codes:

```
field.data <- data.frame(code = c("ACMI", "ELSC", "CAEL", "TACE"), cover = c(12, 13,
14, 11))
field.data
  code cover
1 ACMI    12
2 ELSC    13
3 CAEL    14
4 TACE    11
```

What if I want to sort the dataframe alphabetically by species codes? I would type:

```
field.data[order(field.data[,1]),]
  code cover
1 ACMI    12
3 CAEL    14
2 ELSC    13
4 TACE    11
```

Similarly, to order by species cover I would type:

```
field.data[order(field.data[,2]),]
  code cover
4 TACE    11
1 ACMI    12
2 ELSC    13
3 CAEL    14
```

17.6 `unique`

To find unique values in dataset (and eliminate unwanted repeats) we can use the function `unique`. Here is list of species codes from a bird survey on islands in Southeast Alaska. Notice that here are a large number of repeats.

```
AK.bird <- c("GLGU", "MEGU", "DOCO", "PAJA", "COLO", "BUFF", "COGO", "WHSC", "TUSW",
"GRSC", "GRTE", "REME", "BLOY", "REPH", "SEPL", "LESA", "ROSA", "WESA", "WISN",
"BAEA", "SHOW", "GLGU", "MEGU", "PAJA", "DOCO", "GRSC", "GRTE", "BUFF", "MADU",
"TUSW", "REME", "SEPL", "REPH","ROSA", "LESA", "COSN", "BAEA", "ROHA")
```

Using `unique` we have:

```
unique(AK.bird)
[1] "GLGU" "MEGU" "DOCO" "PAJA" "COLO" "BUFF" "COGO" "WHSC" "TUSW" "GRSC" "GRTE"
[12] "REME" "BLOY" "REPH" "SEPL" "LESA" "ROSA" "WESA" "WISN" "BAEA" "SHOW" "MADU"
[23] "COSN" "ROHA"
```

17.7 `match`

Given two vectors, the function match finds where objects in the second vector appear in the elements of the first vector. For instance:

```
x <- c(6, 5, 4, 3, 2, 7)
y <- c(2, 1, 4, 3, 5, 6)
match(y, x)
[1]  5 NA  3  4  2  1
```

The number 2 (the 1st element in y) is the 5th element of `x`, thus the number 5 is put 1st in the vector `m` created from `match`. The number 1 (the 2nd element of y) does not occur in `x` (it is NA). The number 4 is the 3rd element of `y` and `x`, thus number 3 is placed in the third element of m, and so on.

The value of this function may seem unclear at first, but consider a scenario where I want to convert field data with species codes into a dataset containing species names. Consider the following species list (which includes species not in the field data from § 17.5).

```
species.list <- data.frame(code = c("ACMI", "ASFO", "ELSC", "ERRY", "CAEL",
"CAPA", "TACE"), names = c("Achillea millefolium", "Aster foliaceus", "Elymus
scribneri", "Erigeron rydbergii", "Carex elynoides", "Carex paysonis",
"Taraxacum ceratophorum"))
```

```
species.list
  code                  names
1 ACMI   Achillea millefolium
2 ASFO        Aster foliaceus
3 ELSC       Elymus scribneri
4 ERRY     Erigeron rydbergii
5 CAEL        Carex elynoides
6 CAPA         Carex paysonis
7 TACE Taraxacum ceratophorum
```

Here I give the correct species names to the field codes using the `match` function.

```
m <- match(field.data[,1], species.list[,1])
field.data[,1] <- species.list[,2][m]
field.data
                    code cover
1   Achillea millefolium    12
2       Elymus scribneri    13
3        Carex elynoides    14
4 Taraxacum ceratophorum    11
```

17.8 `which` and `%in%`

We can use the commands `%in%` and `which` together to achieve the same results as `match`. Under the current example we have:

```
m <- which(species.list[,1] %in% field.data[,1])
field.data[,1] <- species.list[,2][m]
field.data
                    code cover
1   Achillea millefolium    12
2       Elymus scribneri    13
3        Carex elynoides    14
4 Taraxacum ceratophorum    11
```

`%in%` returns a logical vector, indicating if a match was located for each element in user-supplied vectors. Thus, unlike `match`, returned values are `TRUE` or `FALSE` but never `NA`.

17.9 `strsplit` and `strtrim`

Elements within a text string can be rearranged, identified or extracted using a number of functions. The function `strsplit` splits a character string into substrings based on user defined criteria. It contains two important arguments.

- The first argument, `x`, specifies the character string to be analyzed.
- The second argument, `split`, is a character criterion that is used for splitting. Letting this argument equal `NULL` (§ 20.219) results in spaces being placed between every character in the string.

```
noquote(strsplit("Achillea millefolium", NULL))
[[1]] A c h i l l e a   m i l l e f o l i u m
```

To split the string whenever the letter `"l"` occurs, I have:

```
noquote(strsplit("Achillea millefolium", "l"))
[[1]] Achi        ea mi       efo   ium
```

The function `noquote()` removes quotes when printing.

The function `strtrim` is useful for extracting characters from vectors. For instance, for the species codes in the `plant` character vector below, the first capital letter indicates whether the species are flowering plants (anthophytes) or mosses (bryophytes). Assume I want to create a new categorical variable distinguishing anthophytes from bryophytes by extracting the first letter. This is defined by specifying `1` in the second `strtrim` argument, `width`.

```
plant <-  c("A_CAAT", "B_CASP", "A_SARI")
strtrim(plant, 1)
[1] "A" "B" "A"
```

17.10 Complex pattern matching: `gsub`, `grep`, and metacharacters

The functions `grep` and `gsub` are specifically designed for pattern matching and replacement within a character vector comprised of multiple text strings. Consider the following character object made up of five strings:

```
sample <- c("amy", "joe", "fred", "mike", "betty")
```

If for some reason we wanted to convert every occurrence of a lower-case 'm' to an upper case 'M' we could use:

```
gsub("m", "M", sample)
[1] "aMy"   "joe"   "fred"  "Mike"  "betty"
```

Here the function `grep` tells us which elements in `sample` contain the letter 'm'.

```
grep("m", sample)
[1] 1 4
```

A **metacharacter** is a keyboard character that has a special (non-literal) meaning to a computer program. In **R** these include the symbols: `\ | () [ { ^ $ * +` and `?`. We can use metacharacters in conjunction with `gsub` and `grep` for the purpose of complex pattern matching and replacement. In using this approach we can also call the **Perl Compatible Regular Expressions** (**PCRE**) library, which has been incorporated into **R**. The PCRE library implements the computer language Perl.

As an example of how metacharacters can be used by the PCRE library we will tell **R** to capitalize the first letter of each element in the object `sample`.

```
gsub("(\\w)(\\w*)", "\\U\\1\\L\\2", sample, perl=TRUE)
[1] "Amy"   "Joe"   "Fred"  "Mike"  "Betty"
```

In the first argument, the string `(\\w)(\\w*)` indicates that I want the function to consider the first letter in each element of `sample`, and all later letters, separately. In the second argument, the string `\\U\\1\\L\\2` indicates that I want the first letter of each element in `sample` to be replaced with an upper case version of itself, and that I want the other letters to be lower case.

The functions `toupper` and `tolower` can be easily used to readily make all the letters in text string upper-case or lower-case, respectively.

```
toupper(sample)
[1] "AMY"   "JOE"   "FRED"  "MIKE"  "BETTY"
```

Here I ask **R** to give me the elements in `sample` which are four or more letters long.

```
grep("[[:alnum:]]{4,}", sample, value = T)
[1] "fred"  "mike"  "betty"
```

The string `[[:alnum:]]` indicates all alphanumeric characters. I am combing this expression with the metacharacter expression `{n,}`. This combination tells **R** to report all elements that have four or more alphanumeric units. The argument `value = T` tells **R** to provide the actual contents of the elements in `sample`, and not the element indices.

For more information type `?grep`.

18 Testing and coercing

There are a number of functions that are designed to test whether an **R** object has particular characteristics, or to coerce an **R** object to have a desired class. For instance, the function `is.numeric` tests whether an object is numeric while the function `as.numeric` coerces an object to be of class numeric.

```
x<-c("a", "b", 4)
is.numeric(x)
[1] FALSE

as.numeric(x)
[1] NA NA  4
Warning message:
NAs introduced by coercion
```

We note that in `as.numeric(x)` the non-numeric parts of `x` are discarded. Testing and coercing functions exist for all important **R**-classes. These include: `vector`, `matrix`, `dataframe`, `array`, `list`, `factor`, `numeric`, `function`, `dist`, `double`, `character` and many others.

Coercion of data to categorical and ordinal classes can be managed using the functions `factor` and `ordered` respectively. For instance:

```
x <- c(1, 2, 1, 2, 1, 2)  #quantitative
is.numeric(x)
[1] TRUE

y <- factor(x)  #categorical
y
[1] 1 2 1 2 1 2
Levels: 1 2

z <- ordered(c(1, 2, 3, 4, 5))  #ordinal
z
[1] 1 2 3 4 5
Levels: 1 < 2 < 3 < 4 < 5
```

All numeric objects in **R** are stored in **double-precision** format, meaning that the object occupies two adjacent locations in computer memory.

```
a <- 1
is.double(a)
[1] TRUE
```

Objects coerced to be integers will be stored with double precision, although one of the storage locations will not be used. As a result integers are not conventional double precision data. This is explained in greater detail in section 20.

```
a <- 1
is.double(as.integer(a))
[1] FALSE
```

19 `NA`, `NaN`, and `NULL`

R identifies missing values (empty cells) as `NA`, which indicates “not available”. Hence the **R** function to identify a missing value is: `is.na`.

For example:

```
x <- c(2, 3, 1, 2, NA, 3, 2)
is.na(x)
[1] FALSE FALSE FALSE FALSE TRUE FALSE FALSE
```

To say “identify all parts of a vector except missing values”, we set a logical test to be true when values are not missing. Because the unary (single argument) operator for "not" in **R** is `!`, the correct command is:

```
!is.na( )
```

For example:

```
!is.na(x)
[1]  TRUE  TRUE  TRUE  TRUE FALSE  TRUE  TRUE
```

There are a number of functions to get rid of missing values. These include `na.omit`.

```
na.omit(x)
[1] 2 3 1 2 3 2
attr(, "na.action")
[1] 5
attr(, "class")
[1] "omit"
```

We see that **R** omitted the missing observation and then told us which observation was omitted.

Functions in **R** are often set up to handle missing data. In many cases, however, it will be desirable to have a complete set of observations for a dataframe, matrix, or vector. Consider the following dataframe which contains plant percent cover for four plant species which are identified with codes.

```
field.data <- data.frame(code=c("ACMI", "ELSC", "CAEL", "CAPA", "TACE"), cover =
c(12, 13, 14, NA, 11))
field.data
 code cover
1 ACMI    12
2 ELSC    13
3 CAEL    14
4 CAPA    NA
5 TACE    11
```

I can check for completeness of the data, i.e. the appearance of missing data for any experimental unit (row) using the `complete.cases` function.

```
complete.cases(field.data)
[1]  TRUE  TRUE  TRUE FALSE TRUE
```

I can omit rows with missing data using `na.omit`.

```
na.omit(field.data)
  code cover
1 ACMI    12
2 ELSC    13
3 CAEL    14
5 TACE    11
```

One shouldn't worry too much about memorizing a million **R** functions. Instead you should develop a basic vocabulary of functions that you will use frequently. For instance, instead of using `na.omit` the example above, I could have gotten the same result using brackets and logical commands.

```
field.data[!is.na(field.data[,2]),]
  code cover
1 ACMI    12
2 ELSC    13
3 CAEL    14
5 TACE    11
```

The final comma in the command above tells **R** that I want to go through the `field.data` dataframe row by row and eliminate rows with missing values.

The designation `NaN` is associated with the current conventions of the IEEE 754-2008 (IEEE is an acronym for Institute of Electrical and Electronics Engineers, and pronounced "I triple E") arithmetic used by **R**. It means "not a number." Mathematical operations which produce `NaN` include:

```
0/0
[1] NaN
```

```
Inf-Inf
[1] NaN
```

```
sin(Inf)
[1] NaN
```

Occasionally one may wish to specify that an **R**-object is `NULL`, meaning that it is *absent*. A `NULL` object can be included as an argument in a function without requiring that it have a particular value or meaning. As with `NA` the `NULL` specification is easy:

```
x <- NULL
```

It should be emphasized that **R**-objects or elements within objects that are `NA` or `NULL` cannot be identified with the logical commands == or `!=`. For instance:

```
x <- NA; y <- NULL
x == NA
[1] NA
y == NULL
logical(0)
```

Instead one should use `is.na` (as above) or `is.null` to identify `NA` or `NULL` elements or objects.

```
is.na(x)
[1] TRUE
is.null(y)
[1] TRUE
```

20 Computers

To acquire a deeper understanding of the workings of **R** we must gain some familiarity with basic principles of computer science.

20.1 Binary numbers, bits and bytes

Computers are designed around bits and bytes. A **bit** is a binary unit of digital information, a 0 or a 1. This convention occurs because conventional computer systems use electronic circuits that exist in only one of two states, on or off. For somewhat arbitrary historical reasons, a **byte** consists of eight bits. Modern computers always work on the addresses at the level of bytes of information.

Two major systems exist to describe larger units of information, based on bytes. The *decimal method,* the most common system, uses powers of 10, allowing implementation of SI prefixes (i.e., kilo = 10^3 = 1000, mega = 10^6 = 1000^2, giga = 10^9 = 1000^3, etc.) (Table 5). The *binary system*, used frequently by Windows to describe RAM, defines byte units in multiples of 1024 (Table 5).

Table 5. Frequently used byte units

Decimal		Binary	
Bytes	Name	Bytes	Name (IEC)
1000	kB kilobyte	1024	KiB kibibyte
1000^2	MB megabyte	1024^2	MiB mebibyte
1000^3	GB gigabyte	1024^3	GiB gibibyte
1000^4	TB terabyte	1024^4	TiB tebibyte
1000^5	PB petabyte	1024^5	PeB pebibyte

In most programs, on most workstations, the results of computations are stored as 32 bits (i.e., 4 bytes, becasue 8 times 4 = 32) or as 64 bits (5 bytes) of information. A computer hard drive with 1 gigabyte (1 billion bytes) of memory will have 1×10^9 bytes = 8×10^9 bits of memory. Double precision storage (used by **R**) requires 64 bits. This allows expression and storage of numerical quantities between approximately 5.0×10^{-324} and capproximately 1.8×10^{308}, and a precision of at least 15 - 17 significant digits (see below).

We can see that the current upper numerical limit in **R** (ver 4.3.0) is somewhere between:

```
1.8 * 10^307
[1] 1.8e+307
```

and

```
1.8 * 10^308
[1] Inf
```

And that the (non-negative) numeric lower limits are between

```
5.0 * 10^-323
[1] 4.940656e-323
```

and

```
5.0 * 10^-324
[1] 0
```

With a single bit we can describe only $2^1 = 2$ distinct digital objects. These are, an object represented by a 0 and an object represented by a 1. It follows that $2^2 = 4$ distinct objects can be described with two bits, $2^3 = 8$ objects can be described with three bits, and so on[13]. We count to ten in binary using: 0 = 0, 1 = 1, 10 = 2, 11 = 3, 100 = 4, 101 = 5, 110 = 6, 111 = 7, 1000 = 8, 1001 = 9, 1010 = 10. Thus, we require four bits to count to ten. Note that the binary sequences for all positive non-zero integers start with one. We have the following guidelines:

1) For the smallest integer, given a particular number of bits, the leftmost placeholder will be a one, and all other bits will be zeros (e.g., 100 = 4).
2) For the next largest integer, a one is placed in the rightmost placeholder occupied by a zero in the previous step (e.g., 101 = 5).
3) For the next largest integer the one inserted in the previous step is moved one placeholder to the left if that bit is zero (e.g. 110 = 6). If the bit to the left is non-zero, then go to step 2 (e.g., 111 = 7). If all bits are ones following (or preceding) step 2, then add a bit, and begin again at step 1 (e.g., 1000 = 8).

The addition of a binary digit represents an increasing power of 2. As a result we say that the rightmost digit in a set of binary digits represents 2^0, the next represents 2^1, then 2^2, and so on. This can be defined with the equation

$$\alpha\beta^k, \tag{1}$$

where α is quantity known as the **significand**, that describes the number of significant digits followed by a modifying number, β (usually 2), and k is called (appropriately) the **exponent.** The number of bits in the significand determines the precision of a binary expression, while the exponent determines minimum and maximum possible number. In a 64 bit double precision format 1 bit is allocated to the sign of the stored item, 53 bits are assigned to the significand, and 11 bits are given to the exponent.

Equation 1 actually represents a **dot product**, i.e., it is the sum of the piecewise multiplication of two vectors. For instance, to find the decimal number version of a single binary bit (consisting of only the right-most digit) we multiply the digit value by the power of two it represents. Thus, as we noted above, $1\times 2^0 = 1$, and $1\times 2^0 = 1$. Accordingly, to find the decimal version of a set of binary values we take the sum of the products of the binary digits and the powers of base 2 that they represent. For instance, the binary number 010101 equals:

$$(0\times 2^5) + (1\times 2^4) + (0\times 2^3) + (1\times 2^2) + (0\times 2^1) + (1\times 2^0) = 0 + 16 + 0 + 4 + 0 + 1 = 21.$$

[13] For instance, images often contain eight bit (one byte) variables describing the colors red, green, and blue. Thus, the color red would be a number between 0 and 255 (i.e. red could have $2^8 = 256$ distinct values). Given that the colors blue and green were also eight bit, there would be $256^3 = 16{,}777{,}216$ color possibilities (combinations) for any pixel in the image.

The function `bin2dec` in *asbio* does the calculation for us.

```
bin2dec(010101)
[1] 21
```

20.2 Floating point arithmetic

Depicting undefinable real numbers (e.g. an irrational number), and certain rational fractional numbers in binary, requires **binary approximation** (Goldberg 1991). One approach is to express numeric values with non-zero fractional parts using **floating point arithmetic**. This framework is used by all conventional software (although its mechanisms are easily revealed in **R**).

As with binary decimal numbers, binary fractional numbers are expressed with respect to a decimal, and the number of digits will (often) be dictated by the significand. Given 13 bits we have the following binary translations for decimal numbers: 1/1 = 1, 1/2 = 0.1, 1/3 = 0.01010101…, 1/4 = 0.01, 1/5 = 0.00110011..., 1/6 = 0.0010101…, 1/7 = 0.001001..., 1/8 = 0.001, 1/9 = 0.000111000111... , 1/10 = 0.000110011....

To obtain decimal fractions from binary fractions we multiply the bits by decreasing inverse powers of base two, starting at 0 (excluding 2^{-0}), and find the sum. For example, back-calculating the decimal value 1/4 from the binary value 0.01 we have:

$$(0 \times 2^0) + (0 \times 2^{-1}) + (1 \times 2^{-2}) = 0 + 0 + 0.25 = 0.25.$$

```
bin2dec(0.01)
[1] 0.25
```

Floating point arithmetic may give unexpected results. For instance:

```
options(digits = 20)
1/10
[1] 0.10000000000000000555
```

Due to the character of the binary floating point 1/10 = 0.1 can only be approximated by a binary number. The approximation is very close (out to the 18th significant digit), but not exactly equal to 0.1. Many other fractional quantities cannot be expressed exactly. Indeed, real (terminal) binary fractions will only exist if the only prime number is in the decimal fraction denominator, and it is 2 (although exception handling allows terminality for many fractions). As other examples, consider

```
1/3
[1] 0.3333333333333333148296
```

```
sqrt(2)^2 == 2
[1] FALSE
```

and even,

```
12.3 - 49.2
[1] -36.9000000000000005684
```

Obviously, such “rounding errors” may result in user-function failures[14].

20.3 Binary characters

Characters can also be expressed in binary. The **American Standard Code for Information Interchange** (**ACSCII**) consists of 128 characters and requires eight bits (one byte). Likewise, **Unicode** has 65,536 characters (the first 128 are the ASCII characters), and requires 16 bits (two bytes)[15]. **R** uses the Unicode system of characters. We can observe the process of binary character assignment using the functions `as.raw()`, `rawToChar()`, and `rawToBits()`.

Here is a list of the fist 128 Unicode characters (i.e. the ASCII characters)

```
rawToChar(as.raw(1:128), multiple = TRUE)
  [1] "\001" "\002" "\003" "\004" "\005" "\006" "\a"   "\b"   "\t"    "\n"   "\v"
 [12] "\f"   "\r"   "\016" "\017" "\020" "\021" "\022" "\023" "\024" "\025"
"\026"
 [23] "\027" "\030" "\031" "\032" "\033" "\034" "\035" "\036" "\037" " "    "!"
 [34] "\""   "#"    "$"    "%"    "&"    "'"    "("    ")"    "*"    "+"    ","
 [45] "-"    "."    "/"    "0"    "1"    "2"    "3"    "4"    "5"    "6"    "7"
 [56] "8"    "9"    ":"    ";"    "<"    "="    ">"    "?"    "@"    "A"    "B"
 [67] "C"    "D"    "E"    "F"    "G"    "H"    "I"    "J"    "K"    "L"    "M"
 [78] "N"    "O"    "P"    "Q"    "R"    "S"    "T"    "U"    "V"    "W"    "X"
 [89] "Y"    "Z"    "["    "\\"   "]"    "^"    "_"    "`"    "a"    "b"    "c"
[100] "d"    "e"    "f"    "g"    "h"    "i"    "j"    "k"    "l"    "m"    "n"
[111] "o"    "p"    "q"    "r"    "s"    "t"    "u"    "v"    "w"    "x"    "y"
[122] "z"    "{"    "|"    "}"    "~"    "\177" "€"
```

[14]Alternatives to binary floating point arithmetic that address this problem exist, but are rarely implemented because: 1) they are less efficient, and 2) currently no IEEE standards have been specified. In order of increasing precision and decreasing efficiency alternative systems include Limited-Precision Decimal, Arbitrary-Precision Decimal, and Symbolic Calculation systems.

[15]This is the number of characters that can be defined with 16 bits. The current number of Unicode characters, however, is actually much larger than 65,536. The 16-bit Unicode Transformation Format (UTF-16) handles these additional characters by using two sixteen bit units.

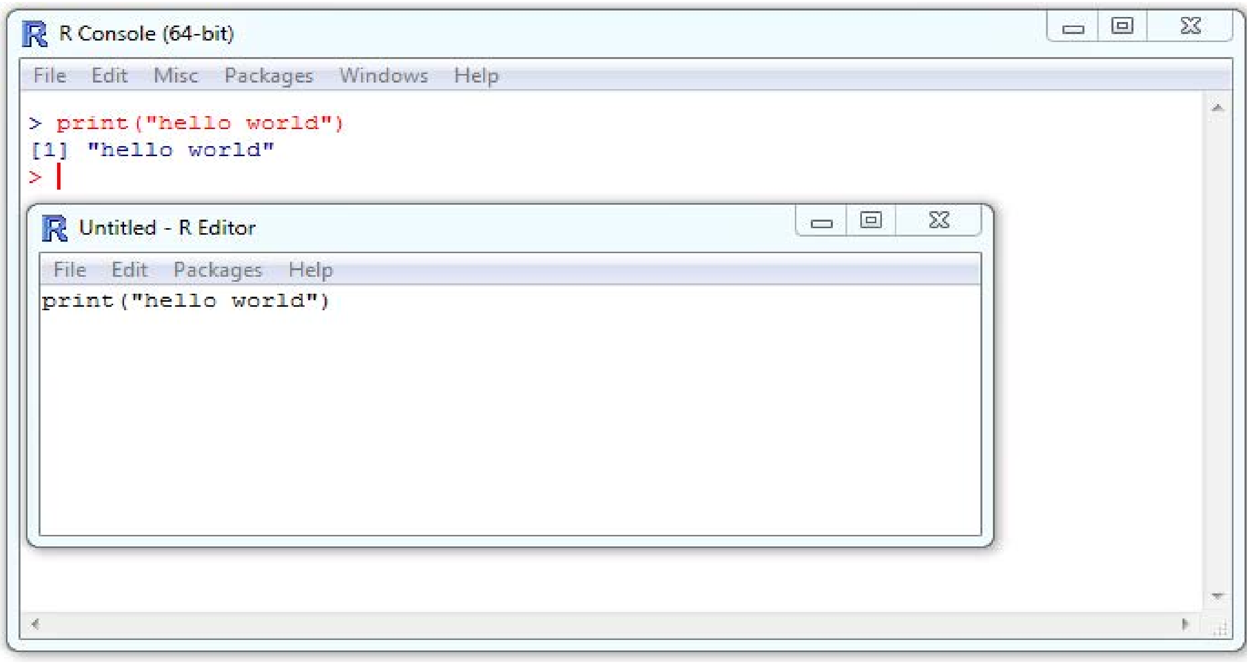
Note that the exclamation point is character number 33. Its 16 bit binary code is:

```
rawToBits(as.raw(33))
[1] 01 00 00 00 00 01 00 00
```

21 Writing functions

Perhaps the most useful thing about **R** is its capacity to implement user-defined functions. At some point you may even wish to compile your functions into an **R**-package. No more will be said on such matters here. Interested readers are directed to the reference for **R**-package construction "Writing **R** Extensions", available at http://cran.r-project.org/doc/manuals/R-exts.html.

Programs like **RWinEdt** (an **R** package plugin for **WinEdt**), **Tinn-R** (a recursive acronym for Tinn is not Notepad, http://www.sciviews.org/Tinn-R), **ESS** (Emacs Speaks Statistics, http://ess.r-project.org) and **RStudio** [16](http://rstudio.org) have been developed primarily to facilitate function writing in **R**[17]. Text editors from these programs provide syntax highlighting of the **R** (and S) code and (often) similar handling for other programming languages, e.g. **C/C++**, **Java**, **Perl**, **Pascal**, **Visual Basic**, and **Fortran**. In addition, some editors, including **R**WinEdt, Tinn-**R,** ESS and **R**Studio allow direct interaction with an **R**-console running on the same computer, or can open **R** and generate an **R**-console. **R-scripts**, accessed with **File>New script** (non-Unix only) or with Ctrl+F+N on the command line prompt, provide another excellent way to edit **R**-code. A single line of code (or selected lines of code) can be sent to the **R**-console from an **R**-script interface using the shortcut Ctrl+R. The entire contents of a script can be selected using Ctrl+A, and then sent to the **R**-console using Ctrl+R (Figure 31).



```
> print("hello world")
[1] "hello world"
>
```

```
print("hello world")
```

Figure 31 Script editor in **R**

In all the text editors described above, functions or groups of functions can be saved as `.R` files. These files can then be read as source code directly in **R** or opened as scripts in the script editor. It is strongly recommended that word processing programs (e.g., MS Word) not be used to create **R** scripts and functions as the resulting

[16] The attributes of RStudio greatly exceed simple function writing (see § 21.12)

[17] Other frequently used text editors with some support for **R** include, but are not limited to, **NppToR** in **Notepad++** (http://sourceforge.net/projects/npptor/) , **Tinn-R** (http://www.sciviews.org/Tinn-R/), **Bluefish** (http://bluefish.openoffice.nl/index.html), **Crimson Editor** (http://www.crimsoneditor.com/), **ConTEXT** http://www.contexteditor.org/), **Eclipse** (http://www.eclipse.org/eclipse/), **ESS** (http://ess.r-project.org/) , **Vim** (http://www.vim.org/), **Geany** (http://www.geany.org/), **jEdit** (http://www.jedit.org/), **Kate** (http://kate-editor.org/), **TextMate** (http://macromates.com/), **gedit** (http://projects.gnome.org/gedit/), **SciTE** (http://www.scintilla.org/SciTE.html), and **RWinEdt** (http://cran.r-project.org/web/packages/RWinEdt/). All websites accessed 4/10/2012.

code may contain hidden formatting characteristics that may affect its implementation in **R**.

21.1 An introductory example

At the risk of sounding repetitive, we specify a function using the function `function`. The arguments for `function` are completely user-defined and will be the argument list for one's personalized function. For instance, in the excerpt `example <- function(x)` the function `example` contains a single argument named `x` (naming conventions for arguments must follow the conventions defined in 4.1). The code for the function itself follows the call to `function`, and the argument list, generally delimited by braces. This results in the format:

```
function.name <- function(argument1, argument2,....argumentn){function contents}
```

Consider the function `Exp.growth` below that solves the function $N_0\lambda^t$, where N_0= initial number of individuals, λ = the rate of increase, and t = the number of time intervals or generations.

```
Exp.growth <- function(N.0, lambda,t){
  Nt <- N.0 * lambda^t
  Nt
}
```

The function requires three arguments: `N.0`, `lambda`, and `t`. The first line of code following the arguments solves the function $N_0\lambda^t$ utilizes the argument definitions and stores the solution as `N.t`. The last line gives the object I want returned by the function, `N.t`. Note that if I didn't specify some "return value", nothing would be returned by the function. If a function has multiple return objects, then one can place them in single suitable container like a list.

To increase clarity one should place the first curly bracket on same line as the arguments, and place last curly bracket on its own line. This convention is followed above. Readability can also be improved by use of spaces. Note that I have inserted two spaces to begin lines containing related operations. This distinguishes these lines from the first (argument) line and the end (return) line. Note also that spaces are placed after commas, and before and after operators, including the assignment operator.

Once I have read the function `Exp.growth` into **R** (by scanning, reading, typing, or pasting it), I will be able to run it by typing the function name and specifying arguments.

Here we run function for N_0= 100, λ = 0.8, and t = 10

```
Exp.growth(N.0 = 100, lambda = 0.8, t = 10)
[1] 10.73742
```

The population size is decreasing because λ is less than one.

21.2 Global variables versus local variables

It is important to note that the arguments and objects created in a function are local variables. That is, they only exist within the confines of the function.

We can use `Exp.growth` to demonstrate that the variable `N.t`, which was defined in the function, is local.

```
Nt
Error: object 'Nt' not found
```

Global variables are (generally) defined outside of functions, and thus can be called within a function as arguments or other sorts of objects. Lexical scoping allows **R** to distinguish global and local variables.

Languages like S that don't have lexical scoping would not "know about" the variables `N.0`, `lamba`, and `t` unless they were defined outside of the function, i.e.,

```
N.0 <- 100; lambda <- 0.8; t <-3
```

Conversely, **R** allows one to define the free variables in the text of the function, e.g.,

```
Exp.growth(100, 0.8,3)
[1] 51.2
```

Global variables can be assigned within functions using the so-called **superassignment operator**, `<<-`.

```
Exp.growth <- function(N.0, lambda,t){
  Nt <<- N.0 * lambda^t
  Nt
}

Exp.growth(N.0 = 100, lambda = 0.8, t = 10)
[1] 10.73742
Nt
[1] 10.73742
rm(Nt)
Nt
Error: object 'Nt' not found
```

|| Example 20 --Summary statistics: variations on a theme

The simple function shown below centers and scales (standardizes) outcomes in the `Downs` dataset (i.e., each element in the data matrix is subtracted from its column mean, and divided by its column standard deviation). The function itself is defined and called within the function `apply`. Recall that the third argument in `apply` must be an existing or user-defined function, e.g., `mean`. We note that braces are not necessary if the "block" of function code only requires a single line, and this line is placed on the same line as the `function` call.

```
stan <- (apply(Downs, 2, function(x){(x - mean(x))/sd(x)}))
stan
             Age     Births      Cases
 [1,] -1.5797549  0.4841299 -0.1698524
 [2,] -1.2553785  1.4397237  0.5774983
 [3,] -1.1626996  1.6535732 -0.1698524
 [4,] -0.4212680  0.7250074 -1.0417617
 [5,] -0.3285890  0.5292520 -0.6680863
 [6,]  0.4128426 -0.5021109 -0.2944109
 [7,]  0.5055216 -0.6008367  1.5739660
 [8,]  0.5982005 -0.7149425  1.6985244
 [9,]  0.9689163 -0.9813779  0.5774983
[10,]  1.0615953 -1.0117986 -0.7926447
[11,]  1.2006137 -1.0206195 -1.2908786
```

Below I create a function called `stats` that will simultaneously calculate a large number of summary statistics.

```
stats <- function(x, digits = 5){
  ds <- data.frame(statistics = round(c(length(x), min(x), max(x),
mean(x), median(x), sd(x), var(x) ,IQR(x), sd(x)/sqrt(length(x)),
kurt(x), skew(x)),
digits))
  rownames(ds) <- c("n", "min", "max", "mean", "median", "sd", "var",
"IQR", "SE", "kurtosis", "skew")
  return(ds)
}
```

The function contains two arguments. A call to a vector of data (`x`), and the number of significant digits (`digits`). Because I have given `digits` the default value 5, only the first argument needs to specified by a user.

Following the arguments, the first three lines of the function create a dataframe called ds. It has one column called "statistics" that will contain eleven statistical summaries of `x`. The summaries are round-ed to the number of digits specified in `digits`.

The next lines of code define the row names of `ds`. These are the names of the statistics calculated by the function.

The last command, `return(ds)`, returns `ds`.

Note that the lines beginning `median(x)`, `digits` and `"SE"` are not indented because they are continuations of the previous line.

Here are summary stats for the `Age` column in `Downs`.

```
stats(Downs$Age)
        statistics
n          11.00000
min        17.00000
max        47.00000
mean       34.04545
median     38.50000
sd         10.78994
var       116.42273
IQR        17.00000
SE          3.25329
kurtosis   -1.41039
skew       -0.40977
```

The lone argument for `stats`, `x`, must be a vector of data. The function, however, can easily be extended to matrices and dataframes. For instance, lets now apply `stats` as the last argument of the `apply` function, to summarize the `stan` dataframe we created above.

```
apply(stan, 2, stats)
$Age                     $Births                  $Cases
         statistics               statistics               statistics
n          11.00000      n          11.00000      n          11.00000
min        -1.57975      min        -1.02062      min        -1.29088
max         1.20061      max         1.65357      max         1.69852
mean        0.00000      mean        0.00000      mean        0.00000
median      0.41284      median     -0.50211      median     -0.16985
sd          1.00000      sd          1.00000      sd          1.00000
var         1.00000      var         1.00000      var         1.00000
IQR         1.57554      IQR         1.47529      IQR         1.30786
SE          0.30151      SE          0.30151      SE          0.30151
kurtosis   -1.41039      kurtosis   -1.28862      kurtosis   -0.63921
skew       -0.40977      skew        0.53721      skew        0.61985
```

The output above is a list. The attributes of the list are the column names of `Downs`. As the result of standardization, three variables now have mean zero, and unit standard deviations and variances.

The function `stats` will work on any **R** object with a numerical class. For instance, try it on the first two columns of `lp`, the loblolly pine dataset.

21.3 `uniroot`

Parameter estimation in statistics often requires (at least implicitly) function optimization. However parameter estimation functions may not have a closed form, because an entire dataset needs to be considered with respect to proposed estimate values. A useful function in these situations is `uniroot` which searches an interval for the zero root of a function. For instance, many location estimators (those which estimate "central" or "typical" values, e.g., the true mean) will be the zero root the function:

$$\sum_{i=1}^{n}(x_i - \hat{\mu})\,, \tag{2}$$

where x_i is the ith observation from a dataset, and $\hat{\mu}$ is an estimator that uses the data to estimate a true location value. We will use `uniroot` to find a location estimate that provides a zero root for this function. To do this we must first create a function defining Eq. 2.

```
f <- function(x, data) sum(data - x)
```

We will evaluate the loblolly tree height data.

```
data <- lp[,1]
```

Here we apply `uniroot`:

```
uniroot(f(data), c(min(data), max(data)))$root
[1] 32.3644
```

This value is identical to the sample mean. Indeed, the sample mean will be always be the zero root of Eq. 2. Normally the difference of the data points and the location estimate is squared. Minimizing this function is called the process of **ordinary least squares**.

21.4 `switch`

A useful command in function writing is `switch`. It evaluates and switches among user-designated alternatives, included as a function argument. The function below switches between five different estimators of location (the typical or central value from a sample). These are the sample mean, a trimmed mean (using 10% trimming), the geometric mean, the median, and Huber's *M*-estimator (see Chapter 4 in the **Foundational and Applied Statistics** text).

```
location <- function(x, estimator){
  switch(estimator,
  mean = mean(x),  # arithmetic mean
  trim = mean(x, trim=0.1),  # trimmed mean κ = 0.1
  geo = exp(mean(log(x))),  # geometric mean
  med = median(x),  # median
  huber = huber.mu(x),  # Huber M-estimator, likelihood maximizing method
  stop("Estimator not included"))
}
```

Here are some data.

```
x <- c(2, 1, 4, 5.6, 7, 6.7, 3, 4.5, 10, 12, 2, 5, 6)
```

I can run the function using any of the four location estimators.

```
location(x, "mean")
[1] 5.292308

location(x, "geo")
[1] 4.357524

location(x, "huber")
[1] 4.959546
```

21.5 Triple dot `...` argument

A particularly handy item for writing **wrapper functions** (functions which embed other functions) is the triple dot (`...`) argument. Imagine you wish to create a wrapper for the function `plot` that allows you to automatically display the results from a simple linear regression. We might create the following:

```
reg.plot <- function(x, y, ...){
  plot(x, y,...)
  lm.temp <- lm(y ~ x)
  coef <- lm.temp$coefficients
  abline(coef[1], coef[2])
}
```

The triple dots in the arguments of `reg.plot`, and the associated triple dots we included in `plot` let us specify any additional argument from `plot` as an argument in `reg.plot`. For instance we could include specification for X and Y axis labels in `reg.plot` with the `plot` arguments `xlab` and `ylab`. For instance:

```
with(Loblolly, reg.plot(age, height, xlab = "age", ylab = "height"))
```

|| Example 21 –Function writing: quantifying biological diversity

In this extended exercise we examine functions for summarizing a community ecology dataset.

Alpha diversity measures the degree of evenness and richness within individual plots in a dataset. Low levels of monodominance and high richness result in high alpha diversity. A large number of alpha diversity indices have been utilized by ecologists (Magurran 1988). The most widely used are **Simpson's index** (D_1, Simpson 1949) and the **Shannon-Weiner index** (H', MacArthur and MacArthur 1961).

$$D_1 = 1 - \sum_i p_i^2 \qquad (3)$$

$$H' = \sum_i p_i \ln p_i \qquad (4)$$

where p_i is the proportional abundance of the *i*th species.

Simpson's index (D_1) has a straightforward interpretation. It is the probability of reaching into a plot and simultaneously pulling out two different species. The Shannon Weiner index (H') does not allow straightforward interpretation, although its values conventionally fall between 1.5 and 3.5, and rarely surpass 4.5 (Magurran 1988, Margalef 1972). D_1 and is sensitive to abundance changes in common species, while H' is sensitive to abundance changes in rare species (Gurevitch et al. 2006). D_1 and H' will both increase with increasing diversity (i.e., increased richness and evenness).

Table 5 Part of a community dataset (six species and five sites) from a Scandinavian *Pinus sylvestris* forest (Väre et al. 1995). Responses are percent ground cover.

	Empetrum nigrum	*Vaccinium myrtillus*	*Vaccinium vitis-idaea*	*Pinus sylvestris*	*Vaccinium uliginosum*	*Betula pubescens*
Site 1	11.13	0	17.8	0.07	1.6	0
Site 2	8.92	2.42	10.28	0.12	0	0
Site 3	6.45	0	14.13	0.07	0.47	0
Site 4	9.3	0	8.5	0.03	0	0
Site 5	3.47	0.25	20.5	0.25	0	0

To read the data into **R** we can use the `data.frame` function, as we have done before, or the `matrix` function (since the variables are all quantitative). Using the `matrix` command we specify how many rows and columns we want and then simply enter the data by rows or columns.

```
ps.data <- matrix(nrow = 5,ncol = 6,data = c(11.13, 0, 17.8, 0.07, 1.6, 0,
8.92, 2.42, 10.28, 0.12, 0, 0, 6.45, 0, 14.13, 0.07, 0.47, 0, 9.3, 0, 8.5,
0.03, 0, 0, 3.47, 0.25, 20.5, 0.25, 0, 0), byrow = TRUE)
```

We can give the matrix the correct row and column names.

```
colnames(ps.data)<-c("Empetrum nigrum", "Vaccinium myrtillus", "Vaccinium vi-
tis-idaea", "Pinus sylvestris", "Vaccinium uliginosum", "Betula pubescens");
rownames(ps.data)<-c("Site 1", "Site 2", "Site 3", "Site 4", "Site 5")
ps.data
```

```
       Empetrum nigrum Vaccinium myrtillus Vaccinium vitis-idaea
Site 1           11.13                0.00                 17.80
Site 2            8.92                2.42                 10.28
Site 3            6.45                0.00                 14.13
Site 4            9.30                0.00                  8.50
Site 5            3.47                0.25                 20.50
       Pinus sylvestris Vaccinium uliginosum Betula pubescens
Site 1             0.07                 1.60                0
Site 2             0.12                 0.00                0
Site 3             0.07                 0.47                0
Site 4             0.03                 0.00                0
Site 5             0.25                 0.00                0
```

Next, let's create a function that can calculate Simpson's Index (Eq. 2.1). First we need to calculate the relative proportion, p_i, of each species at each site. We can use the command `apply` again for this.

```
p.i <- apply(ps.data, 1, function(x){x/sum(x)})
```

As with my first example in this section I have inserted a function where we would normally tell `apply` what to do to the rows or columns of the matrix. In this case I have told the function (within the function `apply`) to divide each element within a particular row by the sum of its respective row.

```
    p.i
                           Site 1      Site 2      Site 3      Site 4
Empetrum nigrum       0.363725490 0.410303588 0.305397727 0.521592821
Vaccinium myrtillus   0.000000000 0.111315547 0.000000000 0.000000000
Vaccinium vitis-idaea 0.581699346 0.472861086 0.669034091 0.476724621
Pinus sylvestris      0.002287582 0.005519779 0.003314394 0.001682557
Vaccinium uliginosum  0.052287582 0.000000000 0.022253788 0.000000000
Betula pubescens      0.000000000 0.000000000 0.000000000 0.000000000
                          Site 5
Empetrum nigrum       0.14180629
Vaccinium myrtillus   0.01021659
Vaccinium vitis-idaea 0.83776052
Pinus sylvestris      0.01021659
Vaccinium uliginosum  0.00000000
Betula pubescens      0.00000000
```

Next I need to: 1) square the proportions, 2) take the sum within each row (each site), and 3) subtract this sum from one.

```
D <- 1 - apply(p.i^2, 2, sum)
```

It looks like we only really need two lines of code to calculate Simpson's index. We can write the function as:

```
Simp.index <- function(x){
  p.i <- apply(x, 1, function(x){x/sum(x)})
  1-apply(p.i^2, 2, sum)
}
```

To run `Simp.index` for the *Pinus sylvestris* data, `ps.data`, I read or type the function into **R** and then type:

```
Simp.index(ps.data)
   Site 1    Site 2    Site 3    Site 4    Site 5
0.5265904 0.5956317 0.4586194 0.5006717 0.2778395
```

Next we will create a function for the Shannon Weiner index. This measure also utilizes p_i; as a result it will be similar to the Simpson's index function.

```
SW.index <- function(x){
  p.i <- apply(x, 1, function(x){x/sum(x)})
  h <- apply(p.i, 1, function(x){log(x) * x})
  -1 * apply(h, 1, function(x){sum(x[!is.na(x)])})
}
```

Note that we run into a problem calculating H' when any $p_i = 0$ because ln(0) is undefined. As a result zeroes in the data will cause the function to fail. To account to for this I told **R** to add p_i elements only when they are <u>not</u> undefined. This is in the line:

```
h <- -1 * apply(h, 1, function(x){sum(x[!is.na(x)])})
```

The line works because an undefined (`NaN`) value is regarded as `NA`.

Here we run the function on `ps.data`.

```
SW.index(ps.data)
   Site 1    Site 2    Site 3    Site 4    Site 5
0.8512311 0.9927535 0.7347475 0.7034007 0.5189526
```

|| Example 22 Advanced mathematical applications -- solving systems of ODEs

Biologists often need to solve systems of dependent differential equations in models involving species interactions (e.g., competition or predation). For instance the Lotka-Volterra competition model has the form:

$$dN_1 / dt = r_{\max 1} N_1 \frac{(K_1 - N_1 - \alpha_{12} N_2)}{K_1}$$
$$dN_2 / dt = r_{\max 2} N_2 \frac{(K_2 - N_2 - \alpha_{21} N_1)}{K_2} \qquad (5)$$

where
t = time,
r_{max1} = the maximum per capita rate of increase for species 1 under ideal conditions,
r_{max2} = the maximum per capita rate of increase for species 2 under ideal conditions,
N_1 = the number of individuals from species 1,
N_2 = the number of individuals from species 2,
K_1 = the carrying capacity for species 1, i.e., the maximum population size of that species that the environment can support.
K_2 = the carrying capacity for species 2,
α_{12} = the competitive effect of species 2 on the growth rate of species 1, and
α_{21} = the competitive effect of species 1 on the growth rate of species 2.

We first bring in the package *deSolve* which contains function for solving **ordinary differential equations (ODEs)**[18].

```
install.packages("deSolve")
library(deSolve)
```

We then define starting values for N_1 and N_2 and model parameters

```
xstart <- c(N1 = 10, N2 = 10)
pars <- list(r1 = 0.5, r2 = 0.4, K1 = 400, K2 = 300, a2.1 = 0.4, a1.2 =
1.1)
```

We then specify the Lotkka-Volterra equations as a function. We will include the argument `time = time` even though it is not used in the function. This is required by ODE evaluators from **deSolve**.

```
LV <- function(time=time, xstart=xstart, pars=pars){
  N1 <- xstart[1]
  N2 <- xstart[2]
  with(as.list(pars),{
    dn1 <- r1 * N1 * ((K1 - N1 - (a1.2 * N2))/K1)
    dn2 <- r2 * N2 * ((K2 - N2 - (a2.1 * N1))/K2)
    res <- list(c(dn1, dn2))
  })
}
```

We will run the Lotka-Volterra function with the function `rk4` from library **deSolve**. The `rk4` function solves simultaneous differential equations using classical Runge-Kutta 4th order integration (Butcher

[18]As opposed to partial differential equations

1987). The method of Euler (the simplest method to find approximate solutions to first order equations) can be specified with the function `euler`. The arguments for `rk4`, in order, are the initial population numbers from species 1 and 2, the time frames to be considered, the function to be evaluated, and the parameter values.

```
out <- as.data.frame(rk4(xstart, time = 1:200, LV, pars))
```

The object `out` contains the number of individuals in species 1 and 2 for time frames 1-200 (Figure 32).

```
plot(out$time, out$N2, xlab = "Time", ylab = "Number of individuals", type
= "l")
lines(out$time, out$N1, type = "l", col = "red", lty = 2)
legend("bottomright", lty = c(1, 2), legend = c("Species 2", "Species 1"),
col = c(1, 2))
```

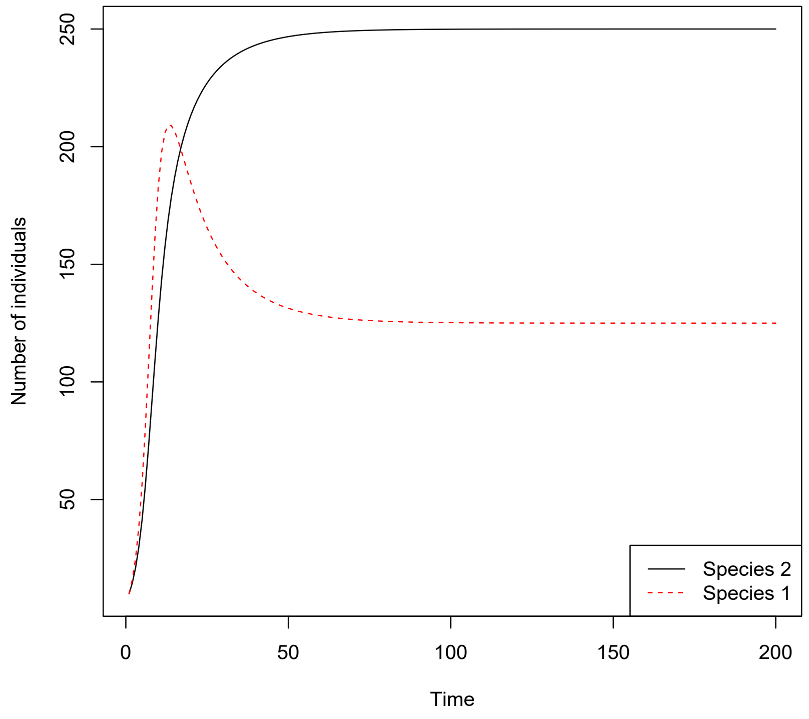


Figure 32 Result of solutions from Lotka Volterra ODEs for t = {1, 2, ..., 200}. Species 1 and 2 coexist, but at levels appreciably below their carrying capacities as a result of interspecific competition.

Functions can obviously be more complicated than these previous examples. Below is a function with some level of complexity, called `radiation.heatl`. Its purpose is to calculate northern hemisphere annual incident solar radiation (MJ $cm^{-2} yr^{-1}$**)** and heatload given slope, aspect, and latitude (all measured in degrees). Heatload is a radiation index based on the idea that the highest amounts of radiation occur on southwest facing slopes because they receive late afternoon sun added to ambient heating from earlier daylight hours (McCune and Keough 2002).

```
radiation.heatl <- function(slope, aspect, lat){
  asp.wrap.rad <- (-1 * abs(aspect - 180)) + 180
  asp.wrap.hl <- abs(180 - abs(aspect - 225))
  rad.lat <- (lat/180) * pi
  rad.asp <- (asp.wrap.rad/180) * pi
  hl.asp <- (asp.wrap.hl/180) * pi
  rad.slope <- (slope/180) * pi
   rad <- 0.339 + 0.808 * (cos(rad.lat) * cos(rad.slope)) - 0.196 *
   (sin(rad.lat) * sin(rad.slope))-0.482 * (cos(rad.asp) * sin(rad.slope))
   hl <- 0.339+0.808 * (cos(rad.lat) * cos(rad.slope)) - 0.196 *
   (sin(rad.lat) * sin(rad.slope))-0.482 * (cos(hl.asp) * sin(rad.slope))
  list(radiation = rad, heat.load = hl)
}
```

After reading the function into **R** I can find the annual incident radiation and heatload for a site with a slope of 20º, with a northeast (30º) aspect, that is located at 40 degrees N latitude, by typing:

```
radiation.heatl(20, 30, 40)
$radiation
[1] 0.7347784

$heat.load
[1] 0.7183095
```

This site receives 0.7347784 mega joules of radiation per cm^2 per year, and has a heat load index of 0.7183095.

21.6 Looping

Loop functions exist in some form in virtually all programming languages. The call to a so-called "for loop" in **R** is made using the command `for`. An **R** for loop requires specification of three entities, in parentheses, following a call to `for`. These are:

1) an index variable, e.g., `i`,
2) the statement `in`, and
3) a sequence that the index variable refers to as loops commence.

The code defining the loop follows, generally (if the loop requires multiple lines) delineated by curly brackets.

In parallel to function writing it is good style to place the first curly bracket on the same line as the call to `for`, and to place the last curly bracket on its own line. For clarity, spaces should also be used to distinguish the loop contents. Thus, we have the basic form:

```
for(i in seq){
  loop contents
}
```

In the loop the *i*th element of something (e.g., matrix column, vector entry, etc.) is defined (or replaced) as the `for` sequence commences. The replacement/definition process takes place in the "loop contents".

|| Example 23

One application for a loop is to make functions with scalar input arguments amenable to vector, matrix or dataframe inputs. For example, what if I wanted to apply the `radiation.heatl` function (which requires scalar inputs) to a three columned dataframe with columns containing slope, aspect, and latitude information, respectively? For instance:

```
x <- data.frame(slope = c(10, 12, 15, 20, 3), aspect = c(148, 110, 0, 30,
130), latitude = c(40, 50, 20, 25, 45))
```

The first step in many loop applications is defining an object to contain the results. Because I will obtain a list with two objects from `radiation.heatl`, I will create two one column matrices to contain my results, one for radiation (I will call this `rad.res`), and one for heatload (I will call this `heat.res`). Because I have five observations, each matrix will have five elements.

```
rad.res <- matrix(ncol = 1, nrow = 5)
heat.res <- matrix(ncol = 1, nrow = 5)
```

Next I create the `for` loop.

```
for(i in 1:5){
  rad.res[i] <-  radiation.heatl(x[i,(1)],x[i,(2)],x[i,(3)])$radiation
  heat.res[i] <-  radiation.heatl(x[i,(1)],x[i,(2)],x[i,(3)])$heat.load
}
```

The function loops around on itself letting `i = 1` during the first loop, `i = 2`, during the second loop, up to `i = 5` on the final loop. Here are the results.

```
rad.res
          [,1]
[1,] 0.9976634
[2,] 0.8500810
[3,] 0.9302991
[4,] 0.8560357
[5,] 0.9185208
```

```
heat.res
          [,1]
[1,] 0.9455112
[2,] 0.7734540
[3,] 0.9668378
[4,] 0.8395667
[5,] 0.9001073
```

Look at the function and try to really I understand what I did, using the information from earlier in this document.

|| Example 24

Another application of a loop is to iteratively build on the results of the previous step in the loop. Consider the following function that counts the number of even entries in a vector of integers.

```
evencount <- function(x){
  res <- 0
  for(i in 1 : length(x)){
    if(x[i]%%2 == 0) res <- res + 1
  }
  res
}
```

Recall that `%%` is the modulus operator in **R**. That is, it finds the remainder in division. By definition the remainder of any even integer divided by two will be zero. At each loop iteration the function adds one to the number in `res` if the current integer in the loop is even (has remainder zero if divided by two).

```
evencount(c(1,2,3))
[1] 1
evencount(c(1,2,3,4,10))
[1] 3
```

|| Example 25

A third loop application is the summarization of data with respect to levels in a categorical variable. Consider the categorical extension to the `Downs` dataset discussed earlier . We have:

```
Categories <- factor(c(rep(1, 6), rep(2, 5)))
cbind(Downs, Categories)
```

What if we wished to statistically summarize the variables in `Downs` (Age, Births, and Cases) simultaneously for each level in the categorical variable `Categories`? One solution is a `for` loop.

We first create an empty list to hold the result:

```
result <- list()
```

The components in the list will be dataframes of summary statistcs. These will be assembled in a for loop that steps through the levels in `Categories`

```
for(i in levels(Categories)){
  temp <- Downs[Categories==i,]
  result[[i]] <- as.data.frame(apply(temp,2,stats))
  names(result[[i]]) <- c("Age","Births","Cases")
}
```

Instead of a numeric sequence, the loop will walk through the levels of `Categories`. This is specified with the code: `for(i in levels(Categories)).` Note that in the first line following the `for` specification, the Downs dataset is subset by levels in categories. The data are then summarized with the function stats that we created in Example 7. Column names for the summary dataframes are given in the last line of the loop.

Here is the loop result:

```
result
$`1`
              Age        Births    Cases
n          6.00000  6.000000e+00  6.00000
min       17.00000  4.834000e+03  9.00000
max       38.50000  2.389600e+04 22.00000
mean      26.25000  1.565483e+04 15.00000
median    25.50000  1.481950e+04 15.50000
sd         7.99844  6.821069e+03  4.38178
var       63.97500  4.652698e+07 19.20000
IQR        9.50000  6.770250e+03  3.25000
SE         3.26535  2.784690e+03  1.78885
kurtosis -0.79755  2.097100e-01  0.92773
skew      0.50457 -4.399500e-01  0.36372

$`2`
              Age        Births     Cases
n          5.00000       5.00000   5.00000
min       39.50000     249.00000   7.00000
max       47.00000    3961.00000  31.00000
mean      43.40000    1617.00000  20.20000
median    44.50000     596.00000  22.00000
sd         3.24808    1721.52011  10.89495
var       10.55000 2963631.50000 118.70000
IQR        5.00000    2625.00000  19.00000
SE         1.45258     769.88720   4.87237
kurtosis -2.48635      -2.20448  -2.64479
skew     -0.32174       0.77477  -0.28092
```

21.7 Looping without `for`

Looping in **R** is also possible using the style of the language C which conventionally uses the functions `while`, `repeat`, and `break`.

|| Example 26

Consider an example in which 2 is added to a base number until the updated number becomes greater then or equal to 10: We have:

```
i <- 1
while (i < 10)i <- i + 2
i
[1] 11
```

Or, alternatively

```
i <- 1
while(TRUE){
 i <- i + 2
 if (i > 9) break
}
i
[1] 11
```

Here the variable `i` took on values 1, 3, 5, 7, 9, and 11 as the loop commenced. When `i` equalled 11 the condition for continuation of the loop failed and the loop was halted.

21.8 Calling and receiving code from other languages

Code from C, C++, Fortran, MATLAB, Python and other languages can be linked to **R** at the command prompt. Indeed, most of the code for **R** is written in C. **R** can also be called from a number of different languages including C, Java, or Python (Lang 2005). For instance, the **R** package *RCytoscape* allows cross communication between the popular Java-driven software molecular network package Cytoscape and the **R**-console. We have already learned that Perl applications can be used to identify and manipulate **R** objects (see § 17.10).

Along with many other modern languages (e.g., Python, Javascript, Mathematica), **R** is generally applied as an **interpreted language**. As a result functions written in **R** must be tacitly translated into binary before they can be executed. This process is in contrast to **compiled languages**, e.g., C, Fortran, and Java. For these languages a compiler (a translation program) is used to transform the **source code** into a **target "object" language**, which is generally binary. The product of the compilation is called an **executable file** (Figure 33). In priniciple, ny programming language can be both compiled or interpreted, so use of the term "interpreted language" here refers to languages that are *usually* interpreted rather than compiled.

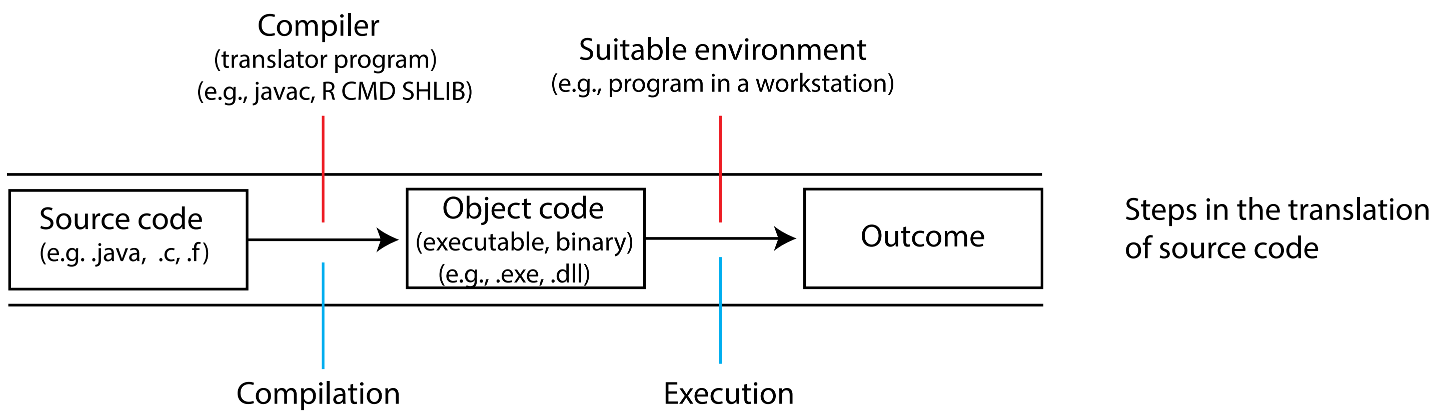


Figure 33 Illustration of translation steps in compiled languages.

Raw Fortran source code is generally saved as an entity called an .f file, C source code is saved as an .c file, and Java source code is saved as a .java file. Windows executable files, complied from source code, will generally have an .exe or .dll extension. **R** contains both Fortran and C compilers. Note, however, that the compilers will only work for Fortran code written as a **subroutine** and C code written in **void** formats. As a result, neither will return a value directly.

To write and compile Fortran and C code in Windows one can save files containing the source code in the **bin** directory of the current version of **R** (where the compilers are located), and then invoke the shell command: `R CMD SHLIB` from a workstation command prompt followed by the name of the file.

The R CMD algorithms located in the **R bin** directory are an important group of functions that are called directly from the command prompt shell (not interactively from the **R**-console). They include `R CMD check`, which checks user designed packages for errors, and `R CMD batch` which creates batch **R** output files (e.g., collections of .pdf files, dataframes or graphs).

Calling Fortran and C for looping

Because its functions are not compiled, **R** requires a large amount of system time for iterative procedures like loops. As a result, it may be expedient to call compiled code, originally written in Fortran or C, for complex looping with large datasets.

Below is a simple example (that could easily be handled without a `for` loop) that compares **R**, Fortran, and C looping. Familiarity with C and Fortran is assumed.

|| Example 27

Here is a Fortran subroutine loop to convert a vector of Fahrenheit measurements to degrees Celsius.

```
      subroutine ftoc(n, x)

      integer n
      double precision x(n)
      integer i

      do 100 i = 1, n
          x(i) = (x(i)-32)*(5./9.)
  100 continue

      end
```

After typing up the code in a text editor we will save it in the **R bin** directory as the file `FtoC.f`. We will then compile it by opening up an operating system command line prompt, going to the **bin** directory (if you are using the 64 bit **R**, be sure to specify the 64 bit version before the 32 bit version in your Windows system search path), and typing:

```
R CMD SHLIB FtoC.f
```

This shell command will create a compiled routine (in a Windows operating system this will be a .dll file, in Unix/Linux it will be an .so file).

Here is an analogous C function for converting ^{0}F to ^{0}C:

```
void ftocc(int *nin, double *x)
{
      int n = nin[0];

      int i;

      for (i=0; i<n; i++)
      x[i] = (x[i] - 32) * 5 / 9;
}
```

We would save the code as the file `ftocc.c` file in the bin directory and run the shell command:

```
R CMD SHLIB ftocc.c
```

will create a compiled routine in the form of a .dll file.
Here is an **R**-wrapper that can call either the Fortran subroutine, `call = "f"`, or the C function, `call = "c"`.

```
F2C <- function(x, call = "f"){
  n <- length(x)
  if(call == "f"){
    dyn.load("C:/Program Files/R/R-3.0.2/bin/x64/ftoc.dll")
    out <- .Fortran("ftoc", n = as.integer(n), x = as.double(x))
  }
  if(call == "c"){
    dyn.load("C:/Program Files/R/R-3.0.2/bin/x64/ftocc.dll", nin = n, x)
    out <- .C("ftocc", n = as.integer(n), x = as.double(x))
  }
  out
}
```

Let's convert 1,000,000 randomly generated Fahrenheit temperatures to Celsius.

```
x <- runif(1000000, 0, 100)
```

Here is a loop using **R** alone.

```
F2CR<-function(x){
  res <- 1 : length(x)
  for(i in 1 : length(x)){
    res[i] <- (x[i] - 32) * (5/9)
  }
  res
}
```

Let's compare the run times.

```
system.time(F2CR(x))
   user  system elapsed
   2.93    0.00    2.95
system.time(F2C(x, call = "f"))
   user  system elapsed
      0       0       0
system.time(F2C(x, call = "c"))
   user  system elapsed
   0.03    0.00    0.03
```

The Fortran and C loops gave the same transformation results (not shown here), but ran much faster. The Fortran subroutine was particularly fast. This is despite the fact that this language greatly predates C (and certainly **R**).

21.9 Functions with animation

Animation can be in **R** used to illustrate a wide range of processes (Xie 2011, Xie and Chang 2008). Functions with animation are generally based on for loops with some method of slowing the loop; usually the function `Sys.sleep()`. Slowing the loop allows examination of the iterative steps defined in the creation of a plot.

|| Example 28

Consider the following function:

```
R.zoom<-function(){ # requires R >= 2.15.1
  for(i in seq(30, 1800, 30)/10){
    dev.hold()
    plot(1:10, 1:10, type = "n", xaxt = "n", yaxt = "n", xlab = "", ylab = "")
    text(5, 5, "R", cex = i, srt = i)
    dev.flush()
    Sys.sleep(.1) #Loop stopped for 0.1 seconds at each iteration
  }
}
```

Using functions from package *animation* (Xie and Chang 2008) one can save an **R** animation as a media file for inclusion in other formats, e.g., webpages, powerpoint presentations, interactive pdf documents, etc.

For instance the code below creates an adobe flash (.swf) file of `Rzoom` to a temporary directory.

```
install.packages("animation")
library(animation)
saveSWF(R.zoom(), swf.name = "Rzoom.swf", interval = 0.1, nmax = 30,
ani.dev = "pdf", ani.type = "pdf",  ani.height = 6, ani.width = 6)
```

The function `saveSWF` requires installation of SWF Tools, and a path in the Windows environment to the tools.

The result, embedded in an .flv file, can be shown by clicking on the flashplayer link below.

As a more practical example we will update Figure 25 to animate a three dimensional plot showing the cover of the plant *Vaccinium vitis-idaea* as a function of pH and % soil N (see || Example 13).

```
rotate.Fig <- function(){
  angle <- 0:360
  for(i in 1:length(angle)){
    dev.hold()
    Fig(angle = angle[i])
    dev.flush()
    Sys.sleep(.1)
   }
}
```

```
library(animation)
saveSWF(rotate.Fig(), swf.name = "rotate.swf", interval = 0.1, nmax = 30,
ani.dev = "pdf", ani.type = "pdf",  ani.height = 6, ani.width = 6)
```

As before, the rotation can be run by clicking on the flashplayer link below.

Of note, we can also create hand-rotatable 3D figures under the *rgl* real-time rendering system (Figure 34).

```
expg <- expand.grid(varechem$pH, varechem$N)
subs <- cbind(varechem$pH, varechem$N)
tf <- (expg[,1] == subs[,1])&(expg[,2] == subs[,2])
y <- ifelse(tf == TRUE, varespec$Vaccviti, NA)
surface <- data.frame(N = expg[,1], pH = expg[,2], vac.vit = y)

library(car)
scatter3d(vac.vit ~ N+pH, data = surface, surface = TRUE, fit = "linear",
zlab = "N", xlab = "pH", ylab = "Vaccinium vitilus (% cover)")
```

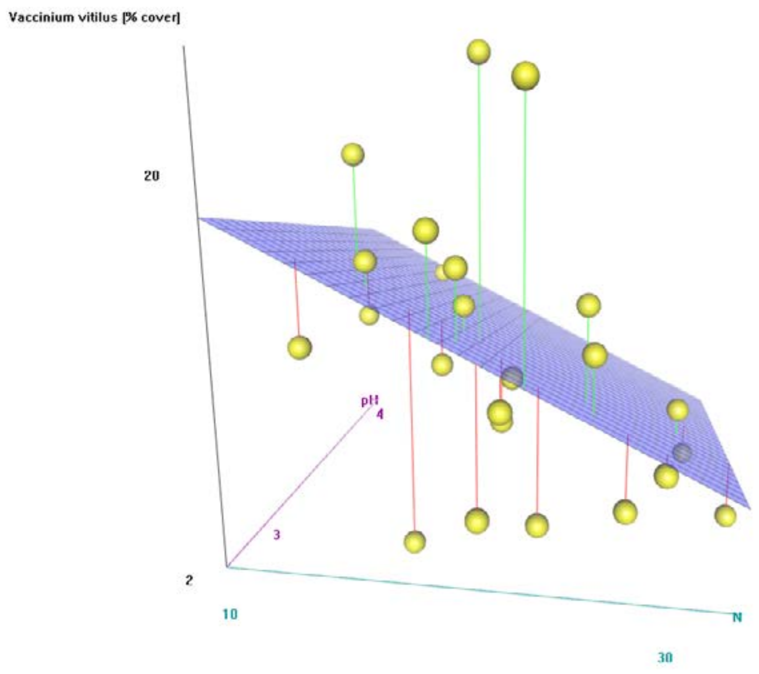


Figure 34 Hand rotatable graphics object.

21.10 Building GUIs

GUIs (**Graphical User Interfaces**) are a mixed bag. A person who is terrified of command line entry will be reassured by their point and click familiarity. However much user flexibility will be lost for controlling functions. In addition, a GUI implementing too many arguments may quickly become visually confusing, and hiding code inside a GUI "black box" is contrary to the "mission statement" of **R**. Command line entry is valuable for two other reasons. First, one can scroll through earlier commands (using the up arrow), and easily repeat or modify earlier steps. Second, command line entry provides an exact record of everything you have done during a particular **R**-session. Despite these caveats the package *asbio* relies on interactive GUIs for pedagogic demonstrations. Type:

```
library(asbio)
book.menu()
```

Devices like those in *asbio* can be created in a number of programming languages including Java and Perl. I used the language **tcltk** (pronounced "tickle tee kay") to create *asbio* GUIs, because tcltk GUIs are easy to build, and an interpreter for tcltk is included with a conventional install of **R**.

tcltk GUIs

An extensive description of the tcltk language and its capacities in **R** are beyond the scope of this book. I include simple examples here (with little code explanation) merely to show the reader that such devices can be easily constructed in **R**.

|| Example 29

Consider a GUI whose only purpose is to destroy itself (Figure 35).

```
require(tcltk)
tt <- tktoplevel()
DM.but <- tkbutton(tt, text = "Exit", command = function() tkdestroy(tt))
tkgrid(DM.but)
```

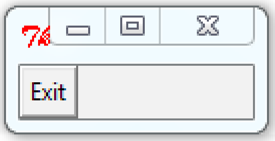


Figure 35 An extremely simple radio button GUI. Click "Exit" (in **R**) to destroy.

- The function `ttoplevel` defines the "toplevel" **widget** (graphical elements that allow a user to interactively change a function), allowing it to be manipulated.
- The `tkbutton` function creates the "Exit" button. The first argument is name of the widget that the button is to be placed upon. The text argument defines the text on the button. The `command` argument defines the function that the button initiates. In this case it is `tkdestroy`, which closes open tcltk widgets.
- The function `tkgrid` places the button on the widget.

We can also use GUIs to run other **R**-functions. For instance the GUI below (Figure 36) calls the function `R.zoom` from § 21.9.

```
tt <- tktoplevel()
but <- tkbutton(tt, text = "Zoom", command = R.zoom)
tkgrid(but)
```

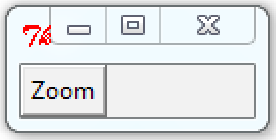


Figure 36 A GUI for calling the function `R.zoom`.

GUIs can contain a number of widgets, including sliders.

| | Example 30

Below is code that defines the function `plot.me`. The function simply plots a large blue dot. Below it is code for a GUI slider. The dot's vertical location is defined by the slider (Figure 37).

```
plot.me <- function(){
  y <- evalq(tclvalue(SliderValue))# Evaluate the expression
  plot(1,as.numeric(y),xlab = "", ylab = "%", xaxt = "n", ylim = c(0,100),
cex = 4, col = 4, pch = 19)
}

slider.env <<- new.env()
tt <- tktoplevel()
SliderValue <- tclVar("50")
SliderValueLabel <- tklabel(tt,text = as.character(tclvalue(SliderValue)))
tkgrid(tklabel(tt, text = "Slider Value : "), SliderValueLabel, tklabel(tt,
text = "%"))
tkconfigure(SliderValueLabel, textvariable = SliderValue)
slider <- tkscale(tt, from=100, to=0, showvalue=F,
                  variable = SliderValue, resolution=1,
                  orient = "vertical", command = substitute(plot.me()))
tkgrid(slider)
```

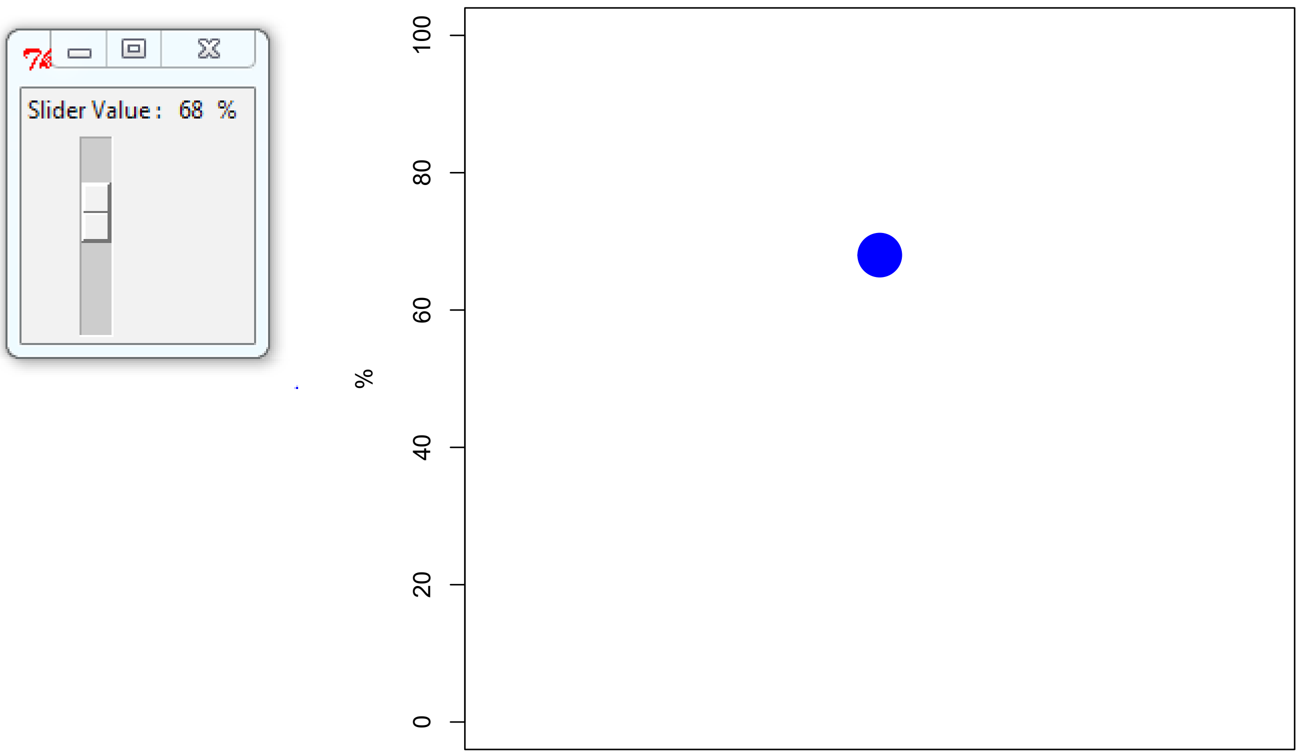


Figure 37 A plotted symbol along with a slider that alters its position.

The superassignment operator `<<-` used above initiates a search through the function environment for an existing definition of the variable being assigned. If the variable is found, then its value is redefined, otherwise assignment takes place with respect to the global environment and will be translated in all functions. Other code specifications include:

- `SliderValue <- tclVar("50")` which creates a variable that can be used interactively, and defines the starting value of the slider to be 50.
- `SliderValueLabel <- tklabel(tt,...` which causes the value of the slider to be formatted for projection
- `tkgrid(tklabel(tt, text = "Slider Value : "),...` which places the slider values,along with text "Slider Value" and "%", above the slider.
- `tkconfigure(SliderValueLabel, textvariable = SliderValue)` which tells **R** that the slider output to be written will come from the variable `SliderValue`.
- `slider <- tkscale(tt, from=100, to=0,...` which defines the range of the slider along with other slider characteristics including the name of the function (`plot.me`) that the slider runs.
- `tkgrid(slider)` which places the slider on the GUI.

For more information on GUIs see the tcltk manual included with a conventional installation of **R** (but written for a non-**R** language framework).

Amazingly, one can call and utilize **R** from a local online server. Further, using **shiny apps** (http://shiny.rstudio.com/), an implementation of Rstudio, one can control R using sliders and widgets. When using such applications R is run unseen and a user need know nothing about the R language (see https://ahoken.shinyapps.io/seeNorm/).

21.11 Functions with `class` and `method`

This is an advanced topic for package developers, but may be of interest to those who wish to embed particular methods for summarizing a family of functions.

It turns out that we are not limited to the pre-existing classes in **R** (e.g., `numeric`, `factor`, etc.). Instead, we can create user-defined classes with associated methods for plotting, printing and summarization. Object classes allow one to customize generic functions, e.g., `plot`, `print`, `summary`, for particular classes. These functions are called with the generic function names e.g., `plot`, `print`, `summary`. Here are functions on my workstation that will be called with `plot`, depending on the class of the object that is being plotted.

```
methods(plot)
 [1] plot.acf*          plot.data.frame*    plot.decomposed.ts* plot.default
 [5] plot.dendrite*     plot.dendrogram*    plot.density*       plot.deSolve*
 [9] plot.ecdf          plot.factor*        plot.formula*       plot.function
[13] plot.hclust*       plot.histogram*     plot.HoltWinters*   plot.isoreg*
[17] plot.lm*           plot.medpolish*     plot.mlm*           plot.pairw
[21] plot.ppr*          plot.prcomp*        plot.princomp*      plot.profile.nls*
[25] plot.shingle*      plot.spec*          plot.stepfun        plot.stl*
[29] plot.table*        plot.trellis*       plot.ts             plot.tskernel*
[33] plot.TukeyHSD*
```

For example, let `x` be an object of class `pairw`. If I type `plot(x)`, then the command `plot.pairw(x)` is run.

The package *asbio* contains a number of functions for summary statistics including the function `G.mean` below which calculates the geometric mean (see Ch. 4 in **Foundational and Applied Statistics** textbook). It might be desirable to create a class called `as.stat` to print such summary statistics in a consistent way.

```
G.mean <- function(x){
  x <- na.omit(x)
  res <- list(stat = (prod(x))^(1/length(x)), name = "Geometric Mean")
  class(res) <- "as.stat"
  res

}
```

```
print.as.stat<-function(x, ...){
  cat("\n")
  cat(x$name, "\n")
  cat(x$stat, "\n")
  invisible(x)
}

x<-c(2, 1, 4, 5.6, 7, 6.7, 3, 4.5, 10, 12, 2, 5, 6)
G.mean(x)

Geometric Mean
4.357524
```

We have gotten rid of some of the clunky default **R** output (for instance the `[1]` is gone). `G.mean` calls the function `print.as.stat` to print its results. Within `print.as.stat` the function `cat` concatenates and prints `G.mean` output, the argument `"\n"` means "put a line break in the output", and the term `invisible` lets additional items be in `print.as.stat` that are not printed, but can still be called. Additional methods can also be made for plotting and other summaries for objects of class `as.stat`. The code for internal functions will not be directly accessible by typing the function name, but can be accessed with the double colon metacharacter (`::`) For instance a user of `as.stat` can see the internal function `print.as.stat` (if it exists) by typing the package name followed by `::print.as.stat`. The triple colon operator (`:::`) allows access to so-called "unexported" objects in a package.

It should be noted that the implementation here describes the **R** S3 system for classes and methods. The so-called S4 system, described in Chambers (2008) requires a much stricter set of conditions for user-classes[19].

21.12 Documenting functions and workflow

A concern with **R** is tracking the characteristics of your functions and workflow. I generally use Rstudio or a text editor like TinnR to create .R script files that can be loaded into **R**, or pasted piecemeal into the **R**-console. However, even with use of notes using `#` it may be difficult to deduce what you have done, particularly given a an extended long separation from the work.

One solution is to create .Rd document files describing functions, translate them into a **LaTex** style .tex documents, and use these to be build a pdf document. LaTex is a high quality typesetting freeware system that is the *de facto* standard for many publishers of scientific documents (see http://www.latex-project.org/).

Consider the function below:

[19]Google has an **R** style guide: http://google-styleguide.googlecode.com/svn/trunk/Rguide.xml that offers good advice for code writing. The webpage recommends S3 over S4 methods for most applications.

```
myfunction <- function(text = "Hello world"){
print(text)
}
```

After entering function, install and load the package *SoDA*,

```
install.packages("SoDA")
library(SoDA)
```

and type

```
promptAll("myfunction")
```

This will create the skeleton of an .Rd documentation file for `myfunction()` that will be placed in your working directory. The document can be completed using any text editor. Now...

- Place the finished file in your R///bin directory,
- Go to a command prompt and navigate to the directory using the MS-DOS command cd
- In the command prompt type `R CMD Rd2pdf myfunction.rd`. This creates a .tex file that is read (in LaTex) to build a .pdf.

The approach requires that both a LaTeX style repository (e.g., MiKTeX), and a Windows **environmental path** to this repository exist on your machine. ALthough normally not a concern for those not developing packages, batches of .Rd files (and other types of R documentation) can be spell-checked using the function `aspell`. The function requires installation of freeware alspell software.

A more sophisticated approach is to use a LaTeX text editor to create an .Rnw file that can be read with either *Sweave* or *knitr*. These programs can write beautiful equations and text (although the LaTeX language can seem daunting initially), distinguish **R** code from documentation, create graphs and tables from **R** code, and correctly place all of these into a .pdf document.

Guidance for *Sweave* can be found at:
http://www.stat.uni-muenchen.de/~leisch/Sweave/

Guidance for *knitr* can be found at:
http://yihui.name/knitr/

Examples for some of my consulting work, documented in this way, can be found with the links below.

Zero-inflated generalized linear models and elk
Dall's sheep population dynamics
Autism neurological genetic networks

Good LaTex editors include TeXnicCenter, which can be customized to call the `R CMD Sweave` script using the **Define Output Profile** dialog box in the **Build** pulldown menu.

|| Example 31

To create *knitr* documentation for an **R** work session we first install and load the *knitr* and *xtabs* packages.

```
install.packages("knitr"); library(knitr)
install.packages("xtable")
```

We then write an empty .Rnw file to our working directory:

```
file.create("stats.Rnw")
```

LaTex documents require a preamble. We open stats.Rnw and type the following:

```
\documentclass{article}
\begin{document}
\title{Stats summary of loblolly pine data}
\maketitle
```

We can, if we wish, now type in some **R** code. We indicate (to Knitr or Sweave) that characters *are* **R** code by beginning a code chunk with `<<>>=` and ending it with `@`.

```
The following code provides a statistical summary of loblolly pine
(\emph{Pinus taeda}) data.

<<>>=
data(Loblolly)
stats <- function(x, digits = 5){
 ds <- data.frame(statistics = round(c(length(x), min(x), max(x),
 mean(x), median(x), sd(x), var(x) ,IQR(x), sd(x)/sqrt(length(x)),
 kurt(x), skew(x)),
 digits))
 rownames(ds) <- c("n", "min", "max", "mean", "median", "sd",
 "var", "IQR", "SE", "kurtosis", "skew")
 return(ds)
}
pine.height <- stats(Loblolly$height)
@
```

We can use the *xtable* library to allow us to make an pretty table of this output. We load the package (and hide the code in the output document that we will create) by typing:

```
Summary stats for tree hieghts are shown in Table 1\\

<<echo=FALSE>>=
library("xtable")
@
```

Two backslashes (i.e. `\\`) is a LaTex carriage return.

We insert the table using:

```
<<label = tab1, results = "asis", echo = FALSE>>=
mat1 <- xtable(as.matrix(pine.height),
caption = "Loblolly pine height summary", label = "tab:one")
print(mat1, table.placement = "H", caption.placement = "top")
@
```

The argument `table.placement = "H"` means: place the table exactly at the indicated location with respect to text.

We can also make on-the-fly graphs:

```
Figure 1 shows a histogram of pine ages
\begin{center}
\begin{figure}[H]

<<out.width="0.8\\linewidth">>=
hist(Loblolly$age)
@

\caption{Distribution of pine ages.}
\end{figure}
\end{center}
```

The argument `center` in `begin` centers the figure. The command `out.width="0.8\\linewidth"` forces the figure width to be 80% of the defined document line width. Figure dimensions will be held constant in this reduction. The quotations and backslashes in this code would be unnecessary in a non-***knitr*** context.

Lets end the document.

```
\end{document}
```

We now save the document. Assuming that stats.Rnw is still in the working directory we go back to

R and type:

```
knit2pdf("stats.Rnw")
```

The document stats.pdf will now be in your working directory. The document is shown here. LaTex/ *knitr* code for the entire example can be found here.

The function `purl` in *knitr* can be used to pull R code from a knit document and compile an .R file of the code. To create such a file for the current example I would type:

```
purl("stats.Rnw")
```

RStudio has a number of outstanding features that simplify writing documentation. For instance, generating html **R**-documentation in RStudio requires no additional LaTex support. Generation of Sweave and knitr pdfs, however, *does* require MikTex-alike installation although this process is greatly simplified in RStudio through the straightforward creation of .Rnw and .Rd files, among other features. Implementation of a simple documentation framework called **R** Markdown is also provided in RStudio, which allows compilation of many output formats including html, pdf, and even MS Word.

22 Exercises

1. The following questions concern the history of and general characteristics of **R**.
   (a) Who were the creators of **R**?
   (b) When was **R** first introduced?
   (c) What languages is **R** derived from/most similar to?
   (d) What features distinguish **R** from other languages and statistical software?
   (e) What are the three operating systems **R** works with?

2. Perform the following operations.
   (a) Leave a note to yourself in the console.
   (b) Identify your working directory.
   (c) Change your working directory.
   (d) Create an object called `x` that contains the numeric entries 1, 2, and 3.
   (e) Examine `x` in the **R** console.
   (f) Make a copy of `x` called `y`.
   (g) List the current objects in your work station.
   (h) Save your history and open the file in a text editor.
   (i) Save your objects using `save.image()`. Close and reopen **R**. Do `x` and `y` still exist?

3. Solve the following mathematical operations using lines of code in **R**. Show code.
   (a) $1 + 3/10 + 2$
   (b) $(1 + 3)/10 + 2$
   (c) $((3 \times 4)/23)^2$
   (d) $\log_2(3^{1/2})$
   (e) $3x^3 + 3x^2 + 2$ where $\mathbf{x} = \{0, 1.5, 4, 6, 8, 10\}$
   (f) $4(\mathbf{x} + \mathbf{y})$ where $\mathbf{x}$ and $\mathbf{y}$ are: $\mathbf{x} = \{0, 1.5, 4, 6, 8\}$ and $\mathbf{y} = \{-2, 0.5, 3, 5, 8\}$.
   (g) $\frac{d}{dx}\tan(x) + 2.3e^{3x}$
   (h) $\frac{d^3}{d^3x}\frac{3}{4x^4}$
   (i) $\int_3^{12} 24x^3 + \ln(x)dx$
   (j) $\int_{-\infty}^{\infty} \frac{1}{\sqrt{2\pi}} e^{-\frac{x^2}{2}} dx$ (i.e., find the area under a standard normal pdf).
   (k) $\int_{-\infty}^{\infty} \frac{x}{\sqrt{2\pi}} e^{-\frac{x^2}{2}} dx$ (i.e., find $E(X)$ for a standard normal pdf).
   (l) $\int_{-\infty}^{\infty} \frac{x^2}{\sqrt{2\pi}} e^{-\frac{x^2}{2}} dx$ (i.e., find $E(X^2)$ for a standard normal pdf).
   (m) Find the arithmetic mean, median, variance, skew and kurtosis of the data $\mathbf{x} = \{0, 1.5, 4, 6, 8, 10\}$. Functions for skew and kurtosis are in the package *asbio*.

4. Read the section on linear algebra in the mathematical Appendix from the **Foundational and Applied Stats** textbook. Let:

$$\mathbf{A} = \begin{bmatrix} 2 & -3 \\ 1 & 0 \end{bmatrix}, \mathbf{b} = \begin{bmatrix} 1 \\ 5 \end{bmatrix}.\ \text{Find:}$$

(a) **Ab**
(b) **bA**
(c) det(**A**)
(d) $\mathbf{A}^{-1}$
(e) **A′**
(f) We can solve systems of linear equations using matrix algebra with the function **Ax** = **b**, and $\mathbf{A}^{-1}\mathbf{b} = \mathbf{x}$. In this notation **A** contains the coefficients from the linear equations (by row), **b** is a vector of solutions given in the individuals equations, and **x** is a vector of solutions sought in the system of models. Thus, for the linear equations:

$$\begin{aligned} x + y &= 2 \\ -x + 3y &= 4 \end{aligned}.$$

We have:

$$\mathbf{A} = \begin{bmatrix} 1 & 1 \\ -1 & 3 \end{bmatrix},\ \mathbf{x} = \begin{bmatrix} x \\ y \end{bmatrix} \text{and } \mathbf{b} = \begin{bmatrix} 2 \\ 4 \end{bmatrix}.$$

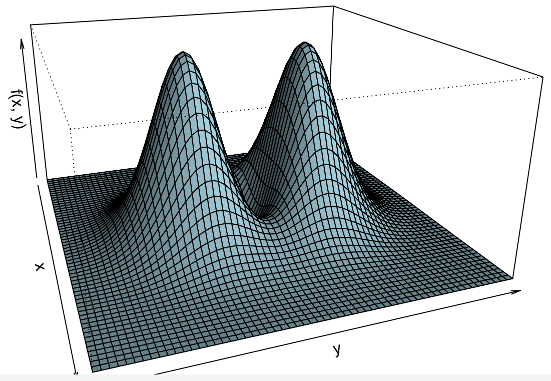
And we find: $\mathbf{x} = \begin{bmatrix} 1/2 \\ 3/2 \end{bmatrix}$.

Solve the system below using linear algebra with **R**:

$$\begin{aligned} 3x + 2y - z &= 1 \\ 2x - 2y + 4z &= -2. \\ -x + 0.5y - z &= 0 \end{aligned}$$

5. The function to the right[20] has the form $f(x, y) = (x^2 + 6y^2)e^{-x^2-y^2}$. Find the area under the function surface between x = 0 and 2 and y = -1 and 2. That is, find:

$$\int_0^2 \int_{-1}^2 (x^2 + 6y^2)e^{-x^2-y^2}\,dydx.$$



[20] code for figure:

```
x <- seq(-3, 3, by = .1); y <- x
f <- function(x, y) {(x^2 + 6 * y^2) * exp(-x^2 - y^2)}
z <- outer(x, y, f)

persp(x, y, z, theta = 70, phi = 20, expand = 0.5, col = "lightblue", ltheta = 120,
shade = 0.75, xlab = "x", ylab = "y", zlab = "f(x, y)")
```

The solution in **R** will require the function `adaptIntegrate` in package *cubature*.

6. Distinguish expressions and assignments in **R**.

7. Complete the following exercises concerning R packages:
   (a) Install the package *asbio.*
   (b) Load the *asbio* package for the current work session.
   (c) Access the help file for `bplot` (a function in *asbio*).
   (d) Load the dataset `fly.sex` from *asbio.*
   (e) Obtain documentation for the dataset `fly.sex`.
   (f) Access the column `longevity` in `fly.sex` using the function `with`

8. The speed of the earth rotating on its axis, *E*, is approximately 1700km/hr, or 1037 mph, at the equator. We can calculate the velocity of the rotation of the earth at any latitude with the equation, $V = \cos(\text{latitude}^o) \times E$. The latitude of Pocatello, Idaho is 42.871 degrees. Use **R** to find the rotational speed of the earth at this latitude. Remember, the function `cos()` assumes inputs are in radians, not degrees.

9. Make a plot showing the relationship between the speed of the earth's rotation and latitude. See question 8 above for more information.
   (a) Create a sequence of numbers (degrees) from 0 to 90. Give this vector a name.
   (b) Convert the vector in (a) from degrees to radians. Give this vector a name.
   (c) Calculate velocities for the vector in (b), give this vector a name.
   (d) Plot these velocities versus latitude, i.e. the vector from (a). Label axes appropriately.

10. Consider the following variables:
```
x <- c(1,2,2.5,3,4,3,5)
y <- c(6,4.3,3,3.1,2,1.7,1)
```

   (a) Make a plot with `x` defining the *X*-axis and `y` on the *Y*-axis.
   (b) Make every point in the scatterplot a different color.
   (c) Make every point a different shape.
   (d) Create a legend describing all the shape and color combinations of all points one through seven (call them Point 1, Point 2, etc.). Type `?legend` for more information.
   (e) Convert from a point to an overplotted line and point plot. Type `?plot` to get more information.
   (f) Change the name of the *X*-axis to "*Abscissa* axis" and the name of the y-axis to "*Ordinate* axis". As indicated, italicize the words "*Abscissa*" and "*Ordinate*" while leaving the word axis in a normal font. Type `?expression`, `?paste` and `?italic` for more information.
   (g) Place the text "Y = -1.203X + 6.539" at coordinates x = 2, y = 2.5. Italicize as indicated. Type `?text` for more information.
   (h) Place a line with a slope of -1.203 and an *Y*-intercept of 6.539 on the plot. Type `?abline` for more information.

11. Load the `C.isotope` dataset from package *asbio*. Create a graphical device holding three plots in a single row, i.e., the three plots will be side by side.
   - In the first plot, show $\delta^{14}C$ as a function of time (`decimal.date`) using a line plot. Use appropriate axis labels.
   - In the second plot, show CO_2 concentration as a function of time in a scatterplot.

- In the third plot, show measurement precision (column four in the dataset) as a function of δ^{14}C.

12. Load the `goats` data set in *asbio*.
    (a) Create a histogram for the variable `NO3`.
    (b) Create a scatterplot of `NO3` as a function of `feces.`
    (c) Make a plot showing `NO3` and `organic.matter` as a simultaneous function of `feces` by adding a second Y axis.
    (d) Change symbol sizes in (b) to reflect the values in `organic.matter`.
    (e) Create a 3D scatterplot depicting `NO3` as a function of `organic.matter and feces`.

13. Load the data set `asthma` in *asbio*. Note that the first and last columns are categorical variables.
    (a) Create a barplot of patient 201 FEV1 responses over time under drug a; i.e., plot row 1 from `asthma`.
    (b) Create a stacked barplot display the FEV1 levels of the 24 patients in the study in treatment "a" using: `a <- asthma[asthma$DRUG == "a",]`. Let bars represent patients.
    (c) Create a legend for the plot in (b)
    (d) Create a stacked barplot (or a beside barplot using `beside = TRUE`) to show how average FEV1 levels for each time frame differed for treatments a, b, and c. To do this you may want to create a 3 x 9 dimension matrix containing means at each time (columns) for each treatment (rows).
    (e) Create a legend to describe (d).
    (f) Make an overplotted line scatterplot showing all FEV levels to be function of time using `matplot()`. Vary symbols types to reflect patients, and vary line and symbol color to reflect the drug treatment.
    (g) Make a legend (or two) to clarify the meaning of symbol types and colors in (f).

14. Load the `fly.sex` dataset from *asbio.*
    (a) Plot longevity as a function of thorax length.
    (b) Distinguish points with respect to treatment types by altering plotting shapes and colors. Add an informative legend.
    (c) Create a boxplot showing longevity as a function of treatment type.
    (d) Create an interval plot (using `bplot()`) showing means and standards errors of longevity for each treatment level.

15. Load the `fly.sex` dataset from *asbio* and use `qplot()` from *ggplot2* to complete the following graphics exercise.
    (a) Plot longevity as a function of thorax length.
    (b) Distinguish points with respect to treatment types by altering plotting shapes and colors.
    (c) Alter axis labels, axis text, panel margins, point size, and legend location using `theme()` and appropriate geoms.

16. Create the following data structures:
    (a) A matrix object with two rows and two columns with the numeric entries 1,2,3,4.
    (b) A dataframe object with two columns; one column containing the numeric entries 1,2,3,4, an one column containing the character entries "a","b","c","d".
    (c) A list containing the objects created in (a) and (b).

17. Access the dataset `cliff.sp` in the library *asbio* which describes cliff vegetation from Yellowstone National Park, USA.
    (a) Use the `names()` function to find the names of the variables.

(b) Show how one would access the first row of data using **R**.
(c) Show how one would access the third column of data using **R**.
(d) Show how one would access the fourth element form the third column using **R**.

18. Consider the data from the table below

Plant height (dm)	Soil % N	Water index (1-10)	Management Type
22.3	12.0	1	A
21	12.5	2	A
24.7	14.3	3	B
25	14.2	4	B
26.3	15.0	5	C
22	14.0	6	C
31	NA	7	D
32	15	8	D
34	13.3	9	E
42	15.2	10	E
28.9	13.6	1	A
33.3	14.7	2	A
35.2	14.3	3	B
36.7	16.1	4	B
34.4	15.8	5	C
33.2	15.3	6	C
35	14.0	7	D
41	14.1	8	D
43	16.3	9	E
44	16.5	10	E

(a) Write the data into an **R** `dataframe`. Use the functions `seq()` and `rep()` to help you.
(b) Simultaneously calculate the column means for plant height and soil N using `apply()`.
(c) Use `complete.cases` to eliminate rows with missing data and rerun (b). Discuss the consequences.
(d) Find the mean and variance of plant heights for each Management Type using `tapply()`.
(e) Create a plot showing plant height as a function of the water index (as a categorical variable) using `boxplot()` or `bplot()`.

19. Create .csv and .txt datasets and read them into **R**.

20. Export the `dataframe` from Q . 19 to your working directory.

21. Given the following dataset provide solutions and **R** code.

```
Q.21 <- data.frame(height.in = c(70, 76, 72, 73, 81, 66, 69, 75, 80, 81, 60, 64,
59, 61, 66, 63, 59, 58, 67, 59), weight.lbs = c(160, 185, 180, 186, 200, 156, 163,
178, 186, 189,140, 156, 136, 141, 158, 154, 135, 120, 145, 117), sex = c(rep("M",
10), rep("F", 10)))
```

(a) Query whether all heights are less than or equal to 80 inches.
(b) Query whether any heights are more than 80 inches.
(c) Find the mean height of females (i.e. F) greater than or equal to 59 inches but less than 63 inches.
(d) The mean weight of males who are 75 or 76 inches tall.

(e) Use `ifelse()` or `if()` to classify heights equal to 58 <u>or</u> 59 as “small”.

22. Consider the dataset from Q. 18.
   (a) Use the function `replace()` to identify samples with soil N less than 13.5% by defining them as `"N-poor"`.
   (b) Use the function `which()` to identify which plant heights are greater than or equal to 33.2 dm.
   (c) Sort plant heights using the function `sort()`.
   (d) Sort the dataset with respect to ascending values of plant height using the function `order()`.

23. Using `match` or `which` and `%in%` replace the code column names in the dataset `cliff.sp` from *asbio* with the correct species names from `sp.list` below.

```
sp.list <- data.frame(code = c("L_ASCA","L_CLCI","L_COSPP","L_COUN",
"L_DEIN","L_LCAT", "L_LCST","L_LEDI","M_POSP","L_STDR","L_THSP","L_TOCA",
"L_XAEL","M_AMSE", "M_CRFI","M_DISP","M_WECO","P_MIGU","P_POAR",
"P_SAOD"), name = c("Aspicilia caesiocineria","Caloplaca citrina",
"Collema spp.", "Collema undulatum", "Dermatocarpon intestiniforme",
"Lecidea atrobrunnea", "Lecidella stigmatea", "Lecanora dispersa",
"Pohlia sp.", "Staurothele drummondii", "Thelidium species",
"Toninia candida", "Xanthoria elegans", "Amblystegium serpens",
"Cratoneuron filicinum", "Dicranella species",  "Weissia controversa",
"Mimulus guttatus", "Poa pattersonii", "Saxifraga odontoloma"))
```

24. Create an object, `x`, containing the letters of the alphabet using: `x <- letters`.
   (a) Verify that x is of class `character` and not classes `logical`, `factor` or `numeric`.
   (b) Coerce `x` to be a `factor` called `y`.
   (c) Coerce `y` to be `numeric` and multiply it by 10.

25. The following questions consider `NA`, `NaN` and `NULL`.
   (a) For the soil N data in Q. 18, identify which elements are *not* missing using `!= NA`. Discuss the results.
   (b) For the soil N data in Q. 18, identify which elements are *not* missing using `!is.na()`. Discuss the results.
   (c) Discuss the printed result for `log(-2)`.

26. The following questions concern binary data and floating point applications.
   (a) Find the binary representation of the number 32 by hand.
   (b) Find the digital numbers for the binary numbers 101101, 101010101, and 0.111 by hand. Verify your answer using `bin2dec`.
   (c) Use `bin2dec` to evaluate different binary representation of the decimal number 1/3. Use 0.0101, 0.01010101, and 0.01010101010101010101. Which provides the most "precise" representation of 1/3? Why?
   (d) Use **R** to find the Unicode binary representation of the letter "A".

27. Divide the values in the first two columns of the dataset in Q. 18 by their respective column sums by specifying an appropriate `function` in the 3rd (function) argument for `apply`.

28. Below is McIntosh’s index of diversity (McIntosh 1967):

$$U = \sqrt{\sum_{i=1}^{S} n_i^2}\ ,$$

where S is the total number of species, and n_i is the number of individuals in the ith species. Write a function to calculate this index. Run it on a sample from a site that contains five species represented by 5, 4, 5, 3, and 2 individuals respectively.

29. Below is the Satterthwaite formula for approximating degrees of freedom for the t distribution.

$$\nu = \frac{\left(\dfrac{S_x^2}{n_X} + \dfrac{S_Y^2}{n_Y}\right)^2}{\dfrac{\left(S_X^2/n_X\right)^2}{n_X - 1} + \dfrac{\left(S_Y^2/n_Y\right)^2}{n_Y - 1}},$$

where S_Y^2 is the sample variance for X, S_Y^2 is the variance for the variable Y, n_X is the sample size for variable X, and n_Y is the sample size for variable Y.

(a) Write a function for this equation that has the variables X and Y as arguments.
(b) Test the function for `x <- c(1,2,3,2,4,5)` and `y <- c(2,3,7,8,9,10,11).`

30. Create a function, implementing `switch()`, that can calculate the first or second derivative of a mathematical expression with respect to `"x"` (see Section 6.1). Test it on `expression(x^3).`

31. Using `apply` and the triple dot operator (`...`) create a function call `colTrim` that calculates trimmed means (`trim` is an argument in `mean`; see Section 6.1) and has flexible NA values (`na.rm` is also an argument in `mean`) for columns in a quantitative matrix or dataframe. Specify two arguments in your function one for `data` one for `...` . Test the function on the first two column of the data in Q. 18 `cliff.sp` dataset in *asbio* specifying both 10% trimming, and the removal of missing values.

32. Solve the systems of ODEs below for $t = \{1,2,...,20\}$.

$$\frac{dx}{dt} = ax + by$$
$$\frac{dy}{dt} = cx + dy$$

Let $a = 3$, $b = 4$, $c = 5$, $d = 6$. Initial values for x and y can be anything but $\{0,0\}$.

33. Create an **R** animation loop using your name that changes font-size, color, and string rotation (plot argument `srt)`, as the loop proceeds.

34. Use a `for` loop to create a 100 x 100 element matrix of random numbers. Accomplish this by completing the following steps.

(a) Create an empty matrix of the correct dimensions to hold the result, and give it a name. For instance, `rand`.
(b) Use a `for` loop to create columns in `rand.` Use the function `runif(100)` to generate 100 random numbers (the contents of one column) based on a uniform probability distribution. Loop to create other columns.

35. More fun with `for` loops. Here are some classic computer science applications.
    (a) A sequence of Fibonacci numbers is based on the function:

$$\begin{aligned}&f(n) = f(n-1) + f(n-2) \quad \text{for } n > 2 \\ &f(1) = f(2) = 1\end{aligned}.$$

    where *n* represents the *n*th step in the sequence.
    Using a `for` loop, create the first 100 numbers in the sequence, i.e. find *f*(1) to *f*(100). As a check, the first 5 numbers in the sequence should be: 1, 1, 2, 3, 5.
    (b) An interesting chaotic recursive sequence has the function:

$$\begin{aligned}&f(n) = f(n - f(n-1)) + f(n - f(n-2)) \quad \text{for } n > 2 \\ &f(1) = f(2) = 1\end{aligned}.$$

    Using a `for` loop, create the first 100 numbers in the sequence, i.e. find *f*(1) to *f*(100). As a check, the first 5 numbers in the sequence should be: 1, 1, 2, 3, 3.

36. Below is a mock dataset of plant height with respect to three treatments.

```
height.data <- data.frame(height = c(20, 30, 40, 40, 40, 20, 15, 10, 15, 20,
50, 35, 40, 50, 60), treatment = rep(1:3, each = 5, times = 1))
```

    (a) Create a function utilizing `tapply()` that simultaneously calculates means, variances, standard deviations, minimums, maximums and medians with respect to a vector of categories. Use it to find these estimates simultaneously for all three treatments in `height.data`.
    (b) Use the function `which()` to find which value in `height.data` is closest to 9.
    (c) Using a `for` loop, create a function that simultaneously calculates means, variances, standard deviations, minimums, maximums and medians for all three treatments.
    (d) Use the function `system.time()` to compare the run time for the functions in (a) and (c). Describe your results.

37. Create a *tcltk* GUI to run the animation function in Q. 33.

38. Create an .rd documentation file for the function in Q. 28. Make a .pdf or .html from the .rd file.

39. Write **R** documentation using *Sweave*, *knitr* or **R** Markdown describing the work done in Q. 8. This will be greatly facilitated through the use of RStudio.

40. Write **R** documentation using *Sweave*, *knitr* or **R** Markdown describing the work done in Q. 9. This will be greatly facilitated through the use of RStudio.

41. Perform a statistical and/or graphical analysis of your own data in **R** and document the workflow using *Sweave*, *knitr* or **R** Markdown.

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