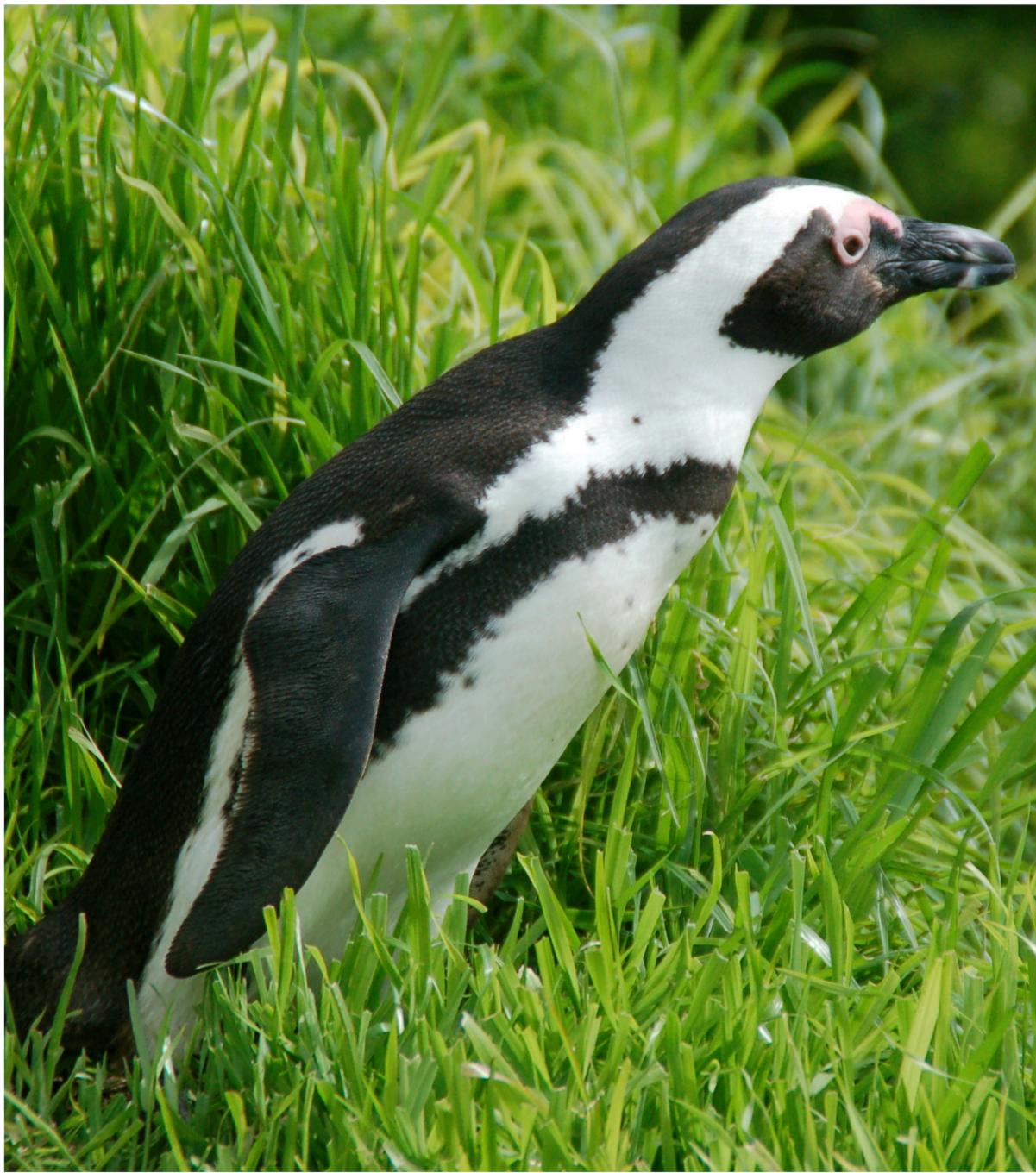


R Programming for Data Science



Roger D. Peng

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This book is for sale at <http://leanpub.com/rprogramming>

This version was published on 2015-09-03



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Also By Roger D. Peng

The Art of Data Science

Exploratory Data Analysis with R

Report Writing for Data Science in R

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Preface

I started using R in 1998 when I was a college undergraduate working on my senior thesis. The version was 0.63. I was an applied mathematics major with a statistics concentration and I was working with Dr. Nicolas Hengartner on an analysis of word frequencies in classic texts (Shakespeare, Milton, etc.). The idea was to see if we could identify the authorship of each of the texts based on how frequently they used certain words. We downloaded the data from Project Gutenberg and used some basic linear discriminant analysis for the modeling. The work was eventually published¹ and was my first ever peer-reviewed publication. I guess you could argue it was my first real “data science” experience.

Back then, no one was using R. Most of my classes were taught with Minitab, SPSS, Stata, or Microsoft Excel. The cool people on the cutting edge of statistical methodology used S-PLUS. I was working on my thesis late one night and I had a problem. I didn’t have a copy of any of those software packages because they were expensive and I was a student. I didn’t feel like trekking over to the computer lab to use the software because it was late at night.

But I had the Internet! After a couple of Yahoo! searches I found a web page for something called R, which I figured was just a play on the name of the S-PLUS package. From what I could tell, R was a “clone” of S-PLUS that was free. I had already written some S-PLUS code for my thesis so I figured I would try to download R and see if I could just run the S-PLUS code.

It didn’t work. At least not at first. It turns out that R is not exactly a clone of S-PLUS and quite a few modifications needed to be made before the code would run in R. In particular, R was missing a lot of statistical functionality that had existed in S-PLUS for a long time already. Luckily, R’s programming language was pretty much there and I was able to more or less re-implement the features that were missing in R.

After college, I enrolled in a PhD program in statistics at the University of California, Los Angeles. At the time the department was brand new and they didn’t have a lot of policies or rules (or classes, for that matter!). So you could kind of do what you wanted, which was good for some students and not so good for others. The Chair of the department, Jan de Leeuw, was a big fan of XLisp-Stat and so all of the department’s classes were taught using XLisp-Stat. I diligently bought my copy of Luke Tierney’s book² and learned to really love XLisp-Stat. It had a number of features that R didn’t have at all, most notably dynamic graphics.

But ultimately, there were only so many parentheses that I could type, and still all of the research-level statistics was being done in S-PLUS. The department didn’t really have a lot of copies of S-PLUS lying around so I turned back to R. When I looked around at my fellow students, I realized that I was basically the only one who had any experience using R. Since there was a budding interest in R

¹<http://amstat.tandfonline.com/doi/abs/10.1198/000313002100#.VQGiSELpagE>

²<http://www.amazon.com/LISP-STAT-Object-Oriented-Environment-Statistical-Probability/dp/0471509167/>

around the department, I decided to start a “brown bag” series where every week for about an hour I would talk about something you could do in R (which wasn’t much, really). People seemed to like it, if only because there wasn’t really anyone to turn to if you wanted to learn about R.

By the time I left grad school in 2003, the department had essentially switched over from XLisp-Stat to R for all its work (although there were a few hold outs). Jan discusses the rationale for the transition in a [paper³](#) in the *Journal of Statistical Software*.

In the next step of my career, I went to the [Department of Biostatistics⁴](#) at the Johns Hopkins Bloomberg School of Public Health, where I have been for the past 12 years. When I got to Johns Hopkins people already seemed into R. Most people had abandoned S-PLUS a while ago and were committed to using R for their research. Of all the available statistical packages, R had the most powerful and expressive programming language, which was perfect for someone developing *new* statistical methods.

However, we didn’t really have a class that taught students how to use R. This was a problem because most of our grad students were coming into the program having never heard of R. Most likely in their undergraduate programs, they used some other software package. So along with Rafael Irizarry, Brian Caffo, Ingo Ruczinski, and Karl Broman, I started a new class to teach our graduate students R and a number of other skills they’d need in grad school.

The class was basically a weekly seminar where one of us talked about a computing topic of interest. I gave some of the R lectures in that class and when I asked people who had heard of R before, almost no one raised their hand. And no one had actually used it before. The main selling point at the time was “It’s just like S-PLUS but it’s free!” A lot of people had experience with SAS or Stata or SPSS. A number of people had used something like Java or C/C++ before and so I often used that a reference frame. No one had ever used a functional-style of programming language like Scheme or Lisp.

To this day, I still teach the class, known a Biostatistics 140.776 (“Statistical Computing”). However, the nature of the class has changed quite a bit over the past 10 years. The population of students (mostly first-year graduate students) has shifted to the point where many of them have been introduced to R as undergraduates. This trend mirrors the overall trend with statistics where we are seeing more and more students do undergraduate majors in statistics (as opposed to, say, mathematics). Eventually, by 2008–2009, when I’d asked how many people had heard of or used R before, everyone raised their hand. However, even at that late date, I still felt the need to convince people that R was a “real” language that could be used for real tasks.

R has grown a lot in recent years, and is being used in so many places now, that I think it’s essentially impossible for a person to keep track of everything that is going on. That’s fine, but it makes “introducing” people to R an interesting experience. Nowadays in class, students are often teaching me something new about R that I’ve never seen or heard of before (they are quite good at Googling around for themselves). I feel no need to “bring people over” to R. In fact it’s quite the opposite—people might start asking questions if I *weren’t* teaching R.

³<http://www.jstatsoft.org/v13/i07>

⁴<http://www.biostat.jhsph.edu>

This book comes from my experience teaching R in a variety of settings and through different stages of its (and my) development. Much of the material has been taken from by Statistical Computing class as well as the [R Programming⁵](#) class I teach through Coursera.

I'm looking forward to teaching R to people as long as people will let me, and I'm interested in seeing how the next generation of students will approach it (and how my approach to them will change). Overall, it's been just an amazing experience to see the widespread adoption of R over the past decade. I'm sure the next decade will be just as amazing.

⁵<https://www.coursera.org/course/rprog>

History and Overview of R

There are only two kinds of languages: the ones people complain about and the ones nobody uses —*Bjarne Stroustrup*

Watch a video of this chapter⁶

What is R?

This is an easy question to answer. R is a dialect of S.

What is S?

S is a language that was developed by John Chambers and others at the old Bell Telephone Laboratories, originally part of AT&T Corp. S was [initiated in 1976](#)⁷ as an internal statistical analysis environment—originally implemented as Fortran libraries. Early versions of the language did not even contain functions for statistical modeling.

In 1988 the system was rewritten in C and began to resemble the system that we have today (this was Version 3 of the language). The book *Statistical Models in S* by Chambers and Hastie (the white book) documents the statistical analysis functionality. Version 4 of the S language was released in 1998 and is the version we use today. The book *Programming with Data* by John Chambers (the green book) documents this version of the language.

Since the early 90's the life of the S language has gone down a rather winding path. In 1993 Bell Labs gave StatSci (later Insightful Corp.) an exclusive license to develop and sell the S language. In 2004 Insightful purchased the S language from Lucent for \$2 million. In 2006, Alcatel purchased Lucent Technologies and is now called Alcatel-Lucent.

Insightful sold its implementation of the S language under the product name S-PLUS and built a number of fancy features (GUIs, mostly) on top of it—hence the “PLUS”. In 2008 Insightful was acquired by TIBCO for \$25 million. As of this writing TIBCO is the current owner of the S language and is its exclusive developer.

The fundamentals of the S language itself has not changed dramatically since the publication of the Green Book by John Chambers in 1998. In 1998, S won the Association for Computing Machinery's Software System Award, a highly prestigious award in the computer science field.

⁶<https://youtu.be/STihTnVSZnI>

⁷<http://cm.bell-labs.com/stat/doc/94.11.ps>

The S Philosophy

The general S philosophy is important to understand for users of S and R because it sets the stage for the design of the language itself, which many programming veterans find a bit odd and confusing. In particular, it's important to realize that the S language had its roots in data analysis, and did not come from a traditional programming language background. Its inventors were focused on figuring out how to make data analysis easier, first for themselves, and then eventually for others.

In [Stages in the Evolution of S⁸](#), John Chambers writes:

“[W]e wanted users to be able to begin in an interactive environment, where they did not consciously think of themselves as programming. Then as their needs became clearer and their sophistication increased, they should be able to slide gradually into programming, when the language and system aspects would become more important.”

The key part here was the transition from *user* to *developer*. They wanted to build a language that could easily service both “people”. More technically, they needed to build language that would be suitable for interactive data analysis (more command-line based) as well as for writing longer programs (more traditional programming language-like).

Back to R

The R language came to use quite a bit after S had been developed. One key limitation of the S language was that it was only available in a commercial package, S-PLUS. In 1991, R was created by Ross Ihaka and Robert Gentleman in the Department of Statistics at the University of Auckland. In 1993 the first announcement of R was made to the public. Ross's and Robert's experience developing R is documented in a 1996 paper in the *Journal of Computational and Graphical Statistics*:

Ross Ihaka and Robert Gentleman. R: A language for data analysis and graphics. *Journal of Computational and Graphical Statistics*, 5(3):299–314, 1996

In 1995, Martin Mächler made an important contribution by convincing Ross and Robert to use the [GNU General Public License⁹](#) to make R free software. This was critical because it allowed for the source code for the entire R system to be accessible to anyone who wanted to tinker with it (more on free software later).

In 1996, a public mailing list was created (the R-help and R-devel lists) and in 1997 the R Core Group was formed, containing some people associated with S and S-PLUS. Currently, the core group controls the source code for R and is solely able to check in changes to the main R source tree. Finally, in 2000 R version 1.0.0 was released to the public.

⁸<http://www.stat.bell-labs.com/S/history.html>

⁹<http://www.gnu.org/licenses/gpl-2.0.html>

Basic Features of R

In the early days, a key feature of R was that its syntax is very similar to S, making it easy for S-PLUS users to switch over. While the R's syntax is nearly identical to that of S's, R's semantics, while superficially similar to S, are quite different. In fact, R is technically much closer to the Scheme language than it is to the original S language when it comes to how R works under the hood.

Today R runs on almost any standard computing platform and operating system. Its open source nature means that anyone is free to adapt the software to whatever platform they choose. Indeed, R has been reported to be running on modern tablets, phones, PDAs, and game consoles.

One nice feature that R shares with many popular open source projects is frequent releases. These days there is a major annual release, typically in October, where major new features are incorporated and released to the public. Throughout the year, smaller-scale bugfix releases will be made as needed. The frequent releases and regular release cycle indicates active development of the software and ensures that bugs will be addressed in a timely manner. Of course, while the core developers control the primary source tree for R, many people around the world make contributions in the form of new feature, bug fixes, or both.

Another key advantage that R has over many other statistical packages (even today) is its sophisticated graphics capabilities. R's ability to create "publication quality" graphics has existed since the very beginning and has generally been better than competing packages. Today, with many more visualization packages available than before, that trend continues. R's base graphics system allows for very fine control over essentially every aspect of a plot or graph. Other newer graphics systems, like lattice and ggplot2 allow for complex and sophisticated visualizations of high-dimensional data.

R has maintained the original S philosophy, which is that it provides a language that is both useful for interactive work, but contains a powerful programming language for developing new tools. This allows the user, who takes existing tools and applies them to data, to slowly but surely become a developer who is creating new tools.

Finally, one of the joys of using R has nothing to do with the language itself, but rather with the active and vibrant user community. In many ways, a language is successful inasmuch as it creates a platform with which many people can create new things. R is that platform and thousands of people around the world have come together to make contributions to R, to develop packages, and help each other use R for all kinds of applications. The R-help and R-devel mailing lists have been highly active for over a decade now and there is considerable activity on web sites like Stack Overflow.

Free Software

A major advantage that R has over many other statistical packages and is that it's free in the sense of free software (it's also free in the sense of free beer). The copyright for the primary source code for R is held by the [R Foundation¹⁰](#) and is published under the [GNU General Public License version](#)

¹⁰<http://www.r-project.org/foundation/>

2.0¹¹.

According to the Free Software Foundation, with *free software*, you are granted the following **four freedoms**¹²

- The freedom to run the program, for any purpose (freedom 0).
- The freedom to study how the program works, and adapt it to your needs (freedom 1). Access to the source code is a precondition for this.
- The freedom to redistribute copies so you can help your neighbor (freedom 2).
- The freedom to improve the program, and release your improvements to the public, so that the whole community benefits (freedom 3). Access to the source code is a precondition for this.

You can visit the [Free Software Foundation's web site](#)¹³ to learn a lot more about free software. The Free Software Foundation was founded by Richard Stallman in 1985 and [Stallman's personal web site](#)¹⁴ is an interesting read if you happen to have some spare time.

Design of the R System

The primary R system is available from the [Comprehensive R Archive Network](#)¹⁵, also known as CRAN. CRAN also hosts many add-on packages that can be used to extend the functionality of R.

The R system is divided into 2 conceptual parts:

1. The “base” R system that you download from CRAN: [Linux](#)¹⁶ [Windows](#)¹⁷ [Mac](#)¹⁸ [Source Code](#)¹⁹
2. Everything else.

R functionality is divided into a number of *packages*.

- The “base” R system contains, among other things, the `base` package which is required to run R and contains the most fundamental functions.
- The other packages contained in the “base” system include `utils`, `stats`, `datasets`, `graphics`, `grDevices`, `grid`, `methods`, `tools`, `parallel`, `compiler`, `splines`, `tcltk`, `stats4`.

¹¹<http://www.gnu.org/licenses/gpl-2.0.html>

¹²<http://www.gnu.org/philosophy/free-sw.html>

¹³<http://www.fsf.org>

¹⁴<https://stallman.org>

¹⁵<http://cran.r-project.org>

¹⁶<http://cran.r-project.org/bin/linux/>

¹⁷<http://cran.r-project.org/bin/windows/>

¹⁸<http://cran.r-project.org/bin/macosx/>

¹⁹<http://cran.r-project.org/src/base/R-3/R-3.1.3.tar.gz>

- There are also “Recommended” packages: `boot`, `class`, `cluster`, `codetools`, `foreign`, `KernSmooth`, `lattice`, `mgcv`, `nlme`, `rpart`, `survival`, `MASS`, `spatial`, `nnet`, `Matrix`.

When you download a fresh installation of R from CRAN, you get all of the above, which represents a substantial amount of functionality. However, there are many other packages available:

- There are over 4000 packages on CRAN that have been developed by users and programmers around the world.
- There are also many packages associated with the [Bioconductor project²⁰](#).
- People often make packages available on their personal websites; there is no reliable way to keep track of how many packages are available in this fashion.
- There are a number of packages being developed on repositories like GitHub and BitBucket but there is no reliable listing of all these packages.

Limitations of R

No programming language or statistical analysis system is perfect. R certainly has a number of drawbacks. For starters, R is essentially based on almost 50 year old technology, going back to the original S system developed at Bell Labs. There was originally little built in support for dynamic or 3-D graphics (but things have improved greatly since the “old days”).

Another commonly cited limitation of R is that objects must generally be stored in physical memory. This is in part due to the scoping rules of the language, but R generally is more of a memory hog than other statistical packages. However, there have been a number of advancements to deal with this, both in the R core and also in a number of packages developed by contributors. Also, computing power and capacity has continued to grow over time and amount of physical memory that can be installed on even a consumer-level laptop is substantial. While we will likely never have enough physical memory on a computer to handle the increasingly large datasets that are being generated, the situation has gotten quite a bit easier over time.

At a higher level one “limitation” of R is that its functionality is based on consumer demand and (voluntary) user contributions. If no one feels like implementing your favorite method, then it’s *your* job to implement it (or you need to pay someone to do it). The capabilities of the R system generally reflect the interests of the R user community. As the community has ballooned in size over the past 10 years, the capabilities have similarly increased. When I first started using R, there was very little in the way of functionality for the physical sciences (physics, astronomy, etc.). However, now some of those communities have adopted R and we are seeing more code being written for those kinds of applications.

If you want to know my general views on the usefulness of R, you can see them here in the following exchange on the R-help mailing list with Douglas Bates and Brian Ripley in June 2004:

²⁰<http://bioconductor.org>

Roger D. Peng: I don't think anyone actually believes that R is designed to make *everyone* happy. For me, R does about 99% of the things I need to do, but sadly, when I need to order a pizza, I still have to pick up the telephone.

Douglas Bates: There are several chains of pizzerias in the U.S. that provide for Internet-based ordering (e.g. www.papajohnsonline.com) so, with the Internet modules in R, it's only a matter of time before you will have a pizza-ordering function available.

Brian D. Ripley: Indeed, the GraphApp toolkit (used for the RGui interface under R for Windows, but Guido forgot to include it) provides one (for use in Sydney, Australia, we presume as that is where the GraphApp author hails from). Alternatively, a Padovian has no need of ordering pizzas with both home and neighbourhood restaurants

At this point in time, I think it would be fairly straightforward to build a pizza ordering R package using something like the `RCurl` or `httr` packages. Any takers?

R Resources

Official Manuals

As far as getting started with R by reading stuff, there is of course this book. Also, available from [CRAN²¹](http://cran.r-project.org) are

- [An Introduction to R²²](http://cran.r-project.org/doc/manuals/r-release/R-intro.html)
- [R Data Import/Export²³](http://cran.r-project.org/doc/manuals/r-release/R-data.html)
- [Writing R Extensions²⁴](http://cran.r-project.org/doc/manuals/r-release/R-exts.html): Discusses how to write and organize R packages
- [R Installation and Administration²⁵](http://cran.r-project.org/doc/manuals/r-release/R-admin.html): This is mostly for building R from the source code)
- [R Internals²⁶](http://cran.r-project.org/doc/manuals/r-release/R-ints.html): This manual describes the low level structure of R and is primarily for developers and R core members
- [R Language Definition²⁷](http://cran.r-project.org/doc/manuals/r-release/R-lang.html): This documents the R language and, again, is primarily for developers

²¹<http://cran.r-project.org>

²²<http://cran.r-project.org/doc/manuals/r-release/R-intro.html>

²³<http://cran.r-project.org/doc/manuals/r-release/R-data.html>

²⁴<http://cran.r-project.org/doc/manuals/r-release/R-exts.html>

²⁵<http://cran.r-project.org/doc/manuals/r-release/R-admin.html>

²⁶<http://cran.r-project.org/doc/manuals/r-release/R-ints.html>

²⁷<http://cran.r-project.org/doc/manuals/r-release/R-lang.html>

Useful Standard Texts on S and R

- Chambers (2008). *Software for Data Analysis*, Springer
- Chambers (1998). *Programming with Data*, Springer: This book is *not* about R, but it describes the organization and philosophy of the current version of the S language, and is a useful reference.
- Venables & Ripley (2002). *Modern Applied Statistics with S*, Springer: This is a standard textbook in statistics and describes how to use many statistical methods in R. This book has an associated R package (the MASS package) that comes with every installation of R.
- Venables & Ripley (2000). *S Programming*, Springer: This book is a little old but is still relevant and accurate. Despite its title, this book is useful for R also.
- Murrell (2005). *R Graphics*, Chapman & Hall/CRC Press: Paul Murrell wrote and designed much of the graphics system in R and this book essentially documents the underlying details. This is not so much a “user-level” book as a developer-level book. But it is an important book for anyone interested in designing new types of graphics or visualizations.
- Wickham (2014). *Advanced R*, Chapman & Hall/CRC Press: This book by Hadley Wickham covers a number of areas including object-oriented programming, functional programming, profiling and other advanced topics.

Other Resources

- Major technical publishers like Springer, Chapman & Hall/CRC have entire series of books dedicated to using R in various applications. For example, Springer has a series of books called *Use R!*.
- A longer list of books can be found on the [CRAN web site²⁸](#).

²⁸<http://www.r-project.org/doc/bib/R-books.html>

Getting Started with R

Installation

The first thing you need to do to get started with R is to install it on your computer. R works on pretty much every platform available, including the widely available Windows, Mac OS X, and Linux systems. If you want to watch a step-by-step tutorial on how to install R for Mac or Windows, you can watch these videos:

- [Installing R on Windows²⁹](#)
- [Installing R on the Mac³⁰](#)

There is also an integrated development environment available for R that is built by RStudio. I really like this IDE—it has a nice editor with syntax highlighting, there is an R object viewer, and there are a number of other nice features that are integrated. You can see how to install RStudio here

- [Installing RStudio³¹](#)

The RStudio IDE is available from [RStudio's web site³²](#).

Getting started with the R interface

After you install R you will need to launch it and start writing R code. Before we get to exactly how to write R code, it's useful to get a sense of how the system is organized. In these two videos I talk about where to write code and how set your working directory, which let's R know where to find all of your files.

- [Writing code and setting your working directory on the Mac³³](#)
- [Writing code and setting your working directory on Windows³⁴](#)

²⁹<http://youtu.be/Ohnk9hcxf9M>

³⁰<https://youtu.be/uxuuWXU-7UQ>

³¹<https://youtu.be/bM7Sz-LADM>

³²<http://rstudio.com>

³³<https://youtu.be/8xT3hmJQskU>

³⁴<https://youtu.be/XBcvH1BplBo>

R Nuts and Bolts

Entering Input

At the R prompt we type expressions. The `<-` symbol is the assignment operator.

```
> x <- 1
> print(x)
[1] 1
> x
[1] 1
> msg <- "hello"
```

The grammar of the language determines whether an expression is complete or not.

```
x <- ## Incomplete expression
```

The `#` character indicates a comment. Anything to the right of the `#` (including the `#` itself) is ignored. This is the only comment character in R. Unlike some other languages, R does not support multi-line comments or comment blocks.

Evaluation

When a complete expression is entered at the prompt, it is evaluated and the result of the evaluated expression is returned. The result may be *auto-printed*.

```
> x <- 5 ## nothing printed
> x       ## auto-printing occurs
[1] 5
> print(x) ## explicit printing
[1] 5
```

The `[1]` shown in the output indicates that `x` is a vector and 5 is its first element.

Typically with interactive work, we do not explicitly print objects with the `print` function; it is much easier to just auto-print them by typing the name of the object and hitting return/enter. However, when writing scripts, functions, or longer programs, there is sometimes a need to explicitly print objects because auto-printing does not work in those settings.

When an R vector is printed you will notice that an index for the vector is printed in square brackets `[]` on the side. For example, see this integer sequence of length 20.

```
> x <- 10:30
> x
[1] 10 11 12 13 14 15 16 17 18 19 20 21
[13] 22 23 24 25 26 27 28 29 30
```

The numbers in the square brackets are not part of the vector itself, they are merely part of the *printed output*.

With R, it's important that one understand that there is a difference between the actual R object and the manner in which that R object is printed to the console. Often, the printed output may have additional bells and whistles to make the output more friendly to the users. However, these bells and whistles are not inherently part of the object.

Note that the `:` operator is used to create integer sequences.

R Objects

R has five basic or “atomic” classes of objects:

- character
- numeric (real numbers)
- integer
- complex
- logical (True/False)

The most basic type of R object is a **vector**. Empty vectors can be created with the `vector()` function. There is really only one rule about vectors in R, which is that **A vector can only contain objects of the same class**.

But of course, like any good rule, there is an exception, which is a *list*, which we will get to a bit later. A list is represented as a vector but can contain objects of different classes. Indeed, that's usually why we use them.

There is also a class for “raw” objects, but they are not commonly used directly in data analysis and I won't cover them here.

Numbers

Numbers in R are generally treated as **numeric objects** (i.e. double precision real numbers). This means that even if you see a number like “1” or “2” in R, which you might think of as integers, they are likely represented behind the scenes as numeric objects (so something like “1.00” or “2.00”). This isn't important most of the time...except when it is.

If you explicitly want an **integer**, you need to specify the **L** suffix. So entering **1** in R gives you a numeric object; entering **1L** explicitly gives you an integer object.

There is also a special number **Inf** which represents infinity. This allows us to represent entities like **1 / 0**. This way, **Inf** can be used in ordinary calculations; e.g. **1 / Inf** is 0.

The value **NaN** represents an undefined value (“not a number”); e.g. **0 / 0**; **NaN** can also be thought of as a missing value (more on that later)

Attributes

R objects can have **attributes**, which are like **metadata** for the object. These metadata can be very useful in that they help to describe the object. For example, column names on a data frame help to tell us what data are contained in each of the columns. Some examples of R object attributes are

- names, dimnames
- dimensions (e.g. matrices, arrays)
- class (e.g. integer, numeric)
- length
- other user-defined attributes/metadata

Attributes of an object (if any) can be accessed using the **attributes()** function. Not all R objects contain attributes, in which case the **attributes()** function returns **NULL**.

Creating Vectors

The **c()** function can be used to create vectors of objects by concatenating things together.

```
> x <- c(0.5, 0.6)      ## numeric
> x <- c(TRUE, FALSE)   ## logical
> x <- c(T, F)          ## logical
> x <- c("a", "b", "c") ## character
> x <- 9:29               ## integer
> x <- c(1+0i, 2+4i)    ## complex
```

Note that in the above example, **T** and **F** are short-hand ways to specify **TRUE** and **FALSE**. However, in general one should try to use the explicit **TRUE** and **FALSE** values when indicating logical values. The **T** and **F** values are primarily there for when you’re feeling lazy.

You can also use the **vector()** function to initialize vectors.

```
> x <- vector("numeric", length = 10)
> x
[1] 0 0 0 0 0 0 0 0 0 0
```

Mixing Objects

There are occasions when different classes of R objects get mixed together. Sometimes this happens by accident but it can also happen on purpose. So what happens with the following code?

```
> y <- c(1.7, "a")    ## character
> y <- c(TRUE, 2)     ## numeric
> y <- c("a", TRUE)   ## character
```

In each case above, we are mixing objects of two different classes in a vector. But remember that the only rule about vectors says this is not allowed. When different objects are mixed in a vector, *coercion* occurs so that every element in the vector is of the same class.

In the example above, we see the effect of *implicit coercion*. What R tries to do is find a way to represent all of the objects in the vector in a reasonable fashion. Sometimes this does exactly what you want and...sometimes not. For example, combining a numeric object with a character object will create a character vector, because numbers can usually be easily represented as strings.

Explicit Coercion

Objects can be explicitly coerced from one class to another using the `as.*` functions, if available.

```
> x <- 0:6
> class(x)
[1] "integer"
> as.numeric(x)
[1] 0 1 2 3 4 5 6
> as.logical(x)
[1] FALSE TRUE TRUE TRUE TRUE TRUE
> as.character(x)
[1] "0" "1" "2" "3" "4" "5" "6"
```

Sometimes, R can't figure out how to coerce an object and this can result in NAs being produced.

```
> x <- c("a", "b", "c")
> as.numeric(x)
Warning: NAs introduced by coercion
[1] NA NA NA
> as.logical(x)
[1] NA NA NA
> as.complex(x)
Warning: NAs introduced by coercion
[1] NA NA NA
```

When nonsensical coercion takes place, you will usually get a warning from R.

Matrices

Matrices are vectors with a *dimension* attribute. The dimension attribute is itself an integer vector of length 2 (number of rows, number of columns)

```
> m <- matrix(nrow = 2, ncol = 3)
> m
[,1] [,2] [,3]
[1,] NA NA NA
[2,] NA NA NA
> dim(m)
[1] 2 3
> attributes(m)
$dim
[1] 2 3
```

Matrices are constructed *column-wise*, so entries can be thought of starting in the “upper left” corner and running down the columns.

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

Matrices can also be created directly from vectors by adding a dimension attribute.

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

Matrices can be created by *column-binding* or *row-binding* with the `cbind()` and `rbind()` functions.

```
> x <- 1:3
> y <- 10:12
> cbind(x, y)
   x  y
[1,] 1 10
[2,] 2 11
[3,] 3 12
> rbind(x, y)
 [,1] [,2] [,3]
x     1     2     3
y     10    11    12
```

Lists

Lists are a special type of vector that can contain elements of different classes. Lists are a very important data type in R and you should get to know them well. Lists, in combination with the various “apply” functions discussed later, make for a powerful combination.

Lists can be explicitly created using the `list()` function, which takes an arbitrary number of arguments.

```
> x <- list(1, "a", TRUE, 1 + 4i)
> x
[[1]]
[1] 1

[[2]]
[1] "a"

[[3]]
[1] TRUE
```

```
[ [4]]  
[1] 1+4i
```

We can also create an empty list of a prespecified length with the `vector()` function

```
> x <- vector("list", length = 5)
```

```
> x
```

```
[ [1]]
```

```
NULL
```

```
[ [2]]
```

```
NULL
```

```
[ [3]]
```

```
NULL
```

```
[ [4]]
```

```
NULL
```

```
[ [5]]
```

```
NULL
```

Factors

Factors are used to represent categorical data and can be unordered or ordered. One can think of a factor as an integer vector where each integer has a *label*. Factors are important in statistical modeling and are treated specially by modelling functions like `lm()` and `glm()`.

Using factors with labels is *better* than using integers because factors are self-describing. Having a variable that has values “Male” and “Female” is better than a variable that has values 1 and 2.

Factor objects can be created with the `factor()` function.

```

> x <- factor(c("yes", "yes", "no", "yes", "no"))
> x
[1] yes yes no yes no
Levels: no yes
> table(x)
x
no yes
2 3
> ## See the underlying representation of factor
> unclass(x)
[1] 2 2 1 2 1
attr(,"levels")
[1] "no" "yes"

```

Often factors will be automatically created for you when you read a dataset in using a function like `read.table()`. Those functions often default to creating factors when they encounter data that look like characters or strings.

The order of the **levels** of a **factor** can be set using the `levels` argument to `factor()`. This can be important in linear modelling because the first level is used as the baseline level.

```

> x <- factor(c("yes", "yes", "no", "yes", "no"))
> x ## Levels are put in alphabetical order
[1] yes yes no yes no
Levels: no yes
> x <- factor(c("yes", "yes", "no", "yes", "no"),
+               levels = c("yes", "no"))
> x
[1] yes yes no yes no
Levels: yes no

```

Missing Values

Missing values are denoted by `NA` or `NaN` for undefined mathematical operations.

- `is.na()` is used to test objects if they are `NA`
- `is.nan()` is used to test for `NaN`
- `NA` values have a class also, so there are integer `NA`, character `NA`, etc.
- A `NaN` value is also `NA` but the converse is not true

```

> ## Create a vector with NAs in it
> x <- c(1, 2, NA, 10, 3)
> ## Return a logical vector indicating which elements are NA
> is.na(x)
[1] FALSE FALSE TRUE FALSE FALSE
> ## Return a logical vector indicating which elements are NaN
> is.nan(x)
[1] FALSE FALSE FALSE FALSE FALSE

> ## Now create a vector with both NA and NaN values
> x <- c(1, 2, NaN, NA, 4)
> is.na(x)
[1] FALSE FALSE TRUE TRUE FALSE
> is.nan(x)
[1] FALSE FALSE TRUE FALSE FALSE

```

Data Frames

Data frames are used to store tabular data in R. They are an important type of object in R and are used in a variety of statistical modeling applications. Hadley Wickham's package `dplyr`³⁵ has an optimized set of functions designed to work efficiently with data frames.

Data frames are represented as a special type of list where every element of the list has to have the same length. Each element of the list can be thought of as a column and the length of each element of the list is the number of rows.

Unlike matrices, data frames can store different classes of objects in each column. Matrices must have every element be the same class (e.g. all integers or all numeric).

In addition to column names, indicating the names of the variables or predictors, data frames have a special attribute called `row.names` which indicate information about each row of the data frame.

Data frames are usually created by reading in a dataset using the `read.table()` or `read.csv()`. However, data frames can also be created explicitly with the `data.frame()` function or they can be coerced from other types of objects like lists.

Data frames can be converted to a matrix by calling `data.matrix()`. While it might seem that the `as.matrix()` function should be used to coerce a data frame to a matrix, almost always, what you want is the result of `data.matrix()`.

³⁵<https://github.com/hadley/dplyr>

```
> x <- data.frame(foo = 1:4, bar = c(T, T, F, F))
> x
  foo   bar
1  1  TRUE
2  2  TRUE
3  3 FALSE
4  4 FALSE
> nrow(x)
[1] 4
> ncol(x)
[1] 2
```

Names

R objects can have names, which is very useful for writing readable code and self-describing objects. Here is an example of assigning names to an integer vector.

```
> x <- 1:3
> names(x)
NULL
> names(x) <- c("New York", "Seattle", "Los Angeles")
> x
  New York      Seattle Los Angeles
    1           2           3
> names(x)
[1] "New York"     "Seattle"      "Los Angeles"
```

Lists can also have names, which is often very useful.

```
> x <- list("Los Angeles" = 1, Boston = 2, London = 3)
> x
$`Los Angeles`
[1] 1

$Boston
[1] 2

$London
[1] 3
> names(x)
[1] "Los Angeles" "Boston"      "London"
```

Matrices can have both column and row names.

```
> m <- matrix(1:4, nrow = 2, ncol = 2)
> dimnames(m) <- list(c("a", "b"), c("c", "d"))
> m
   c d
a 1 3
b 2 4
```

Column names and row names can be set separately using the `colnames()` and `rownames()` functions.

```
> colnames(m) <- c("h", "f")
> rownames(m) <- c("x", "z")
> m
   h f
x 1 3
z 2 4
```

Note that for data frames, there is a separate function for setting the row names, the `row.names()` function. Also, data frames do not have column names, they just have names (like lists). So to set the column names of a data frame just use the `names()` function. Yes, I know its confusing. Here's a quick summary:

Object	Set column names	Set row names
data frame	<code>names()</code>	<code>row.names()</code>
matrix	<code>colnames()</code>	<code>rownames()</code>

Summary

There are a variety of different builtin-data types in R. In this chapter we have reviewed the following

- atomic classes: numeric, logical, character, integer, complex as in atom, basic building blocks
- vectors, lists
- factors
- missing values
- data frames and matrices

All R objects can have attributes that help to describe what is in the object. Perhaps the most useful attribute is names, such as column and row names in a data frame, or simply names in a vector or list. Attributes like dimensions are also important as they can modify the behavior of objects, like turning a vector into a matrix.

Getting Data In and Out of R

Reading and Writing Data

Watch a video of this section³⁶

There are a few principal functions reading data into R.

- `read.table`, `read.csv`, for reading tabular data
- `readLines`, for reading lines of a text file
- `source`, for reading in R code files (inverse of `dump`)
- `dget`, for reading in R code files (inverse of `dput`)
- `load`, for reading in saved workspaces
- `unserialize`, for reading single R objects in binary form

There are of course, many R packages that have been developed to read in all kinds of other datasets, and you may need to resort to one of these packages if you are working in a specific area.

There are analogous functions for writing data to files

- `write.table`, for writing tabular data to text files (i.e. CSV) or connections
- `writeLines`, for writing character data line-by-line to a file or connection
- `dump`, for dumping a textual representation of multiple R objects
- `dput`, for outputting a textual representation of an R object
- `save`, for saving an arbitrary number of R objects in binary format (possibly compressed) to a file.
- `serialize`, for converting an R object into a binary format for outputting to a connection (or file).

Reading Data Files with `read.table()`

The `read.table()` function is one of the most commonly used functions for reading data. The help file for `read.table()` is worth reading in its entirety if only because the function gets used a lot (run `?read.table` in R). I know, I know, everyone always says to read the help file, but this one is actually worth reading.

The `read.table()` function has a few important arguments:

³⁶https://youtu.be/Z_dc_FADyi4

- `file`, the name of a file, or a connection
- `header`, logical indicating if the file has a header line
- `sep`, a string indicating how the columns are separated
- `colClasses`, a character vector indicating the class of each column in the dataset
- `nrows`, the number of rows in the dataset. By default `read.table()` reads an entire file.
- `comment.char`, a character string indicating the comment character. This defaults to "#". If there are no commented lines in your file, it's worth setting this to be the empty string "".
- `skip`, the number of lines to skip from the beginning
- `stringsAsFactors`, should character variables be coded as factors? This defaults to TRUE because back in the old days, if you had data that were stored as strings, it was because those strings represented levels of a categorical variable. Now we have lots of data that is text data and they don't always represent categorical variables. So you may want to set this to be FALSE in those cases. If you *always* want this to be FALSE, you can set a global option via `options(stringsAsFactors = FALSE)`. I've never seen so much heat generated on discussion forums about an R function argument than the `stringsAsFactors` argument. Seriously.

For small to moderately sized datasets, you can usually call `read.table` without specifying any other arguments

```
> data <- read.table("foo.txt")
```

In this case, R will automatically

- skip lines that begin with a #
- figure out how many rows there are (and how much memory needs to be allocated)
- figure what type of variable is in each column of the table.

Telling R all these things directly makes R run faster and more efficiently. The `read.csv()` function is identical to `read.table` except that some of the defaults are set differently (like the `sep` argument).

Reading in Larger Datasets with `read.table`

[Watch a video of this section³⁷](#)

With much larger datasets, there are a few things that you can do that will make your life easier and will prevent R from choking.

- Read the help page for `read.table`, which contains many hints

³⁷<https://youtu.be/BJYYIJO3UFI>

- Make a rough calculation of the memory required to store your dataset (see the next section for an example of how to do this). If the dataset is larger than the amount of RAM on your computer, you can probably stop right here.
- Set `comment.char = ""` if there are no commented lines in your file.
- Use the `colClasses` argument. Specifying this option instead of using the default can make `'read.table'` run MUCH faster, often twice as fast. In order to use this option, you have to know the class of each column in your data frame. If all of the columns are “numeric”, for example, then you can just set `colClasses = "numeric"`. A quick and dirty way to figure out the classes of each column is the following:

```
> initial <- read.table("datatable.txt", nrows = 100)
> classes <- sapply(initial, class)
> tabAll <- read.table("datatable.txt", colClasses = classes)
```

- Set `nrows`. This doesn’t make R run faster but it helps with memory usage. A mild overestimate is okay. You can use the Unix tool `wc` to calculate the number of lines in a file.

`word count`

In general, when using R with larger datasets, it’s also useful to know a few things about your system.

- How much memory is available on your system?
- What other applications are in use? Can you close any of them?
- Are there other users logged into the same system?
- What operating system are you using? Some operating systems can limit the amount of memory a single process can access

Calculating Memory Requirements for R Objects

Because R stores all of its objects physical memory, it is important to be cognizant of how much memory is being used up by all of the data objects residing in your workspace. One situation where it’s particularly important to understand memory requirements is when you are reading in a new dataset into R. Fortunately, it’s easy to make a back of the envelope calculation of how much memory will be required by a new dataset.

For example, suppose I have a data frame with 1,500,000 rows and 120 columns, all of which are numeric data. Roughly, how much memory is required to store this data frame? Well, on most modern computers **double precision floating point numbers**³⁸ are stored using 64 bits of memory, or 8 bytes. Given that information, you can do the following calculation

³⁸http://en.wikipedia.org/wiki/Double-precision_floating-point_format

$$\begin{aligned} 1,500,000 \times 120 \times 8 \text{ bytes/numeric} &= 1,440,000,000 \text{ bytes} \\ &= 1,440,000,000 / 2^{20} \text{ bytes/MB} \\ &= 1,373.29 \text{ MB} \\ &= 1.34 \text{ GB} \end{aligned}$$

So the dataset would require about 1.34 GB of RAM. Most computers these days have at least that much RAM. However, you need to be aware of

- what other programs might be running on your computer, using up RAM
- what other R objects might already be taking up RAM in your workspace

Reading in a large dataset for which you do not have enough RAM is one easy way to freeze up your computer (or at least your R session). This is usually an unpleasant experience that usually requires you to kill the R process, in the best case scenario, or reboot your computer, in the worst case. So make sure to do a rough calculation of memory requirements before reading in a large dataset. You'll thank me later.

Using the `readr` Package

The `readr` package is recently developed by Hadley Wickham to deal with reading in large flat files quickly. The package provides replacements for functions like `read.table()` and `read.csv()`. The analogous functions in `readr` are `read_table()` and `read_csv()`. These functions are even *much* faster than their base R analogues and provide a few other nice features such as progress meters.

For the most part, you can use `read_table()` and `read_csv()` pretty much anywhere you might use `read.table()` and `read.csv()`. In addition, if there are non-fatal problems that occur while reading in the data, you will get a warning and the returned data frame will have some information about which rows/observations triggered the warning. This can be very helpful for “debugging” problems with your data before you get neck deep in data analysis.

Using Textual and Binary Formats for Storing Data

[Watch a video of this chapter³⁹](#)

There are a variety of ways that data can be stored, including structured text files like CSV or tab-delimited, or more complex binary formats. However, there is an intermediate format that is textual, but not as simple as something like CSV. The format is native to R and is somewhat readable because of its textual nature.

One can create a more descriptive representation of an R object by using the `dput()` or `dump()` functions. The `dump()` and `dput()` functions are useful because the resulting textual format is editable, and in the case of corruption, potentially recoverable. Unlike writing out a table or CSV file, `dump()` and `dput()` preserve the *metadata* (sacrificing some readability), so that another user doesn't have to specify it all over again. For example, we can preserve the class of each column of a table or the levels of a factor variable.

Textual formats can work much better with version control programs like subversion or git which can only track changes meaningfully in text files. In addition, textual formats can be longer-lived; if there is corruption somewhere in the file, it can be easier to fix the problem because one can just open the file in an editor and look at it (although this would probably only be done in a worst case scenario!). Finally, textual formats adhere to the [Unix philosophy⁴⁰](#), if that means anything to you.

There are a few downsides to using these intermediate textual formats. The format is not very space-efficient, because all of the metadata is specified. Also, it is really only partially readable. In some instances it might be preferable to have data stored in a CSV file and then have a separate code file that specifies the metadata.

Using `dput()` and `dump()`

One way to pass data around is by deparsing the R object with `dput()` and reading it back in (parsing it) using `get()`.

³⁹<https://youtu.be/5mIPigbNDfk>

⁴⁰<http://www.catb.org/esr/writings/taoup/>

```
> ## Create a data frame
> y <- data.frame(a = 1, b = "a")
> ## Print 'dput' output to console
> dput(y)
structure(list(a = 1, b = structure(1L, .Label = "a", class = "factor")), .Names =
  c("a",
  "b"), row.names = c(NA, -1L), class = "data.frame")
```

Notice that the `dput()` output is in the form of R code and that it preserves metadata like the class of the object, the row names, and the column names.

The output of `dput()` can also be saved directly to a file.

```
> ## Send 'dput' output to a file
> dput(y, file = "y.R")
> ## Read in 'dput' output from a file
> new.y <- dget("y.R")
> new.y
  a b
1 1 a
```

Multiple objects can be deparsed at once using the `dump` function and read back in using `source`.

```
> x <- "foo"
> y <- data.frame(a = 1L, b = "a")
```

We can `dump()` R objects to a file by passing a character vector of their names.

```
> dump(c("x", "y"), file = "data.R")
> rm(x, y)
```

The inverse of `dump()` is `source()`.

```
> source("data.R")
> str(y)
'data.frame':       1 obs. of  2 variables:
$ a: int 1
$ b: Factor w/ 1 level "a": 1
> x
[1] "foo"
```

Binary Formats

The complement to the textual format is the binary format, which is sometimes necessary to use for efficiency purposes, or because there's just no useful way to represent data in a textual manner. Also, with numeric data, one can often lose precision when converting to and from a textual format, so it's better to stick with a binary format.

The key functions for converting R objects into a binary format are `save()`, `save.image()`, and `serialize()`. Individual R objects can be saved to a file using the `save()` function.

```
> a <- data.frame(x = rnorm(100), y = runif(100))
> b <- c(3, 4.4, 1 / 3)
>
> ## Save 'a' and 'b' to a file
> save(a, b, file = "mydata.rda")
>
> ## Load 'a' and 'b' into your workspace
> load("mydata.rda")
```

If you have a lot of objects that you want to save to a file, you can save all objects in your workspace using the `save.image()` function.

```
> ## Save everything to a file
> save.image(file = "mydata.RData")
>
> ## load all objects in this file
> load("mydata.RData")
```

Notice that I've used the `.rda` extension when using `save()` and the `.RData` extension when using `save.image()`. This is just my personal preference; you can use whatever file extension you want. The `save()` and `save.image()` functions do not care. However, `.rda` and `.RData` are fairly common extensions and you may want to use them because they are recognized by other software.

The `serialize()` function is used to convert individual R objects into a binary format that can be communicated across an arbitrary connection. This may get sent to a file, but it could get sent over a network or other connection.

When you call `serialize()` on an R object, the output will be a raw vector coded in hexadecimal format.

```
> x <- list(1, 2, 3)
> serialize(x, NULL)
[1] 58 0a 00 00 00 02 00 03 02 01 00 02 03 00 00 00 00 13 00 00 00 03 00
[24] 00 00 0e 00 00 00 01 3f f0 00 00 00 00 00 00 00 00 00 0e 00 00 00 01
[47] 40 00 00 00 00 00 00 00 00 00 00 00 0e 00 00 00 01 40 08 00 00 00 00 00
[70] 00
```

If you want, this can be sent to a file, but in that case you are better off using something like `save()`.

The benefit of the `serialize()` function is that it is the only way to perfectly represent an R object in an exportable format, without losing precision or any metadata. If that is what you need, then `serialize()` is the function for you.

Interfaces to the Outside World

[Watch a video of this chapter⁴¹](#)

Data are read in using *connection* interfaces. Connections can be made to files (most common) or to other more exotic things.

- `file`, opens a connection to a file
- `gzfile`, opens a connection to a file compressed with gzip
- `bzfile`, opens a connection to a file compressed with bzip2
- `url`, opens a connection to a webpage

In general, connections are powerful tools that let you navigate files or other external objects. Connections can be thought of as a translator that lets you talk to objects that are outside of R. Those outside objects could be anything from a data base, a simple text file, or a web service API. Connections allow R functions to talk to all these different external objects without you having to write custom code for each object.

File Connections

Connections to text files can be created with the `file()` function.

```
> str(file)
function (description = "", open = "", blocking = TRUE, encoding = getOption("en\
coding"),
  raw = FALSE)
```

The `file()` function has a number of arguments that are common to many other connection functions so it's worth going into a little detail here.

- `description` is the name of the file
- `open` is a code indicating what mode the file should be opened in

The `open` argument allows for the following options:

⁴¹<https://youtu.be/Pb01WoJRUtY>

- “r” open file in read only mode
- “w” open a file for writing (and initializing a new file)
- “a” open a file for appending
- “rb”, “wb”, “ab” reading, writing, or appending in binary mode (Windows)

In practice, we often don’t need to deal with the connection interface directly as many functions for reading and writing data just deal with it in the background.

For example, if one were to explicitly use connections to read a CSV file in to R, it might look like this,

```
> ## Create a connection to 'foo.txt'  
> con <- file("foo.txt")  
>  
> ## Open connection to 'foo.txt' in read-only mode  
> open(con, "r")  
>  
> ## Read from the connection  
> data <- read.csv(con)  
>  
> ## Close the connection  
> close(con)
```

which is the same as

```
> data <- read.csv("foo.txt")
```

In the background, `read.csv()` opens a connection to the file `foo.txt`, reads from it, and closes the connection when its done.

The above example shows the basic approach to using connections. Connections must be opened, then the are read from or written to, and then they are closed.

Reading Lines of a Text File

Text files can be read line by line using the `readLines()` function. This function is useful for reading text files that may be unstructured or contain non-standard data.

```
> ## Open connection to gz-compressed text file
> con <- gzfile("words.gz")
> x <- readLines(con, 10)
> x
[1] "1080"      "10-point"   "10th"       "11-point"   "12-point"   "16-point"
[7] "18-point"   "1st"        "2"          "20-point"
```

For more structured text data like CSV files or tab-delimited files, there are other functions like `read.csv()` or `read.table()`.

The above example used the `gzfile()` function which is used to create a connection to files compressed using the gzip algorithm. This approach is useful because it allows you to read from a file without having to uncompress the file first, which would be a waste of space and time.

There is a complementary function `writeLines()` that takes a character vector and writes each element of the vector one line at a time to a text file.

Reading From a URL Connection

The `readLines()` function can be useful for reading in lines of webpages. Since web pages are basically text files that are stored on a remote server, there is conceptually not much difference between a web page and a local text file. However, we need R to negotiate the communication between your computer and the web server. This is what the `url()` function can do for you, by creating a `url` connection to a web server.

This code might take time depending on your connection speed.

```
> ## Open a URL connection for reading
> con <- url("http://www.jhsph.edu", "r")
>
> ## Read the web page
> x <- readLines(con)
>
> ## Print out the first few lines
> head(x)
[1] "<!DOCTYPE html>"
[2] "<html lang=\"en\">"
[3] ""
[4] "<head>"
[5] "<meta charset=\"utf-8\" />"
[6] "<title>Johns Hopkins Bloomberg School of Public Health</title>"
```

While reading in a simple web page is sometimes useful, particularly if data are embedded in the web page somewhere. However, more commonly we can use URL connection to read in specific data files that are stored on web servers.

Using URL connections can be useful for producing a reproducible analysis, because the code essentially documents where the data came from and how they were obtained. This approach is preferable to opening a web browser and downloading a dataset by hand. Of course, the code you write with connections may not be executable at a later date if things on the server side are changed or reorganized.

Subsetting R Objects

Watch a video of this section⁴²

There are three operators that can be used to extract subsets of R objects.

- The `[` operator always returns an object of the **same class as the original**. It can be used to select multiple elements of an object
- The `[` operator is used to extract elements of **a list or a data frame**. It can only be used to extract a single element and the class of the returned object will not necessarily be a list or data frame.
- The `$` operator is used to extract elements of **a list or data frame by literal name**. Its semantics are similar to that of `[[]`.

Subsetting a Vector

Vectors are basic objects in R and they can be subsetted using the `[` operator.

```
> x <- c("a", "b", "c", "c", "d", "a")
> x[1]    ## Extract the first element
[1] "a"
> x[2]    ## Extract the second element
[1] "b"
```

The `[` operator can be used to extract multiple elements of a vector by passing the operator an integer sequence. Here we extract the first four elements of the vector.

```
> x[1:4]
[1] "a" "b" "c" "c"
```

The sequence does not have to be in order; you can specify any arbitrary integer vector.

```
> x[c(1, 3, 4)]      c for choose
[1] "a" "c" "c"
```

We can also pass a logical sequence to the `[` operator to extract elements of a vector that satisfy a given condition. For example, here we want the elements of `x` that come lexicographically *after* the letter “a”.

⁴²<https://youtu.be/VfZUZGUgHqg>

```
> u <- x > "a"
> u
[1] FALSE TRUE TRUE TRUE TRUE FALSE
> x[u]
[1] "b" "c" "c" "d"
```

Another, more compact, way to do this would be to skip the creation of a logical vector and just subset the vector directly with the logical expression.

```
> x[x > "a"]
[1] "b" "c" "c" "d"
```

Subsetting a Matrix

[Watch a video of this section⁴³](#)

Matrices can be subsetted in the usual way with (i,j) type indices. Here, we create simple 2×3 matrix with the `matrix` function.

```
> x <- matrix(1:6, 2, 3)
> x
     [,1] [,2] [,3]
[1,]    1    3    5
[2,]    2    4    6
```

We can access the $(1, 2)$ or the $(2, 1)$ element of this matrix using the appropriate indices.

```
> x[1, 2]
[1] 3
> x[2, 1]
[1] 2
```

Indices can also be missing. This behavior is used to access entire rows or columns of a matrix.

```
> x[1, ] ## Extract the first row
[1] 1 3 5
> x[, 2] ## Extract the second column
[1] 3 4
```

Dropping matrix dimensions

By default, when a single element of a matrix is retrieved, it is returned as a vector of length 1 rather than a 1×1 matrix. Often, this is exactly what we want, but this behavior can be turned off by setting `drop = FALSE`.

⁴³<https://youtu.be/FzjXesh9tRw>

```
> x <- matrix(1:6, 2, 3)
> x[1, 2]
[1] 3
> x[1, 2, drop = FALSE]
[,1]
[1,]    3
```

Similarly, when we extract a single row or column of a matrix, R by default drops the dimension of length 1, so instead of getting a \$1\times 3\$ matrix after extracting the first row, we get a vector of length 3. This behavior can similarly be turned off with the `drop = FALSE` option.

```
> x <- matrix(1:6, 2, 3)
> x[1, ]
[1] 1 3 5
> x[1, , drop = FALSE]
[,1] [,2] [,3]
[1,]    1     3     5
```

Be careful of R's automatic dropping of dimensions. This is a feature that is often quite useful during interactive work, but can later come back to bite you when you are writing longer programs or functions.

Subsetting Lists

Watch a video of this section⁴⁴

Lists in R can be subsetted using all three of the operators mentioned above, and all three are used for different purposes.

```
> x <- list(foo = 1:4, bar = 0.6)
> x
$foo
[1] 1 2 3 4

$bar
[1] 0.6
```

The `[[` operator can be used to extract *single* elements from a list. Here we extract the first element of the list.

⁴⁴<https://youtu.be/DStKguVpuDI>

```
> x[[1]]  
[1] 1 2 3 4
```

The `[[` operator can also use named indices so that you don't have to remember the exact ordering of every element of the list. You can also use the `$` operator to extract elements by `name`.

```
> x[["bar"]]  
[1] 0.6  
> x$bar  
[1] 0.6
```

Notice you don't need the quotes when you use the `$` operator.

One thing that differentiates the `[[` operator from the `$` is that the `[[` operator can be used with *computed* indices. The `$` operator can only be used with literal names.

```
> x <- list(foo = 1:4, bar = 0.6, baz = "hello")  
> name <- "foo"  
>  
> ## computed index for "foo"  
> x[[name]]  
[1] 1 2 3 4  
>  
> ## element "name" doesn't exist! (but no error here)  
> x$name  
NULL  
>  
> ## element "foo" does exist  
> x$foo  
[1] 1 2 3 4
```

Subsetting Nested Elements of a List

The `[[` operator can take an integer sequence if you want to extract a nested element of a list.

```
> x <- list(a = list(10, 12, 14), b = c(3.14, 2.81))
>
> ## Get the 3rd element of the 1st element
> x[[c(1, 3)]]
[1] 14
>
> ## Same as above
> x[[1]][[3]]
[1] 14
>
> ## 1st element of the 2nd element
> x[[c(2, 1)]]
[1] 3.14
```

Extracting Multiple Elements of a List

The [operator can be used to extract *multiple* elements from a list. For example, if you wanted to extract the first and third elements of a list, you would do the following

```
> x <- list(foo = 1:4, bar = 0.6, baz = "hello")
> x[c(1, 3)]
$foo
[1] 1 2 3 4

$baz
[1] "hello"
```

Note that `x[c(1, 3)]` is NOT the same as `x[[c(1, 3)]]`.

Remember that the [operator always returns an object of the same class as the original. Since the original object was a list, the [operator returns a list. In the above code, we returned a list with two elements (the first and the third).

Partial Matching

[Watch a video of this section⁴⁵](#)

Partial matching of names is allowed with [[and \$. This is often very useful during interactive work if the object you're working with has very long element names. You can just abbreviate those names and R will figure out what element you're referring to.

⁴⁵<https://youtu.be/q3BNhHHVCu4>

```
> x <- list(aardvark = 1:5)
> x$a
[1] 1 2 3 4 5
> x[["a"]]
NULL
> x[["a", exact = FALSE]]
[1] 1 2 3 4 5
```

In general, this is fine for interactive work, but you shouldn't resort to partial matching if you are writing longer scripts, functions, or programs. In those cases, you should refer to the full element name if possible. That way there's no ambiguity in your code.

Removing NA Values

[Watch a video of this section⁴⁶](#)

A common task in data analysis is removing missing values (NAs).

```
> x <- c(1, 2, NA, 4, NA, 5)
> bad <- is.na(x)
> print(bad)
[1] FALSE FALSE TRUE FALSE TRUE FALSE
> x[!bad]
[1] 1 2 4 5
```

What if there are multiple R objects and you want to take the subset with no missing values in any of those objects?

```
> x <- c(1, 2, NA, 4, NA, 5)
> y <- c("a", "b", NA, "d", NA, "f")
> good <- complete.cases(x, y)
> good
[1] TRUE TRUE FALSE TRUE FALSE TRUE
> x[good]
[1] 1 2 4 5
> y[good]
[1] "a" "b" "d" "f"
```

You can use `complete.cases` on data frames too.

⁴⁶<https://youtu.be/TtJxmwXbwo0>

```
> head(airquality)
   Ozone Solar.R Wind Temp Month Day
1     41      190  7.4   67     5    1
2     36      118  8.0   72     5    2
3     12      149 12.6   74     5    3
4     18      313 11.5   62     5    4
5     NA       NA 14.3   56     5    5
6     28       NA 14.9   66     5    6
> good <- complete.cases(airquality)
> head(airquality[good, ])
   Ozone Solar.R Wind Temp Month Day
1     41      190  7.4   67     5    1
2     36      118  8.0   72     5    2
3     12      149 12.6   74     5    3
4     18      313 11.5   62     5    4
7     23      299  8.6   65     5    7
8     19      99   13.8   59     5    8
```

Head is first few rows, defaults to first 6 rows

Vectorized Operations

Watch a video of this chapter⁴⁷

Many operations in R are *vectorized*, meaning that operations occur in parallel in certain R objects. This allows you to write code that is efficient, concise, and easier to read than in non-vectorized languages.

The simplest example is when adding two vectors together.

```
> x <- 1:4  
> y <- 6:9  
> z <- x + y  
> z  
[1] 7 9 11 13
```

Natural, right? Without vectorization, you'd have to do something like

```
z <- numeric(length(x))  
for(i in seq_along(x)) {  
  z <- x[i] + y[i]  
}  
z  
[1] 13
```

If you had to do that every time you wanted to add two vectors, your hands would get very tired from all the typing.

Another operation you can do in a vectorized manner is logical comparisons. So suppose you wanted to know which elements of a vector were greater than 2. You could do the following.

```
> x  
[1] 1 2 3 4  
> x > 2  
[1] FALSE FALSE TRUE TRUE
```

Here are other vectorized logical operations.

⁴⁷<https://youtu.be/YH3qtw7mTyA>

```
> x >= 2
[1] FALSE TRUE TRUE TRUE
> x < 3
[1] TRUE TRUE FALSE FALSE
> y == 8
[1] FALSE FALSE TRUE FALSE
```

Notice that these logical operations return a logical vector of TRUE and FALSE.

Of course, subtraction, multiplication and division are also vectorized.

```
> x - y
[1] -5 -5 -5 -5
> x * y
[1]  6 14 24 36
> x / y
[1] 0.1666667 0.2857143 0.3750000 0.4444444
```

Vectorized Matrix Operations

Matrix operations are also vectorized, making for nicely compact notation. This way, we can do element-by-element operations on matrices without having to loop over every element.

```
> x <- matrix(1:4, 2, 2)
> y <- matrix(rep(10, 4), 2, 2)
>
> ## element-wise multiplication
> x * y
[,1] [,2]
[1,]    10    30
[2,]    20    40
>
> ## element-wise division
> x / y
[,1] [,2]
[1,]  0.1  0.3
[2,]  0.2  0.4
>
> ## true matrix multiplication
> x %*% y
[,1] [,2]
[1,]    40    40
[2,]    60    60
```

Dates and Times

R has developed a special representation for dates and times. Dates are represented by the Date class and times are represented by the POSIXct or the POSIXlt class. Dates are stored internally as the number of days since 1970-01-01 while times are stored internally as the number of seconds since 1970-01-01.

It's not important to know the internal representation of dates and times in order to use them in R. I just thought those were fun facts.

Dates in R

[Watch a video of this section⁴⁸](#)

Dates are represented by the Date class and can be coerced from a character string using the `as.Date()` function. This is a common way to end up with a Date object in R.

```
> ## Coerce a 'Date' object from character
> x <- as.Date("1970-01-01")
> x
[1] "1970-01-01"
```

You can see the internal representation of a Date object by using the `unclass()` function.

```
> unclass(x)
[1] 0
> unclass(as.Date("1970-01-02"))
[1] 1
```

Times in R

[Watch a video of this section⁴⁹](#)

Times are represented by the POSIXct or the POSIXlt class. POSIXct is just a very large integer under the hood. It uses a useful class when you want to store times in something like a data frame. POSIXlt

⁴⁸<https://youtu.be/opYexVgjwkE>

⁴⁹<https://youtu.be/8HENCYXwZoU>

is a list underneath and it stores a bunch of other useful information like the day of the week, day of the year, month, day of the month. This is useful when you need that kind of information.

There are a number of generic functions that work on dates and times to help you extract pieces of dates and/or times.

- `weekdays`: give the day of the week
- `months`: give the month name
- `quarters`: give the quarter number (“Q1”, “Q2”, “Q3”, or “Q4”)

Times can be coerced from a character string using the `as.POSIXlt` or `as.POSIXct` function.

```
> x <- Sys.time()
> x
[1] "2015-04-13 10:09:17 EDT"
> class(x)    ## 'POSIXct' object
[1] "POSIXct" "POSIXt"
```

The `POSIXlt` object contains some useful metadata.

```
> p <- as.POSIXlt(x)
> names(unclass(p))
[1] "sec"      "min"      "hour"     "mday"     "mon"      "year"      "wday"
[8] "yday"     "isdst"    "zone"     "gmtoff"
> p$wday      ## day of the week
[1] 1
```

You can also use the `POSIXct` format.

```
> x <- Sys.time()
> x          ## Already in 'POSIXct' format
[1] "2015-04-13 10:09:17 EDT"
> unclass(x) ## Internal representation
[1] 1428934157
> x$sec       ## Can't do this with 'POSIXct'!
Error in x$sec: $ operator is invalid for atomic vectors
> p <- as.POSIXlt(x)
> p$sec       ## That's better
[1] 17.16238
```

Finally, there is the `strptime()` function in case your dates are written in a different format. `strptime()` takes a character vector that has dates and times and converts them into to a `POSIXlt` object.

```
> datestring <- c("January 10, 2012 10:40", "December 9, 2011 9:10")
> x <- strptime(datestring, "%B %d, %Y %H:%M")
> x
[1] "2012-01-10 10:40:00 EST" "2011-12-09 09:10:00 EST"
> class(x)
[1] "POSIXlt" "POSIXt"
```

The weird-looking symbols that start with the % symbol are the formatting strings for dates and times. I can *never* remember the formatting strings. Check `?strptime` for details. It's probably not worth memorizing this stuff.

Operations on Dates and Times

[Watch a video of this section⁵⁰](#)

You can use mathematical operations on dates and times. Well, really just + and -. You can do comparisons too (i.e. ==, <=)

```
> x <- as.Date("2012-01-01")
> y <- strptime("9 Jan 2011 11:34:21", "%d %b %Y %H:%M:%S")
> x-y
Warning: Incompatible methods ("-.Date", "-.POSIXt") for "-"
Error in x - y: non-numeric argument to binary operator
> x <- as.POSIXlt(x)
> x-y
Time difference of 356.3095 days
```

The nice thing about the date/time classes is that they keep track of all the annoying things about dates and times, like leap years, leap seconds, daylight savings, and time zones.

Here's an example where a leap year gets involved.

```
> x <- as.Date("2012-03-01")
> y <- as.Date("2012-02-28")
> x-y
Time difference of 2 days
```

Here's an example where two different time zones are in play (unless you live in GMT timezone, in which case they will be the same!).

⁵⁰<https://youtu.be/vEmWJrpP1KM>

```
> ## My local time zone
> x <- as.POSIXct("2012-10-25 01:00:00")
> y <- as.POSIXct("2012-10-25 06:00:00", tz = "GMT")
> y-x
Time difference of 1 hours
```

Summary

- Dates and times have special classes in R that allow for numerical and statistical calculations
- Dates use the Date class
- Times use the POSIXct and POSIXlt class
- Character strings can be coerced to Date/Time classes using the `strptime` function or the `as.Date`, `as.POSIXlt`, or `as.POSIXct`

Managing Data Frames with the dplyr package

[Watch a video of this chapter⁵¹](#)

Data Frames

The *data frame* is a key data structure in statistics and in R. The basic structure of a data frame is that there is one observation per row and each column represents a variable, a measure, feature, or characteristic of that observation. R has an internal implementation of data frames that is likely the one you will use most often. However, there are packages on CRAN that implement data frames via things like relational databases that allow you to operate on very very large data frames (but we won't discuss them here).

Given the importance of managing data frames, it's important that we have good tools for dealing with them. In previous chapters we have already discussed some tools like the `subset()` function and the use of `[` and `$` operators to extract subsets of data frames. However, other operations, like filtering, re-ordering, and collapsing, can often be tedious operations in R whose syntax is not very intuitive. The `dplyr` package is designed to mitigate a lot of these problems and to provide a highly optimized set of routines specifically for dealing with data frames.

The dplyr Package

The `dplyr` package was developed by Hadley Wickham of RStudio and is an optimized and distilled version of his `plyr` package. The `dplyr` package does not provide any “new” functionality to R per se, in the sense that everything `dplyr` does could already be done with base R, but it *greatly* simplifies existing functionality in R.

One important contribution of the `dplyr` package is that it provides a “grammar” (in particular, verbs) for data manipulation and for operating on data frames. With this grammar, you can sensibly communicate what it is that you are doing to a data frame that other people can understand (assuming they also know the grammar). This is useful because it provides an abstraction for data manipulation that previously did not exist. Another useful contribution is that the `dplyr` functions are **very** fast, as many key operations are coded in C++.

⁵¹<https://youtu.be/aywFompr1F4>

dplyr Grammar

Some of the key “verbs” provided by the `dplyr` package are

- `select`: return a subset of the columns of a data frame, using a flexible notation
- `filter`: extract a subset of rows from a data frame based on logical conditions
- `arrange`: reorder rows of a data frame
- `rename`: rename variables in a data frame
- `mutate`: add new variables/columns or transform existing variables
- `summarise / summarize`: generate summary statistics of different variables in the data frame, possibly within strata
- `%>%`: the “pipe” operator is used to connect multiple verb actions together into a pipeline

The `dplyr` package has a number of its own data types that it takes advantage of. For example, there is a handy `print` method that prevents you from printing a lot of data to the console. Most of the time, these additional data types are transparent to the user and do not need to be worried about.

Common dplyr Function Properties

All of the functions that we will discuss in this Chapter will have a few common characteristics. In particular,

1. The first argument is a data frame.
2. The subsequent arguments describe what to do with the data frame specified in the first argument, and you can refer to columns in the data frame directly without using the `$` operator (just use the column names).
3. The return result of a function is a new data frame
4. Data frames must be properly formatted and annotated for this to all be useful. In particular, the data must be `tidy`⁵². In short, there should be one observation per row, and each column should represent a feature or characteristic of that observation.

Installing the dplyr package

The `dplyr` package can be installed from CRAN or from GitHub using the `devtools` package and the `install_github()` function. The GitHub repository will usually contain the latest updates to the package and the development version.

To install from CRAN, just run

⁵²<http://www.jstatsoft.org/v59/i10/paper>

```
> install.packages("dplyr")
```

To install from GitHub you can run

```
> install_github("hadley/dplyr")
```

After installing the package it is important that you load it into your R session with the `library()` function.

```
> library(dplyr)
```

```
Attaching package: 'dplyr'
```

```
The following object is masked from 'package:stats':
```

```
filter
```

```
The following objects are masked from 'package:base':
```

```
intersect, setdiff, setequal, union
```

You may get some warnings when the package is loaded because there are functions in the `dplyr` package that have the same name as functions in other packages. For now you can ignore the warnings.

select()

For the examples in this chapter we will be using a dataset containing air pollution and temperature data for the [city of Chicago](#)⁵³ in the U.S. The dataset is available from my web site.

After unzipping the archive, you can load the data into R using the `readRDS()` function.

```
> chicago <- readRDS("chicago.rds")
```

You can see some basic characteristics of the dataset with the `dim()` and `str()` functions.

⁵³http://www.biostat.jhsph.edu/~rpeng/leanpub/rprog/chicago_data.zip

```
> dim(chicago)
[1] 6940     8
> str(chicago)
'data.frame':   6940 obs. of  8 variables:
 $ city      : chr  "chic" "chic" "chic" "chic" ...
 $ tmpd      : num  31.5 33 33 29 32 40 34.5 29 26.5 32.5 ...
 $ dptp      : num  31.5 29.9 27.4 28.6 28.9 ...
 $ date      : Date, format: "1987-01-01" "1987-01-02" ...
 $ pm25tmean2: num  NA NA NA NA NA NA NA NA NA ...
 $ pm10tmean2: num  34 NA 34.2 47 NA ...
 $ o3tmean2  : num  4.25 3.3 3.33 4.38 4.75 ...
 $ no2tmean2 : num  20 23.2 23.8 30.4 30.3 ...
```

The `select()` function can be used to select columns of a data frame that you want to focus on. Often you'll have a large data frame containing "all" of the data, but any *given* analysis might only use a subset of variables or observations. The `select()` function allows you to get the few columns you might need.

Suppose we wanted to take the first 3 columns only. There are a few ways to do this. We could for example use numerical indices. But we can also use the names directly.

```
> names(chicago)[1:3]
[1] "city" "tmpd" "dptp"
> subset <- select(chicago, city:dptp)
> head(subset)
  city tmpd  dptp
1 chic 31.5 31.500
2 chic 33.0 29.875
3 chic 33.0 27.375
4 chic 29.0 28.625
5 chic 32.0 28.875
6 chic 40.0 35.125
```

Note that the `:` normally cannot be used with names or strings, but inside the `select()` function you can use it to specify a range of variable names.

You can also *omit* variables using the `select()` function by using the negative sign. With `select()` you can do

```
> select(chicago, -(city:dptp))
```

which indicates that we should include every variable *except* the variables `city` through `dptp`. The equivalent code in base R would be

```
> i <- match("city", names(chicago))
> j <- match("dptp", names(chicago))
> head(chicago[, -(i:j)])
```

Not super intuitive, right?

The `select()` function also allows a special syntax that allows you to specify variable names based on patterns. So, for example, if you wanted to keep every variable that ends with a “2”, we could do

```
> subset <- select(chicago, ends_with("2"))
> str(subset)
'data.frame': 6940 obs. of 4 variables:
 $ pm25tmean2: num NA NA NA NA NA NA NA NA NA ...
 $ pm10tmean2: num 34 NA 34.2 47 NA ...
 $ o3tmean2 : num 4.25 3.3 3.33 4.38 4.75 ...
 $ no2tmean2 : num 20 23.2 23.8 30.4 30.3 ...
```

Or if we wanted to keep every variable that starts with a “d”, we could do

```
> subset <- select(chicago, starts_with("d"))
> str(subset)
'data.frame': 6940 obs. of 2 variables:
 $ dptp: num 31.5 29.9 27.4 28.6 28.9 ...
 $ date: Date, format: "1987-01-01" "1987-01-02" ...
```

You can also use more general regular expressions if necessary. See the help page (`?select`) for more details.

`filter()`

The `filter()` function is used to extract subsets of rows from a data frame. This function is similar to the existing `subset()` function in R but is quite a bit faster in my experience.

Suppose we wanted to extract the rows of the `chicago` data frame where the levels of PM2.5 are greater than 30 (which is a reasonably high level), we could do

```
> chic.f <- filter(chicago, pm25tmean2 > 30)
> str(chic.f)
'data.frame': 194 obs. of 8 variables:
 $ city      : chr "chic" "chic" "chic" "chic" ...
 $ tmpd      : num 23 28 55 59 57 57 75 61 73 78 ...
 $ dptp      : num 21.9 25.8 51.3 53.7 52 56 65.8 59 60.3 67.1 ...
 $ date      : Date, format: "1998-01-17" "1998-01-23" ...
 $ pm25tmean2: num 38.1 34 39.4 35.4 33.3 ...
 $ pm10tmean2: num 32.5 38.7 34 28.5 35 ...
 $ o3tmean2  : num 3.18 1.75 10.79 14.3 20.66 ...
 $ no2tmean2 : num 25.3 29.4 25.3 31.4 26.8 ...
```

You can see that there are now only 194 rows in the data frame and the distribution of the pm25tmean2 values is.

```
> summary(chic.f$pm25tmean2)
   Min. 1st Qu. Median     Mean 3rd Qu.    Max.
30.05    32.12   35.04   36.63   39.53   61.50
```

We can place an arbitrarily complex logical sequence inside of `filter()`, so we could for example extract the rows where PM2.5 is greater than 30 *and* temperature is greater than 80 degrees Fahrenheit.

```
> chic.f <- filter(chicago, pm25tmean2 > 30 & tmpd > 80)
> select(chic.f, date, tmpd, pm25tmean2)
      date tmpd pm25tmean2
1 1998-08-23  81  39.60000
2 1998-09-06  81  31.50000
3 2001-07-20  82  32.30000
4 2001-08-01  84  43.70000
5 2001-08-08  85  38.83750
6 2001-08-09  84  38.20000
7 2002-06-20  82  33.00000
8 2002-06-23  82  42.50000
9 2002-07-08  81  33.10000
10 2002-07-18 82  38.85000
11 2003-06-25 82  33.90000
12 2003-07-04  84  32.90000
13 2005-06-24  86  31.85714
14 2005-06-27  82  51.53750
15 2005-06-28  85  31.20000
16 2005-07-17  84  32.70000
17 2005-08-03  84  37.90000
```

Now there are only 17 observations where both of those conditions are met.

arrange()

The `arrange()` function is used to reorder rows of a data frame according to one of the variables/columns. Reordering rows of a data frame (while preserving corresponding order of other columns) is normally a pain to do in R. The `arrange()` function simplifies the process quite a bit.

Here we can order the rows of the data frame by date, so that the first row is the earliest (oldest) observation and the last row is the latest (most recent) observation.

```
> chicago <- arrange(chicago, date)
```

We can now check the first few rows

```
> head(select(chicago, date, pm25tmean2), 3)
      date pm25tmean2
1 1987-01-01      NA
2 1987-01-02      NA
3 1987-01-03      NA
```

and the last few rows.

```
> tail(select(chicago, date, pm25tmean2), 3)
      date pm25tmean2
6938 2005-12-29    7.45000
6939 2005-12-30   15.05714
6940 2005-12-31   15.00000
```

Columns can be arranged in descending order too by using the special `desc()` operator.

```
> chicago <- arrange(chicago, desc(date))
```

Looking at the first three and last three rows shows the dates in descending order.

```
> head(select(chicago, date, pm25tmean2), 3)
      date pm25tmean2
1 2005-12-31 15.00000
2 2005-12-30 15.05714
3 2005-12-29 7.45000
> tail(select(chicago, date, pm25tmean2), 3)
      date pm25tmean2
6938 1987-01-03       NA
6939 1987-01-02       NA
6940 1987-01-01       NA
```

rename()

Renaming a variable in a data frame in R is surprisingly hard to do! The `rename()` function is designed to make this process easier.

Here you can see the names of the first five variables in the `chicago` data frame.

```
> head(chicago[, 1:5], 3)
  city tmpd dptp      date pm25tmean2
1 chic   35 30.1 2005-12-31 15.00000
2 chic   36 31.0 2005-12-30 15.05714
3 chic   35 29.4 2005-12-29  7.45000
```

The `dptp` column is supposed to represent the dew point temperature and the `pm25tmean2` column provides the PM2.5 data. However, these names are pretty obscure or awkward and probably be renamed to something more sensible.

```
> chicago <- rename(chicago, dewpoint = dptp, pm25 = pm25tmean2)
> head(chicago[, 1:5], 3)
  city tmpd dewpoint      date     pm25
1 chic   35    30.1 2005-12-31 15.00000
2 chic   36    31.0 2005-12-30 15.05714
3 chic   35    29.4 2005-12-29  7.45000
```

The syntax inside the `rename()` function is to have the new name on the left-hand side of the `=` sign and the old name on the right-hand side.

I leave it as an exercise for the reader to figure how you do this in base R without `dplyr`.

mutate()

The `mutate()` function exists to compute transformations of variables in a data frame. Often, you want to create new variables that are derived from existing variables and `mutate()` provides a clean interface for doing that.

For example, with air pollution data, we often want to *detrend* the data by subtracting the mean from the data. That way we can look at whether a given day's air pollution level is higher than or less than average (as opposed to looking at its absolute level).

Here we create a `pm25detrend` variable that subtracts the mean from the `pm25` variable.

```
> chicago <- mutate(chicago, pm25detrend = pm25 - mean(pm25, na.rm = TRUE))
> head(chicago)
#> #>   city tmpd dewpoint      date    pm25 pm10tmean2  o3tmean2 no2tmean2
#> #>   1 chic   35     30.1 2005-12-31 15.00000    23.5  2.531250 13.25000
#> #>   2 chic   36     31.0 2005-12-30 15.05714    19.2  3.034420 22.80556
#> #>   3 chic   35     29.4 2005-12-29  7.45000    23.5  6.794837 19.97222
#> #>   4 chic   37     34.5 2005-12-28 17.75000    27.5  3.260417 19.28563
#> #>   5 chic   40     33.6 2005-12-27 23.56000    27.0  4.468750 23.50000
#> #>   6 chic   35     29.6 2005-12-26  8.40000     8.5 14.041667 16.81944
#> #>   pm25detrend
#> #>   1   -1.230958
#> #>   2   -1.173815
#> #>   3   -8.780958
#> #>   4    1.519042
#> #>   5    7.329042
#> #>   6   -7.830958
```

There is also the related `transmute()` function, which does the same thing as `mutate()` but then *drops all non-transformed variables*.

Here we detrend the PM10 and ozone (O₃) variables.

```
> head(transmute(chicago,
+                  pm10detrend = pm10tmean2 - mean(pm10tmean2, na.rm = TRUE),
+                  o3detrend = o3tmean2 - mean(o3tmean2, na.rm = TRUE)))
#> #>   pm10detrend  o3detrend
#> #>   1   -10.395206 -16.904263
#> #>   2   -14.695206 -16.401093
#> #>   3   -10.395206 -12.640676
#> #>   4   -6.395206 -16.175096
#> #>   5   -6.895206 -14.966763
#> #>   6  -25.395206  -5.393846
```

Note that there are only two columns in the transmuted data frame.

group_by()

The `group_by()` function is used to generate summary statistics from the data frame within strata defined by a variable. For example, in this air pollution dataset, you might want to know what the average annual level of PM2.5 is. So the stratum is the year, and that is something we can derive from the `date` variable. In conjunction with the `group_by()` function we often use the `summarize()` function (or `summarise()` for some parts of the world).

The general operation here is a combination of splitting a data frame into separate pieces defined by a variable or group of variables (`group_by()`), and then applying a summary function across those subsets (`summarize()`).

First, we can create a `year` variable using `as.POSIXlt()`.

```
> chicago <- mutate(chicago, year = as.POSIXlt(date)$year + 1900)
```

Now we can create a separate data frame that splits the original data frame by year.

```
> years <- group_by(chicago, year)
```

Finally, we compute summary statistics for each year in the data frame with the `summarize()` function.

```
> summarize(years, pm25 = mean(pm25, na.rm = TRUE),
+           o3 = max(o3tmean2, na.rm = TRUE),
+           no2 = median(no2tmean2, na.rm = TRUE))
Source: local data frame [19 x 4]
```

	year	pm25	o3	no2
1	1987	NaN	62.96966	23.49369
2	1988	NaN	61.67708	24.52296
3	1989	NaN	59.72727	26.14062
4	1990	NaN	52.22917	22.59583
5	1991	NaN	63.10417	21.38194
6	1992	NaN	50.82870	24.78921
7	1993	NaN	44.30093	25.76993
8	1994	NaN	52.17844	28.47500
9	1995	NaN	66.58750	27.26042
10	1996	NaN	58.39583	26.38715
11	1997	NaN	56.54167	25.48143

```
12 1998 18.26467 50.66250 24.58649
13 1999 18.49646 57.48864 24.66667
14 2000 16.93806 55.76103 23.46082
15 2001 16.92632 51.81984 25.06522
16 2002 15.27335 54.88043 22.73750
17 2003 15.23183 56.16608 24.62500
18 2004 14.62864 44.48240 23.39130
19 2005 16.18556 58.84126 22.62387
```

`summarize()` returns a data frame with `year` as the first column, and then the annual averages of `pm25`, `o3`, and `no2`.

In a slightly more complicated example, we might want to know what are the average levels of ozone (`o3`) and nitrogen dioxide (`no2`) within quintiles of `pm25`. A slicker way to do this would be through a regression model, but we can actually do this quickly with `group_by()` and `summarize()`.

First, we can create a categorical variable of `pm25` divided into quintiles.

```
> qq <- quantile(chicago$pm25, seq(0, 1, 0.2), na.rm = TRUE)
> chicago <- mutate(chicago, pm25.quint = cut(pm25, qq))
```

Now we can group the data frame by the `pm25.quint` variable.

```
> quint <- group_by(chicago, pm25.quint)
```

Finally, we can compute the mean of `o3` and `no2` within quintiles of `pm25`.

```
> summarize(quint, o3 = mean(o3tmean2, na.rm = TRUE),
+            no2 = mean(no2tmean2, na.rm = TRUE))
Source: local data frame [6 x 3]
```

	pm25.quint	o3	no2
1	(1.7,8.7]	21.66401	17.99129
2	(8.7,12.4]	20.38248	22.13004
3	(12.4,16.7]	20.66160	24.35708
4	(16.7,22.6]	19.88122	27.27132
5	(22.6,61.5]	20.31775	29.64427
6	NA	18.79044	25.77585

From the table, it seems there isn't a strong relationship between `pm25` and `o3`, but there appears to be a positive correlation between `pm25` and `no2`. More sophisticated statistical modeling can help to provide precise answers to these questions, but a simple application of `dplyr` functions can often get you most of the way there.

%>%

The pipeline operator `%>%` is very handy for stringing together multiple `dplyr` functions in a sequence of operations. Notice above that every time we wanted to apply more than one function, the sequence gets buried in a sequence of nested function calls that is difficult to read, i.e.

```
> third(second(first(x)))
```

This nesting is not a natural way to think about a sequence of operations. The `%>%` operator allows you to string operations in a left-to-right fashion, i.e.

```
> first(x) %>% second %>% third
```

Take the example that we just did in the last section where we computed the mean of `o3` and `no2` within quintiles of `pm25`. There we had to

1. create a new variable `pm25.quint`
2. split the data frame by that new variable
3. compute the mean of `o3` and `no2` in the sub-groups defined by `pm25.quint`

That can be done with the following sequence in a single R expression.

```
> mutate(chicago, pm25.quint = cut(pm25, qq)) %>%
+     group_by(pm25.quint) %>%
+     summarize(o3 = mean(o3tmean2, na.rm = TRUE),
+               no2 = mean(no2tmean2, na.rm = TRUE))
Source: local data frame [6 x 3]
```

	pm25.quint	o3	no2
1	(1.7,8.7]	21.66401	17.99129
2	(8.7,12.4]	20.38248	22.13004
3	(12.4,16.7]	20.66160	24.35708
4	(16.7,22.6]	19.88122	27.27132
5	(22.6,61.5]	20.31775	29.64427
6	NA	18.79044	25.77585

This way we don't have to create a set of temporary variables along the way or create a massive nested sequence of function calls.

Notice in the above code that I pass the `chicago` data frame to the first call to `mutate()`, but then afterwards I do not have to pass the first argument to `group_by()` or `summarize()`. Once you travel down the pipeline with `%>%`, the first argument is taken to be the output of the previous element in the pipeline.

Another example might be computing the average pollutant level by month. This could be useful to see if there are any seasonal trends in the data.

```
> mutate(chicago, month = as.POSIXlt(date)$mon + 1) %>%
+     group_by(month) %>%
+     summarize(pm25 = mean(pm25, na.rm = TRUE),
+             o3 = max(o3tmean2, na.rm = TRUE),
+             no2 = median(no2tmean2, na.rm = TRUE))
Source: local data frame [12 x 4]
```

	month	pm25	o3	no2
1	1	17.76996	28.22222	25.35417
2	2	20.37513	37.37500	26.78034
3	3	17.40818	39.05000	26.76984
4	4	13.85879	47.94907	25.03125
5	5	14.07420	52.75000	24.22222
6	6	15.86461	66.58750	25.01140
7	7	16.57087	59.54167	22.38442
8	8	16.93380	53.96701	22.98333
9	9	15.91279	57.48864	24.47917
10	10	14.23557	47.09275	24.15217
11	11	15.15794	29.45833	23.56537
12	12	17.52221	27.70833	24.45773

Here we can see that o3 tends to be low in the winter months and high in the summer while no2 is higher in the winter and lower in the summer.

Summary

The dplyr package provides a concise set of operations for managing data frames. With these functions we can do a number of complex operations in just a few lines of code. In particular, we can often conduct the beginnings of an exploratory analysis with the powerful combination of `group_by()` and `summarize()`.

Once you learn the dplyr grammar there are a few additional benefits

- dplyr can work with other data frame “backends” such as SQL databases. There is an SQL interface for relational databases via the DBI package
- dplyr can be integrated with the data.table package for large fast tables

The dplyr package is handy way to both simplify and speed up your data frame management code. It’s rare that you get such a combination at the same time!

Control Structures

[Watch a video of this section⁵⁴](#)

Control structures in R allow you to control the flow of execution of a series of R expressions. Basically, control structures allow you to put some “logic” into your R code, rather than just always executing the same R code every time. Control structures allow you to respond to inputs or to features of the data and execute different R expressions accordingly.

Commonly used control structures are

- `if` and `else`: testing a condition and acting on it
- `for`: execute a loop a fixed number of times
- `while`: execute a loop *while* a condition is true
- `repeat`: execute an infinite loop (must `break` out of it to stop)
- `break`: break the execution of a loop
- `next`: skip an iteration of a loop

Most control structures are not used in interactive sessions, but rather when writing functions or longer expressions. However, these constructs do not have to be used in functions and it's a good idea to become familiar with them before we delve into functions.

if-else

[Watch a video of this section⁵⁵](#)

The `if-else` combination is probably the most commonly used control structure in R (or perhaps any language). This structure allows you to test a condition and act on it depending on whether it's true or false.

For starters, you can just use the `if` statement.

⁵⁴https://youtu.be/BPNLjUDZ8_o

⁵⁵<https://youtu.be/ZaBtJPYYGwg>

```
if(<condition>) {
    ## do something
}
## Continue with rest of code
```

The above code does nothing if the condition is false. If you have an action you want to execute when the condition is false, then you need an **else** clause.

```
if(<condition>) {
    ## do something
}
else {
    ## do something else
}
```

You can have a series of tests by following the initial **if** with any number of **else if**s.

```
if(<condition1>) {
    ## do something
} else if(<condition2>) {
    ## do something different
} else {
    ## do something different
}
```

Here is an example of a valid if/else structure.

```
## Generate a uniform random number
x <- runif(1, 0, 10)
if(x > 3) {
    y <- 10
} else {
    y <- 0
}
```

The value of **y** is set depending on whether **x > 3** or not. This expression can also be written a different, but equivalent, way in R.

```
y <- if(x > 3) {  
  10  
} else {  
  0  
}
```

Neither way of writing this expression is more correct than the other. Which one you use will depend on your preference and perhaps those of the team you may be working with.

Of course, the `else` clause is not necessary. You could have a series of `if` clauses that always get executed if their respective conditions are true.

```
if(<condition1>) {  
  
}  
  
if(<condition2>) {  
  
}
```

for Loops

Watch a video of this section⁵⁶

For loops are pretty much the only looping construct that you will need in R. While you may occasionally find a need for other types of loops, in my experience doing data analysis, I've found very few situations where a `for` loop wasn't sufficient.

In R, `for` loops take an iterator variable and assign it successive values from a sequence or vector. `For` loops are most commonly used for iterating over the elements of an object (list, vector, etc.)

```
> for(i in 1:10) {  
+   print(i)  
+ }  
[1] 1  
[1] 2  
[1] 3  
[1] 4  
[1] 5  
[1] 6  
[1] 7
```

⁵⁶<https://youtu.be/FbT1dGXCCxU>

```
[1] 8  
[1] 9  
[1] 10
```

This loop takes the `i` variable and in each iteration of the loop gives it values 1, 2, 3, ..., 10, executes the code within the curly braces, and then the loop exits.

The following three loops all have the same behavior.

```
> x <- c("a", "b", "c", "d")  
>  
> for(i in 1:4) {  
+     ## Print out each element of 'x'  
+     print(x[i])  
+ }  
[1] "a"  
[1] "b"  
[1] "c"  
[1] "d"
```

The `seq_along()` function is commonly used in conjunction with for loops in order to generate an integer sequence based on the length of an object (in this case, the object `x`).

```
> ## Generate a sequence based on length of 'x'  
> for(i in seq_along(x)) {  
+     print(x[i])  
+ }  
[1] "a"  
[1] "b"  
[1] "c"  
[1] "d"
```

It is not necessary to use an index-type variable.

```
> for(letter in x) {  
+     print(letter)  
+ }  
[1] "a"  
[1] "b"  
[1] "c"  
[1] "d"
```

For one line loops, the curly braces are not strictly necessary.

```
> for(i in 1:4) print(x[i])  
[1] "a"  
[1] "b"  
[1] "c"  
[1] "d"
```

However, I like to use curly braces even for one-line loops, because that way if you decide to expand the loop to multiple lines, you won't be burned because you forgot to add curly braces (and you *will* be burned by this).

Nested for loops

for loops can be nested inside of each other.

```
x <- matrix(1:6, 2, 3)  
  
for(i in seq_len(nrow(x))) {  
    for(j in seq_len(ncol(x))) {  
        print(x[i, j])  
    }  
}
```

Nested loops are commonly needed for multidimensional or hierarchical data structures (e.g. matrices, lists). Be careful with nesting though. Nesting beyond 2 to 3 levels often makes it difficult to read/understand the code. If you find yourself in need of a large number of nested loops, you may want to break up the loops by using functions (discussed later).

while Loops

Watch a video of this section⁵⁷

While loops begin by testing a condition. If it is true, then they execute the loop body. Once the loop body is executed, the condition is tested again, and so forth, until the condition is false, after which the loop exits.

```
> count <- 0
> while(count < 10) {
+     print(count)
+     count <- count + 1
+
[1] 0
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
[1] 6
[1] 7
[1] 8
[1] 9
```

While loops can potentially result in infinite loops if not written properly. Use with care!

Sometimes there will be more than one condition in the test.

```
> z <- 5
> set.seed(1)
>
> while(z >= 3 && z <= 10) {
+     coin <- rbinom(1, 1, 0.5)
+
+     if(coin == 1) { ## random walk
+         z <- z + 1
+     } else {
+         z <- z - 1
+     }
+ }
> print(z)
[1] 2
```

⁵⁷<https://youtu.be/VqrS1Wghq1c>

Conditions are always evaluated from left to right. For example, in the above code, if `z` were less than 3, the second test would not have been evaluated.

repeat Loops

Watch a video of this section⁵⁸

`repeat` initiates an infinite loop right from the start. These are not commonly used in statistical or data analysis applications but they do have their uses. The only way to exit a repeat loop is to call `break`.

One possible paradigm might be in an iterative algorithm where you may be searching for a solution and you don't want to stop until you're close enough to the solution. In this kind of situation, you often don't know in advance how many iterations it's going to take to get "close enough" to the solution.

```
x0 <- 1
tol <- 1e-8

repeat {
  x1 <- computeEstimate()

  if(abs(x1 - x0) < tol) { ## Close enough?
    break
  } else {
    x0 <- x1
  }
}
```

Note that the above code will not run if the `computeEstimate()` function is not defined (I just made it up for the purposes of this demonstration).

The loop above is a bit dangerous because there's no guarantee it will stop. You could get in a situation where the values of `x0` and `x1` oscillate back and forth and never converge. Better to set a hard limit on the number of iterations by using a `for` loop and then report whether convergence was achieved or not.

next, break

`next` is used to skip an iteration of a loop.

⁵⁸<https://youtu.be/SajmdYr30SY>

```
for(i in 1:100) {  
  if(i <= 20) {  
    ## Skip the first 20 iterations  
    next  
  }  
  ## Do something here  
}
```

`break` is used to exit a loop immediately, regardless of what iteration the loop may be on.

```
for(i in 1:100) {  
  print(i)  
  
  if(i > 20) {  
    ## Stop loop after 20 iterations  
    break  
  }  
}
```

Summary

- Control structures like `if`, `while`, and `for` allow you to control the flow of an R program
- Infinite loops should generally be avoided, even if (you believe) they are theoretically correct.
- Control structures mentioned here are primarily useful for writing programs; for command-line interactive work, the “apply” functions are more useful.

Functions

Writing functions is a core activity of an R programmer. It represents the key step of the transition from a mere “user” to a developer who creates new functionality for R. Functions are often used to encapsulate a sequence of expressions that need to be executed numerous times, perhaps under slightly different conditions. Functions are also often written when code must be shared with others or the public.

The writing of a function allows a developer to create an interface to the code, that is explicitly specified with a set of parameters. This interface provides an abstraction of the code to potential users. This abstraction simplifies the users’ lives because it relieves them from having to know every detail of how the code operates. In addition, the creation of an interface allows the developer to communicate to the user the aspects of the code that are important or are most relevant.

Functions in R

Functions in R are “first class objects”, which means that they can be treated much like any other R object. Importantly,

- Functions can be passed as arguments to other functions. This is very handy for the various apply functions, like `lapply()` and `sapply()`.
- Functions can be nested, so that you can define a function inside of another function

If you’re familiar with common language like C, these features might appear a bit strange. However, they are really important in R and can be useful for data analysis.

Your First Function

Functions are defined using the `function()` directive and are stored as R objects just like anything else. In particular, they are R objects of class “function”.

Here’s a simple function that takes no arguments and does nothing.

```
> f <- function() {
+     ## This is an empty function
+
> ## Functions have their own class
> class(f)
[1] "function"
> ## Execute this function
> f()
NULL
```

Not very interesting, but it's a start. The next thing we can do is create a function that actually has a non-trivial *function body*.

```
> f <- function() {
+     cat("Hello, world!\n")
+
> f()
Hello, world!
```

The last aspect of a basic function is the *function arguments*. These are the options that you can specify to the user that the user may explicitly set. For this basic function, we can add an argument that determines how many times “Hello, world!” is printed to the console.

```
> f <- function(num) {
+     for(i in seq_len(num)) {
+         cat("Hello, world!\n")
+
+     }
+
> f(3)
Hello, world!
Hello, world!
Hello, world!
```

Obviously, we could have just cut-and-pasted the `cat("Hello, world!\n")` code three times to achieve the same effect, but then we wouldn't be programming, would we? Also, it would be unneighborly of you to give your code to someone else and force them to cut-and-paste the code however many times the need to see “Hello, world!”.

In general, if you find yourself doing a lot of cutting and pasting, that's usually a good sign that you might need to write a function.

Finally, the function above doesn't *return* anything. It just prints "Hello, world!" to the console `num` number of times and then exits. But often it is useful if a function returns something that perhaps can be fed into another section of code.

This next function returns the total number of characters printed to the console.

```
> f <- function(num) {  
+   hello <- "Hello, world!\n"  
+   for(i in seq_len(num)) {  
+     cat(hello)  
+   }  
+   chars <- nchar(hello) * num  
+   chars  
+ }  
> meaningoflife <- f(3)  
Hello, world!  
Hello, world!  
Hello, world!  
> print(meaningoflife)  
[1] 42
```

In the above function, we didn't have to indicate anything special in order for the function to return the number of characters. In R, the return value of a function is always the very last expression that is evaluated. Because the `chars` variable is the last expression that is evaluated in this function, that becomes the return value of the function.

Note that there is a `return()` function that can be used to return an explicitly value from a function, but it is rarely used in R (we will discuss it a bit later in this chapter).

Finally, in the above function, the user must specify the value of the argument `num`. If it is not specified by the user, R will throw an error.

```
> f()  
Error in f(): argument "num" is missing, with no default
```

We can modify this behavior by setting a *default value* for the argument `num`. Any function argument can have a default value, if you wish to specify it. Sometimes, argument values are rarely modified (except in special cases) and it makes sense to set a default value for that argument. This relieves the user from having to specify the value of that argument every single time the function is called.

Here, for example, we could set the default value for `num` to be 1, so that if the function is called without the `num` argument being explicitly specified, then it will print "Hello, world!" to the console once.

```

> f <- function(num = 1) {
+   hello <- "Hello, world!\n"
+   for(i in seq_len(num)) {
+     cat(hello)
+   }
+   chars <- nchar(hello) * num
+   chars
+ }
> f()    ## Use default value for 'num'
Hello, world!
[1] 14
> f(2)  ## Use user-specified value
Hello, world!
Hello, world!
[1] 28

```

Remember that the function still returns the number of characters printed to the console.

At this point, we have written a function that

- has one *formal argument* named `num` with a *default value* of 1. The *formal arguments* are the arguments included in the function definition. The `formals()` function returns a list of all the formal arguments of a function
- prints the message “Hello, world!” to the console a number of times indicated by the argument `num`
- *returns* the number of characters printed to the console

Functions have *named arguments* which can optionally have default values. Because all function arguments have names, they can be specified using their name.

```

> f(num = 2)
Hello, world!
Hello, world!
[1] 28

```

Specifying an argument by its name is sometimes useful if a function has many arguments and it may not always be clear which argument is being specified. Here, our function only has one argument so there's no confusion.

Argument Matching

Calling an R function with arguments can be done in a variety of ways. This may be confusing at first, but it's really handing when doing interactive work at the command line. R functions arguments can be matched *positionally* or by name. Positional matching just means that R assigns the first value to the first argument, the second value to second argument, etc. So in the following call to `rnorm()`

```
> str(rnorm)
function (n, mean = 0, sd = 1)
> mydata <- rnorm(100, 2, 1)          ## Generate some data
```

100 is assigned to the `n` argument, 2 is assigned to the `mean` argument, and 1 is assigned to the `sd` argument, all by positional matching.

The following calls to the `sd()` function (which computes the empirical standard deviation of a vector of numbers) are all equivalent. Note that `sd()` has two arguments: `x` indicates the vector of numbers and `na.rm` is a logical indicating whether missing values should be removed or not.

```
> ## Positional match first argument, default for 'na.rm'
> sd(mydata)
[1] 0.9033251
> ## Specify 'x' argument by name, default for 'na.rm'
> sd(x = mydata)
[1] 0.9033251
> ## Specify both arguments by name
> sd(x = mydata, na.rm = FALSE)
[1] 0.9033251
```

When specifying the function arguments by name, it doesn't matter in what order you specify them. In the example below, we specify the `na.rm` argument first, followed by `x`, even though `x` is the first argument defined in the function definition.

```
> ## Specify both arguments by name
> sd(na.rm = FALSE, x = mydata)
[1] 0.9033251
```

You can mix positional matching with matching by name. When an argument is matched by name, it is "taken out" of the argument list and the remaining unnamed arguments are matched in the order that they are listed in the function definition.

```
> sd(na.rm = FALSE, mydata)
[1] 0.9033251
```

Here, the `mydata` object is assigned to the `x` argument, because it's the only argument not yet specified.

Below is the argument list for the `lm()` function, which fits linear models to a dataset.

```
> args(lm)
function (formula, data, subset, weights, na.action, method = "qr",
  model = TRUE, x = FALSE, y = FALSE, qr = TRUE, singular.ok = TRUE,
  contrasts = NULL, offset, ...)
NULL
```

The following two calls are equivalent.

```
lm(data = mydata, y ~ x, model = FALSE, 1:100)
lm(y ~ x, mydata, 1:100, model = FALSE)
```

Even though it's legal, I don't recommend messing around with the order of the arguments too much, since it can lead to some confusion.

Most of the time, named arguments are useful on the command line when you have a long argument list and you want to use the defaults for everything except for an argument near the end of the list. Named arguments also help if you can remember the name of the argument and not its position on the argument list. For example, plotting functions often have a lot of options to allow for customization, but this makes it difficult to remember exactly the position of every argument on the argument list.

Function arguments can also be *partially* matched, which is useful for interactive work. The order of operations when given an argument is

1. Check for exact match for a named argument
2. Check for a partial match
3. Check for a positional match

Partial matching should be avoided when writing longer code or programs, because it may lead to confusion if someone is reading the code. However, partial matching is very useful when calling functions interactively that have very long argument names.

In addition to not specifying a default value, you can also set an argument value to `NULL`.

```
f <- function(a, b = 1, c = 2, d = NULL) {  
}
```

You can check to see whether an R object is `NULL` with the `is.null()` function. It is sometimes useful to allow an argument to take the `NULL` value, which might indicate that the function should take some specific action.

Lazy Evaluation

Arguments to functions are evaluated *lazily*, so they are evaluated only as needed in the body of the function.

In this example, the function `f()` has two arguments: `a` and `b`.

```
> f <- function(a, b) {  
+     a^2  
+ }  
> f(2)  
[1] 4
```

This function never actually uses the argument `b`, so calling `f(2)` will not produce an error because the `2` gets positionally matched to `a`. This behavior can be good or bad. It's common to write a function that doesn't use an argument and not notice it simply because R never throws an error.

This example also shows lazy evaluation at work, but does eventually result in an error.

```
> f <- function(a, b) {  
+     print(a)  
+     print(b)  
+ }  
> f(45)  
[1] 45  
Error in print(b): argument "b" is missing, with no default
```

Notice that “45” got printed first before the error was triggered. This is because `b` did not have to be evaluated until after `print(a)`. Once the function tried to evaluate `print(b)` the function had to throw an error.

The . . . Argument

There is a special argument in R known as the `...` argument, which indicate a variable number of arguments that are usually passed on to other functions. The `...` argument is often used when extending another function and you don't want to copy the entire argument list of the original function.

For example, a custom plotting function may want to make use of the default `plot()` function along with its entire argument list. The function below changes the default for the `type` argument to the value `type = "l"` (the original default was `type = "p"`).

```
myplot <- function(x, y, type = "l", ...) {
  plot(x, y, type = type, ...)      ## Pass '...' to 'plot' function
}
```

Generic functions use `...` so that extra arguments can be passed to methods.

```
> mean
function (x, ...)
UseMethod("mean")
<bytecode: 0x7fe7bc5cf988>
<environment: namespace:base>
```

The `...` argument is necessary when the number of arguments passed to the function cannot be known in advance. This is clear in functions like `paste()` and `cat()`.

```
> args(paste)
function (..., sep = " ", collapse = NULL)
NULL
> args(cat)
function (..., file = "", sep = " ", fill = FALSE, labels = NULL,
  append = FALSE)
NULL
```

Because both `paste()` and `cat()` print out text to the console by combining multiple character vectors together, it is impossible for those functions to know in advance how many character vectors will be passed to the function by the user. So the first argument to either function is `...`.

Arguments Coming After the . . . Argument

One catch with `...` is that any arguments that appear *after* `...` on the argument list must be named explicitly and cannot be partially matched or matched positionally.

Take a look at the arguments to the `paste()` function.

```
> args(paste)
function (..., sep = " ", collapse = NULL)
NULL
```

With the `paste()` function, the arguments `sep` and `collapse` must be named explicitly and in full if the default values are not going to be used.

Here I specify that I want “a” and “b” to be pasted together and separated by a colon.

```
> paste("a", "b", sep = ":")
[1] "a:b"
```

If I don’t specify the `sep` argument in full and attempt to rely on partial matching, I don’t get the expected result.

```
> paste("a", "b", se = ":")
[1] "a b :"
```

Summary

- Functions can be defined using the `function()` directive and are assigned to R objects just like any other R object
- Functions have can be defined with named arguments; these function arguments can have default values
- Functions arguments can be specified by name or by position in the argument list
- Functions always return the last expression evaluated in the function body
- A variable number of arguments can be specified using the special `...` argument in a function definition.

Scoping Rules of R

A Diversion on Binding Values to Symbol

[Watch a video of this section⁵⁹](#)

How does R know which value to assign to which symbol? When I type

```
> lm <- function(x) { x * x }
> lm
function(x) { x * x }
```

how does R know what value to assign to the symbol `lm`? Why doesn't it give it the value of `lm` that is in the `stats` package?

When R tries to bind a value to a symbol, it searches through a series of environments to find the appropriate value. When you are working on the command line and need to retrieve the value of an R object, the order in which things occur is roughly

1. Search the global environment (i.e. your workspace) for a symbol name matching the one requested.
2. Search the namespaces of each of the packages on the search list

The search list can be found by using the `search()` function.

```
> search()
[1] ".GlobalEnv"          "package:knitr"      "package:stats"
[4] "package:graphics"    "package:grDevices" "package:utils"
[7] "package:datasets"     "Autoloads"        "package:base"
```

The *global environment* or the user's workspace is always the first element of the search list and the `base` package is always the last. For better or for worse, the order of the packages on the search list matters, particularly if there are multiple objects with the same name in different packages.

Users can configure which packages get loaded on startup so if you are writing a function (or a package), you cannot assume that there will be a set list of packages available in a given order. When a user loads a package with `library()` the namespace of that package gets put in position 2 of the search list (by default) and everything else gets shifted down the list.

Note that R has separate namespaces for functions and non-functions so it's possible to have an object named `c` and a function named `c()`.

⁵⁹<https://youtu.be/ujdm01Vsrmo>

Scoping Rules

The scoping rules for R are the main feature that make it different from the original S language (in case you care about that). This may seem like an esoteric aspect of R, but it's one of its more interesting and useful features.

The scoping rules of a language determine how a value is associated with a *free variable* in a function. R uses *lexical scoping*⁶⁰ or *static scoping*. An alternative to lexical scoping is *dynamic scoping* which is implemented by some languages. Lexical scoping turns out to be particularly useful for simplifying statistical computations

Related to the scoping rules is how R uses the *search list* to bind a value to a symbol

Consider the following function.

```
> f <- function(x, y) {
+     x^2 + y / z
+ }
```

This function has 2 formal arguments x and y. In the body of the function there is another symbol z. In this case z is called a *free variable*.

The scoping rules of a language determine how values are assigned to free variables. Free variables are not formal arguments and are not local variables (assigned inside the function body).

Lexical scoping in R means that

the values of free variables are searched for in the environment in which the function was defined.

Okay then, what is an environment?

An *environment* is a collection of (symbol, value) pairs, i.e. x is a symbol and 3.14 might be its value. Every environment has a parent environment and it is possible for an environment to have multiple “children”. The only environment without a parent is the *empty environment*.

A function, together with an environment, makes up what is called a *closure* or *function closure*. Most of the time we don't need to think too much about a function and its associated environment (making up the closure), but occasionally, this setup can be very useful. The function closure model can be used to create functions that “carry around” data with them.

How do we associate a value to a free variable? There is a search process that occurs that goes as follows:

⁶⁰[http://en.wikipedia.org/wiki/Scope_\(computer_science\)#Lexical_scope_vs._dynamic_scope](http://en.wikipedia.org/wiki/Scope_(computer_science)#Lexical_scope_vs._dynamic_scope)

- If the value of a symbol is not found in the environment in which a function was defined, then the search is continued in the *parent environment*.
- The search continues down the sequence of parent environments until we hit the *top-level environment*; this usually the global environment (workspace) or the namespace of a package.
- After the top-level environment, the search continues down the search list until we hit the *empty environment*.

If a value for a given symbol cannot be found once the empty environment is arrived at, then an error is thrown.

One implication of this search process is that it can be affected by the number of packages you have attached to the search list. The more packages you have attached, the more symbols R has to sort through in order to assign a value. That said, you'd have to have a pretty large number of packages attached in order to notice a real difference in performance.

Lexical Scoping: Why Does It Matter?

[Watch a video of this section⁶¹](#)

Typically, a function is defined in the global environment, so that the values of free variables are just found in the user's workspace. This behavior is logical for most people and is usually the "right thing" to do. However, in R you can have functions defined *inside other functions* (languages like C don't let you do this). Now things get interesting—in this case the environment in which a function is defined is the body of another function!

Here is an example of a function that returns another function as its return value. Remember, in R functions are treated like any other object and so this is perfectly valid.

```
> make.power <- function(n) {
+   pow <- function(x) {
+     x^n
+   }
+   pow
+ }
```

The `make.power()` function is a kind of "constructor function" that can be used to construct other functions.

⁶¹<https://youtu.be/yYzPhtF6--A>

```
> cube <- make.power(3)
> square <- make.power(2)
> cube(3)
[1] 27
> square(3)
[1] 9
```

Let's take a look at the `cube()` function's code.

```
> cube
function(x) {
  x^n
}
<environment: 0x7fb01c174350>
```

Notice that `cube()` has a free variable `n`. What is the value of `n` here? Well, its value is taken from the environment where the function was defined. When I defined the `cube()` function it was when I called `make.power(3)`, so the value of `n` at that time was 3.

We can explore the environment of a function to see what objects are there and their values.

```
> ls(environment(cube))
[1] "n"    "pow"
> get("n", environment(cube))
[1] 3
```

We can also take a look at the `square()` function.

```
> ls(environment(square))
[1] "n"    "pow"
> get("n", environment(square))
[1] 2
```

Lexical vs. Dynamic Scoping

We can use the following example to demonstrate the difference between lexical and dynamic scoping rules.

```
> y <- 10
>
> f <- function(x) {
+     y <- 2
+     y^2 + g(x)
+ }
>
> g <- function(x) {
+     x*y
+ }
```

What is the value of the following expression?

`f(3)`

With **lexical scoping** the value of `y` in the function `g` is looked up in the environment in which the function was defined, in this case the global environment, so the value of `y` is 10. With **dynamic scoping**, the value of `y` is looked up in the environment from which the function was *called* (sometimes referred to as the *calling environment*). In R the calling environment is known as the *parent frame*. In this case, the value of `y` would be 2.

When a function is *defined* in the global environment and is subsequently *called* from the global environment, then the defining environment and the calling environment are the same. This can sometimes give the appearance of dynamic scoping.

Consider this example.

```
> g <- function(x) {
+     a <- 3
+     x+a+y
+     ## 'y' is a free variable
+ }
> g(2)
Error in g(2): object 'y' not found
> y <- 3
> g(2)
[1] 8
```

Here, `y` is defined in the global environment, which also happens to be where the function `g()` is defined.

There are numerous other languages that support lexical scoping, including

- Scheme

- Perl
- Python
- Common Lisp (all languages converge to Lisp, right?)

Lexical scoping in R has consequences beyond how free variables are looked up. In particular, it's the reason that all objects must be stored in memory in R. This is because all functions must carry a pointer to their respective defining environments, which could be *anywhere*. In the S language (R's close cousin), free variables are always looked up in the global workspace, so everything can be stored on the disk because the "defining environment" of all functions is the same.

Application: Optimization

[Watch a video of this section⁶²](#)

NOTE: This section requires some knowledge of statistical inference and modeling. If you do not have such knowledge, feel free to skip this section.

Why is any of this information about lexical scoping useful?

Optimization routines in R like `optim()`, `nlm()`, and `optimize()` require you to pass a function whose argument is a vector of parameters (e.g. a log-likelihood, or a cost function). However, an objective function that needs to be minimized might depend on a host of other things besides its parameters (like data). When writing software which does optimization, it may also be desirable to allow the user to hold certain parameters fixed. The scoping rules of R allow you to abstract away much of the complexity involved in these kinds of problems.

Here is an example of a "constructor" function that creates a negative log-likelihood function that can be minimized to find maximum likelihood estimates in a statistical model.

```
> make.NegLogLik <- function(data, fixed = c(FALSE, FALSE)) {
+     params <- fixed
+     function(p) {
+         params[!fixed] <- p
+         mu <- params[1]
+         sigma <- params[2]
+
+         ## Calculate the Normal density
+         a <- -0.5*length(data)*log(2*pi*sigma^2)
+         b <- -0.5*sum((data-mu)^2) / (sigma^2)
+         -(a + b)
+     }
+ }
```

⁶²<https://youtu.be/GCNZrffYLFi>

Note: Optimization functions in R *minimize* functions, so you need to use the negative log-likelihood.

Now we can generate some data and then construct our negative log-likelihood.

```
> set.seed(1)
> normals <- rnorm(100, 1, 2)
> nLL <- make.NegLogLik(normals)
> nLL
function(p) {
  params[!fixed] <- p
  mu <- params[1]
  sigma <- params[2]

  ## Calculate the Normal density
  a <- -0.5*length(data)*log(2*pi*sigma^2)
  b <- -0.5*sum((data-mu)^2) / (sigma^2)
  -(a + b)
}
<environment: 0x7fb01c5aa0e0>
>
> ## What's in the function environment?
> ls(environment(nLL))
[1] "data"   "fixed"  "params"
```

Now that we have our `nLL()` function, we can try to minimize it with `optim()` to estimate the parameters.

```
> optim(c(mu = 0, sigma = 1), nLL)$par
      mu      sigma
1.218239 1.787343
```

You can see that the algorithm converged and obtained an estimate of `mu` and `sigma`.

We can also try to estimate one parameter while holding another parameter fixed. Here we fix `sigma` to be equal to 2.

```
> nLL <- make.NegLogLik(normals, c(FALSE, 2))
> optimize(nLL, c(-1, 3))$minimum
[1] 1.217775
```

Because we now have a one-dimensional problem, we can use the simpler `optimize()` function rather than `optim()`.

We can also try to estimate `sigma` while holding `mu` fixed at 1.

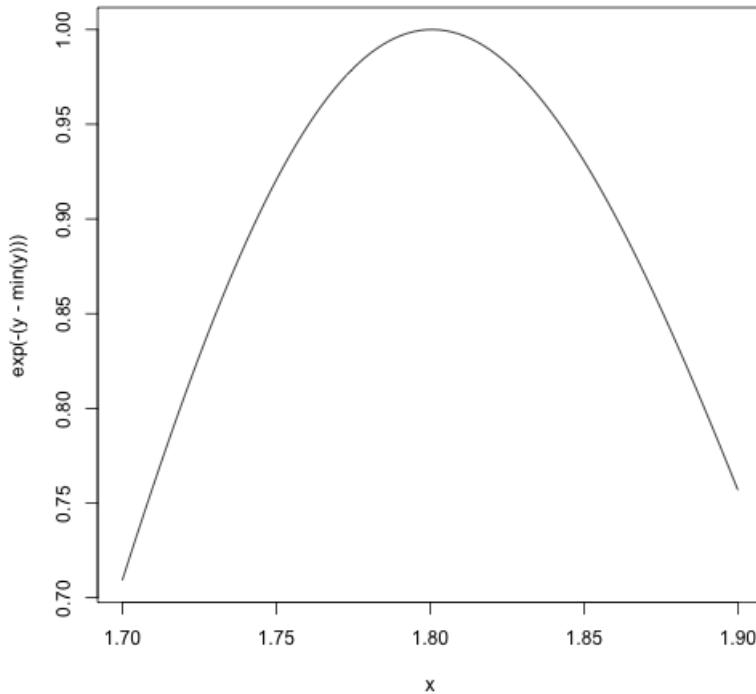
```
> nLL <- make.NegLogLik(normals, c(1, FALSE))
> optimize(nLL, c(1e-6, 10))$minimum
[1] 1.800596
```

Plotting the Likelihood

Another nice feature that you can take advantage of is plotting the negative log-likelihood to see how peaked or flat it is.

Here is the function when `mu` is fixed.

```
> ## Fix 'mu' to be equal to 1
> nLL <- make.NegLogLik(normals, c(1, FALSE))
> x <- seq(1.7, 1.9, len = 100)
>
> ## Evaluate 'nLL()' at every point in 'x'
> y <- sapply(x, nLL)
> plot(x, exp(-(y - min(y))), type = "l")
```



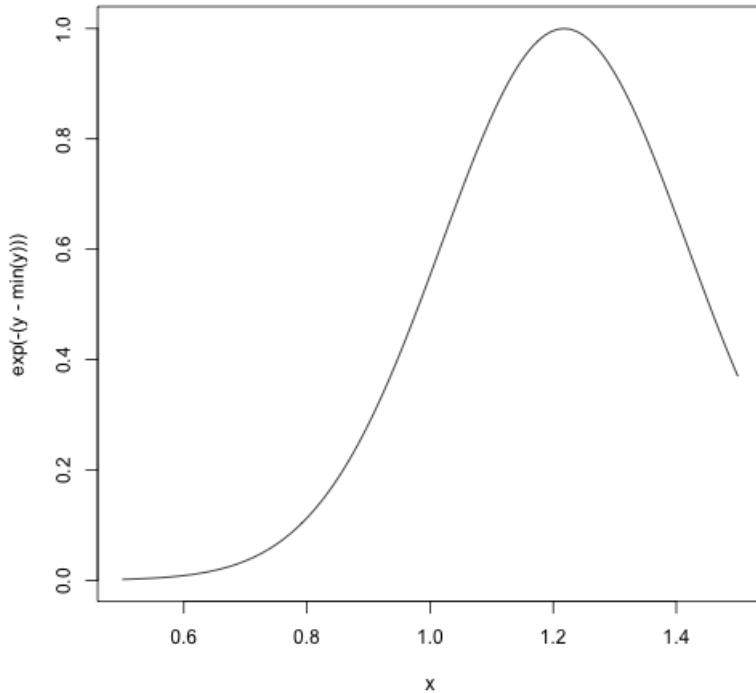
plot of chunk nLLFixMu

Here is the function when `sigma` is fixed.

```

> ## Fix 'sigma' to be equal to 2
> nLL <- make.NegLogLik(normals, c(FALSE, 2))
> x <- seq(0.5, 1.5, len = 100)
>
> ## Evaluate 'nLL()' at every point in 'x'
> y <- sapply(x, nLL)
> plot(x, exp(-(y - min(y))), type = "l")

```



plot of chunk nLLFixSigma

Summary

- Objective functions can be “built which contain all of the necessary data for evaluating the function
- No need to carry around long argument lists — useful for interactive and exploratory work.
- Code can be simplified and cleaned up
- Reference: Robert Gentleman and Ross Ihaka (2000). “Lexical Scope and Statistical Computing,” *JCGS*, 9, 491–508.

Coding Standards for R

[Watch a video of this chapter⁶³](#)

Coding standards are by no means universal and are often the subject of irrational flame wars on various language- or project-specific mailing lists. Nevertheless, I will just give you the standards that I use and the rationale behind them.

Always use text files / text editor. I think we can all agree on this one. Using text files and a text editor is fundamental to coding. If you're writing your code in an editor like Microsoft Word, you need to stop. Interactive development environments like RStudio have nice text editors built in, but there are many others out there.

Indent your code. Indenting is very important for the readability of your code. Some programming languages actually require it as part of their syntax, but R does not. Nevertheless, indenting is very important. How much you should indent is up for debate, but I think each indent should be a minimum of 4 spaces, and ideally **it should be 8 spaces**.

Limit the width of your code. I like to limit the width of my text editor so that the code I write doesn't fly off into the wilderness on the right hand side. This limitation, along with the 8 space indentation, forces you to write code that is clean, readable, and naturally broken down into modular units. In particular, this combination limits your ability to write very long functions with many different levels of nesting.

Limit the length of individual functions. If you are writing functions, it's usually a good idea to not let your functions run for pages and pages. Typically, purpose of a function is to execute one activity or idea. If your function is doing lots of things, it probably needs to be broken into multiple functions. My rule of thumb is that a function should not take up more than one page of your editor (of course, this depends on the size of your monitor).

⁶³<http://youtu.be/MSPKE1y3cyQ>

Loop Functions

Looping on the Command Line

Writing `for` and `while` loops is useful when programming but not particularly easy when working interactively on the command line. Multi-line expressions with curly braces are just not that easy to sort through when working on the command line. R has some functions which implement looping in a compact form to make your life easier.

- `lapply()`: Loop over a list and evaluate a function on each element
- `sapply()`: Same as `lapply` but try to simplify the result
- `apply()`: Apply a function over the margins of an array
- `tapply()`: Apply a function over subsets of a vector
- `mapply()`: Multivariate version of `lapply`

An auxiliary function `split` is also useful, particularly in conjunction with `lapply`.

`lapply()`

[Watch a video of this section⁶⁴](#)

The `lapply()` function does the following simple series of operations:

1. it loops over a list, iterating over each element in that list
2. it applies a *function* to each element of the list (a function that you specify)
3. and returns a list (the 1 is for “list”).

This function takes three arguments: (1) a list `x`; (2) a function (or the name of a function) `FUN`; (3) other arguments via its `...` argument. If `X` is not a list, it will be coerced to a list using `as.list()`.

The body of the `lapply()` function can be seen here.

⁶⁴https://youtu.be/E1_NlFb0E4g

```
> lapply
function (X, FUN, ...)
{
  FUN <- match.fun(FUN)
  if (!is.vector(X) || is.object(X))
    X <- as.list(X)
  .Internal(lapply(X, FUN))
}
<bytecode: 0x7fcc8388f758>
<environment: namespace:base>
```

Note that the actual looping is done internally in C code for efficiency reasons.

It's important to remember that `lapply()` always returns a list, regardless of the class of the input.

Here's an example of applying the `mean()` function to all elements of a list. If the original list has names, the the names will be preserved in the output.

```
> x <- list(a = 1:5, b = rnorm(10))
> lapply(x, mean)
$a
[1] 3

$b
[1] 0.1322028
```

Notice that here we are passing the `mean()` function as an argument to the `lapply()` function. Functions in R can be used this way and can be passed back and forth as arguments just like any other object. When you pass a function to another function, you do not need to include the open and closed parentheses () like you do when you are *calling* a function.

Here is another example of using `lapply()`.

```
> x <- list(a = 1:4, b = rnorm(10), c = rnorm(20, 1), d = rnorm(100, 5))
> lapply(x, mean)
$a
[1] 2.5

$b
[1] 0.248845

$c
[1] 0.9935285
```

```
$d  
[1] 5.051388
```

You can use `lapply()` to evaluate a function multiple times each with a different argument. Below, is an example where I call the `runif()` function (to generate uniformly distributed random variables) four times, each time generating a different number of random numbers.

```
> x <- 1:4  
> lapply(x, runif)  
[[1]]  
[1] 0.02778712  
  
[[2]]  
[1] 0.5273108 0.8803191  
  
[[3]]  
[1] 0.37306337 0.04795913 0.13862825  
  
[[4]]  
[1] 0.3214921 0.1548316 0.1322282 0.2213059
```

When you pass a function to `lapply()`, `lapply()` takes elements of the list and passes them as the *first argument* of the function you are applying. In the above example, the first argument of `runif()` is `n`, and so the elements of the sequence `1:4` all got passed to the `n` argument of `runif()`.

Functions that you pass to `lapply()` may have other arguments. For example, the `runif()` function has a `min` and `max` argument too. In the example above I used the default values for `min` and `max`. How would you be able to specify different values for that in the context of `lapply()`?

Here is where the `...` argument to `lapply()` comes into play. Any arguments that you place in the `...` argument will get passed down to the function being applied to the elements of the list.

Here, the `min = 0` and `max = 10` arguments are passed down to `runif()` every time it gets called.

```
> x <- 1:4
> lapply(x, runif, min = 0, max = 10)
[[1]]
[1] 2.263808

[[2]]
[1] 1.314165 9.815635

[[3]]
[1] 3.270137 5.069395 6.814425

[[4]]
[1] 0.9916910 1.1890256 0.5043966 9.2925392
```

So now, instead of the random numbers being between 0 and 1 (the default), they are all between 0 and 10.

The `lapply()` function and its friends make heavy use of *anonymous* functions. Anonymous functions are like members of [Project Mayhem](#)⁶⁵—they have no names. These are functions generated “on the fly” as you are using `lapply()`. Once the call to `lapply()` is finished, the function disappears and does not appear in the workspace.

Here I am creating a list that contains two matrices.

```
> x <- list(a = matrix(1:4, 2, 2), b = matrix(1:6, 3, 2))
> x
$a
 [,1] [,2]
[1,]    1    3
[2,]    2    4

$b
 [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6
```

Suppose I wanted to extract the first column of each matrix in the list. I could write an anonymous function for extracting the first column of each matrix.

⁶⁵http://en.wikipedia.org/wiki/Fight_Club

```
> lapply(x, function(elt) { elt[,1] })
$a
[1] 1 2

$b
[1] 1 2 3
```

Notice that I put the `function()` definition right in the call to `lapply()`. This is perfectly legal and acceptable. You can put an arbitrarily complicated function definition inside `lapply()`, but if it's going to be more complicated, it's probably a better idea to define the function separately.

For example, I could have done the following.

```
> f <- function(elt) {
+     elt[, 1]
+ }
> lapply(x, f)
$a
[1] 1 2

$b
[1] 1 2 3
```

Now the function is no longer anonymous; its name is `f`. Whether you use an anonymous function or you define a function first depends on your context. If you think the function `f` is something you're going to need a lot in other parts of your code, you might want to define it separately. But if you're just going to use it for this call to `lapply()`, then it's probably simpler to use an anonymous function.

sapply()

The `sapply()` function behaves similarly to `lapply()`; the only real difference is in the return value. `sapply()` will try to **simplify** the result of `lapply()` if possible. Essentially, `sapply()` calls `lapply()` on its input and then applies the following algorithm:

- If the result is a list where every element is length 1, then a vector is returned
- If the result is a list where every element is a vector of the same length (> 1), a matrix is returned.
- If it can't figure things out, a list is returned

Here's the result of calling `lapply()`.

```
> x <- list(a = 1:4, b = rnorm(10), c = rnorm(20, 1), d = rnorm(100, 5))
> lapply(x, mean)
$a
[1] 2.5

$b
[1] -0.251483

$c
[1] 1.481246

$d
[1] 4.968715
```

Notice that `lapply()` returns a list (as usual), but that each element of the list has length 1. Here's the result of calling `sapply()` on the same list.

```
> sapply(x, mean)
      a          b          c          d
2.500000 -0.251483 1.481246 4.968715
```

Because the result of `lapply()` was a list where each element had length 1, `sapply()` collapsed the output into a numeric vector, which is often more useful than a list.

split()

[Watch a video of this section⁶⁶](#)

The `split()` function takes a vector or other objects and splits it into groups determined by a factor or list of factors.

The arguments to `split()` are

```
> str(split)
function (x, f, drop = FALSE, ...)
```

str(function) is a simple help in command line that
details the arguments needed

where

- `x` is a vector (or list) or data frame

⁶⁶<https://youtu.be/TjwE5b0fOcs>

- `f` is a factor (or coerced to one) or a list of factors
- `drop` indicates whether empty factors levels should be dropped

The combination of `split()` and a function like `lapply()` or `sapply()` is a common paradigm in R. The basic idea is that you can take a data structure, split it into subsets defined by another variable, and apply a function over those subsets. The results of applying the function over the subsets are then collated and returned as an object. This sequence of operations is sometimes referred to as “map-reduce” in other contexts.

Here we simulate some data and split it according to a factor variable. Note that we use the `gl()` function to “generate levels” in a factor variable.

```
> x <- c(rnorm(10), runif(10), rnorm(10, 1))
> f <- gl(3, 10)
> split(x, f)
$`1`
[1]  0.3981302 -0.4075286  1.3242586 -0.7012317 -0.5806143 -1.0010722
[7] -0.6681786  0.9451850  0.4337021  1.0051592
```

```
$`2`
[1]  0.34822440  0.94893818  0.64667919  0.03527777  0.59644846  0.41531800
[7]  0.07689704  0.52804888  0.96233331  0.70874005
```

```
$`3`
[1]  1.13444766  1.76559900  1.95513668  0.94943430  0.69418458
[6]  1.89367370 -0.04729815  2.97133739  0.61636789  2.65414530
```

A common idiom is `split` followed by an `lapply`.

```
> lapply(split(x, f), mean)
$`1`
[1] 0.07478098

$`2`
[1] 0.5266905

$`3`
[1] 1.458703
```

Splitting a Data Frame

```
> library(datasets)
> head(airquality)
  Ozone Solar.R Wind Temp Month Day
1    41     190  7.4   67      5    1
2    36     118  8.0   72      5    2
3    12     149 12.6   74      5    3
4    18     313 11.5   62      5    4
5    NA      NA 14.3   56      5    5
6    28      NA 14.9   66      5    6
```

We can split the `airquality` data frame by the `Month` variable so that we have separate sub-data frames for each month.

```
> s <- split(airquality, airquality$Month)
> str(s)
List of 5
$ 5:'data.frame':      31 obs. of  6 variables:
..$ Ozone  : int [1:31] 41 36 12 18 NA 28 23 19 8 NA ...
..$ Solar.R: int [1:31] 190 118 149 313 NA NA 299 99 19 194 ...
..$ Wind   : num [1:31] 7.4 8 12.6 11.5 14.3 14.9 8.6 13.8 20.1 8.6 ...
..$ Temp   : int [1:31] 67 72 74 62 56 66 65 59 61 69 ...
..$ Month  : int [1:31] 5 5 5 5 5 5 5 5 5 5 ...
..$ Day    : int [1:31] 1 2 3 4 5 6 7 8 9 10 ...
$ 6:'data.frame':      30 obs. of  6 variables:
..$ Ozone  : int [1:30] NA NA NA NA NA 29 NA 71 39 ...
..$ Solar.R: int [1:30] 286 287 242 186 220 264 127 273 291 323 ...
..$ Wind   : num [1:30] 8.6 9.7 16.1 9.2 8.6 14.3 9.7 6.9 13.8 11.5 ...
..$ Temp   : int [1:30] 78 74 67 84 85 79 82 87 90 87 ...
..$ Month  : int [1:30] 6 6 6 6 6 6 6 6 6 6 ...
..$ Day    : int [1:30] 1 2 3 4 5 6 7 8 9 10 ...
$ 7:'data.frame':      31 obs. of  6 variables:
..$ Ozone  : int [1:31] 135 49 32 NA 64 40 77 97 97 85 ...
..$ Solar.R: int [1:31] 269 248 236 101 175 314 276 267 272 175 ...
..$ Wind   : num [1:31] 4.1 9.2 9.2 10.9 4.6 10.9 5.1 6.3 5.7 7.4 ...
..$ Temp   : int [1:31] 84 85 81 84 83 83 88 92 92 89 ...
..$ Month  : int [1:31] 7 7 7 7 7 7 7 7 7 7 ...
..$ Day    : int [1:31] 1 2 3 4 5 6 7 8 9 10 ...
$ 8:'data.frame':      31 obs. of  6 variables:
..$ Ozone  : int [1:31] 39 9 16 78 35 66 122 89 110 NA ...
..$ Solar.R: int [1:31] 83 24 77 NA NA NA 255 229 207 222 ...
..$ Wind   : num [1:31] 6.9 13.8 7.4 6.9 7.4 4.6 4 10.3 8 8.6 ...
..$ Temp   : int [1:31] 81 81 82 86 85 87 89 90 90 92 ...
```

```
..$ Month : int [1:31] 8 8 8 8 8 8 8 8 8 ...
..$ Day   : int [1:31] 1 2 3 4 5 6 7 8 9 10 ...
$ 9: 'data.frame':      30 obs. of  6 variables:
..$ Ozone : int [1:30] 96 78 73 91 47 32 20 23 21 24 ...
..$ Solar.R: int [1:30] 167 197 183 189 95 92 252 220 230 259 ...
..$ Wind  : num [1:30] 6.9 5.1 2.8 4.6 7.4 15.5 10.9 10.3 10.9 9.7 ...
..$ Temp  : int [1:30] 91 92 93 93 87 84 80 78 75 73 ...
..$ Month : int [1:30] 9 9 9 9 9 9 9 9 9 9 ...
..$ Day   : int [1:30] 1 2 3 4 5 6 7 8 9 10 ...
```

Then we can take the column means for `Ozone`, `Solar.R`, and `Wind` for each sub-data frame.

```
> lapply(s, function(x) {
+   colMeans(x[, c("Ozone", "Solar.R", "Wind")])
+ })
$`5`
  Ozone  Solar.R      Wind
NA       NA 11.62258

$`6`
  Ozone  Solar.R      Wind
NA 190.16667 10.26667

$`7`
  Ozone  Solar.R      Wind
NA 216.483871 8.941935

$`8`
  Ozone  Solar.R      Wind
NA       NA 8.793548

$`9`
  Ozone  Solar.R      Wind
NA 167.4333 10.1800
```

Using `sapply()` might be better here for a more readable output.

```
> sapply(s, function(x) {
+     colMeans(x[, c("Ozone", "Solar.R", "Wind")])
+ })
      5       6       7       8       9
Ozone    NA    NA    NA    NA    NA
Solar.R   NA 190.16667 216.483871      NA 167.4333
Wind     11.62258 10.26667  8.941935 8.793548 10.1800
```

Unfortunately, there are NAs in the data so we cannot simply take the means of those variables. However, we can tell the `colMeans` function to remove the NAs before computing the mean.

```
> sapply(s, function(x) {
+     colMeans(x[, c("Ozone", "Solar.R", "Wind")],
+               na.rm = TRUE)
+ })
      5       6       7       8       9
Ozone  23.61538 29.44444 59.115385 59.961538 31.44828
Solar.R 181.29630 190.16667 216.483871 171.857143 167.43333
Wind    11.62258 10.26667  8.941935 8.793548 10.18000
```

Occasionally, we may want to split an R object according to levels defined in more than one variable. We can do this by creating an interaction of the variables with the `interaction()` function.

```
> x <- rnorm(10)
> f1 <- gl(2, 5)
> f2 <- gl(5, 2)
> f1
[1] 1 1 1 1 1 2 2 2 2 2
Levels: 1 2
> f2
[1] 1 1 2 2 3 3 4 4 5 5
Levels: 1 2 3 4 5
> ## Create interaction of two factors
> interaction(f1, f2)
[1] 1.1 1.1 1.2 1.2 1.3 2.3 2.4 2.4 2.5 2.5
Levels: 1.1 2.1 1.2 2.2 1.3 2.3 1.4 2.4 1.5 2.5
```

With multiple factors and many levels, creating an interaction can result in many levels that are empty.

```
> str(split(x, list(f1, f2)))
List of 10
$ 1.1: num [1:2] 1.512 0.083
$ 2.1: num(0)
$ 1.2: num [1:2] 0.567 -1.025
$ 2.2: num(0)
$ 1.3: num 0.323
$ 2.3: num 1.04
$ 1.4: num(0)
$ 2.4: num [1:2] 0.0991 -0.4541
$ 1.5: num(0)
$ 2.5: num [1:2] -0.6558 -0.0359
```

Notice that there are 4 categories with no data. But we can drop empty levels when we call the `split()` function.

```
> str(split(x, list(f1, f2), drop = TRUE))
List of 6
$ 1.1: num [1:2] 1.512 0.083
$ 1.2: num [1:2] 0.567 -1.025
$ 1.3: num 0.323
$ 2.3: num 1.04
$ 2.4: num [1:2] 0.0991 -0.4541
$ 2.5: num [1:2] -0.6558 -0.0359
```

tapply

[Watch a video of this section⁶⁷](#)

`tapply()` is used to apply a function over subsets of a vector. It can be thought of as a combination of `split()` and `sapply()` for vectors only. I've been told that the "t" in `tapply()` refers to "table", but that is unconfirmed.

```
> str(tapply)
function (X, INDEX, FUN = NULL, ..., simplify = TRUE)
```

The arguments to `tapply()` are as follows:

- X is a vector

⁶⁷<https://youtu.be/6YEPWjbk3GA>

- INDEX is a factor or a list of factors (or else they are coerced to factors)
- FUN is a function to be applied
- ... contains other arguments to be passed FUN
- simplify, should we simplify the result?

Given a vector of numbers, one simple operation is to take group means.

```
> ## Simulate some data
> x <- c(rnorm(10), runif(10), rnorm(10, 1))
> ## Define some groups with a factor variable
> f <- gl(3, 10)
> f
[1] 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3
Levels: 1 2 3
> tapply(x, f, mean)
      1          2          3
0.1896235 0.5336667 0.9568236
```

We can also take the group means without simplifying the result, which will give us a list. For functions that return a single value, usually, this is not what we want, but it can be done.

```
> tapply(x, f, mean, simplify = FALSE)
$`1`
[1] 0.1896235

$`2`
[1] 0.5336667

$`3`
[1] 0.9568236
```

We can also apply functions that return more than a single value. In this case, `tapply()` will not simplify the result and will return a list. Here's an example of finding the range of each sub-group.

```
> tapply(x, f, range)
$`1`
[1] -1.869789  1.497041

$`2`
[1] 0.09515213 0.86723879

$`3`
[1] -0.5690822  2.3644349
```

apply()

[Watch a video of this section⁶⁸](#)

The `apply()` function is used to evaluate a function (often an anonymous one) over the margins of an array. It is most often used to apply a function to the rows or columns of a matrix (which is just a 2-dimensional array). However, it can be used with general arrays, for example, to take the average of an array of matrices. Using `apply()` is not really faster than writing a loop, but it works in one line and is highly compact.

```
> str(apply)
function (X, MARGIN, FUN, ...)
```

The arguments to `apply()` are

- `X` is an array
- `MARGIN` is an integer vector indicating which margins should be “retained”.
- `FUN` is a function to be applied
- `...` is for other arguments to be passed to `FUN`

Here I create a 20 by 10 matrix of Normal random numbers. I then compute the mean of each column.

```
> x <- matrix(rnorm(200), 20, 10)
> apply(x, 2, mean) ## Take the mean of each column
[1]  0.02218266 -0.15932850  0.09021391  0.14723035 -0.22431309
[6] -0.49657847  0.30095015  0.07703985 -0.20818099  0.06809774
```

I can also compute the sum of each row.

⁶⁸https://youtu.be/F54ixFPq_xQ

```
> apply(x, 1, sum)    ## Take the mean of each row
[1] -0.48483448  5.33222301 -3.33862932 -1.39998450  2.37859098
[6]  0.01082604 -6.29457190 -0.26287700  0.71133578 -3.38125293
[11] -4.67522818  3.01900232 -2.39466347 -2.16004389  5.33063755
[16] -2.92024635  3.52026401 -1.84880901 -4.10213912  5.30667310
```

Note that in both calls to `apply()`, the return value was a vector of numbers.

You've probably noticed that the second argument is either a 1 or a 2, depending on whether we want row statistics or column statistics. What exactly *is* the second argument to `apply()`?

The `MARGIN` argument essentially indicates to `apply()` which dimension of the array you want to preserve or retain. So when taking the mean of each column, I specify

```
> apply(x, 2, mean)
```

because I want to collapse the first dimension (the rows) by taking the mean and I want to preserve the number of columns. Similarly, when I want the row sums, I run

```
> apply(x, 1, sum)
```

because I want to collapse the columns (the second dimension) and preserve the number of rows (the first dimension).

Col/Row Sums and Means

For the special case of column/row sums and column/row means of matrices, we have some useful shortcuts.

- `rowSums = apply(x, 1, sum)`
- `rowMeans = apply(x, 1, mean)`
- `colSums = apply(x, 2, sum)`
- `colMeans = apply(x, 2, mean)`

The shortcut functions are heavily optimized and hence are *much* faster, but you probably won't notice unless you're using a large matrix. Another nice aspect of these functions is that they are a bit more descriptive. It's arguably more clear to write `colMeans(x)` in your code than `apply(x, 2, mean)`.

Other Ways to Apply

You can do more than take sums and means with the `apply()` function. For example, you can compute quantiles of the rows of a matrix using the `quantile()` function.

```
> x <- matrix(rnorm(200), 20, 10)
> ## Get row quantiles
> apply(x, 1, quantile, probs = c(0.25, 0.75))
      [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
25% -1.0884151 -0.6693040 0.2908481 -0.4602083 -1.0432010 -1.12773555
75%  0.1843547  0.8210295 1.3667301  0.4424153  0.3571219  0.03653687
      [,7]      [,8]      [,9]      [,10]     [,11]     [,12]
25% -1.4571706 -0.2406991 -0.3226845 -0.329898 -0.8677524 -0.2023664
75% -0.1705336  0.6504486 1.1460854  1.247092  0.4138139  0.9145331
      [,13]     [,14]     [,15]     [,16]     [,17]     [,18]
25% -0.9796050 -1.3551031 -0.1823252 -1.260911898 -0.9954289 -0.3767354
75%  0.5448777 -0.5396766  0.7795571  0.002908451  0.4323192  0.7542638
      [,19]     [,20]
25% -0.8557544 -0.7000363
75%  0.5440158  0.5432995
```

Notice that I had to pass the `probs = c(0.25, 0.75)` argument to `quantile()` via the `...` argument to `apply()`.

For a higher dimensional example, I can create an array of \$2\times 2\times 10\$ matrices and then compute the average of the matrices in the array.

```
> a <- array(rnorm(2 * 2 * 10), c(2, 2, 10))
> apply(a, c(1, 2), mean)
      [,1]      [,2]
[1,] 0.1681387 -0.1039673
[2,] 0.3519741 -0.4029737
```

In the call to `apply()` here, I indicated via the `MARGIN` argument that I wanted to preserve the first and second dimensions and to collapse the third dimension by taking the mean.

There is a faster way to do this specific operation via the `colMeans()` function.

```
> rowMeans(a, dims = 2)    ## Faster
      [,1]      [,2]
[1,] 0.1681387 -0.1039673
[2,] 0.3519741 -0.4029737
```

In this situation, I might argue that the use of `rowMeans()` is less readable, but it is substantially faster with large arrays.

mapply()

[Watch a video of this section⁶⁹](#)

The `mapply()` function is a multivariate apply of sorts which applies a function in parallel over a set of arguments. Recall that `lapply()` and friends only iterate over a single R object. What if you want to iterate over multiple R objects in parallel? This is what `mapply()` is for.

```
> str(mapply)
function (FUN, ..., MoreArgs = NULL, SIMPLIFY = TRUE, USE.NAMES = TRUE)
```

The arguments to `mapply()` are

- `FUN` is a function to apply
- `...` contains R objects to apply over
- `MoreArgs` is a list of other arguments to `FUN`.
- `SIMPLIFY` indicates whether the result should be simplified

The `mapply()` function has a different argument order from `lapply()` because the function to apply comes first rather than the object to iterate over. The R objects over which we apply the function are given in the `...` argument because we can apply over an arbitrary number of R objects.

For example, the following is tedious to type

```
list(rep(1, 4), rep(2, 3), rep(3, 2), rep(4, 1))
```

With `mapply()`, instead we can do

```
> mapply(rep, 1:4, 4:1)
[[1]]
[1] 1 1 1 1

[[2]]
[1] 2 2 2

[[3]]
[1] 3 3

[[4]]
[1] 4
```

This passes the sequence `1:4` to the first argument of `rep()` and the sequence `4:1` to the second argument.

Here's another example for simulating random Normal variables.

⁶⁹https://youtu.be/z8jC_h7S0VE

```

> noise <- function(n, mean, sd) {
+     rnorm(n, mean, sd)
+ }
> ## Simulate 5 random numbers
> noise(5, 1, 2)
[1] -0.5196913  3.2979182 -0.6849525  1.7828267  2.7827545
>
> ## This only simulates 1 set of numbers, not 5
> noise(1:5, 1:5, 2)
[1] -1.670517  2.796247  2.776826  5.351488  3.422804

```

Here we can use `mapply()` to pass the sequence `1:5` separately to the `noise()` function so that we can get 5 sets of random numbers, each with a different length and mean.

```

> mapply(noise, 1:5, 1:5, 2)
[[1]]
[1] 0.8260273

[[2]]
[1] 4.764568 2.336980

[[3]]
[1] 4.6463819 2.5582108 0.9412167

[[4]]
[1] 3.978149 1.550018 -1.192223 6.338245

[[5]]
[1] 2.826182 1.347834 6.990564 4.976276 3.800743

```

The above call to `mapply()` is the same as

```

> list(noise(1, 1, 2), noise(2, 2, 2),
+       noise(3, 3, 2), noise(4, 4, 2),
+       noise(5, 5, 2))
[[1]]
[1] 0.644104

[[2]]
[1] 1.148037 3.993318

[[3]]

```

```
[1] 4.4553214 -0.4532612 3.7067970
[[4]]
[1] 5.4536273 5.3365220 -0.8486346 3.5292851
[[5]]
[1] 8.959267 6.593589 1.581448 1.672663 5.982219
```

Vectorizing a Function

The `mapply()` function can be used to automatically “vectorize” a function. What this means is that it can be used to take a function that typically only takes single arguments and create a new function that can take vector arguments. This is often needed when you want to plot functions.

Here’s an example of a function that computes the sum of squares given some data, a mean parameter and a standard deviation. The formula is $\sum_{i=1}^n (x_i - \mu)^2 / \sigma^2$.

```
> sumsq <- function(mu, sigma, x) {
+   sum(((x - mu) / sigma)^2)
+ }
```

This function takes a mean `mu`, a standard deviation `sigma`, and some data in a vector `x`.

In many statistical applications, we want to minimize the sum of squares to find the optimal `mu` and `sigma`. Before we do that, we may want to evaluate or plot the function for many different values of `mu` or `sigma`. However, passing a vector of `mus` or `sigmas` won’t work with this function because it’s not vectorized.

```
> x <- rnorm(100)      ## Generate some data
> sumsq(1:10, 1:10, x) ## This is not what we want
[1] 110.2594
```

Note that the call to `sumsq()` only produced one value instead of 10 values.

However, we can do what we want to do by using `mapply()`.

```
> mapply(sumsq, 1:10, 1:10, MoreArgs = list(x = x))
[1] 196.2289 121.4765 108.3981 104.0788 102.1975 101.2393 100.6998
[8] 100.3745 100.1685 100.0332
```

There’s even a function in R called `Vectorize()` that automatically can create a vectorized version of your function. So we could create a `vsumsq()` function that is fully vectorized as follows.

```
> vsumsq <- Vectorize(sumsq, c("mu", "sigma"))
> vsumsq(1:10, 1:10, x)
[1] 196.2289 121.4765 108.3981 104.0788 102.1975 101.2393 100.6998
[8] 100.3745 100.1685 100.0332
```

Pretty cool, right?

Summary

- The loop functions in R are very powerful because they allow you to conduct a series of operations on data using a compact form
- The operation of a loop function involves iterating over an R object (e.g. a list or vector or matrix), applying a function to each element of the object, and collating the results and returning the collated results.
- Loop functions make heavy use of anonymous functions, which exist for the life of the loop function but are not stored anywhere
- The `split()` function can be used to divide an R object into subsets determined by another variable which can subsequently be looped over using loop functions.

Debugging

Something's Wrong!

Watch a video of this section⁷⁰ (note that this video differs slightly from the material presented here)

R has a number of ways to indicate to you that something's not right. There are different levels of indication that can be used, ranging from mere notification to fatal error. Executing any function in R may result in the following *conditions*.

- **message**: A generic notification/diagnostic message produced by the `message()` function; execution of the function continues
- **warning**: An indication that something is wrong but not necessarily fatal; execution of the function continues. Warnings are generated by the `warning()` function
- **error**: An indication that a fatal problem has occurred and execution of the function stops. Errors are produced by the `stop()` function.
- **condition**: A generic concept for indicating that something unexpected has occurred; programmers can create their own custom conditions if they want.

Here is an example of a warning that you might receive in the course of using R.

```
> log(-1)
Warning in log(-1): NaNs produced
[1] NaN
```

This warning lets you know that taking the log of a negative number results in a `NaN` value because you can't take the log of negative numbers. Nevertheless, R doesn't give an error, because it has a useful value that it can return, the `NaN` value. The warning is just there to let you know that something unexpected happen. Depending on what you are programming, you may have intentionally taken the log of a negative number in order to move on to another section of code.

Here is another function that is designed to print a message to the console depending on the nature of its input.

⁷⁰<https://youtu.be/LHQxbRInyycc>

```
> printmessage <- function(x) {  
+     if(x > 0)  
+         print("x is greater than zero")  
+     else  
+         print("x is less than or equal to zero")  
+     invisible(x)  
+ }
```

This function is simple—it prints a message telling you whether x is greater than zero or less than or equal to zero. It also returns its input *invisibly*, which is a common practice with “print” functions. Returning an object invisibly means that the return value does not get auto-printed when the function is called.

Take a hard look at the function above and see if you can identify any bugs or problems.

We can execute the function as follows.

```
> printmessage(1)  
[1] "x is greater than zero"
```

The function seems to work fine at this point. No errors, warnings, or messages.

```
> printmessage(NA)  
Error in if (x > 0) print("x is greater than zero") else print("x is less than o\  
r equal to zero"): missing value where TRUE/FALSE needed
```

What happened?

Well, the first thing the function does is test if $x > 0$. But you can’t do that test if x is a NA or NaN value. R doesn’t know what to do in this case so it stops with a fatal error.

We can fix this problem by anticipating the possibility of NA values and checking to see if the input is NA with the `is.na()` function.

```
> printmessage2 <- function(x) {  
+     if(is.na(x))  
+         print("x is a missing value!")  
+     else if(x > 0)  
+         print("x is greater than zero")  
+     else  
+         print("x is less than or equal to zero")  
+     invisible(x)  
+ }
```

Now we can run the following.

```
> printmessage2(NA)
[1] "x is a missing value!"
```

And all is fine.

Now what about the following situation.

```
> x <- log(c(-1, 2))
Warning in log(c(-1, 2)): NaNs produced
> printmessage2(x)
Warning in if (is.na(x)) print("x is a missing value!") else if (x > 0)
print("x is greater than zero") else print("x is less than or equal to
zero"): the condition has length > 1 and only the first element will be
used
[1] "x is a missing value!"
```

Now what?? Why are we getting this warning? The warning says “the condition has length > 1 and only the first element will be used”.

The problem here is that I passed `printmessage2()` a vector `x` that was of length 2 rather than length 1. Inside the body of `printmessage2()` the expression `is.na(x)` returns a vector that is tested in the `if` statement. However, `if` cannot take vector arguments so you get a warning. The fundamental problem here is that `printmessage2()` is not *vectorized*.

We can solve this problem two ways. One is by simply not allowing vector arguments. The other way is to vectorize the `printmessage2()` function to allow it to take vector arguments.

For the first way, we simply need to check the length of the input.

```
> printmessage3 <- function(x) {
+   if(length(x) > 1L)
+     stop("'x' has length > 1")
+   if(is.na(x))
+     print("x is a missing value!")
+   else if(x > 0)
+     print("x is greater than zero")
+   else
+     print("x is less than or equal to zero")
+   invisible(x)
+ }
```

Now when we pass `printmessage3()` a vector we should get an error.

```
> printmessage3(1:2)
Error in printmessage3(1:2): 'x' has length > 1
```

Vectorizing the function can be accomplished easily with the `Vectorize()` function.

```
> printmessage4 <- Vectorize(printmessage2)
> out <- printmessage4(c(-1, 2))
[1] "x is less than or equal to zero"
[1] "x is greater than zero"
```

You can see now that the correct messages are printed without any warning or error. Note that I stored the return value of `printmessage4()` in a separate R object called `out`. This is because when I use the `Vectorize()` function it no longer preserves the invisibility of the return value.

Figuring Out What's Wrong

The primary task of debugging any R code is correctly diagnosing what the problem is. When diagnosing a problem with your code (or somebody else's), it's important first understand what you were expecting to occur. Then you need to identify what *did* occur and how did it deviate from your expectations. Some basic questions you need to ask are

- What was your input? How did you call the function?
- What were you expecting? Output, messages, other results?
- What did you get?
- How does what you get differ from what you were expecting?
- Were your expectations correct in the first place?
- Can you reproduce the problem (exactly)?

Being able to answer these questions is important not just for your own sake, but in situations where you may need to ask someone else for help with debugging the problem. Seasoned programmers will be asking you these exact questions.

Debugging Tools in R

[Watch a video of this section⁷¹](#)

R provides a number of tools to help you with debugging your code. The primary tools for debugging functions in R are

⁷¹<https://youtu.be/h9rs6-Cwwto>

- `traceback()`: prints out the function call stack after an error occurs; does nothing if there's no error
- `debug()`: flags a function for "debug" mode which allows you to step through execution of a function one line at a time
- `browser()`: suspends the execution of a function wherever it is called and puts the function in debug mode
- `trace()`: allows you to insert debugging code into a function a specific places
- `recover()`: allows you to modify the error behavior so that you can browse the function call stack

These functions are interactive tools specifically designed to allow you to pick through a function. There's also the more blunt technique of inserting `print()` or `cat()` statements in the function.

Using `traceback()`

[Watch a video of this section⁷²](#)

The `traceback()` function prints out the *function call stack* after an error has occurred. The function call stack is the sequence of functions that was called before the error occurred.

For example, you may have a function `a()` which subsequently calls function `b()` which calls `c()` and then `d()`. If an error occurs, it may not be immediately clear in which function the error occurred. The `traceback()` function shows you how many levels deep you were when the error occurred.

```
> mean(x)
Error in mean(x) : object 'x' not found
> traceback()
1: mean(x)
```

Here, it's clear that the error occurred inside the `mean()` function because the object `x` does not exist.

The `traceback()` function must be called immediately after an error occurs. Once another function is called, you lose the traceback.

Here is a slightly more complicated example using the `lm()` function for linear modeling.

⁷²<https://youtu.be/VT9ZxCp6o-I>

```
> lm(y ~ x)
Error in eval(expr, envir, enclos) : object 'y' not found
> traceback()
7: eval(expr, envir, enclos)
6: eval(predvars, data, env)
5: model.frame.default(formula = y ~ x, drop.unused.levels = TRUE)
4: model.frame(formula = y ~ x, drop.unused.levels = TRUE)
3: eval(expr, envir, enclos)
2: eval(mf, parent.frame())
1: lm(y ~ x)
```

You can see now that the error did not get thrown until the 7th level of the function call stack, in which case the `eval()` function tried to evaluate the formula $y \sim x$ and realized the object `y` did not exist.

Looking at the traceback is useful for figuring out roughly where an error occurred but it's not useful for more detailed debugging. For that you might turn to the `debug()` function.

Using `debug()`

The `debug()` function initiates an interactive debugger (also known as the “browser” in R) for a function. With the debugger, you can step through an R function one expression at a time to pinpoint exactly where an error occurs.

The `debug()` function takes a function as its first argument. Here is an example of debugging the `lm()` function.

```
> debug(lm)      ## Flag the 'lm()' function for interactive debugging
> lm(y ~ x)
debugging in: lm(y ~ x)
debug: {
  ret.x <- x
  ret.y <- y
  cl <- match.call()
  ...
  if (!qr)
    z$qr <- NULL
  z
}
Browse[2]>
```

Now, every time you call the `lm()` function it will launch the interactive debugger. To turn this behavior off you need to call the `undebug()` function.

The debugger calls the browser at the very top level of the function body. From there you can step through each expression in the body. There are a few special commands you can call in the browser:

- n executes the current expression and moves to the next expression
- c continues execution of the function and does not stop until either an error or the function exits
- Q quits the browser

Here's an example of a browser session with the lm() function.

```
Browse[2]> n    ## Evaluate this expression and move to the next one
debug: ret.x <- x
Browse[2]> n
debug: ret.y <- y
Browse[2]> n
debug: cl <- match.call()
Browse[2]> n
debug: mf <- match.call(expand.dots = FALSE)
Browse[2]> n
debug: m <- match(c("formula", "data", "subset", "weights", "na.action",
"offset"), names(mf), 0L)
```

While you are in the browser you can execute any other R function that might be available to you in a regular session. In particular, you can use ls() to see what is in your current environment (the function environment) and print() to print out the values of R objects in the function environment.

You can turn off interactive debugging with the undbug() function.

```
undbug(lm)    ## Unflag the 'lm()' function for debugging
```

Using recover()

The recover() function can be used to modify the error behavior of R when an error occurs. Normally, when an error occurs in a function, R will print out an error message, exit out of the function, and return you to your workspace to await further commands.

With recover() you can tell R that when an error occurs, it should halt execution at the exact point at which the error occurred. That can give you the opportunity to poke around in the environment in which the error occurred. This can be useful to see if there are any R objects or data that have been corrupted or mistakenly modified.

```
> options(error = recover)      ## Change default R error behavior
> read.csv("nosuchfile")       ## This code doesn't work
Error in file(file, "rt") : cannot open the connection
In addition: Warning message:
In file(file, "rt") :
  cannot open file 'nosuchfile': No such file or directory
```

Enter a frame number, or 0 to exit

```
1: read.csv("nosuchfile")
2: read.table(file = file, header = header, sep = sep, quote = quote, dec =
3: file(file, "rt")
```

Selection:

The `recover()` function will first print out the function call stack when an error occurs. Then, you can choose to jump around the call stack and investigate the problem. When you choose a frame number, you will be put in the browser (just like the interactive debugger triggered with `debug()`) and will have the ability to poke around.

Summary

- There are three main indications of a problem/condition: `message`, `warning`, `error`; only an `error` is fatal
- When analyzing a function with a problem, make sure you can reproduce the problem, clearly state your expectations and how the output differs from your expectation
- Interactive debugging tools `traceback`, `debug`, `browser`, `trace`, and `recover` can be used to find problematic code in functions
- Debugging tools are not a substitute for thinking!

Profiling R Code

Let's solve the problem but let's not make it worse by guessing. —*Gene Kranz, Apollo 13 Lead Flight Director*

[Watch a video of this section⁷³](#)

R comes with a profiler to help you optimize your code and improve its performance. In general, it's usually a bad idea to focus on optimizing your code at the very beginning of development. Rather, in the beginning it's better to focus on translating your ideas into code and writing code that's coherent and readable. The problem is that heavily optimized code tends to be obscure and difficult to read, making it harder to debug and revise. Better to get all the bugs out first, then focus on optimizing.

Of course, when it comes to optimizing code, the question is what should you optimize? Well, clearly should optimize the parts of your code that are running slowly, but how do we know what parts those are?

This is what the profiler is for. Profiling is a systematic way to examine how much time is spent in different parts of a program.

Sometimes profiling becomes necessary as a project grows and layers of code are placed on top of each other. Often you might write some code that runs fine once. But then later, you might put that same code in a big loop that runs 1,000 times. Now the original code that took 1 second to run is taking 1,000 seconds to run! Getting that little piece of original code to run faster will help the entire loop.

It's tempting to think you just *know* where the bottlenecks in your code are. I mean, after all, you write it! But trust me, I can't tell you how many times I've been surprised at where exactly my code is spending all its time. The reality is that *profiling is better than guessing*. Better to collect some data than to go on hunches alone. Ultimately, getting the biggest impact on speeding up code depends on knowing where the code spends most of its time. This cannot be done without some sort of rigorous performance analysis or profiling.

We should forget about small efficiencies, say about 97% of the time: premature optimization is the root of all evil —*Donald Knuth*

The basic principles of optimizing your code are:

- Design first, then optimize
- Remember: Premature optimization is the root of all evil
- Measure (collect data), don't guess.
- If you're going to be scientist, you need to apply the same principles here!

⁷³<https://youtu.be/pHFgb12uG5s>

Using `system.time()`

The `system.time()` function takes an arbitrary R expression as input (can be wrapped in curly braces) and returns the amount of time taken to evaluate the expression. The `system.time()` function computes the time (in seconds) needed to execute an expression and if there's an error, gives the time until the error occurred. The function returns an object of class `proc_time` which contains two useful bits of information:

- *user time*: time charged to the CPU(s) for this expression
- *elapsed time*: “wall clock” time, the amount of time that passes for *you* as you’re sitting there

Usually, the user time and elapsed time are relatively close, for straight computing tasks. But there are a few situations where the two can diverge, sometimes dramatically. The elapsed time may be *greater than* the user time if the CPU spends a lot of time waiting around. This commonly happens if your R expression invokes some input or output, which depends on the activity of the file system and the disk (or the Internet, if using a network connection).

The elapsed time may be *smaller than* the user time if your machine has multiple cores/processors (and is capable of using them). For example, multi-threaded BLAS libraries (vecLib/Accelerate, ATLAS, ACML, MKL) can greatly speed up linear algebra calculations and are commonly installed on even desktop systems these days. Also, parallel processing done via something like the `parallel` package can make the elapsed time smaller than the user time. When you have multiple processors/cores/machines working in parallel, the amount of time that the collection of CPUs spends working on a problem is the same as with a single CPU, but because they are operating in parallel, there is a savings in elapsed time.

Here's an example of where the elapsed time is greater than the user time.

```
## Elapsed time > user time
system.time(readLines("http://www.jhsph.edu"))
  user  system elapsed
 0.004   0.002   0.431
```

Most of the time in this expression is spent waiting for the connection to the web server and waiting for the data to travel back to my computer. This doesn't involve the CPU and so the CPU simply waits around for things to get done. Hence, the user time is small.

In this example, the elapsed time is smaller than the user time.

```
## Elapsed time < user time
> hilbert <- function(n) {
+   i <- 1:n
+   1 / outer(i - 1, i, "+")
+ }
> x <- hilbert(1000)
> system.time(svd(x))
  user  system elapsed
 1.035   0.255   0.462
```

In this case I ran a singular value decomposition on the matrix in `x`, which is a common linear algebra procedure. Because my computer is able to split the work across multiple processors, the elapsed time is about half the user time.

Timing Longer Expressions

You can time longer expressions by wrapping them in curly braces within the call to `system.time()`.

```
> system.time({
+   n <- 1000
+   r <- numeric(n)
+   for(i in 1:n) {
+     x <- rnorm(n)
+     r[i] <- mean(x)
+   }
+ })
  user  system elapsed
 0.088   0.001   0.091
```

If your expression is getting pretty long (more than 2 or 3 lines), it might be better to either break it into smaller pieces or to use the profiler. The problem is that if the expression is too long, you won't be able to identify which part of the code is causing the bottleneck.

The R Profiler

[Watch a video of this section⁷⁴](#)

Using `system.time()` allows you to test certain functions or code blocks to see if they are taking excessive amounts of time. However, this approach assumes that you already know where the

⁷⁴<https://youtu.be/BZVcMPtJ4A>

problem is and can call `system.time()` on it that piece of code. What if you don't know where to start?

This is where the profiler comes in handy. The `Rprof()` function starts the profiler in R. Note that R must be compiled with profiler support (but this is usually the case). In conjunction with `Rprof()`, we will use the `summaryRprof()` function which summarizes the output from `Rprof()` (otherwise it's not really readable). Note that you should NOT use `system.time()` and `Rprof()` together, or you will be sad.

`Rprof()` keeps track of the function call stack at regularly sampled intervals and tabulates how much time is spent inside each function. By default, the profiler samples the function call stack every 0.02 seconds. This means that if your code runs very quickly (say, under 0.02 seconds), the profiler is not useful. But if your code runs that fast, you probably don't need the profiler.

The profiler is started by calling the `Rprof()` function.

```
> Rprof()    ## Turn on the profiler
```

You don't need any other arguments. By default it will write its output to a file called `Rprof.out`. You can specify the name of the output file if you don't want to use this default.

Once you call the `Rprof()` function, everything that you do from then on will be measured by the profiler. Therefore, you usually only want to run a single R function or expression once you turn on the profiler and then immediately turn it off. The reason is that if you mix too many function calls together when running the profiler, all of the results will be mixed together and you won't be able to sort out where the bottlenecks are. In reality, I usually only run a single function with the profiler on.

The profiler can be turned off by passing `NULL` to `Rprof()`.

```
> Rprof(NULL)    ## Turn off the profiler
```

The raw output from the profiler looks something like this. Here I'm calling the `lm()` function on some data with the profiler running.

```
## lm(y ~ x)

sample.interval=10000
"list" "eval" "eval" "model.frame.default" "model.frame" "eval" "eval" "lm"
"na.omit" "model.frame.default" "model.frame" "eval" "eval" "lm"
"na.omit" "model.frame.default" "model.frame" "eval" "eval" "lm"
```

```
"na.omit" "model.frame.default" "model.frame" "eval" "eval" "lm"
"lm.fit" "lm"
"lm.fit" "lm"
"lm.fit" "lm"
```

At each line of the output, the profiler writes out the function call stack. For example, on the very first line of the output you can see that the code is 8 levels deep in the call stack. This is where you need the `summaryRprof()` function to help you interpret this data.

Using `summaryRprof()`

The `summaryRprof()` function tabulates the R profiler output and calculates how much time is spent in which function. There are two methods for normalizing the data.

- “by.total” divides the time spend in each function by the total run time
- “by.self” does the same as “by.total” but first subtracts out time spent in functions above the current function in the call stack. I personally find this output to be much more useful.

Here is what `summaryRprof()` reports in the “by.total” output.

	total.time	total.pct	self.time	self.pct
“lm”	7.41	100.00	0.30	4.05
“lm.fit”	3.50	47.23	2.99	40.35
“model.frame.default”	2.24	30.23	0.12	1.62
“eval”	2.24	30.23	0.00	0.00
“model.frame”	2.24	30.23	0.00	0.00
“na.omit”	1.54	20.78	0.24	3.24
“na.omit.data.frame”	1.30	17.54	0.49	6.61
“lapply”	1.04	14.04	0.00	0.00
“[.data.frame”	1.03	13.90	0.79	10.66
“[”	1.03	13.90	0.00	0.00
“as.list.data.frame”	0.82	11.07	0.82	11.07
“as.list”	0.82	11.07	0.00	0.00

Because `lm()` is the function that I called from the command line, of course 100% of the time is spent somewhere in that function. However, what this doesn't show is that if `lm()` immediately calls another function (like `lm.fit()`, which does most of the heavy lifting), then in reality, most of the time is spent in *that* function, rather than in the top-level `lm()` function.

The “`by.self`” output corrects for this discrepancy.

```
$by.self
      self.time self.pct total.time total.pct
"lm.fit"        2.99   40.35     3.50    47.23
"as.list.data.frame" 0.82   11.07     0.82   11.07
"[ .data.frame" 0.79   10.66     1.03   13.90
"structure"     0.73    9.85     0.73    9.85
"na.omit.data.frame" 0.49    6.61     1.30   17.54
"list"          0.46    6.21     0.46    6.21
"lm"            0.30    4.05     7.41  100.00
"model.matrix.default" 0.27    3.64     0.79   10.66
"na.omit"       0.24    3.24     1.54   20.78
"as.character" 0.18    2.43     0.18    2.43
"model.frame.default" 0.12    1.62     2.24   30.23
"anyDuplicated.default" 0.02    0.27     0.02    0.27
```

Now you can see that only about 4% of the runtime is spent in the actual `lm()` function, whereas over 40% of the time is spent in `lm.fit()`. In this case, this is no surprise since the `lm.fit()` function is the function that actually fits the linear model.

You can see that a reasonable amount of time is spent in functions not necessarily associated with linear modeling (i.e. `as.list.data.frame`, `[.data.frame`). This is because the `lm()` function does a bit of pre-processing and checking before it actually fits the model. This is common with modeling functions—the preprocessing and checking is useful to see if there are any errors. But those two functions take up over 1.5 seconds of runtime. What if you want to fit this model 10,000 times? You’re going to be spending a lot of time in preprocessing and checking.

The final bit of output that `summaryRprof()` provides is the sampling interval and the total runtime.

```
$sample.interval
[1] 0.02
```

```
$sampling.time
[1] 7.41
```

Summary

- `Rprof()` runs the profiler for performance analysis of R code

- `summaryRprof()` summarizes the output of `Rprof()` and gives percent of time spent in each function (with two types of normalization)
- Good to break your code into functions so that the profiler can give useful information about where time is being spent
- C or Fortran code is not profiled

Simulation

Generating Random Numbers

Watch a video of this section⁷⁵

Simulation is an important (and big) topic for both statistics and for a variety of other areas where there is a need to introduce randomness. Sometimes you want to implement a statistical procedure that requires random number generation or sampling (i.e. Markov chain Monte Carlo, the bootstrap, random forests, bagging) and sometimes you want to simulate a system and random number generators can be used to model random inputs.

R comes with a set of pseudo-random number generators that allow you to simulate from well-known probability distributions like the Normal, Poisson, and binomial. Some example functions for probability distributions in R

- `rnorm`: generate random Normal variates with a given mean and standard deviation
- `dnorm`: evaluate the Normal probability density (with a given mean/SD) at a point (or vector of points)
- `pnorm`: evaluate the cumulative distribution function for a Normal distribution
- `rpois`: generate random Poisson variates with a given rate

For each probability distribution there are typically four functions available that start with a “r”, “d”, “p”, and “q”. The “r” function is the one that actually simulates random numbers from that distribution. The other functions are prefixed with a

- d for density
- r for random number generation
- p for cumulative distribution
- q for quantile function (inverse cumulative distribution)

If you’re only interested in simulating random numbers, then you will likely only need the “r” functions and not the others. However, if you intend to simulate from arbitrary probability distributions using something like rejection sampling, then you will need the other functions too.

Probably the most common probability distribution to work with is the Normal distribution (also known as the Gaussian). Working with the Normal distributions requires using these four functions

⁷⁵<https://youtu.be/tzz4flrajr0>

```
dnorm(x, mean = 0, sd = 1, log = FALSE)
pnorm(q, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
qnorm(p, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
rnorm(n, mean = 0, sd = 1)
```

Here we simulate standard Normal random numbers with mean 0 and standard deviation 1.

```
> ## Simulate standard Normal random numbers
> x <- rnorm(10)
> x
[1] 0.01874617 -0.18425254 -1.37133055 -0.59916772 0.29454513
[6] 0.38979430 -1.20807618 -0.36367602 -1.62667268 -0.25647839
```

We can modify the default parameters to simulate numbers with mean 20 and standard deviation 2.

```
> x <- rnorm(10, 20, 2)
> x
[1] 22.20356 21.51156 19.52353 21.97489 21.48278 20.17869 18.09011
[8] 19.60970 21.85104 20.96596
> summary(x)
   Min. 1st Qu. Median     Mean 3rd Qu.    Max.
18.09    19.75   21.22   20.74   21.77   22.20
```

If you wanted to know what was the probability of a random Normal variable of being less than, say, 2, you could use the `pnorm()` function to do that calculation.

```
> pnorm(2)
[1] 0.9772499
```

You never know when that calculation will come in handy.

Setting the random number seed

When simulating any random numbers it is essential to set the *random number seed*. Setting the random number seed with `set.seed()` ensures reproducibility of the sequence of random numbers.

For example, I can generate 5 Normal random numbers with `rnorm()`.

```
> set.seed(1)
> rnorm(5)
[1] -0.6264538  0.1836433 -0.8356286  1.5952808  0.3295078
```

Note that if I call `rnorm()` again I will of course get a different set of 5 random numbers.

```
> rnorm(5)
[1] -0.8204684  0.4874291  0.7383247  0.5757814 -0.3053884
```

If I want to reproduce the original set of random numbers, I can just reset the seed with `set.seed()`.

```
> set.seed(1)
> rnorm(5)      ## Same as before
[1] -0.6264538  0.1836433 -0.8356286  1.5952808  0.3295078
```

In general, you should **always set the random number seed when conducting a simulation!** Otherwise, you will not be able to reconstruct the exact numbers that you produced in an analysis.

It is possible to generate random numbers from other probability distributions like the Poisson. The Poisson distribution is commonly used to model data that come in the form of counts.

```
> rpois(10, 1)    ## Counts with a mean of 1
[1] 0 0 1 1 2 1 1 4 1 2
> rpois(10, 2)    ## Counts with a mean of 2
[1] 4 1 2 0 1 1 0 1 4 1
> rpois(10, 20)   ## Counts with a mean of 20
[1] 19 19 24 23 22 24 23 20 11 22
```

Simulating a Linear Model

[Watch a video of this section⁷⁶](#)

Simulating random numbers is useful but sometimes we want to simulate values that come from a specific *model*. For that we need to specify the model and then simulate from it using the functions described above.

Suppose we want to simulate from the following linear model

$$y = \beta_0 + \beta_1 x + \varepsilon$$

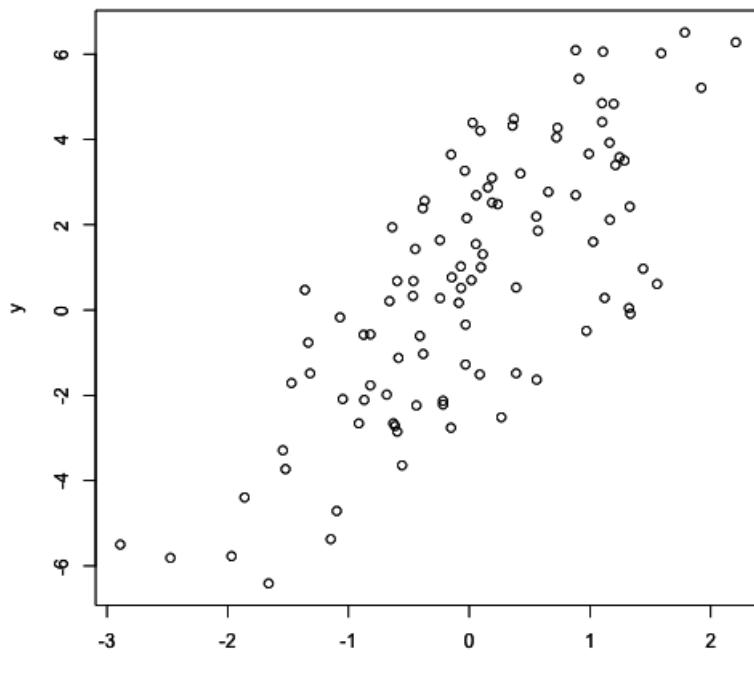
where $\varepsilon \sim \mathcal{N}(0, 2^2)$. Assume $x \sim \mathcal{N}(0, 1^2)$, $\beta_0 = 0.5$ and $\beta_1 = 2$. The variable x might represent an important predictor of the outcome y . Here's how we could do that in R.

⁷⁶<https://youtu.be/p7kSSSsv4ms>

```
> ## Always set your seed!
> set.seed(20)
>
> ## Simulate predictor variable
> x <- rnorm(100)
>
> ## Simulate the error term
> e <- rnorm(100, 0, 2)
>
> ## Compute the outcome via the model
> y <- 0.5 + 2 * x + e
> summary(y)
   Min. 1st Qu. Median  Mean 3rd Qu. Max.
-6.4080 -1.5400  0.6789  0.6893  2.9300  6.5050
```

We can plot the results of the model simulation.

```
> plot(x, y)
```



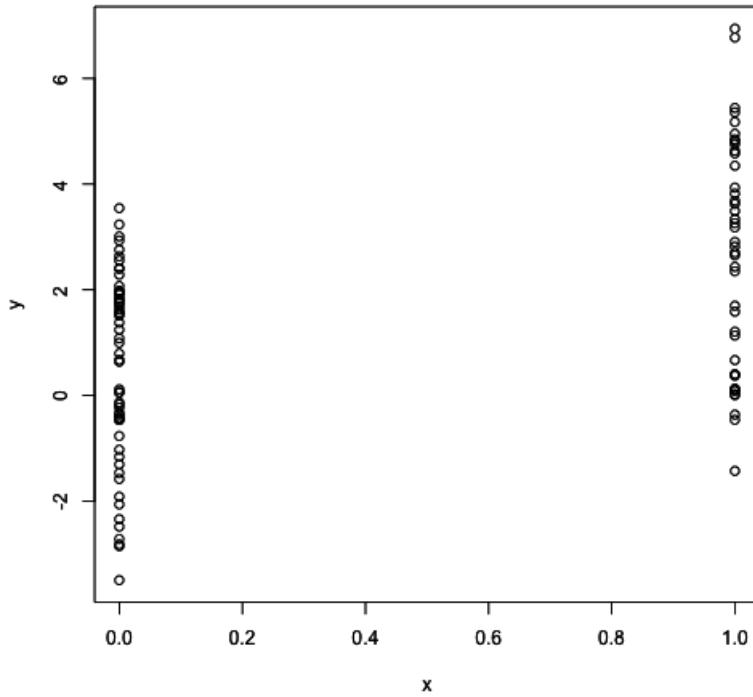
plot of chunk Linear Model

What if we wanted to simulate a predictor variable x that is binary instead of having a Normal distribution. We can use the `rbinom()` function to simulate binary random variables.

```
> set.seed(10)
> x <- rbinom(100, 1, 0.5)
> str(x)      ## 'x' is now 0s and 1s
int [1:100] 1 0 0 1 0 0 0 0 1 0 ...
```

Then we can proceed with the rest of the model as before.

```
> e <- rnorm(100, 0, 2)
> y <- 0.5 + 2 * x + e
> plot(x, y)
```



plot of chunk Linear Model Binary

We can also simulate from *generalized linear model* where the errors are no longer from a Normal distribution but come from some other distribution. For example, suppose we want to simulate from a Poisson log-linear model where

$$Y \sim \text{Poisson}(\mu)$$

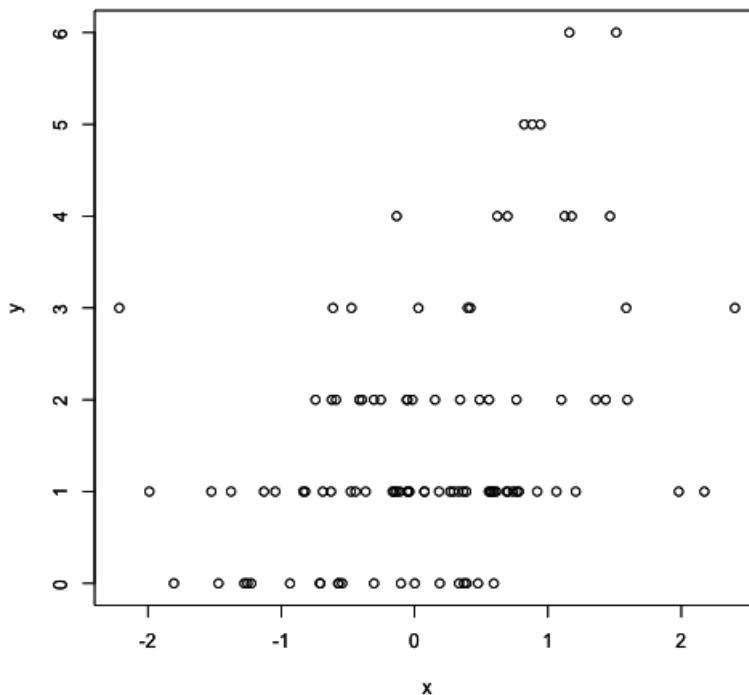
$$\log \mu = \beta_0 + \beta_1 x$$

and $\beta_0 = 0.5$ and $\beta_1 = 0.3$. We need to use the `rpois()` function for this

```
> set.seed(1)
>
> ## Simulate the predictor variable as before
> x <- rnorm(100)
```

Now we need to compute the log mean of the model and then exponentiate it to get the mean to pass to `rpois()`.

```
> log.mu <- 0.5 + 0.3 * x
> y <- rpois(100, exp(log.mu))
> summary(y)
   Min. 1st Qu. Median    Mean 3rd Qu.    Max.
 0.00    1.00    1.00    1.55    2.00    6.00
> plot(x, y)
```



plot of chunk Poisson Log-Linear Model

You can build arbitrarily complex models like this by simulating more predictors or making transformations of those predictors (e.g. squaring, log transformations, etc.).

Random Sampling

[Watch a video of this section⁷⁷](#)

The `sample()` function draws randomly from a specified set of (scalar) objects allowing you to sample from arbitrary distributions of numbers.

```
> set.seed(1)
> sample(1:10, 4)
[1] 3 4 5 7
> sample(1:10, 4)
[1] 3 9 8 5
>
> ## Doesn't have to be numbers
> sample(letters, 5)
[1] "q" "b" "e" "x" "p"
>
> ## Do a random permutation
> sample(1:10)
[1] 4 7 10 6 9 2 8 3 1 5
> sample(1:10)
[1] 2 3 4 1 9 5 10 8 6 7
>
> ## Sample w/replacement
> sample(1:10, replace = TRUE)
[1] 2 9 7 8 2 8 5 9 7 8
```

To sample more complicated things, such as rows from a data frame or a list, you can sample the indices into an object rather than the elements of the object itself.

Here's how you can sample rows from a data frame.

⁷⁷<https://youtu.be/-7GA10KWDJg>

```
> library(datasets)
> data(airquality)
> head(airquality)
  Ozone Solar.R Wind Temp Month Day
1    41     190  7.4   67      5    1
2    36     118  8.0   72      5    2
3    12     149 12.6   74      5    3
4    18     313 11.5   62      5    4
5    NA      NA 14.3   56      5    5
6    28      NA 14.9   66      5    6
```

Now we just need to create the index vector indexing the rows of the data frame and sample directly from that index vector.

```
> set.seed(20)
>
> ## Create index vector
> idx <- seq_len(nrow(airquality))
>
> ## Sample from the index vector
> samp <- sample(idx, 6)
> airquality[samp, ]
  Ozone Solar.R Wind Temp Month Day
135    21     259 15.5   76      9   12
117    168     238  3.4   81      8   25
43     NA      250  9.2   92      6   12
80     79     187  5.1   87      7   19
144    13     238 12.6   64      9   21
146    36     139 10.3   81      9   23
```

Other more complex objects can be sampled in this way, as long as there's a way to index the sub-elements of the object.

Summary

- Drawing samples from specific probability distributions can be done with “r” functions
- Standard distributions are built in: Normal, Poisson, Binomial, Exponential, Gamma, etc.
- The `sample()` function can be used to draw random samples from arbitrary vectors
- Setting the random number generator seed via `set.seed()` is critical for reproducibility

Data Analysis Case Study: Changes in Fine Particle Air Pollution in the U.S.

This chapter presents an example data analysis looking at changes in fine particulate matter (PM) air pollution in the United States using the Environmental Protection Agencies freely available national monitoring data. The purpose of the chapter is to just show how the various tools that we have covered in this book can be used to read, manipulate, and summarize data so that you can develop statistical evidence for relevant real-world questions.

[Watch a video of this chapter⁷⁸](#)

Synopsis

In this chapter we aim to describe the changes in fine particle (PM2.5) outdoor air pollution in the United States between the years 1999 and 2012. Our overall hypothesis is that outdoor PM2.5 has decreased on average across the U.S. due to nationwide regulatory requirements arising from the Clean Air Act. To investigate this hypothesis, we obtained PM2.5 data from the U.S. Environmental Protection Agency which is collected from monitors sited across the U.S. We specifically obtained data for the years 1999 and 2012 (the most recent complete year available). From these data, we found that, on average across the U.S., levels of PM2.5 have decreased between 1999 and 2012. At one individual monitor, we found that levels have decreased and that the variability of PM2.5 has decreased. Most individual states also experienced decreases in PM2.5, although some states saw increases.

Loading and Processing the Raw Data

From the [EPA Air Quality System⁷⁹](#) we obtained data on fine particulate matter air pollution (PM2.5) that is monitored across the U.S. as part of the nationwide PM monitoring network. We obtained the files for the years 1999 and 2012.

Reading in the 1999 data

We first read in the 1999 data from the raw text file included in the zip archive. The data is a delimited file where fields are delimited with the | character and missing values are coded as blank fields. We skip some commented lines in the beginning of the file and initially we do not read the header data.

⁷⁸<https://youtu.be/VE-6bQvyfTQ>

⁷⁹http://aqsdr1.epa.gov/aqsweb/aqstmp/airdata/download_files.html

```
> pm0 <- read.table("pm25_data/RD_501_88101_1999-0.txt", comment.char = "#", header = FALSE, sep = "|", na.strings = "")
```

After reading in the 1999 we check the first few rows (there are 117,421) rows in this dataset.

```
> dim(pm0)
[1] 117421      28
> head(pm0[, 1:13])
   V1 V2 V3 V4 V5     V6 V7 V8 V9 V10      V11 V12 V13
1 RD I 1 27 1 88101 1 7 105 120 19990103 00:00    NA
2 RD I 1 27 1 88101 1 7 105 120 19990106 00:00    NA
3 RD I 1 27 1 88101 1 7 105 120 19990109 00:00    NA
4 RD I 1 27 1 88101 1 7 105 120 19990112 00:00 8.841
5 RD I 1 27 1 88101 1 7 105 120 19990115 00:00 14.920
6 RD I 1 27 1 88101 1 7 105 120 19990118 00:00 3.878
```

We then attach the column headers to the dataset and make sure that they are properly formatted for R data frames.

```
> cnames <- readLines("pm25_data/RD_501_88101_1999-0.txt", 1)
> cnames <- strsplit(cnames, "|", fixed = TRUE)
> ## Ensure names are properly formatted
> names(pm0) <- make.names(cnames[[1]])
> head(pm0[, 1:13])
   X..RD Action.Code State.Code County.Code Site.ID Parameter POC
1      RD          I           1         27       1    88101     1
2      RD          I           1         27       1    88101     1
3      RD          I           1         27       1    88101     1
4      RD          I           1         27       1    88101     1
5      RD          I           1         27       1    88101     1
6      RD          I           1         27       1    88101     1
   Sample.Duration Unit Method      Date Start.Time Sample.Value
1                  7 105    120 19990103      00:00        NA
2                  7 105    120 19990106      00:00        NA
3                  7 105    120 19990109      00:00        NA
4                  7 105    120 19990112      00:00 8.841
5                  7 105    120 19990115      00:00 14.920
6                  7 105    120 19990118      00:00 3.878
```

The column we are interested in is the `Sample.Value` column which contains the PM2.5 measurements. Here we extract that column and print a brief summary.

```
> x0 <- pm0$Sample.Value
> summary(x0)
  Min. 1st Qu. Median     Mean 3rd Qu.    Max.    NA's
  0.00    7.20   11.50   13.74   17.90  157.10  13217
```

Missing values are a common problem with environmental data and so we check to see what proportion of the observations are missing (i.e. coded as NA).

```
> mean(is.na(x0)) ## Are missing values important here?
[1] 0.1125608
```

Because the proportion of missing values is relatively low (0.1125608), we choose to ignore missing values for now.

Reading in the 2012 data

We then read in the 2012 data in the same manner in which we read the 1999 data (the data files are in the same format).

```
> pm1 <- read.table("pm25_data/RD_501_88101_2012-0.txt", comment.char = "#",
+ header = FALSE, sep = "|", na.strings = "", nrow = 1304290)
```

We also set the column names (they are the same as the 1999 dataset) and extract the Sample.Value column from this dataset.

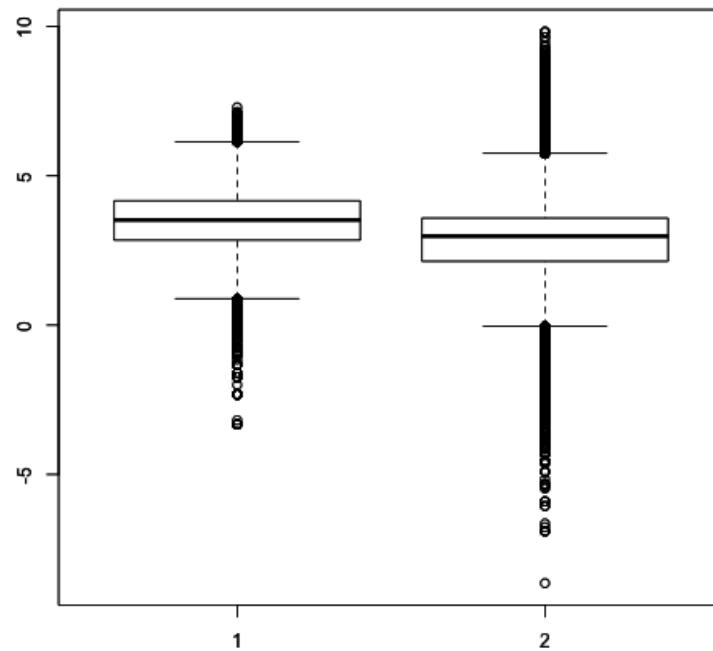
```
> names(pm1) <- make.names(cnames[[1]])
> x1 <- pm1$Sample.Value
```

Results

Entire U.S. analysis

In order to show aggregate changes in PM across the entire monitoring network, we can make boxplots of all monitor values in 1999 and 2012. Here, we take the log of the PM values to adjust for the skew in the data.

```
> boxplot(log2(x0), log2(x1))
Warning in boxplot.default(log2(x0), log2(x1)): NaNs produced
Warning in bplt(at[i], wid = width[i], stats = z$stats[, i], out = z$out[z
$group == : Outlier (-Inf) in boxplot 1 is not drawn
Warning in bplt(at[i], wid = width[i], stats = z$stats[, i], out = z$out[z
$group == : Outlier (-Inf) in boxplot 2 is not drawn
```



plot of chunk boxplot log values

```
> summary(x0)
   Min. 1st Qu. Median     Mean 3rd Qu.    Max.    NA's
  0.00    7.20   11.50   13.74   17.90  157.10  13217
> summary(x1)
   Min. 1st Qu. Median     Mean 3rd Qu.    Max.    NA's
-10.00    4.00   7.63    9.14   12.00  909.00  73133
```

Interestingly, from the summary of x1 it appears there are some negative values of PM, which in general should not occur. We can investigate that somewhat to see if there is anything we should worry about.

```
> negative <- x1 < 0
> mean(negative, na.rm = T)
[1] 0.0215034
```

There is a relatively small proportion of values that are negative, which is perhaps reassuring. In order to investigate this a step further we can extract the date of each measurement from the original data frame. The idea here is that perhaps negative values occur more often in some parts of the year than other parts. However, the original data are formatted as character strings so we convert them to R's Date format for easier manipulation.

```
> dates <- pm1$Date
> dates <- as.Date(as.character(dates), "%Y%m%d")
```

We can then extract the month from each of the dates with negative values and attempt to identify when negative values occur most often.

```
> missing.months <- month.name[as.POSIXlt(dates)$mon + 1]
> tab <- table(factor(missing.months, levels = month.name))
> round(100 * tab / sum(tab))
```

January	February	March	April	May	June	July
15	13	15	13	14	13	8
August	September	October	November	December		
6	3	0	0	0		

From the table above it appears that bulk of the negative values occur in the first six months of the year (January–June). However, beyond that simple observation, it is not clear why the negative values occur. That said, given the relatively low proportion of negative values, we will ignore them for now.

Changes in PM levels at an individual monitor

So far we have examined the change in PM levels on average across the country. One issue with the previous analysis is that the monitoring network could have changed in the time period between 1999 and 2012. So if for some reason in 2012 there are more monitors concentrated in cleaner parts of the country than there were in 1999, it might appear the PM levels decreased when in fact they didn't. In this section we will focus on a single monitor in New York State to see if PM levels *at that monitor* decreased from 1999 to 2012.

Our first task is to identify a monitor in New York State that has data in 1999 and 2012 (not all monitors operated during both time periods). First we subset the data frames to only include data from New York (State.Code == 36) and only include the County.Code and the Site.ID (i.e. monitor number) variables.

```
> site0 <- unique(subset(pm0, State.Code == 36, c(County.Code, Site.ID)))
> site1 <- unique(subset(pm1, State.Code == 36, c(County.Code, Site.ID)))
```

Then we create a new variable that combines the county code and the site ID into a single string.

```
> site0 <- paste(site0[,1], site0[,2], sep = ".")
> site1 <- paste(site1[,1], site1[,2], sep = ".")
> str(site0)
chr [1:33] "1.5" "1.12" "5.73" "5.80" "5.83" "5.110" ...
> str(site1)
chr [1:18] "1.5" "1.12" "5.80" "5.133" "13.11" "29.5" ...
```

Finally, we want the intersection between the sites present in 1999 and 2012 so that we might choose a monitor that has data in both periods.

```
> both <- intersect(site0, site1)
> print(both)
[1] "1.5"      "1.12"     "5.80"     "13.11"    "29.5"     "31.3"     "63.2008"
[8] "67.1015"  "85.55"   "101.3"
```

Here (above) we can see that there are 10 monitors that were operating in both time periods. However, rather than choose one at random, it might best to choose one that had a reasonable amount of data in each year.

```
> ## Find how many observations available at each monitor
> pm0$county.site <- with(pm0, paste(County.Code, Site.ID, sep = "."))
> pm1$county.site <- with(pm1, paste(County.Code, Site.ID, sep = "."))
> cnt0 <- subset(pm0, State.Code == 36 & county.site %in% both)
> cnt1 <- subset(pm1, State.Code == 36 & county.site %in% both)
```

Now that we have subsetted the original data frames to only include the data from the monitors that overlap between 1999 and 2012, we can split the data frames and count the number of observations at each monitor to see which ones have the most observations.

```

> ## 1999
> sapply(split(cnt0, cnt0$county.site), nrow)
  1.12      1.5    101.3   13.11    29.5    31.3    5.80  63.2008 67.1015
    61      122     152      61       61     183      61      122     122
  85.55
    7
> ## 2012
> sapply(split(cnt1, cnt1$county.site), nrow)
  1.12      1.5    101.3   13.11    29.5    31.3    5.80  63.2008 67.1015
    31      64      31      31      33      15      31      30      31
  85.55
    31

```

A number of monitors seem suitable from the output, but we will focus here on County 63 and site ID 2008.

```

> both.county <- 63
> both.id <- 2008
>
> ## Choose county 63 and site ID 2008
> pm1sub <- subset(pm1, State.Code == 36 & County.Code == both.county & Site.ID \
== both.id)
> pm0sub <- subset(pm0, State.Code == 36 & County.Code == both.county & Site.ID \
== both.id)

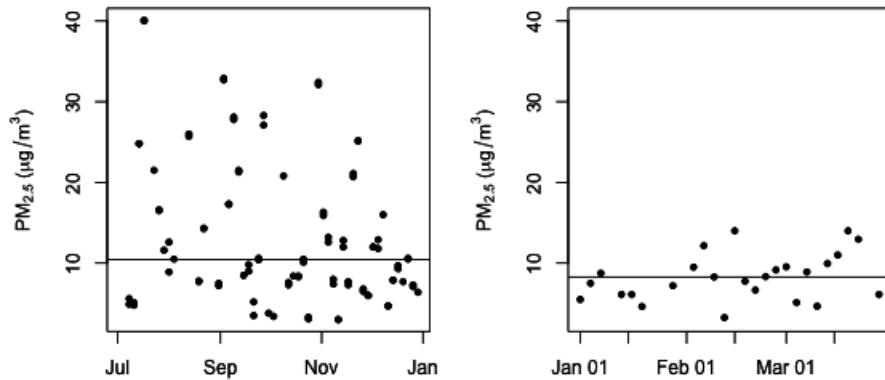
```

Now we plot the time series data of PM for the monitor in both years.

```

> dates1 <- as.Date(as.character(pm1sub$date), "%Y%m%d")
> x1sub <- pm1sub$sample.value
> dates0 <- as.Date(as.character(pm0sub$date), "%Y%m%d")
> x0sub <- pm0sub$sample.value
>
> ## Find global range
> rng <- range(x0sub, x1sub, na.rm = T)
> par(mfrow = c(1, 2), mar = c(4, 5, 2, 1))
> plot(dates0, x0sub, pch = 20, ylim = rng, xlab = "", ylab = expression(PM[2.5] \
* (" * mu * g/m^3 * ")))
> abline(h = median(x0sub, na.rm = T))
> plot(dates1, x1sub, pch = 20, ylim = rng, xlab = "", ylab = expression(PM[2.5] \
* (" * mu * g/m^3 * ")))
> abline(h = median(x1sub, na.rm = T))

```



plot of chunk unnamed-chunk-11

From the plot above, we can see that median levels of PM (horizontal solid line) have decreased a little from 10.45 in 1999 to 8.29 in 2012. However, perhaps more interesting is that the variation (spread) in the PM values in 2012 is much smaller than it was in 1999. This suggests that not only are median levels of PM lower in 2012, but that there are fewer large spikes from day to day. One issue with the data here is that the 1999 data are from July through December while the 2012 data are recorded in January through April. It would have been better if we'd had full-year data for both years as there could be some seasonal confounding going on.

Changes in state-wide PM levels

Although ambient air quality standards are set at the federal level in the U.S. and hence affect the entire country, the actual reduction and management of PM is left to the individual states. States that are not “in attainment” have to develop a plan to reduce PM so that they are in attainment (eventually). Therefore, it might be useful to examine changes in PM at the state level. This analysis falls somewhere in between looking at the entire country all at once and looking at an individual monitor.

What we do here is calculate the mean of PM for each state in 1999 and 2012.

```
> ## 1999
> mn0 <- with(pm0, tapply(Sample.Value, State.Code, mean, na.rm = TRUE))
> ## 2012
> mn1 <- with(pm1, tapply(Sample.Value, State.Code, mean, na.rm = TRUE))
>
> ## Make separate data frames for states / years
> d0 <- data.frame(state = names(mn0), mean = mn0)
> d1 <- data.frame(state = names(mn1), mean = mn1)
> mrg <- merge(d0, d1, by = "state")
> head(mrg)
```

```

state    mean.x    mean.y
1       1 19.956391 10.126190
2      10 14.492895 11.236059
3      11 15.786507 11.991697
4      12 11.137139  8.239690
5      13 19.943240 11.321364
6      15  4.861821  8.749336

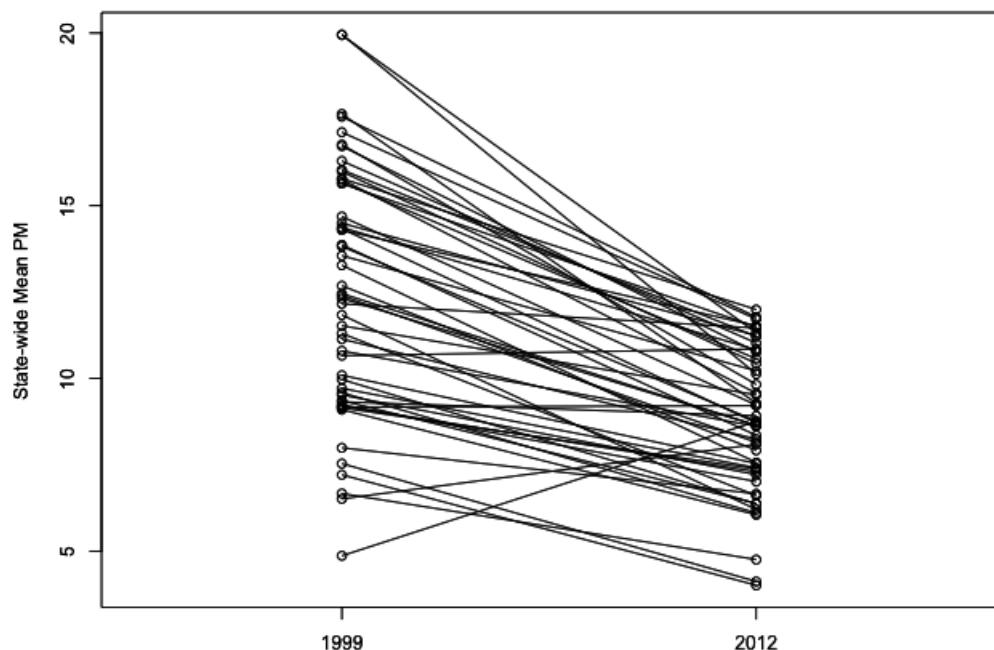
```

Now make a plot that shows the 1999 state-wide means in one “column” and the 2012 state-wide means in another columns. We then draw a line connecting the means for each year in the same state to highlight the trend.

```

> par(mfrow = c(1, 1))
> rng <- range(mrg[,2], mrg[,3])
> with(mrg, plot(rep(1, 52), mrg[, 2], xlim = c(.5, 2.5), ylim = rng, xaxt = "n" \
, xlab = "", ylab = "State-wide Mean PM"))
> with(mrg, points(rep(2, 52), mrg[, 3]))
> segments(rep(1, 52), mrg[, 2], rep(2, 52), mrg[, 3])
> axis(1, c(1, 2), c("1999", "2012"))

```



plot of chunk unnamed-chunk-13

From the plot above we can see that many states have decreased the average PM levels from 1999 to 2012 (although a few states actually increased their levels).