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Reproducible Research with R and RStudio

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Forward

FILL IN

Preface

FILL IN

List of Figures

List of Tables

9.1 Coefficient Estimates Predicting Examination Scores in Swiss Cantons (1888) Found Using Bayesian Normal Linear Regres- sion	40
---	----



x



Contents

I	Getting Started	1
1	Introducing Reproducible Research	3
1.1	What is reproducible research?	3
1.2	Why should research be reproducible?	3
1.2.1	For Science	3
1.2.2	For You	3
1.3	Who should read this book?	4
1.3.1	Students	4
1.3.2	Researchers	4
1.3.3	Industry practitioners	4
1.4	Why use R/RStudio for reproducible research?	4
1.4.1	Complete integration of data gathering, analysis, and presentation.	5
1.4.1.1	Presentation	5
1.5	Book overview	5
1.5.1	What this book is not.	5
1.5.2	How to read this book.	6
1.5.3	How this book was written	7
1.5.4	Contents overview.	7
2	Getting Started with Reproducible Research	9
2.1	The Big Picture: A workflow for reproducible research	9
2.1.1	Data Gathering	9
2.1.2	Data Analysis	9
2.1.3	Data Presentation	9
2.2	Practical tips for reproducible research	9
2.2.1	Document everything	9
2.2.2	Work hard so you can be lazy	10
2.2.3	Everything is a (text) file	10
2.2.4	All files should be human readable	10
2.2.5	Research projects are many files tied together	10
2.2.6	Have a plan to organize, store, and make your files available	10
2.3	Introduction to the tools of reproducible research covered in this book	10

2.3.1	R/RStudio	10
2.3.2	knitr	10
2.3.3	Cloud storage & versioning	10
2.3.4	The command line	10
2.3.5	Markup languages: L ^A T _E X & Markdown/HTML	10
3	Chapter 3:	11
4	Chapter 4:	13
II	Data Gathering and Storage	15
5	Gathering Data with R	17
5.1	Organize Your Data Gathering	17
5.2	Importing locally stored data sets	19
5.2.1	Single files	19
5.2.2	Looping through multiple files	19
5.3	Importing data sets from the internet	19
5.3.1	Data from non-secure (http) URLs	19
5.3.2	Data from secure (https) URLs	19
5.3.3	Compressed data stored online	19
5.3.4	Data APIs & feeds	20
5.4	Basic web scraping	21
5.4.1	Scraping tables	21
5.4.2	Gathering and parsing text	21
6	Storing, Collaborating, Accessing Files, Versioning	23
6.1	Saving data in reproducible formats	24
6.2	Storing data in the cloud	24
6.3	Dropbox	24
6.3.1	Version control	25
6.3.2	Accessing Data	25
6.4	GitHub	26
6.4.0.1	Setting Up GitHub	27
6.4.0.2	Version Control in GitHub	27
7	Chapter 7:	29
III	Analysis and Results	31
8	CStatistical Modelling and ‘knitr’	33
8.1	Incorporating analyses into the markup	33
8.1.1	Full code in the main document	33
8.1.1.1	L ^A T _E X	33
8.1.1.2	Markdown	33
8.1.2	Showing code & results inline	33

8.1.2.1	\LaTeX	34
8.1.2.2	Markdown	34
8.1.3	Sourcing R code from another file	34
8.1.3.1	Source from a local file	35
8.1.3.2	Source from a non-secure URL (<code>http</code>)	35
8.1.3.3	Source from a secure URL (<code>https</code>)	35
8.2	Saving output objects for future use	36
8.3	Including highlighted syntax in the output	36
8.3.1	\LaTeX	36
8.3.2	Markdown/HTML	36
8.4	Debugging	36
9	Showing Results with Tables	37
9.1	Table Basics	38
9.1.1	Tables in \LaTeX	38
9.1.2	Tables in Markdown/HTML	38
9.2	Creating tables from R objects	38
9.2.1	<code>xtable</code> & <code>texreg</code> basics with supported class objects	38
9.2.1.1	<code>xtable</code> for \LaTeX	38
9.2.1.2	<code>xtable</code> for Markdown	38
9.2.2	<code>xtable</code> with non-supported class objects	38
9.2.3	Basic <code>knitr</code> syntax for tables	40
9.3	Tables with <code>apsrtable</code>	41
10	Chapter 10:	43
IV	Presentation Documents	45
11	Presenting with \LaTeX	47
11.1	The Basics	47
11.1.1	Editors	47
11.1.2	The Header	47
11.1.3	Headings	47
11.1.4	Footnotes & Bibliographies	47
11.1.4.1	Footnotes	47
11.1.4.2	Bibliographies	47
12	Chapter 12:	51
12.0.5	Editors	51
13	Presenting on the Web and Beyond with Markdown/HTML	53
13.1	The Basics	53
13.1.1	Headings	53
13.1.2	Footnotes and bibliographies with MultiMarkdown	54
13.1.3	Math	54
13.1.4	Drawing figures with CSS	54

13.2 Simple webpages	54
13.2.1 RPubS	54
13.2.2 Hosting webpages with Dropbox	54
13.3 Presentations with Slidify	54
13.4 Reproducible websites	54
13.4.1 Blogging with Tumblr	54
13.4.2 Jekyll-Bootstrap and GitHub	54
13.4.3 Jekyll and Github Pages	54
13.5 Using Markdown for non-HTML output with Pandoc	54
14 Chapter 14:	55
Bibliography	57
Index	59



Part I

Getting Started



1

Introducing Reproducible Research

CONTENTS

1.1	What is reproducible research?	3
1.2	Why should research be reproducible?	3
1.2.1	For Science	3
1.2.2	For You	3
1.3	Who should read this book?	4
1.3.1	Students	4
1.3.2	Researchers	4
1.3.3	Industry practitioners	4
1.4	Why use R/RStudio for reproducible research?	4
1.4.1	Complete integration of data gathering, analysis, and presentation.	5
1.4.1.1	Presentation	5
1.5	Book overview	5
1.5.1	What this book is not.	5
1.5.2	How to read this book.	6
1.5.3	How this book was written	6
1.5.4	Contents overview.	7

FILL IN

1.1 What is reproducible research?

1.2 Why should research be reproducible?

Incorporating high reproducibility into your research is important for science and it also makes the research process easier for the researcher.

1.2.1 For Science

1.2.2 For You

Working to make your research reproducible from the start makes the research process easier. A third person may or may not actually reproduce your research even if you make it easy to do so. But, it's almost certain that you will reproduce parts or even all of your research. Virtually no actual research

process is completely linear. We almost never gather data, run our analyses, and present our results without also going backwards to add variables, make changes to our statistical models, create new graphs, and so on. Whether these changes are because of journal reviewers' or conference participants comments or we discovery that new and better data has been made available since beginning the project, designing our research to be reproducible from the start makes it much easier to make these changes.

Changes made to one part of a research project have a way of cascading through the other parts. For example, adding a new variable to a largely completed analysis requires gathering new data and merging it into existing data sets. If we are using data imputation or matching methods this can lead to adjustments to the entire data set. We then have to update our statistical models and the tables and graphs we use to present results. Adding a new variable essentially forces us to reproduce large portions of our research. If we made it easier for others to reproduce our research we also made it easier for us to do this.

COMPLETE

1.3 Who should read this book?

1.3.1 Students

1.3.2 Researchers

1.3.3 Industry practitioners

1.4 Why use R/RStudio for reproducible research?

R

Why use a statistical programming language like R for reproducible research? R is more than just a statistics program, like , Stata, or SPSS. It can be used to integrate all stages of the research process not just the statistical analysis stage. COMPLETE

The way we interact with R or any other programming and markup language promotes reproducibility more than our interactions with Graphical User Interface (GUI) programs like SPSS¹ and Microsoft Word. When we write (and save) R code we are being forced to explicitly express the steps we take to accomplish a goal in an easily documented way. When we achieve

¹I know you can write scripts in statistical programs like SPSS, but doing so is not encouraged by the interface and we often have to learn multiple languages just to write scripts that run analyses, create graphics, and deal with matrices.

a goal by clicking through drop down menus in GUI programs, the steps we take are lost. To document them requires considerable extra effort.

RStudio

Why use an Integrated Development Environment (IDE), especially RStudio for reproducible research? RStudio allows us to have all of the R's advantages, but in a more visually navigable way. Think of it as a happy medium between R's text-based interface and a pure GUI. COMPLETE

RStudio also has a very tight integration with technologies such as `knitr` and `LATEX` that makes the presentation of reproducible presentation of results.

1.4.1 Complete integration of data gathering, analysis, and presentation.

1.4.1.1 Presentation

There are many `LATEX` editors available, both open source and paid, as well as other ways to compile `LATEX` documents, including directly through the command line. **R** is capable of compiling `LATEX` documents through .

RStudio is actually as a very nice `LATEX` editor. For creating documents that integrate markup and **R** code, at the moment it pretty much can't be beat. It has full syntax highlighting, even for documents with `knitr` code (which it can collapse when you just want to work on the text). It can spell check `LATEX` documents. It handles `knitr` code chunks beautifully making it easy to navigate through complex documents and run individual chunks.

Even if you aren't creating documents that integrate **R** code, *R* is still a decent full functioning `LATEX` editor. It can insert common commands like `\section*{}` for unnumbered sections. Most importantly it easily compile `LATEX` documents and show you a preview.

1.5 Book overview

1.5.1 What this book is not.

This book describes a workflow for reproducible research primarily using R and RStudio. It is designed to give you the necessary tools to use this workflow for your own research. It is not designed to be a complete introduction to R, RStudio, GitHub, the command line, or any other program that is a part of this workflow. Instead it shows you how these tools can fit together to make your research more reproducible.

To get the most out of these individual programs I point you to other resources that cover these programs in more detail.

That being said, my goal in this for this book to be self-sufficient to the extent that a reader without a detailed understanding of these programs will be able to understand and use the commands and procedures I cover in this book. While learning how to use R and the other programs I often encountered examples that included commands, variables, and other things that were not well explained in the texts that I was reading. This caused me to waste many hours trying to figure out, for example, what the `$` is used for (preview: it's the 'component selector'). I hope to save you from this wasted time by either providing a brief explanation of these possibly frustratingly mysterious conventions and/or pointing you in the direction of a good explanation.

To that end, I can recommend a number of books for that cover more of the nitty-gritty of R and the command line.

- Michael J. Crawley's encyclopaedic R book, appropriately titled, **The R Book** published by Wiley.
- Norman Matloff's tour through the programming language aspects of R called **The Art of R Programming: A Tour of Statistical Design Software** published by No Starch Press.
- For an excellent introduction to the command line in Linux and Mac, though with pretty clear implications for Windows users if they are running PowerShell (see Chapter 2) see William E. Shotts Jr.'s book *The Linux Command Line: A Complete Introduction* also published by No Starch Press.
- The RStudio website (<http://rstudio.org/docs/>) has a number of useful tutorials on how to use `knitr` with `LATEX` and Markdown.

1.5.2 How to read this book.

This book tells a story. It has a beginning, middle, and end. So, unlike a reference book it can and should be read like a novel, taking you through an empirical research processes from an empty folder maybe called **Research Paper** to a completed set of documents that showcase your findings.

That being said, readers with more experience using tools like R or `LATEX`) may want to skip over the nitty-gritty parts of the book that describe how to manipulate data frames or compile a `LATEX`) document into a PDF. Please feel free to do this.

If you are experienced with R in particular you may want to skip over Chapter 3: Getting Started with R/RStudio.

1.5.3 How this book was written

This book practices what it preaches. It can be reproduced. It was written using the programs and methods that it describes. Full documentation and source files can be found at the Book's **GitHub** repository.

Feel free to read and even copy (within reason and with attribution, of course) the Book's source code. You can find it at <https://github.com/christophergandrud/Rep-Res-Book>. This is especially useful if you want to know how to do something in the book that I don't directly cover in the text.

In the same spirit, I encourage you to make your research files—not just data, but analysis code and markup—available for other researchers to learn from.

Not only does reproducibility help us evaluate past work, but it also pushes forward knowledge in the scientific community.

1.5.4 Contents overview.

2

Getting Started with Reproducible Research

CONTENTS

2.1	The Big Picture: A workflow for reproducible research	9
2.1.1	Data Gathering	9
2.1.2	Data Analysis	9
2.1.3	Data Presentation	9
2.2	Practical tips for reproducible research	9
2.2.1	Document everything	9
2.2.2	Work hard so you can be lazy	10
2.2.3	Everything is a (text) file	10
2.2.4	All files should be human readable	10
2.2.5	Research projects are many files tied together	10
2.2.6	Have a plan to organize, store, and make your files available	10
2.3	Introduction to the tools of reproducible research covered in this book	10
2.3.1	R/RStudio	10
2.3.2	knitr	10
2.3.3	Cloud storage & versioning	10
2.3.4	The command line	10
2.3.5	Markup languages: \LaTeX & Markdown/HTML	10

2.1 The Big Picture: A workflow for reproducible research

2.1.1 Data Gathering

2.1.2 Data Analysis

2.1.3 Data Presentation

2.2 Practical tips for reproducible research

2.2.1 Document everything

We'll discuss this more later in this chapter, but one important part of reproducible research with **R** is to *record your session info*. Many things in **R** stay the same over time, which makes it easy to recreate for future researchers to recreate what was done in the past. However, things do change from one

version of **R** to another. Also, the way **R** functions may be slightly different on different operating systems. Finally, you may have **R** set to load packages by default. These packages might be necessary to run your code, but other people might not be able to easily know this from just looking at your source code. The `sessionInfo` command prints a record of all of these things.

2.2.2 Work hard so you can be lazy

2.2.3 Everything is a (text) file

2.2.4 All files should be human readable

2.2.5 Research projects are many files tied together

2.2.6 Have a plan to organize, store, and make your files available

2.3 Introduction to the tools of reproducible research covered in this book

2.3.1 R/RStudio

2.3.2 knitr

2.3.3 Cloud storage & versioning

2.3.4 The command line

2.3.5 Markup languages: \LaTeX & Markdown/HTML

3

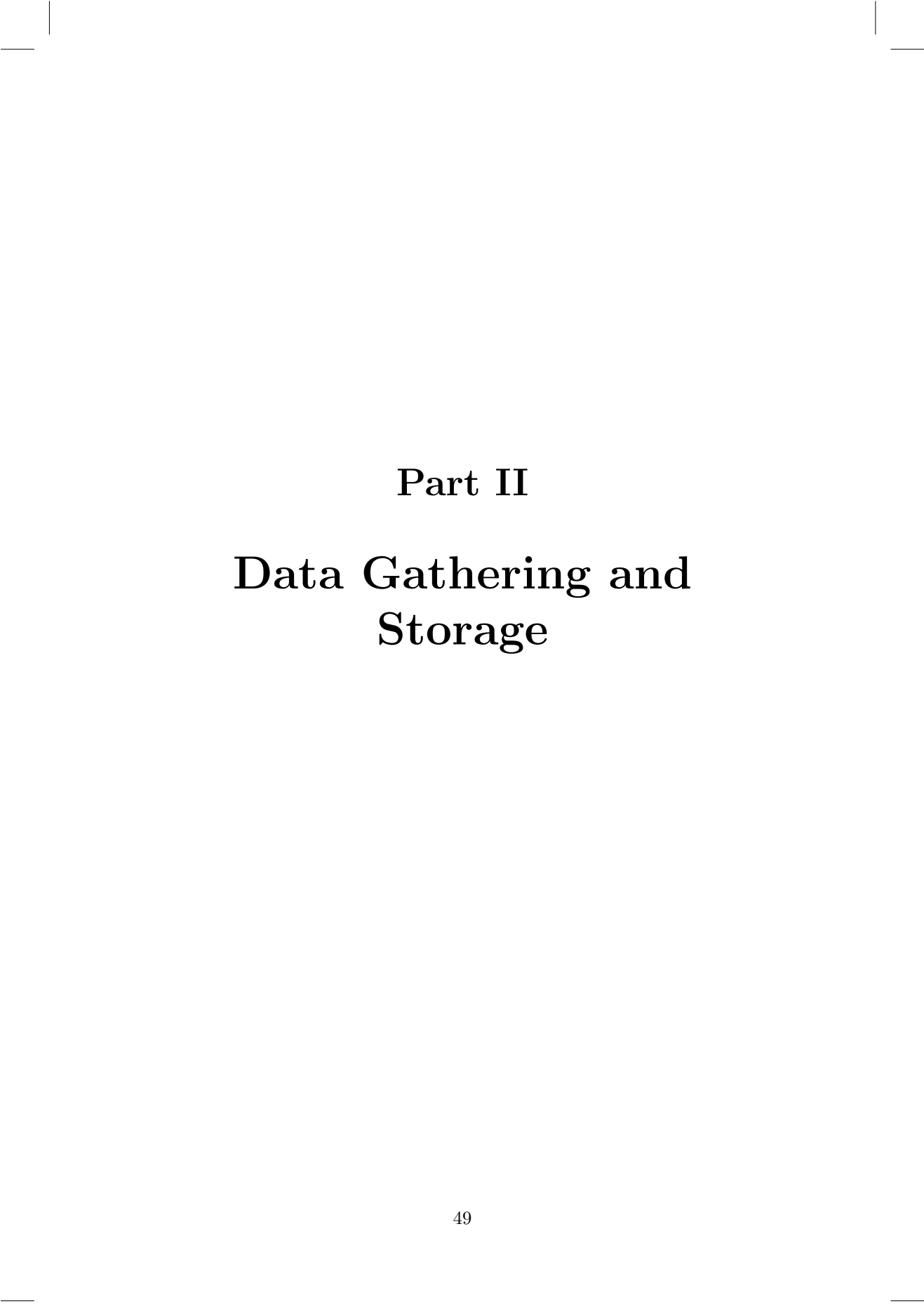
Chapter 3:

CONTENTS

4

Chapter 4:

CONTENTS



Part II

Data Gathering and Storage



5

Gathering Data with R

CONTENTS

5.1	Organize Your Data Gathering	17
5.2	Importing locally stored data sets	18
5.2.1	Single files	19
5.2.2	Looping through multiple files	19
5.3	Importing data sets from the internet	19
5.3.1	Data from non-secure (http) URLs	19
5.3.2	Data from secure (https) URLs	19
5.3.3	Compressed data stored online	19
5.3.4	Data APIs & feeds	20
5.4	Basic web scraping	20
5.4.1	Scraping tables	21
5.4.2	Gathering and parsing text	21

There are many practical issues involved in gathering data that can make replication easier or harder. As with all of the steps in this book: document everything. Replication will be easier if your documentation—source code—can be understood and executed by a computer. Of course there are data gathering situations that simply require manually pointing and clicking, talking with subjects in an experiment, and so on. The best we can do in these situations is just describe our data gathering process in detail CITE. Nonetheless, R's automated data gathering capabilities are extensive and often under utilized. Learning how to take full advantage of them greatly increases replicability and can even save researchers considerable time and effort.

5.1 Organize Your Data Gathering

Before getting into the details of using R to automate data gathering, let's start from where all data gathering should start: a plan to organize the process. Clearly organizing your data gathering process from the start of a research project improves the possibility of replicability and can save significant effort over the course of the project.

A key principle of replicable data gathering with R, like replicable research in general is segmenting the process into discrete files that can be run by a

common Make file. The Make file's output is the data set(s) that we use in the statistical analyses. There are two types of files that the Make file runs: data clean up files and merging files. Data clean up files bring raw (the rawer the better) individual data sources into R and transform them into something that can be merge with data from the other sources. Some of the R tools for data clean up were covered in Chapter 3. In this chapter we mostly cover the ways to bring raw data into R. We don't explicitly cover the process of merging data sets together in this book GET CITE. Merging files are executed by the Make file after it runs the clean up files.

Data gathering Make files usually only need one or two commands `setwd` and `source`. As we talked about in the previous chapter, `setwd` simply tells R where to look for and place files. `source` tells R to run code in some file.¹

If we plan to gather data from two different data sources—DATA1 and DATA2—stored in the directory DIRECTORY our Make file might look like this:

```
# Example Make file
setwd("~/DIRECTORY/")

# Clean up raw data files.
source("CleanDATA1.R")
source("CleanDATA2.R")

# Merge cleaned data files
source("MergeDATA1.DATA2.R")
```

You can save the output data set using the `write.table` command placed in the merge file or the Make file.

¹The `source` command is used more in the Chapter 8.

5.2 Importing locally stored data sets

5.2.1 Single files

5.2.2 Looping through multiple files

5.3 Importing data sets from the internet

5.3.1 Data from non-secure (http) URLs

5.3.2 Data from secure (https) URLs

5.3.3 Compressed data stored online

Sometimes data files can be very large, making them difficult to store and download without compressing them. There are a number of compression methods such as Zip and tar archives. Zip files have the extension `.zip` and tar archives use extensions such as `.tar` and `.gz`. In most cases² we can easily download, decompress, and create dataframe objects from these files directly in **R**.

To do this we need to:³

- create a temporary file with `tempfile` to store the zipped file which we will remove with the `unlink` command at the end,
- download the file with `download.file`,
- decompress the file with one of the `connections` commands in base **R**,⁴
- read the file with `read.table`.

The reason that we have to go through so many extra steps is that compressed files are more than just a single file, but can contain more than one file as well as metadata.

Let's download a compressed file called `uds_summary.csv` from [2]. It is in a zipped file called `uds_summary.csv.gz`. The file's URL address is `http://www.unified-democracy-scores.org/files/uds_summary.csv.gz`

²Some formats that require the *foreign* package to open are more difficult. This is because functions such as `read.dta` for opening Stata `.dta` files only accept file names or URLs as arguments, not connections, which we create for unzipped files.

³The description of this process is based on a Stack Overflow comment by Dirk Eddelbuettel (see [#tab-top](http://stackoverflow.com/questions/3053833/using-r-to-download-zipped-data-file-extract-and-import-data?answertab=votes), accessed 16 July 2012).

⁴To find a full list of commands type `?connections` in to the **R** console.

```
# For simplicity, store the URL in an object called 'url'.
url <- "http://www.unified-democracy-scores.org/files/uds_summary.csv.gz"

# Create a temporary file called 'temp' to put the zip file into.
temp <- tempfile()

# Download the compressed file into the temporary file.
download.file(url, temp)

# Decompress the file and convert it into a dataframe class object called
# 'data'.
data <- read.csv(gzfile(temp, "uds_summary.csv"))

## Warning: seek on a gzfile connection returned an internal
error

## Warning: seek on a gzfile connection returned an internal
error

# Delete the temporary file.
unlink(temp)
```

5.3.4 Data APIs & feeds

There are growing number of commands that can gather data directly from their sources and import them into **R**. Needless to say, this is great for reproducible research since it not only makes the data gathering process easier (you don't have to download a ton of Excel files and fiddle around with them before even getting the data into **R**), but it also makes replicating the data gathering process much more straightforward. Some examples include:

- The *openair* package, which beyond providing a number of tools for analysing air quality data also has the ability to directly gather data directly from sources such as Kings College London's London Air (<http://www.londonair.org.uk/>) database with the `importKCL` command.

5.4 Basic web scraping

5.4.1 Scraping tables

5.4.2 Gathering and parsing text

6

Storing, Collaborating, Accessing Files, Versioning

CONTENTS

6.1	Saving data in reproducible formats	24
6.2	Storing data in the cloud	24
6.3	Dropbox	24
6.3.1	Version control	24
6.3.2	Accessing Data	25
6.4	GitHub	25
6.4.0.1	Setting Up GitHub	26
6.4.0.2	Version Control in GitHub	27

A stumbling block to actually reproducing a piece of research is getting a hold of the datasets and the codebooks that describe the data used in an analysis.

Researchers often face a number of data management issues that, beyond making their research difficult to reproduce, can make doing the initial research difficult.

First, there is the problem of **storing** the data so that it is protected against computer failure—virus infections, spilling coffee on your laptop, and so on.

Fourth, we almost never create a data set or write a paper perfectly all at once. We may make changes and then realize that we liked an earlier version, or parts of an earlier version better. This is a particularly important issue in data management where we may transform our data in unintended ways and want to go back to an earlier version. Collaborative projects can have regular incidents of one author accidentally deleting something in a file that another author needed, for example.

To deal with these issues we need to store our data in a system that has **version control**. Version control systems keep track of changes we make to our files and allow us to access previous versions if we like.

the data set can often grow and become disorganized. Perhaps even during a data transformation This creates problems

You can solve all of these problems in a couple of different ways using free or low cost cloud-based storage formats. In this chapter we will learn how to use Dropbox and GitHub for data:

- storage,

- accessing,
- collaboration,
- version control.

6.1 Saving data in reproducible formats

Before getting into the details of cloud-based data storage, let's just consider what type of formats you should actually save your data in. A key issue for reproducibility is that others be able to not only get ahold of the exact data you used in your analysis, but be able to understand and use the data not only now, but in the future. Some file formats make this easier than others.

R is able to read (and write) a very wide variety of file formats, mostly through the `foreign` package in `base R`. This includes

6.2 Storing data in the cloud

Storing data locally—on your computer—or on a flash drive is generally more prone to loss than storing data on remote servers, often referred to as ‘the cloud’.

6.3 Dropbox

The easiest types of cloud storage for your research are services like Dropbox and Google Drive. These services typically involve a folder based on your computer's hard drive that is automatically synced with a similar folder on a cloud-based server. Typically you can sign up for the service for free and receive a limited amount of storage space (usually a few gigabytes, which should be plenty if your research is made up of text files.).

Most of these services not only store your data in the cloud, but also provide some way to share files and maybe even includes basic version control. I am going to focus on using Dropbox because it currently offers a complete set of features that allow you to store, version, collaborate, and access your data.

6.3.1 Version control

Dropbox has a simple version control system. Every time you save a document on Dropbox a new version is created. One the Dropbox website

6.3.2 Accessing Data

There are two similar, but importantly different ways to access data stored on Dropbox. All files stored on Dropbox have a URL address through which they can be access from computer connected to the internet. Some of these files can be easily loaded directly into R, while others must me manually (point-and-click) downloaded onto your computer and then loaded into R. The key factor is whether or not the files are located in your **Dropbox's** *Public* folder. Files in the *Public* folder can be downloaded directly into R. Files not in the *Public* folder have to be downloaded manually.¹

Either way you find a file's URL address by first right-clicking on the file icon in you Dropbox folder. If the file is stored in the *Public* folder, you go to Dropbox then **Copy Public Link**. This copies the URL into your clipboard from where you can paste it into your R source code (or wherever). Once you have the URL you can load the file directly into R using the `read.table` command for dataframes (see Chapter 5) or the `source` command for source files (see Chapter 8).

If the file is not in your *Public* folder you also go to Dropbox after right-clicking. Then choose **Get Link**. This will open a webpage in your default web browser from where you can download the file. You can copy and paste the page's URL from your browser's address bar.

You can also get these URL links through the online version of your Dropbox. First log into the Dropbox website. When you hover your curser over a file (or folder) name you will see a chain icon appear on the far right. Clicking on this icon will get you the link.

Storing files in the *Public* folder clearly makes replication easier because the files can be downloaded and run directly in R.

Note that you cannot save files through the URL link. You must save files in the Dropbox folder on your computer.

¹This is not completely true. It is possible to create a web scraper (see Chapter GET) that could download a data file from a file not in your *Public* folder. However, this is kind of a hassle and not practical, especially since the accessing files from the *Public* folder is so easy.

6.4 GitHub

Dropbox does a fine job of meeting our four basic criteria for reproducible data storage. GitHub meets these criteria and more.

GitHub was not explicitly designed to host research projects or even data. It was designed to host ‘socially coded’ computer programs. It built an interface on top of the git version control system that makes it easy relatively easy for a number of collaborators to work together to build a computer program. This seems very far from reproducible research.

However, remember that as reproducible researchers we are just building projects out of interconnected text files. This is exactly the same as computer programming. and like computer programers, we need ways to store, version control, access, and collaborate on our text files. Because GitHub is very actively used by people with very similar needs (who are also really good programmers), the interface offers many highly developed and robust features for reproducible researchers.

As is usually the case, GitHub’s added features mean that it takes a longer time than Dropbox to set up and become familiar. So we need good reasons to want to invest the time needed to learn GitHub rather than just sticking with Dropbox or a similar service. Here is a list of GitHub’s key features relative to Dropbox for reproducible research:

- Git is directly integrated into RStudio projects (**RStudio** also supports the subversion version control system, but I don’t cover that here).
- Dropbox’s version control system only lets you see the file names, the times they were created, who created them, and revert back to specific versions. git tracks every change you make in a way that makes it relatively easy to find the version you want. The GitHub website and GUI programs for Mac and Windows provide nice interfaces for examining specific changes. You can also use the command line to see changes.
- Dropbox creates a new version every time you save a file, which can make it difficult to actually find the version you want. git’s version control system only creates a new version when you tell it to.
- Dropbox does not merge conflicting versions of a file together. This can be annoying when you are collaborating on project and more than one author is making changes to documents. GitHub identifies conflicts and lets you reconcile them.
- The GitHub website has an “Issues” area where you can note and discuss issues you have while doing your research. Basically this is an interactive to-do list for your research project.

6.4.0.1 Setting Up GitHub

There are a number of ways to set up GitHub on your computer. I will briefly cover both the command line version (available for Windows, Mac, and Linux) and the GUI² version currently available only for Windows and Mac.

6.4.0.2 Version Control in GitHub

GitHub's version control system is much more comprehensive than Dropbox's. However, it also has a steeper learning curve.

Reverting to an old version of a file

You can use the `git checkout` command to revert to a previous version of a document, because you accidentally deleted something important or made other changes you don't like. To 'checkout' a particular version of a file type:

```
git checkout COMMITREF FILENAME
```

Now the previous version of the file is in your working directory, where you can commit it as usual.

Let's break down the code. `FILENAME` is the name of the file that you want to change³ and `COMMITREF` is the reference that git gave to the commit you want to revert back to. The reference is easy to find and copy in GitHub. On the file's GitHub page click on the **History** button. This will show you all of the commits. By clicking on **Browse Code** you can see what the file at that commit looks like. Above this button is another with a series of numbers and letters. This is the commit's SHA (Secure Hash Algorithm). For our purposes, it is the commit's reference number. Click on the **Copy SHA** button to the left of the SHA to copy it. You can then paste it as an argument to your `git checkout` command.

More Practice with Command Line GitHub

If you want more practice setting up GitHub in the command line, GitHub and the website Code School have an interactive tutorial that you might find interesting. You can find it at: <http://try.github.com/levels/1/challenges/4>.

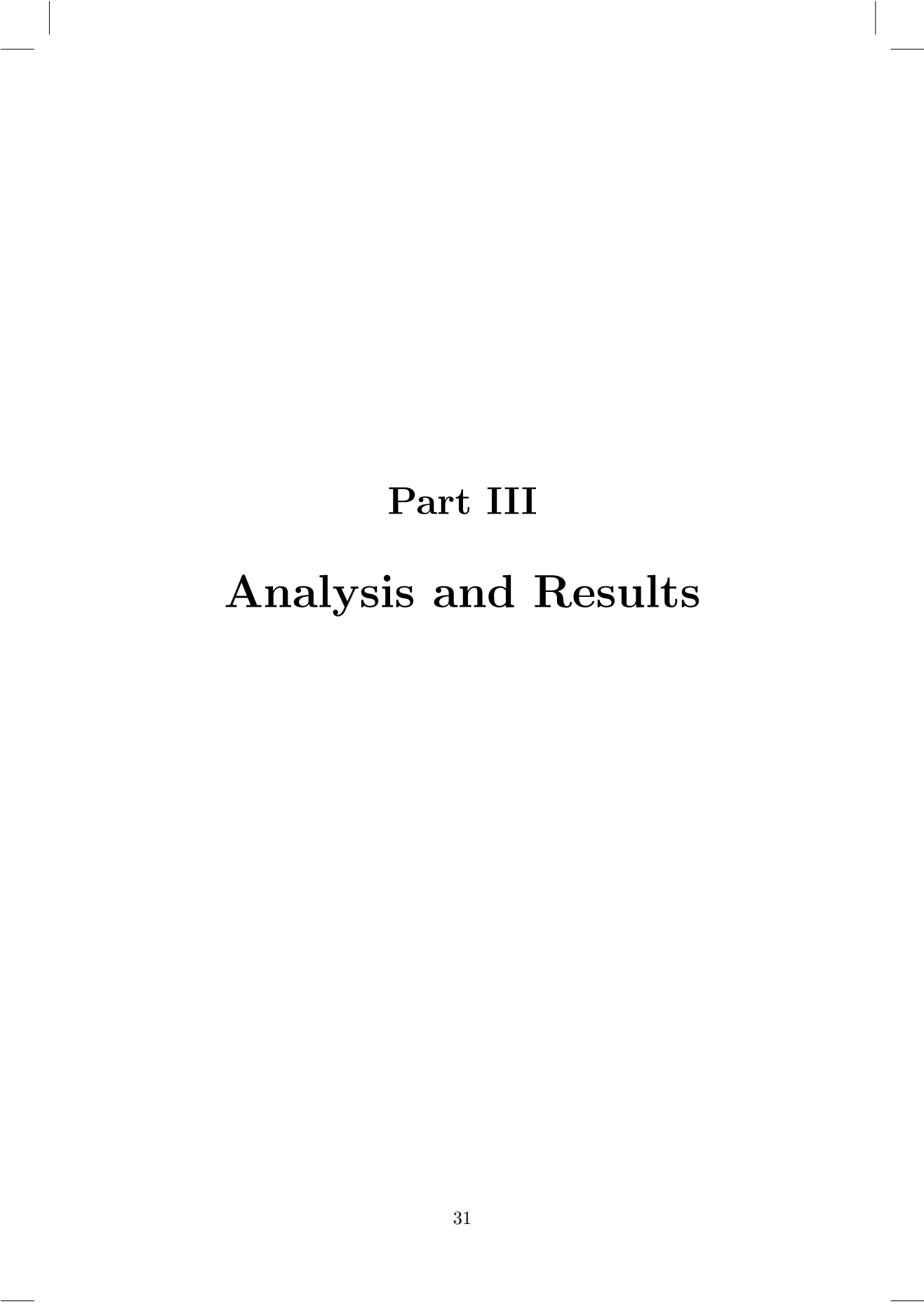
²Graphical User Interface, i.e. not the command line version, but the one with windows that you navigate with your mouse.

³If it is in a repository's subdirectory you will need to include this in the file name.

7

Chapter 7:

CONTENTS



Part III

Analysis and Results



8

CStatistical Modelling and ‘knitr’

CONTENTS

8.1	Incorporating analyses into the markup	33
8.1.1	Full code in the main document	33
8.1.1.1	LaTeX	33
8.1.1.2	Markdown	33
8.1.2	Showing code & results inline	33
8.1.2.1	LaTeX	33
8.1.2.2	Markdown	34
8.1.3	Sourcing R code from another file	34
8.1.3.1	Source from a local file	35
8.1.3.2	Source from a non-secure URL (<code>http</code>)	35
8.1.3.3	Source from a secure URL (<code>https</code>)	35
8.2	Saving output objects for future use	35
8.3	Including highlighted syntax in the output	36
8.3.1	LaTeX	36
8.3.2	Markdown/HTML	36
8.4	Debugging	36

8.1 Incorporating analyses into the markup

8.1.1 Full code in the main document

8.1.1.1 LaTeX

8.1.1.2 Markdown

8.1.2 Showing code & results inline

Sometimes we want to have some **R** code or output to show up in the text of our documents. We may want to include stylized code in our text when we discuss how we did an analysis. We may want to report the mean of some variable in our text.

8.1.2.1 **L^AT_EX**

Static code

If we just want to include a code snippet in our text we can simply use the **L^AT_EX** command `\tt`. This sets our text to ‘typewriter’ font, the standard font for inline code in **L^AT_EX** (I use it in this book, as you’ve probably noticed).

Dynamic code

If we want to dynamically show the results of some **R** code in our text we can use the `\Sexpr` command. This is a pseudo-**L^AT_EX** command. Its structure is more like a **L^AT_EX** command’s structure than `knitr` in that we enclose our **R** code in curly brackets (`{}`) rather than the usual ‘`<<>>= . . . @`’ syntax for code chunks.

For example

8.1.2.2 **Markdown**

Static code

To include static code inline in an **R Markdown** document we enclose the code in single backticks (`“`).

Dynamic code

To include dynamic code in an **R Markdown** document we use the backticks as before but include a the letter `r` after the first one.

8.1.3 **Sourcing R code from another file**

There are a number of reasons that you might want to have your **R** source code located in a separate file from your markup even if you plan to compile them together with `knitr`.

First, it can be unwieldy to edit both your markup and long **R** source code chunks in the same document, even with **RStudio**’s handy `knitr` code collapsing and chunk management options. There are just too many things going on in one document.

Second, you may want to use the same code in multiple documents—an article and presentation for example. It is nice to not have to copy and paste the same code into multiple places, but have multiple documents link to the same source code. Plus if you make changes to the source code, these changes will automatically be made across all of your presentation documents. You don’t need to make the same changes multiple times.

Third, other researchers trying to replicate your work might only be interested in specific parts of your analysis. If you have the analysis broken into separate and clearly labeled files it is easier for these researchers to find the

specific bits of code that they are interested compared to digging through long markup files.

8.1.3.1 Source from a local file

Usually in the early stages of research you may want to source analysis files located on your computer. Doing this is simple. The `knitr` syntax is the same as above. The only change is that instead of writing all of our code in the chunk we save it to its own file and use the `source` command in *base R* to access it. For example:

8.1.3.2 Source from a non-secure URL (http)

Sourcing from your local computer is fine if you are working alone and do not want others to access your code. Once you start collaborating and generally wanting people to be able to replicate your code, you need to use another method.¹

The simplest solution to these issues is to host the replication code in your **Dropbox** public folder. You can find the file’s public URL the same way we did in Chapter 6. Now use the `source` command the same way as before. For example:

8.1.3.3 Source from a secure URL (https)

If you are using **GitHub** or another service that uses secure URLs the steps are generally the same, but you need to use the `source_url` command in the *devtools* package. For **GitHub** based source code we find the file’s URL the same way we did in Chapter 6. Remember to get the URL for the *raw* version of the file.

¹Sure you can make the replication code accessible for download and either instruct others to change the working directory to the replication file or have them change the directory information as necessary. However, this usually just adds an extra complicating step that makes replication harder. It is also a pain if you are collaborating and each author has to constantly change the directories.

8.2 Saving output objects for future use

8.3 Including highlighted syntax in the output

8.3.1 \LaTeX

8.3.2 Markdown/HTML

8.4 Debugging

9

Showing Results with Tables

CONTENTS

9.1	Table Basics	38
9.1.1	Tables in \LaTeX	38
9.1.2	Tables in Markdown/HTML	38
9.2	Creating tables from R objects	38
9.2.1	<code>xtable</code> & <code>texreg</code> basics with supported class objects	38
9.2.1.1	<code>xtable</code> for \LaTeX	38
9.2.1.2	<code>xtable</code> for Markdown	38
9.2.2	<code>xtable</code> with non-supported class objects	38
9.2.3	Basic <code>knitr</code> syntax for tables	40
9.3	Tables with <code>apsrtable</code>	41

Graphs and other visual methods, discussed in the next chapter, can often be a more effective way to present results than tables.¹ Nonetheless, tables of results, descriptive statistics, and so on can sometimes be an important part of communicating research findings.

Creating tables by hand can be tedious no matter what program you are using to type up your results. Even more tedious is making changes to hand-created tables when you make changes to your data and models. Creating these tables can actually introduce new errors—post-analysis!—if you incorrectly copy what is in your R output. This is a very real possibility. The mind can go numb doing that sort of work. Also, creating tables by hand is not very reproducible.

Fortunately, we don't actually need to create tables by hand. There are many ways to have R do the work for us. The goal of this chapter is to learn how to **automate table creation** for documents produced with both \LaTeX and Markdown/HTML. There are a number of ways to turn R objects into tables written in \LaTeX or HTML markup. In this chapter I mostly focus on the `xtable` and `texreg` packages. `xtable` can create tables for both of these markup languages. `texreg` only produces output for \LaTeX . `knitr` allows us to incorporate these tables directly into our documents.

Warning: Automating table creation removes the possibility of adding errors to our analyses by incorrectly copying R output, which is a big potential problem in hand-created tables. Be warned, it is not an error free process. We could easily create inaccurate tables through coding errors. For example, we

¹This is especially true of the small-print, high-density coefficient estimate tables that are sometimes descriptively called 'train schedule' tables.

may incorrectly merge together columns in so that our id variables no longer match the data they are supposed to.

So, as always, it is important to ‘eyeball’ the output. Does it make sense? If we picked a couple values in the R output do they match what is in our final table? If not, we need to go back to the code and see where things have gone wrong. With that caveat, let's start making tables.

9.1 Table Basics

Before getting into the details of how to create tables from R objects we need to first learn how generic tables are created in \LaTeX and Markdown/HTML.

9.1.1 Tables in \LaTeX

9.1.2 Tables in Markdown/HTML

9.2 Creating tables from R objects

9.2.1 `xtable` & `texreg` basics with supported class objects

9.2.1.1 `xtable` for \LaTeX

9.2.1.2 `xtable` for Markdown

9.2.2 `xtable` with non-supported class objects

`xtable` and other commands in similar packages are very convenient for making tables from objects in supported classes.² With supported class objects `xtable` knows where to look for the vectors containing the things—coefficient names, standard errors, and so on—that it needs to create the table. With unsupported classes, however, it doesn't know where to look for these things. We need to help it out.

`xtable` does have a way of dealing with `matrix` and `dataframe` class objects. The rows of these objects become the rows of the table and the columns become the table columns. So, to create tables with non-supported class objects we need to

1. find and extract the information from the unsupported class object that we want in the table,
2. convert this information into a matrix or dataframe where the rows

²To see a full list of classes that `xtable` supports type `methods(xtable)` into the R console.

and columns of the object correspond to the rows and columns of the table that we want,

3. use `xtable` with this object to create the table.

Imagine that we want to create a results table showing the covariate names, coefficient means, and quantiles for marginal posterior distributions from a Bayesian normal linear regression using the `zelig` command [1] and data from the *swiss* dataframe.³ We run our model:

```
# Load required library
library(Zelig)

# Run model
NBModel <- zelig(Examination ~ Education, model = "normal.bayes",
                 data = swiss, cite = FALSE)

# Find NBModel's class
class(NBModel)

## [1] "MCMCZelig"
```

Using the `class` command we found that the model output object is an `MCMCZelig` class object. This class is not supported by `xtable`. If we try to create a summary table called *NBTable* of the results we will get the following error:

```
## Error: no applicable method for 'xtable' applied to an object
of class
## "MCMCZelig"
```

With unsupported class objects we have to create the summary ourselves and extract the things that we want from it manually. This is where a good knowledge of vectors comes in handy.

First, let's create a summary of our output object *NBModel*:

```
NBModelSum <- summary(NBModel)

## Warning: closing unused connection 4
##
(/var/folders/bf/fgxf1t3x6_b-cbb6fjkw9gf80000gn/T//RtmpB0Y1iM/file1ca1261c0f57)
```

We created a new object of the class `summary.MCMCZelig`. We're still not there yet as this object contains not just the covariate names and so on but also information we don't want to include in our results table like the formula that

³This dataframe is loaded by default.

we used. The second step is to extract a matrix from inside *NBModelSum* called *summary* with the component selector (`$`). This matrix is where the things we want in our table are located. I find it easier to work with dataframes, so we'll also convert the matrix into a dataframe.

```
NBSumDataFrame <- data.frame(NBModelSum$summary)
```

Here is what our model results dataframe looks like:

```
##           Mean      SD   X2.5.   X50.  X97.5.
## (Intercept) 10.1397 1.31673  7.5579 10.1566 12.7058
## Education    0.5786 0.09118  0.3963  0.5781  0.7609
## sigma2       34.9703 7.81260 22.9567 33.8782 53.2172
```

Now we have a dataframe object that `xtable` can handle. After a little cleaning up (see the chapter's source code for more details) we can use *NBSumDataFrame* with `xtable` as before to create the following table:

	Mean	2.5%	50%	97.5%
(Intercept)	10.14	7.56	10.16	12.71
Education	0.58	0.40	0.58	0.76
sigma2	34.97	22.96	33.88	53.22

TABLE 9.1

Coefficient Estimates Predicting Examination Scores in Swiss Cantons (1888)
Found Using Bayesian Normal Linear Regression

It may take a bit of hunting to find what you want, but a similar process can be used to create tables from objects of virtually any class.⁴ Hunting for what you want is generally easier by clicking on the object in RStudio's workspace pane.

9.2.3 Basic knitr syntax for tables

So far we have only looked at how to create \LaTeX and HTML tables from R objects. How can we knit these tables into our presentation documents?

The most important `knitr` chunk option for showing the markup created by these packages as tables is `results`. The `results` option can have three values:

- `markup`,
- `asis`,

⁴This process can also be used to create graphics.

- `hide`.

`hide` clearly hides the results of whatever we have in our code chunk; no results show up.

9.3 Tables with `apsrtable`

10

Chapter 10:

CONTENTS

Part IV

Presentation Documents



11

Presenting with L^AT_EX

CONTENTS

11.1 The Basics	47
11.1.1 Editors	47
11.1.2 The Header	47
11.1.3 Headings	47
11.1.4 Footnotes & Bibliographies	47
11.1.4.1 Footnotes	47
11.1.4.2 Bibliographies	47

11.1 The Basics

11.1.1 Editors

11.1.2 The Header

11.1.3 Headings

11.1.4 Footnotes & Bibliographies

11.1.4.1 Footnotes

Plain, non-bibliographic footnotes are easy to create in L^AT_EX. Simply place `\footnote{` where you would like the footnote number to appear in the text. Then type in the footnote's text and of course remember to close it with a `}`. L^AT_EX does the rest, including formatting and numbering.

11.1.4.2 Bibliographies

Citing R Packages with BibTeX

Researchers are pretty good about consistently citing others' articles and data. However, citing the R packages used in an analysis is very inconsistent. This is unfortunate not only because correct attribution is not being given but also because it makes reproducibility harder because it obscures important steps that were taken in the research process. Fortunately, R actually includes the tools to quickly generate citations, including the version of the package you are using. It can also add them directly to an existing bibliography file.

You can automatically create citations for R packages using the `citation`

command in *base* R. For example if we want the citation information for the *Zelig* package we would simply type:

```
citation("ggplot2")

##
## To cite ggplot2 in publications, please use:
##
## H. Wickham. ggplot2: elegant graphics for data analysis.
## Springer New York, 2009.
##
## A BibTeX entry for LaTeX users is
##
## @Book{,
##   author = {Hadley Wickham},
##   title = {ggplot2: elegant graphics for data analysis},
##   publisher = {Springer New York},
##   year = {2009},
##   isbn = {978-0-387-98140-6},
##   url = {http://had.co.nz/ggplot2/book},
## }
```

This gives us both the plain citation as well as the BibTeX version for use in L^AT_EX and MultiMarkdown documents. If you only want the BibTeX version of the citation we can use the `toBibtex` command in the *utils* package.

```
toBibtex(citation("ggplot2"))

## @Book{,
##   author = {Hadley Wickham},
##   title = {ggplot2: elegant graphics for data analysis},
##   publisher = {Springer New York},
##   year = {2009},
##   isbn = {978-0-387-98140-6},
##   url = {http://had.co.nz/ggplot2/book},
## }
```

You can append the citation to your existing BibTeX file using the `sink` command in *base* R. This command diverts our output and/or the messages to a file. For example, imagine that our existing BibTeX file is called `biblio.bib`. To add the *Zelig* package citation:

```
# Divert output to biblio.bib
sink(file = "biblio.bib",
      append = TRUE, type = c("output"))
```



```
)  
toBibtex(citation("ggplot2")) sink()
```

This places the citation at the end of our `biblio.bib` file. It is very important to include the argument `append = TRUE`. If you don't you will erase the existing file. The argument `type = c("output")` tells R to include only the output, not the messages.

An even faster way to add citations to a bibliography is with `write.bibtex` command in the *knitcitations* package. To add the *Zelig* citation to our `biblio.bib` file we only need to enter:

```
# Load package  
library(knitcitations)  
  
# Write Zelig citation and  
# to biblio.bib  
write.bibtex(entry = c("ggplot2"),  
             file = "bibliography.bib", append = TRUE)
```

In Chapter 13 we'll look at the `knitcitations` package in more detail.

12

Chapter 12:

CONTENTS

12.0.5 Editors	51
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12.0.5 Editors

13

Presenting on the Web and Beyond with Markdown/HTML

CONTENTS

13.1 The Basics	53
13.1.1 Headings	53
13.1.2 Footnotes and bibliographies with MultiMarkdown	53
13.1.3 Math	54
13.1.4 Drawing figures with CSS	54
13.2 Simple webpages	54
13.2.1 RPubS	54
13.2.2 Hosting webpages with Dropbox	54
13.3 Presentations with Slidify	54
13.4 Reproducible websites	54
13.4.1 Blogging with Tumblr	54
13.4.2 Jekyll-Bootstrap and GitHub	54
13.4.3 Jekyll and Github Pages	54
13.5 Using Markdown for non-HTML output with Pandoc	54

13.1 The Basics

13.1.1 Headings

Headings in Markdown are extremely simple. To create a line in the style of the topmost heading—maybe a title—just place one hash mark (#) at the beginning of the line. The second tier heading just gets two hashes (##) and so on. You can also put the hash mark(s) at the end of the heading, but this is not necessary.

13.1.2 Footnotes and bibliographies with MultiMarkdown

13.1.3 Math

13.1.4 Drawing figures with CSS

13.2 Simple webpages

13.2.1 RPubS

13.2.2 Hosting webpages with Dropbox

13.3 Presentations with Slidify

13.4 Reproducible websites

13.4.1 Blogging with Tumblr

13.4.2 Jekyll-Bootstrap and GitHub

see <http://jfisher-usgs.github.com/r/2012/07/03/knitr-jekyll/>

13.4.3 Jekyll and Github Pages

13.5 Using Markdown for non-HTML output with Pandoc

Markdown syntax is very simple. So simple, you may be tempted to write many or all of your presentation documents in Markdown. This presents the obvious problem of how to convert your markdown documents to other markup languages if, for example, you would want to create a \LaTeX formatted PDF.

Pandoc can help solve this problem. Pandoc is a command line program that can convert files written in Markdown, HTML, \LaTeX , and a number of other markup languages¹ to any of the other formats.

To use Pandoc first install it by following the instructions at <http://johnmacfarlane.net/pandoc/installing.html>. Luckily you do not need to open a shell window in addition to **R** to run Pandoc. Instead you can run all Pandoc commands in **R** with the `system` command.

For example,

¹See the Pandoc website for more details: <http://johnmacfarlane.net/pandoc/>

14

Chapter 14:

CONTENTS

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Index

SAS, 4