

An Introduction to Quantitative Text Analysis for Linguistics

Reproducible Research using R

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Table of contents

License	3
Credits	4
Acknowledgements	4
Build information	4
Preface	5
Rationale	5
Aims	6
Approach	7
Structure	7
Book level	7
Chapter level	8
Resources	9
Getting started	10
R and IDEs	10
R packages	11
Git and GitHub	12
Getting help	13
Conventions	14
Prose	14
Code blocks	15
Callouts	16
Activities	17
Summary	18
To the instructor	18
I Orientation	19
1 Text analysis	21
1.1 Enter science	21
1.2 Data analysis	23
1.2.1 Emergence of data science	23
1.2.2 Data science toolbelt	23
1.2.3 Quant everywhere	24

1.3	Language analysis	25
1.3.1	Qualities and quantities	25
1.3.2	The nature of data	26
1.4	Text analysis	28
1.4.1	Aims	28
1.4.2	Approaches	29
1.4.3	Implementation	29
1.4.4	Applications	31
	Activities	33
	Summary	33
II	Foundations	34
2	Data	36
2.1	Data	36
2.1.1	Populations and samples	37
2.1.2	Corpora	38
2.1.3	Other considerations	39
2.2	Information	45
2.2.1	Organization	45
2.2.2	Transformation	48
2.3	Documentation	58
2.3.1	Data origin	59
2.3.2	Data dictionaries	59
	Activities	60
	Summary	61
3	Analysis	63
3.1	Describe	64
3.1.1	Central tendency	65
3.1.2	Dispersion	66
3.1.3	Distributions	68
3.1.4	Association	76
3.2	Analyze	81
3.2.1	Explore	81
3.2.2	Predict	83
3.2.3	Infer	85
3.3	Communicate	88
3.3.1	Report	88
3.3.2	Document	88
	Activities	89
	Summary	89

4 Research	92
4.1 Frame	93
4.2 Connect	93
4.2.1 Research area	93
4.2.2 Research problem	94
4.3 Define	96
4.3.1 Research aim	96
4.3.2 Research question	96
4.4 Blueprint	98
4.4.1 Plan	99
4.4.2 Scaffold	101
Activities	104
Summary	104
III Preparation	106
5 Acquire	108
5.1 Downloads	109
5.1.1 Manual	109
5.1.2 Programmatic	114
5.2 APIs	121
Activities	130
Summary	131
6 Curate	132
6.1 Unstructured	133
6.1.1 Reading data	133
6.1.2 Orientation	133
6.1.3 Tidy the data	136
6.2 Structured	139
6.2.1 Reading datasets	139
6.2.2 Orientation	140
6.2.3 Tidy the dataset	142
6.3 Semi-structured	148
6.3.1 Reading data	148
6.3.2 Orientation	148
6.3.3 Tidy the data	151
6.4 Documentation	159
Activities	160
Summary	161

7 Transform	162
7.1 Preparation	162
7.1.1 Normalization	164
7.1.2 Tokenization	168
7.2 Enrichment	172
7.2.1 Generation	174
7.2.2 Recoding	179
7.2.3 Integration	182
Activities	191
Summary	192
IV Analysis	193
8 Explore	195
8.1 Orientation	196
8.1.1 Goals and approach	196
8.2 Analysis	197
8.2.1 Descriptive analysis	199
8.2.2 Unsupervised learning	226
Activities	258
Summary	258
9 Predict	260
9.1 Orientation	260
9.1.1 Research goal	261
9.1.2 Approach	262
9.2 Analysis	264
9.2.1 Text classification	266
9.2.2 Text regression	298
Activities	321
Summary	322
10 Infer	323
10.1 Orientation	323
10.1.1 Research goal	324
10.1.2 Approach	324
10.2 Analysis	327
10.2.1 Categorical	328
10.2.2 Numeric	364
Activities	394
Summary	395

V Communication	396
11 Contribute	398
11.1 Goals	399
11.2 Write ups	399
11.2.1 Contents	399
11.2.2 Structure	402
11.3 Reproducibility	403
Activities	406
Summary	406
References	408
Appendices	416
A Data	416
A.1 ANC	416
A.2 BNC	416
A.3 CABNC	416
A.4 CEDEL2	416
A.5 ENNTT	416

Welcome

The goal of this textbook is to provide readers with foundational knowledge and practical skills in quantitative text analysis using the R programming language.

By the end of this textbook, readers will be able to identify, interpret and evaluate data analysis procedures and results to support research questions within language science. Additionally, readers will gain experience in designing and implementing research projects that involve processing and analyzing textual data employing modern programming strategies. This textbook aims to instill a strong sense of reproducible research practices, which are critical for promoting transparency, verification, and sharing of research findings.

This textbook is geared towards advanced undergraduates, graduate students, and researchers looking to expand their methodological toolbox. It assumes no prior knowledge of programming or quantitative methods and prioritizes practical application and intuitive understanding over technical details.

About the author

Dr. Jerid Francom is Associate Professor of Spanish and Linguistics at Wake Forest University. His research focuses on the use of language corpora from a variety of sources (news, social media, and other internet sources) to better understand the linguistic and cultural similarities and differences between language varieties for both scholarly and pedagogical projects. He has published on topics including the development, annotation, and evaluation of linguistic corpora and analyzed corpora through corpus, psycholinguistic, and computational methodologies. He also has experience working with and teaching statistical programming with R.

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¹<https://francojc.github.io/>

Credits

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Build information

This textbook was built with the `quarto` package (Allaire 2023) and the `bookdown` package (Xie 2023a) for R. The source code for this book is available on GitHub³.

This version of the textbook was built with R version 4.3.2 (2023-10-31) on macOS Ventura 13.6.3 with the following packages:

package	version	source
dplyr	1.1.4	CRAN (R 4.3.2)
ggplot2	3.4.4	CRAN (R 4.3.2)
here	1.0.1	CRAN (R 4.3.0)
kableExtra	1.4.0	CRAN (R 4.3.2)
knitr	1.45	CRAN (R 4.3.2)
qtlrkit	0.9.2	Github (qtlr/qtlrkit@e6c0ee871482c503bd8b159c5ea4dd562383fa66)
readr	2.1.5	CRAN (R 4.3.2)
reprex	2.1.0	CRAN (R 4.3.2)
rmarkdown	2.25	CRAN (R 4.3.1)
rstudioapi	0.15.0	CRAN (R 4.3.1)
scales	1.3.0	CRAN (R 4.3.2)
stringr	1.5.1	CRAN (R 4.3.2)
tibble	3.2.1	CRAN (R 4.3.2)
tidyverse	1.3.1	CRAN (R 4.3.2)
tinytable	0.0.5	CRAN (R 4.3.2)

²<https://fontawesome.com/>

³<https://github.com/qtlr/book>

Preface

The journey of a thousand miles begins with one step.

— Lao Tzu

Outcomes

- Comprehend the book's rationale, learning goals, and pedagogical approach.
- Navigate and engage with the book's structure and content effectively.
- Set up the computing environment and utilize textbook and support resources for an optimal learning experience.

The purpose of this chapter is to present the rationale behind this textbook, outline the key learning objectives, describe the pedagogical approach, and identify the intended audience. Additionally, this chapter will provide readers with a guide to the book's structure and the scope of its content, as well as instructions for the instructor and a summary of supporting resources available. Finally, this chapter will provide readers with information on setting up their computing environment and where to seek support.

Rationale

Data science, an interdisciplinary field that combines knowledge and skills from statistics, computer science, and domain-specific expertise to extract meaningful insight from structured and unstructured data, has emerged as an exciting and rapidly growing field in recent years, driven in large part by the increase in computing power available to the average individual and the abundance of electronic data now available through the internet. These advances have become an integral part of the modern scientific landscape, with data-driven insights now being used to inform decision-making in a wide variety of academic fields, including linguistics and language-related disciplines.

This textbook seeks to meet this growing demand by providing an introduction to the fundamental concepts and practical programming skills from data science applied to the task of quantitative text analysis. It is intended primarily for undergraduate students, but may also be useful for graduates and researchers seeking to expand their methodological toolbox. The textbook takes a pedagogical approach which assumes no prior experience with statistics

or programming, making it an accessible resource for novices beginning their exploration of quantitative text analysis methods.

Aims

The overarching goal of this textbook is to provide readers with foundational knowledge and practical skills to conduct and evaluate quantitative text analysis using the R programming language and other open source tools and technologies. The specific aims are to develop the reader's proficiency in three main areas:

- **Data literacy:** Identify, interpret and evaluate data analysis procedures and results

Throughout this textbook we will explore topics which will help you understand how data analysis methods derive insight from data. In this process you will be encouraged to critically evaluate connections across linguistic and language-related disciplines using data analysis knowledge and skills. Data literacy is an invaluable skillset for academics and professionals but also is an indispensable aptitude for in the 21st century citizens to navigate and actively participate in the 'Information Age' in which we live (Carmi et al. 2020).

- **Research skills:** Design, implement, and communicate quantitative research

This aim does not differ significantly, in spirit, from common learning outcomes in a research methods course. However, working with text will incur a series of key steps in the selection, collection, and preparation of the data that are unique to text analysis projects. In addition, I will stress the importance of research documentation and creating reproducible research as an integral part of modern scientific inquiry (Buckheit and Donoho 1995).

- **Programming skills:** Apply programmatic strategies to develop and collaborate on reproducible research projects

Modern data analysis, and by extension, text analysis is conducted using programming. There are various key reasons for this: a programming approach (1) affords researchers unlimited research freedom –if you can envision it, you can program it, (2) underlies well-documented and reproducible research (Gandrud 2015), and (3) invites researchers to engage more intimately with the data and the methods for analysis.

These aims are important for linguistics students because they provide a foundation for concepts and in the skills required to succeed in the rapidly evolving landscape of 21st-century research. These abilities enable researchers to evaluate and conduct high-quality empirical investigation across linguistic fields on a wide variety of topics. Moreover, these skills go beyond

linguistics research; they are widely applicable across many disciplines where quantitative data analysis and programming are becoming increasingly important. Thus, this textbook provides students with a comprehensive introduction to quantitative text analysis that is relevant to linguistics research and that equips them with valuable skills for their future careers.

Approach

The approach taken in this textbook is designed to accommodate linguistics students and researchers with little to no prior experience with programming or quantitative methods. With this in mind the objective is connect conceptual understanding with practical application. Real-world data and research tasks relevant to linguistics are used throughout the book to provide context and to motivate the learning process⁴. Furthermore, as an introduction to the field, the textbook focuses on the most common and fundamental methods and techniques for quantitative text analysis and prioritizes breadth over depth and intuitive understanding over technical explanations. On the programming side, the **Tidyverse** approach to programming in R will be adopted. This approach provides a consistent syntax across different packages and is known for its legibility, making it easier for readers to understand and write code. Together, these strategies form an approach that is intended to provide readers with an accessible resource to gain a foothold in the field and to equip them with the knowledge and skills to apply quantitative text analysis in their own research.

Structure

The aims and approach described above is reflected in the overall structure of the book and each chapter.

Book level

At the book level, there are five interdependent parts:

Part I “Orientation” provides the necessary background knowledge to situate quantitative text analysis in the wider context of data analysis and linguistic research and to provide a clearer picture of what text analysis entails and its range of applications.

⁴Research data and questions are primarily based on English for wide accessibility as it is the *de facto* language of academics and research. However, the methods and techniques presented in this textbook are applicable to many other languages.

The subsequent parts are directly aligned with the data analysis process. The building blocks of this process are reflected in ‘**Data to Insight Hierarchy (DIKI)**’ visualized in Figure 1⁵.

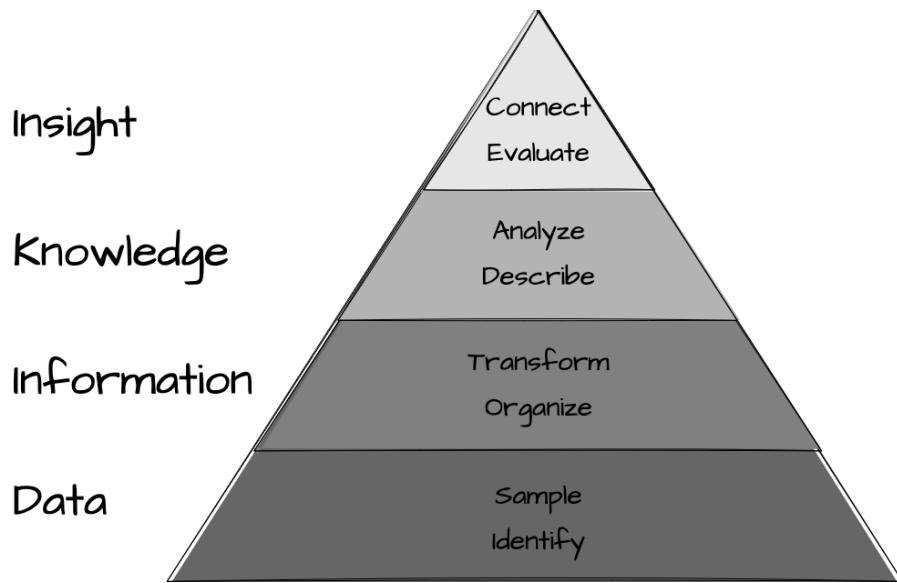


Figure 1: Data to Insight Hierarchy (DIKI)

The DIKI Hierarchy highlights the stages and intermediate steps required to derive insight from data. Part II “Foundations” provides a conceptual introduction to the DIKI Hierarchy and establishes foundational knowledge about data, information, knowledge, and insight which is fundamental to developing a viable research plan.

Parts III “Preparation” and IV “Analysis” focus on the implementation process. Part III covers the steps involved in preparing data for analysis, including data acquisition, curation, and transformation. Part IV covers the steps involved in conducting analysis, including exploratory, predictive, and inferential data analysis.

The final part, Part V “Communication”, covers the final stage of the data analysis process, which is to communicate the results of the analysis. This includes the structure and content of research reports as well as the process of publishing, sharing, and collaborating on research.

⁵Adapted from Ackoff (1989) and Rowley (2007).

Chapter level

At the chapter level, both conceptual and programming skills are developed in stages⁶. The chapter-level structure is consistent across chapters and can be seen in Table 1.

Table 2: The general structure of a chapter

Component	Purpose	Resource	Stage
Outcomes Overview	Identify the learning objectives for the chapter Provide a brief introduction to the chapter topic	Textbook	Introduction
Coding Lessons	Teach programming techniques with hands-on interactive exercises	GitHub	Skills
Content	Combine conceptual discussions and programming skills, incorporating thought-provoking questions, relevant studies, and advanced topic references	Textbook	Knowledge
Recipes	Offer step-by-step programming examples related to the chapter and relevant for the upcoming lab	Resources website	Comprehension
Labs	Allow readers to apply chapter-specific concepts and techniques to practical tasks	GitHub	Application
Summary	Review the key concepts and skills covered in the chapter	Textbook	Review

Each chapter will begin with a list of key learning outcomes followed by a brief introduction to the chapter's content. The goal is to orient the reader to the chapter. Next there will be a prompt to complete the interactive coding lesson(s) to introduce readers to key programming concepts related to the chapter through hands-on experience and then the main content of the chapter will follow. The content will be a combination of conceptual discussions and programming skills, incorporating thought-provoking questions ('💡 Consider this'), relevant studies ('📄 Case study'), and advanced topic references ('📌 Dive deeper'). Together these components form the skills and knowledge phase.

The next phase is the application phase. This phase will include step-by-step programming demonstrations related to the chapter (Recipes) and lab exercises that allow readers to apply their knowledge and skills chapter-related tasks. Finally, the chapters conclude with a summary of the key concepts and skills covered in the chapter and in the associated activites.

⁶These stages attempt to capture the general progression of learning reflected in Bloom's Taxonomy (see Krathwohl (2002) for a description and revision).

Resources

The description and location of the available resources to support the aims and approach of this textbook appear in Table 2.

Table 3: Resources available to support the aims and approach of this textbook

Resource	Description	Location
Textbook	Prose discussion, figures/ tables, R code, case studies, and thought and practical exercises	Physical/ Online ⁷
qtalrkit ⁸	R package with functions for accessing data and datasets, as well as various useful functions developed specifically for this textbook	CRAN/ GitHub ⁹
Resources Kit	Programming tutorials (Recipes), guides to enhance the reader's recognition of how programming strategies are implemented, and other supplementary materials ¹⁰	Online ¹¹
Lessons	A set of interactive R programming lessons (Swirl)	GitHub ¹²
Labs	A set of lab exercises designed to guide the reader through practical hands-on programming applications	GitHub ¹³

Getting started

Before jumping in to this and subsequent chapter's textbook activities, it is important to prepare your computing environment and understand how to take advantage of the resources available, both those directly and indirectly associated with the textbook.

R and IDEs

Programming is the backbone for modern quantitative research. Among the many programming languages available, R is a popular open-source language and software environment for

⁷<https://qtalr.github.io/book/>

⁸The *qtalrkit* package (Francom 2023) is not yet available on CRAN but will be in the future.

⁹<https://github.com/qtalr/qtalrkit>

¹⁰Including Instructor materials and Errata for the textbook.

¹¹<https://qtalr.github.io/qtalrkit/>

¹²<https://github.com/qtalr/>

¹³<https://github.com/qtalr/>

statistical computing. R is popular with statisticians and has been adopted as the *de facto* language by many other fields in natural and social sciences, including linguistics. It is freely downloadable from The R Project for Statistical Programming¹⁴ website and is available for macOS, Linux, and Windows¹⁵ operating systems.

Successfully installing R is rarely the last step in setting up your R-enabled computing environment. The majority of R users also install an **integrated development environment** (IDE). An IDE, such as RStudio¹⁶ or Visual Studio Code¹⁷, provide a **graphical user interface** (GUI) for working with R. In effect, IDEs provide a dashboard for working with R and are designed to make it easier to write and execute R code. IDEs also provide a number of other useful features such as syntax highlighting, code completion, and debugging. IDEs are not required to work with R but they are *highly* recommended.

Choosing to install R and an IDE directly on your personal computer, which is known as your **local environment**, is not the only option to work with R. Other options include working with R in a **remote environment** or a **virtual environment**.

Guides

For more information and instructions on setting up an R environment consult the Setting up an R environment^a guide.

^a<https://qtalr.github.io/qtalrkit/articles/guide-1.html>

There are trade-offs in terms of cost, convenience, and flexibility when choosing to work with R in a local, remote, or virtual environment. The choice is yours and you can always change your mind later. The important thing is to get started and begin learning R. Furthermore, any of the approaches described here will be compatible with this textbook.

R packages

As you progress in your R programming experience, you'll find yourself leveraging code from other R users, which is typically provided as packages. Packages are sets of functions and/or datasets that are freely accessible for download, designed to perform a specific set of interrelated tasks. They enhance the capabilities of R. Official R packages can be found in repositories like CRAN¹⁸ (Comprehensive R Archive Network), while other packages can be obtained from code-sharing platforms such as GitHub¹⁹.

¹⁴<https://www.r-project.org/>

¹⁵<https://cloud.r-project.org/>

¹⁶<https://posit.co/products/open-source/rstudio/>

¹⁷<https://code.visualstudio.com/>

¹⁸<https://cran.r-project.org/>

¹⁹<https://github.com/>

💡 Consider this

The Comprehensive R Archive Network (CRAN) includes groupings of popular packages related to a given applied programming task called Task Views^a. Explore the available CRAN Task Views listings. Note the variety of areas (tasks) that are covered in this listing. Now explore in more detail one of the following task views which are directly related to topics covered in this textbook noting the associated packages and their descriptions: (1) Cluster, (2) MachineLearning, (3) NaturalLanguageProcessing, or (4) ReproducibleResearch.

^a<https://cran.r-project.org/web/views/>

You will download a number of packages at different stages of this textbook, but there is a set of packages that will be key to have from the get go. Once you have access to a working R/RStudio environment, you can proceed to install the following packages.

↳ Guides

For instructions on how to install the `qtalrkit` package from GitHub and download and use the interactive R programming lessons for this textbook, see the Getting started^a guide.

^a<https://qtalr.github.io/qtalrkit/articles/qtalrkit.html>

Install the following packages from CRAN.

- `tidyverse` (Wickham 2023b)
- `remotes` (Csárdi et al. 2023)
- `tinytex` (Xie 2023b)
- `swirl` (Kross et al. 2020)

You can do this by running the following code in an R console:

```
# install key packages from CRAN
install.packages(c("tidyverse", "remotes", "tinytex", "swirl"))
```

Git and GitHub

↳ Guides

For more information and instructions on setting up version control and interacting with GitHub consult the Setting up Git and GitHub^a guide.

^a<https://qtalr.github.io/qtalrkit/articles/guide-2.html>

GitHub²⁰ is a code sharing website. Modern computing is highly collaborative and GitHub is a very popular platform for sharing and collaborating on coding projects. The lab exercises for this textbook²¹ are shared on GitHub. To access and complete these exercises you will need to sign up for a (free) GitHub account²² and then set up the version control software `git` on your computing environment, if it is not already.

Getting help

The technologies employed in this approach to text analysis will include a somewhat steep learning curve. And in all honesty, the learning never stops! Both seasoned programmers and beginners alike need assistance. Fortunately there is a very large community of programmers who have developed many official support resources and who actively contribute to official and unofficial discussion forums. Together these resources provide many avenues for overcoming challenges.

In Table 3, I provide a list of steps for seeking help with R.

Table 4: Recommended order for seeking help with R

Order	Resource	Description
1	Official R Documentation	Access the official documentation by running <code>help(package = "package_name")</code> in an R console. Use the <code>?</code> operator followed by the package or function name. Check out available Vignettes by running <code>browseVignettes("package_name")</code> .
2	Web Search	Look for package documentation and vignettes on the web. A popular site for this is R-Universe.
3	RStudio IDE Help Toolbar	If you're using RStudio IDE, use the "Help" toolbar menu. It provides links to help resources, guides, and manuals.
4	Online Discussion Forums	Sites like Stack Overflow and RStudio Community are great platforms where the programming community asks and answers questions related to real-world issues.
5	Post Questions with Reprex	When posting a question, especially those involving coding issues or errors, provide enough background and include a reproducible example (reprex) - a minimal piece of code that demonstrates your issue. This helps others understand and answer your question effectively.

²⁰<https://github.com/>

²¹<https://github.com/stars/francojc/lists/labs>

²²https://github.com/signup?ref_cta=Sign+up&ref_loc=header+logged+out&ref_page=%2F&source=header-home

Guides

For information on how to create a minimal reproducible example with the `reprex` package (Bryan et al. 2024), consult the Creating reproducible examples^a guide.

^a<https://qtalr.github.io/qtalrkit/articles/guide-3.html>

The take-home message here is that you are not alone. There are many people world-wide that are learning to program and/ or contribute to the learning of others. The more you engage with these resources and communities the more successful your learning will be. As soon as you are able, pay it forward. Posting questions and offering answers helps the community and engages and refines your skills –a win-win.

Conventions

To facilitate the learning process, this textbook will employ a number of conventions. These conventions are intended to help the reader navigate the text and to signal the reader’s attention to important concepts and information.

Prose

The following typographic conventions are used throughout the text:

- *Italics*
 - Filenames, file extensions, directory paths, and URLs.
- **Fixed-width**
 - Package names, function names, variable names, and in-line code including expressions and operators.
- **Bold**
 - Key concepts when first introduced.
- **Linked text**²³
 - Links to internal and external resources, footnotes, and citations including references to R packages when first introduced.

²³<https://qtalr.github.io/qtalrkit/>

Code blocks

More lengthy code will be presented in code blocks, as seen in Example 0.1.

Example 0.1.

```
# A function that takes a name and returns a greeting
greetings <- function(name) {
  paste("Hello", name)
}

greetings(name = "Jerid") # apply function to a name

> [1] "Hello Jerid"
```

There are a couple of things to note about the code in Example 0.1. First, it shows the code that is run in R as well as the output that is returned. The code will appear in a box and the output will appear below the box. Both code and output will appear in fixed-width font. Output which is text will be prefixed with `>`. Second, the `#` symbol is used to signal a **code comment**, a human-facing description. Everything right of a `#` is not run as code. In this textbook you will see code comments above code on a separate line and to the right of code on the same line. It is good practice to comment your code to enhance readability and to help others understand what your code is doing.

All figures, tables, and images in this textbook are generated by code blocks but only code for those elements that are relevant for discussion will be shown. However, if you wish to see the code for any element in this textbook, you can visit the GitHub repository <https://qtalr.github.io/book/>.

When a reference to a file and its contents is made, it will appear as in File 0.1.

File 0.1 example.R R script

```
# Load libraries
library(tidyverse)

# Add 1 and 1
1 + 1
```

Callouts

Callouts are used to signal the reader's attention to content, activity, and other important sections. The following callouts are used in this textbook:

Content

Outcomes

Learning outcomes for the chapter appear here.

Consider this

Points for you to consider and questions to explore appear here.

Case study

Case studies for applying conceptual knowledge and coding skills covered in the chapter appear here.

Dive deeper

Links to additional resources for diving deeper into the topic appear here.

Activities

Lessons

Links to swirl lessons for practicing coding skills for the chapter appear here.

Recipe

Links to demonstration programming tasks on the qtalr site for the chapter appear here.

Lab

Links to lab exercises for applying conceptual knowledge and coding skills on the qtalr GitHub repository for the chapter appear here.

Other

Tip

Tips for using R and related tools appear here.

⚠ Warning

Warnings for using R and related tools appear here.

Activities

At this point you should have a working R environment with the core packages including `qtalrkit` installed. You should also have verified that you have a working Git environment and that you have a GitHub account. If you have not completed these tasks, return to the guides listed above in “Getting started” of this Preface and complete them before proceeding.

The following activities are designed to help you become familiar with the tools and resources that you will be using throughout this textbook. These and subsequent activities are designed to be completed in the order that they are presented in this textbook.

➤ Lessons

What: Intro to Swirl^a

How: In the R console load `swirl`, run `swirl()`, and follow prompts to select the lesson.

Why: To familiarize you with navigating, selecting, and completing `swirl` lessons for interactive R programming tutorials.

^a<https://github.com/qtalr/lessons>

cook Recipe

What: Literate Programming and Quarto^a

How: Read Recipe 0, complete comprehension check, and prepare for Lab 0.

Why: To introduce the concept of Literate Programming and how to create literate documents using R and Quarto.

^a<https://qtalr.github.io/qtalrkit/articles/recipe-0.html>

lab Lab

What: Writing with code^a

How: Clone, fork, and complete the steps in Lab 0.

Why: To put literate programming techniques covered in Recipe 0 into practice. Specifically, you will create and edit a Quarto document and render a report in PDF format.

^a<https://github.com/qtalr/lab-00>

Summary

This preface outlines the textbook's underlying principles, learning goals, teaching methods, and target audience. The chapter also offers advice on how to navigate the book's layout, comprehend its subject matter, and make use of supplementary materials. With this foundation, you're now prepared to delve into quantitative text analysis. I hope you enjoy the journey!

To the instructor

For recommendations on how to use this textbook in your course and to access additional resources, visit the Instructor Guide²⁴ on the companion website.

²⁴<https://qtalr.github.io/qtalrkit/articles/instructor-guide.html>

Part I

Orientation

In this part, I introduce fundamental concepts that are essential for understanding text analysis in its research and methodological context. We start by pointing to the limitations of human cognition in processing vast amounts of information and that underscore the need for scientific methods to objectively analyze data. A brief history of quantitative data analysis highlights the commonalities between text analysis and other quantitative methods. We then discuss the role of quantitative methods in language research, and how text analysis contributes to the field. As we transition into the subsequent parts of the textbook, these initial insights will serve as a backbone for the entire text analysis process.

1 Text analysis

Everything about science is changing because of the impact of information technology and the data deluge.

— Jim Gray

▀ Outcomes

- Understand the role and goals of data analysis both within and outside of academia.
- Describe the various approaches to quantitative language research.
- Identify the applications of text analysis in different contexts.

In this chapter, I will aim to introduce the topic of text analysis and provide the context needed to understand how text analysis fits in a larger universe of science and the ever-ubiquitous methods of data science, with attention to how linguistics and language-related studies employ data analysis down to the particular area of text analysis.

➤ Lessons

What: Workspace, Vectors^a

How: In an R console load `swirl`, run `swirl()`, and follow prompts to select the lesson.

Why: To examine your local workspace in RStudio and understand the relationship between your R workspace and the file system of your computing environment. To explore the key building blocks of the R programming language.

^a<https://github.com/qtalr/lessons>

1.1 Enter science

The world around us is full of actions and interactions so numerous that it is difficult to truly comprehend. As individuals, we see and experience this world, gaining knowledge and building heuristic understanding of how it works and how we can interact with it. This happens regardless of one's educational background. As humans, we are designed for this. Our minds process countless sensory inputs, which enable skills and abilities that we often take for granted, such as predicting what will happen if someone is about to knock a wine glass off a table and onto a concrete floor. Even if we have never encountered this specific situation before, our

minds somehow instinctively make an effort to warn the potential glass-breaker before it is too late.

You have most likely not stopped to consider where this predictive knowledge comes from. If you have, you may have simply attributed it to ‘common sense’. Despite its commonality, it is an incredible display of the brain’s capacity to monitor the environment, make connections between events and observations, and store that information without making a big fuss to inform our conscious mind about its processes.

Our brains are efficient but not infallible along to key fronts. First, our brains are not supercomputers. They do not store every experience in raw form; we do not have access to the records of our experience like we would imagine a computer would have access to the records logged in a database. Where our brains do excel is in making associations and predictions that help us (most of the time) navigate the complex world we inhabit.

Second, our brains are prone to bias. Given our particular and limited experiences and the way our brains process information, we are prone to biases that can influence our understanding of the world. For example, we are prone to confirmation bias, the tendency to seek out information that confirms our beliefs and ignore information that contradicts them. We are also prone to the availability heuristic, the tendency to overestimate the likelihood of events that are more easily recalled. These are just two of many biases that can influence our understanding of the world.

These points are key – our brains are doing some amazing work, but that work can give us the impression that we understand the world better and in more detail than we actually do. In this way, what we think the world is like and what the world is actually like can be two different things. This is where science comes in.

💡 Consider this

How might your own experiences and biases influence your understanding of the world? What are some ways that you can mitigate these biases? Is ever possible to be completely objective? How might biases influence the way you approach text analysis?

Science starts with a question, identifies and collects data, careful selected slices of the complex world, submits this data to analysis through clearly defined and reproducible procedures, and reports the results for others to evaluate. This process is repeated, modifying, and manipulating the procedures, asking new questions and positing new explanations, all in an effort to make inroads to bring the complex into tangible view.

In essence what science does is attempt to subvert our inherent limitations by drawing on carefully and purposefully collected samples of observable experience and letting the analysis of these observations speak, even if it goes against our intuitions (those powerful but sometime spurious heuristics that our brains use to make sense of the world).

1.2 Data analysis

1.2.1 Emergence of data science

This science I've described is the one you are likely quite familiar with and, if you are like me, this description of science conjure visions of white coats, labs, and petri dishes. While science's foundation still stands strong in the 21st century, a series of intellectual and technological events mid-20th century set in motion changes that have changed aspects about how science is done, not why it is done. We could call this Science 2.0, but let's use the more popularized term **data science**.

The recognized beginnings of data science are attributed to work in the "Statistics and Data Analysis Research" department at Bell Labs during the 1960s. Although primarily conceptual and theoretic at the time, a framework for quantitative data analysis took shape that would anticipate what would come: sizable datasets which would "[...] require advanced statistical and computational techniques [...] and the software to implement them." (Chambers 2020) This framework emphasized both the inference-based research of traditional science, but also embraced exploratory research and recognized the need to address practical considerations that would arise when working with and deriving insight from an abundance of machine-readable data.

Fast-forward to the 21st century, a world in which machine-readable data is truly in abundance. With increased computing power, the emergence of the world wide web, and wide adoption of mobile devices electronic communication skyrocketed around the globe. To put this in perspective, in 2019 it was estimated that every minute 511 thousand tweets were posted, 18.1 million text messages were sent, and 188 million emails were sent ("Data Never Sleeps 7.0 Infographic" 2019). The data flood has not been limited to language, there are more sensors and recording devices than ever before which capture evermore swaths of the world we live in (Desjardins 2019).

Where increased computing power gave rise to the influx of data, it is also one of the primary methods for gathering, preparing, transforming, analyzing, and communicating insight derived from this data (Donoho 2017). The vision laid out in the 1960s at Bell Labs had come to fruition.

1.2.2 Data science toolbelt

Data science is not predicated on data alone. Turning data into insight takes computing skills, statistical knowledge, and domain expertise. This triad has been popularly represented as a Venn diagram such as in Figure 1.1.

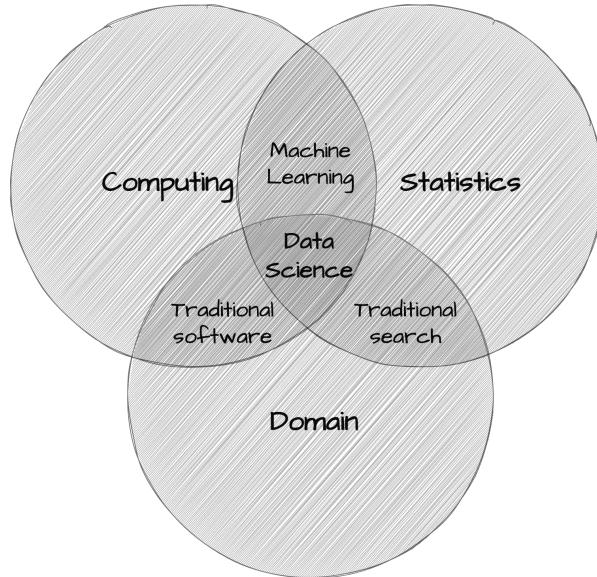


Figure 1.1: Data Science Venn Diagram adapted from Drew Conway¹.

The **computing skills** component of data science is the ability to write code to perform the data analysis process. This is the primary approach for working with data at scale. The **statistical knowledge** component of data science is the ability to apply statistical methods to data to derive insight by bringing patterns and relationships in the data into view. **Domain expertise** provides researchers insight at key junctures in the development of a research project and aid researchers in evaluating results.

This triad of skills in combination with reproducible research practices is the foundational toolbelt of data science (Hicks and Peng 2019). **Reproducible research** entails the use of computational tools to automate the process of data analysis. This automation is achieved by writing code that can be executed to replicate the data analysis. This code can then be shared through code sharing repositories, where it can be viewed, downloaded, and executed by others. This adds transparency to the process and allows others to build on previous work enhancing scientific progress along the way (Baker 2016).

1.2.3 Quant everywhere

Equipped with the data science toolbelt, the interest in deriving insight from data is now almost ubiquitous. The science of data has now reached deep into all aspects of life where making sense of the world is sought. Predicting whether a loan applicant will get a loan (Bao, Lianju, and Yue 2019), whether a lump is cancerous (Saxena and Gyanchandani 2020), what films to recommend based on your previous viewing history (Gomez-Uribe and Hunt 2015),

what players a sports team should sign (Lewis 2004), now all incorporate a common set of data analysis tools.

The data science toolbelt also underlies well-known public-facing language applications. From the language-capable chat applications, plagiarism detection software, machine translation algorithms, and search engines, tangible results of quantitative approaches to language are becoming standard fixtures in our lives.

The spread of quantitative data analysis too has taken root in academia. Even in areas that on first blush don't appear readily approachable in a quantitative manner, such as fields in the social sciences and humanities, data science is making important and sometimes disciplinary changes to the way that academic research is conducted.

This textbook focuses in on a domain that cuts across many of these fields; namely language. At this point let's turn to quantitative approaches to language analysis as we work closer to contextualizing text analysis in the field of linguistics.

1.3 Language analysis

1.3.1 Qualities and quantities

Language is a defining characteristic of our species. Since antiquity, language has attracted interest across disciplines and schools of thought. In the early 20th century, the development of the rigorous approach to study of language as a field in its own right took root (Campbell 2001), yet a plurality of theoretical views and methodological approaches remained. Contemporary linguistics bares this complex history and even today, it is far from theoretically and methodologically unified discipline.

Either based on the tenets of theoretical frameworks and/ or the objects of study of particular fields, methodological approaches to language research vary. On the one hand, some language research commonly applies qualitative assessment of language structure and/ or use. **Qualitative approaches** describe and account for characteristics, or “qualities”, that can be observed, but not measured (*e.g.* introspective methods, ethnographic methods, *etc.*)

On the other hand, other language research programs employ quantitative research methods either out of necessity given the object of study (phonetics, psycholinguistics, *etc.*) or based on theoretical principles (Cognitive Linguistics, Connectionism, *etc.*). **Quantitative approaches** involve “quantities” of properties that can be observed and measured (*e.g.* frequency of use, reaction time, *etc.*).

Case study

Manning (2003) discusses the use of probabilistic models in syntax to account for the variability in language usage and the presence of both hard and soft constraints in gram-

mar. The paper touches on the statistical methods in text analysis, the importance of distinguishing between external and internal language, and the limitations of Generative Grammar. Overall, the paper suggests that usage-based and formal syntax can learn from each other to better understand language variation and change.

These latter research areas and theoretical paradigms employ methods that share much of the common data analysis toolbox described in the previous section. In effect, this establishes a common methodological language between other language-based research fields but also with research outside of linguistics.

1.3.2 The nature of data

In quantitative language analysis there is a key methodological distinction that has downstream effects in terms of procedure but also in terms of interpretation. The key distinction that we need to make at this point, which will provide context for our introduction to quantitative text analysis, comes down to the approach to collecting language data and the nature of that data. This distinction is between experimental data and observational data.

Experimental approaches start with a intentionally designed hypothesis and lay out a research methodology with appropriate instruments and a plan to collect data that shows promise for shedding light on the likelihood of the hypothesis. Experimental approaches are conducted under controlled contexts, usually a lab environment, in which participants are recruited to perform a language related task with stimuli that have been carefully curated by researchers to elicit some aspect of language behavior of interest. Experimental approaches to language research are heavily influenced by procedures adapted from psychology. This link is logical as language is a central area of study in cognitive psychology. This approach looks much like the white-coat science that we made reference to earlier but, as in most quantitative research, has now taken advantage of the data analysis toolbelt to collect and organize much larger quantities of data and conduct statistically more robust analysis procedures and communicate findings more efficiently.

Observational approaches are a bit more of a mixed bag in terms of the rationale for the study; they may either start with a testable hypothesis or in other cases may start with a more open-ended research question to explore. But a more fundamental distinction between the two approaches is drawn in the amount of control the researcher exerts on the contexts and conditions in which the language behavior data to be collected is produced. Observational approaches seek out records of language behavior that is produced by language speakers for communicative purposes in natural(-istic) contexts. This may take place in labs (language development, language disorders, *etc.*), but more often than not, language is collected from sources where speakers are performing language as part of their daily lives –whether that be posting on social media, speaking on the telephone, making political speeches, writing class essays, reporting the latest news for a newspaper, or crafting the next novel destined to be

a New York Times best-seller. What is more, data collected from the ‘wild’ varies more in structure relative to data collected in experimental approaches and requires a number of organizational steps to prepare the data to sync up with the data analysis toolbelt.

I liken this distinction between experimental and observational data collection to the difference between farming and foraging. Experimental approaches are like farming; the groundwork for a research plan is designed, much as a field is prepared for seeding, then the researcher performs a series of tasks to produce data, just as a farmer waters and cares for the crops, the results of the process bear fruit, data in our case, and this data is harvested. Observational approaches are like foraging; the researcher scans the available environmental landscape for viable sources of data from all the naturally existing sources, these sources are assessed as to their usefulness and value to address the research question, the most viable is selected, and then the data is collected.

The data acquired from both of these approaches have their trade-offs, just as farming and foraging. Experimental approaches directly elicit language behavior in highly controlled conditions. This directness and level of control has the benefit of allowing researchers to precisely track how particular experimental conditions effect language behavior. As these conditions are an explicit part of the design and therefore the resulting language behavior can be more precisely attributed to the experimental manipulation.

The primary shortcoming of experimental approaches is that there is a level of artificialness to this directness and control. Whether it is the language materials used in the task, the task itself, or the fact that the procedure takes place under supervision the language behavior elicited can diverge quite significantly from language behavior performed in natural communicative settings.

Observational approaches show complementary strengths and shortcomings. Whereas experimental approaches may diverge from natural language use, observational approaches strive to identify and collect language behavior data in natural, uncontrolled, and unmonitored contexts, as seen in Figure 1.2. In this way, observational approaches do not have to question to what extent the language behavior data is or is not performed as a natural communicative act.

On the flipside, the contexts in which natural language communication take place are complex relative to experimental contexts. Language collected from natural contexts are nested within the complex workings of a complex world and as such inevitably include a host of factors and conditions which can prove challenging to disentangle from the language phenomenon of interest but must be addressed in order to draw reliable associations and conclusions.

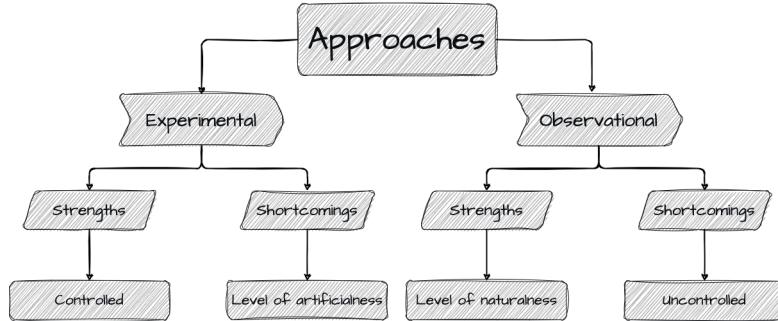


Figure 1.2: Trade-offs between experimental and observational data collection methods.

The upshot, then, is two-fold: (1) data collection methods matter for research design and interpretation and (2) there is no single best approach to data collection, each have their strengths and shortcomings.

In the ideal, a robust science of language will include insight from both experimental and observational approaches (Gilquin and Gries 2009). And evermore there is greater appreciation for the complementary nature of experimental and observational approaches and a growing body of research which highlights this recognition.

1.4 Text analysis

In a nutshell, **text analysis** is the process of leveraging the data science toolbelt to derive insight from textual data collected through observational methods. In the next subsections, I will unpack this definition and discuss the primary components that make up text analysis including research approaches and technical implementation, as well as practical applications.

1.4.1 Aims

Text analysis is a multifaceted research methodology. It can be used to facilitate the qualitative exploration of smaller, human-digestible textual information, but is more often employed quantitatively to bring to the surface patterns and relationships in large samples of textual data that would be otherwise difficult, if not impossible, to identify manually.

The aims of text analysis are as varied as the research questions that can be asked of language data. Some research questions are data-driven, where the researcher is interested in exploring and uncovering patterns and relationships in the data. Other research questions are theory-driven, where the researcher is interested in testing a hypothesis or evaluating a theory. In either case, the researcher is interested in gaining insight from the data.

The relationship(s) of interest in text analysis may be language internal, where the researcher is interested in the patterns and relationships between linguistic features or language external, where the researcher is interested in the patterns and relationships between linguistic features and some external variable.

1.4.2 Approaches

Text being text, there are a series of **data preparation** steps that must be taken to ready the data for analysis, whatever the aim may be. In addition to collecting the data, the data must be organized, cleaned, and transformed into a format that is amenable to statistical analysis.

The statistical and evaluative approach employed in the analysis is dependent on the aim of the research. For research aimed at exploring and uncovering patterns and relationships in a data-driven manner, **Exploratory Data Analysis** (EDA) is employed. EDA combines descriptive statistics, visualizations, and statistical learning methods in an iterative and interactive way to provide the researcher the ability to identify patterns and relationships and to evaluate whether and why they are meaningful.

Predictive Data Analysis (PDA), applied in research for outcome prediction, is a supervised machine learning task. It uses feature sets to predict an outcome variable. Its primary evaluation metric is the prediction accuracy on new data. However, for many text analysis tasks, human interpretation is crucial to provide context and assess the significance of the results.

Research aimed at explaining relationships between variables and the population from which the sample was drawn will adopt an **Inferential Data Analysis** (IDA) approach. IDA is a theory-driven process that employs statistical models for hypothesis testing. The extent to which the results can be confidently generalized to the population is the primary evaluation metric.

As we see, text analysis can be used for a variety of purposes; from data-driven exploration and discovery to hypothesis testing and generalization.

1.4.3 Implementation

Text analysis branch of data science. As such, it takes advantage of the data science toolbelt to derive insight from data. It is important to note, that while all of the components of the data science toolbelt are present in text analysis, the relative importance of each varies with the stage research. Computing skills being the most important at the data and information stages, statistical knowledge being the most important to derive knowledge, and domain knowledge leading the way towards insight.

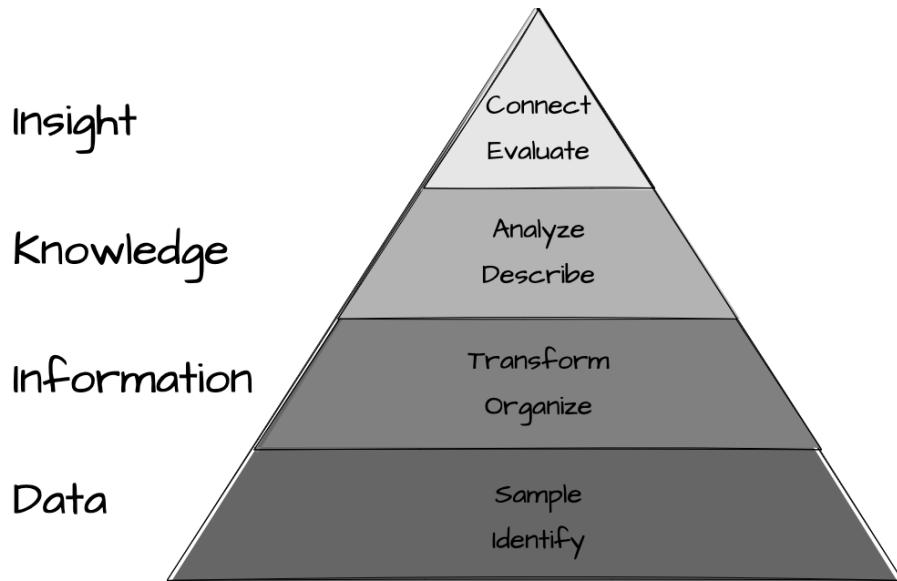


Figure 1.3: Data to Insight Hierarchy (DIKI)

Text is a rather raw form of data. It is more often than not unstructured, meaning that it is not organized in a way that such that it can be easily analyzed. The collection, organization, and transformation of text data is a key component of text analysis and computers are well-suited for this task, as we will see in Chapter 2 and Part III “Preparation”.

Once text is transformed to a dataset that can be analyzed, we lean on statistical methods to gain perspective on the relationship(s) of interest. By and large, these methods are the same as those used in other areas of data science. We will provide an overview of these methods in Chapter 3 and do a deeper dive in Part IV “Analysis”.

With the results of the analysis in hand, the researcher must interpret the results and evaluate their significance in disciplinary context. This is where domain knowledge comes to the fore. The researcher must be able to interpret the results in light of the research question and the context in which the data was collected and communicate the value of the results to the broader community. Domain knowledge also plays a vital role in framing the research question and designing the research methodology, as we will see in Chapter 4. Then we will return to the role of domain knowledge in interpreting and communicating the results in Part V “Communication”.

To ensure that the results of text analysis projects are replicable and transparent, programming strategies and documentation play an integral role at each stage of the implementation of a research project. While there are a number of programming languages that can be used for text analysis, R is widely adopted in linguistics research and is the language of choice for this textbook.

R is a free and open-source programming language that is specifically designed for statistical computing and graphics. It has a large and active community of users and developers, and a robust ecosystem of packages which make it a powerful and flexible language that is well-suited for core text analysis tasks: data collection, organization, transformation, analysis, and visualization.

When combined with Quarto for literate programming and GitHub for version control and collaboration, R provides a robust and reproducible workflow for text analysis projects. We will scaffold your R and general computing skills in the first parts of this textbook and then apply and develop these skills as we move into the steps of implementing text analysis projects.

1.4.4 Applications

So what are some applications of text analysis? Most public facing applications stem from Computational Linguistic research, often known as **Natural Language Processing** (NLP) by practitioners. Whether it be using search engines, online translators, submitting your paper to plagiarism detection software, *etc.* many of the text analysis methods we will cover are at play.

 **Consider this**

What are some other public facing applications of text analysis that you are aware of?

In academia the use of quantitative text analysis is even more widespread, despite the lack of public fanfare. In linguistics, text analysis research often falls under **Corpus Linguistics** (CL). And this approach is applied to a wide range of topics and research questions in both theoretical and applied linguistics fields and subfields, as seen in Example 1.1 and Example 1.2.

Example 1.1. Theoretical linguistics

- Hay (2002) use a corpus study to investigate the role of frequency and phonotactics in affix ordering in English.
- Riehemann (2001) explores the extent to which idiomatic expressions (*e.g.* ‘raise hell’) are lexical or syntactic units.
- Bresnan (2007) investigate the claim that possessed deverbal nouns in English (*e.g.* ‘the city’s destruction’) are subject to a syntactic constraint that requires the possessor to be affected by the action denoted by the deverbal noun.

Example 1.2. Applied linguistics

- Wulff, Stefanowitsch, and Gries (2007) explore differences between British and American English at the lexico-syntactic level in the *into*-causative construction (*e.g.* ‘He tricked me into employing him.’).

- Eisenstein et al. (2012) track the geographic spread of neologisms (*e.g.* ‘bruh’, ‘af’, ‘—’) from city to city in the United States using Twitter data collected between 6/2009 and 5/2011.
- Bychkovska and Lee (2017) investigates possible differences between L1-English and L1-Chinese undergraduate students’ use of lexical bundles, multiword sequences which are extended collocations (*e.g.* ‘as the result of’), in argumentative essays.
- Jaeger and Snider (2007) use a corpus study to investigate the phenomenon of syntactic persistence, the increased tendency for speakers to use a particular syntactic form over an alternate when the syntactic form has been recently processed.
- Voigt et al. (2017) explore potential racial disparities in officer respect in police body camera footage.
- Olohan (2008) investigate the extent to which translated texts differ from native texts do to ‘explicitation’.

So too, text analysis is used in a variety of fields outside of linguistics where insight from language is sought, as seen in Example 1.3.

Example 1.3. Language-related fields

- Kloumann et al. (2012) explore the extent to which languages are positively, neutrally, or negatively biased.
- Mosteller and Wallace (1963) provide a method for solving the authorship debate surrounding The Federalist papers.
- Conway et al. (2012) investigate whether the established drop in language complexity of rhetoric in election seasons is associated with election outcomes.

Consider this

Language is a key component of human communication and interaction. What are some other areas of research in and outside linguistics that you think could be explored using text analysis methods?

These studies in Examples 1.1, 1.2, and 1.3 are just a few illustrations of the contributions of text analysis as the primary method to gain a deeper understanding of language structure, function, variation, and acquisition.

As a method, however, text analysis can also be used to support other research methods. For example, text analysis can be used collect data, generate authentic materials, provide linguistic annotation, and to generate hypotheses, for either qualitative and/ or quantitative approaches. Together these efforts contribute to a more robust language science by incorporating externally valid data and providing methodological triangulation (Francom 2022).

In sum, the applications highlighted in this section underscore the versatility of text analysis as a research method. Whether it be in the public sphere or in academia, text analysis methods furnish a set of powerful tools for gaining insight into the nature of language.

Activities

The following activities build on your introduction to R and Quarto in the preface. In these activities you will uncover more features offered by Quarto which will enhance your ability to produce comprehensive reproducible research documents. You will apply the capabilities of Quarto in a practical context conveying the objectives and key discoveries from a primary research article.

Recipe

What: Academic writing with Quarto^a

How: Read Recipe 1, complete comprehension check, and prepare for Lab 1.

Why: To explore additional functionality in Quarto: numbered sections, table of contents, in-line citations and a document-final references list, and cross-referenced tables and figures.

^a<https://qtalr.github.io/qtalrkit/articles/recipe-1.html>

Lab

What: Crafting scholarly documents^a

How: Clone, fork, and complete the steps in Lab 1.

Why: To put into practice Quarto functionality to communicate the aim(s) and main finding(s) from a primary research article.

^a<https://github.com/qtalr/lab-01>

Summary

In this chapter, I started with some general observations about the difficulty of making sense of a complex world. The standard approach to overcoming inherent human limitations in sense making is science. In the 21st century the toolbelt for doing scientific research and exploration has grown in terms of the amount of data available, the statistical methods for analyzing the data, and the computational power to manage, store, and share the data, methods, and results from quantitative research. The methods and tools for deriving insight from data have made significant inroads in and outside academia, and increasingly figure in the quantitative investigation of language. Text analysis is a particular branch of this enterprise based on observational data from real-world language and is used in a wide variety of fields.

In the end I hope that you enjoy this exploration into text analysis. Although the learning curve at times may seem steep –the experience you will gain will not only improve your data literacy, research skills, and programmatic skills but also enhance your appreciation for the richness of human language and its important role in our everyday lives.

Part II

Foundations

Before working on the specifics of a data project, it is important to establish a fundamental understanding of the characteristics of each of the levels in the “Data, Information, Knowledge, and Insight Hierarchy (DIKI)” (see Figure 1.3) and the roles each of these levels have in deriving insight from data. In Chapter 2 we will explore the Data and Information levels drawing a distinction between two main types of data (populations and samples) and then cover how data is structured and transformed to generate information (datasets) that is fit for statistical analysis. In Chapter 3 I will outline the importance and distinct types of statistical procedures (descriptive and analytic) that are commonly used in text analysis. Chapter 4 aims to tie these concepts together and cover the required steps for preparing a research blueprint to guide the implementation of a text analysis project.

2 Data

The goal is to turn data into information, and information into insight.

— Carly Fiorina

▀ Outcomes

- Describe the difference between data and information.
- Understand how the tidy approach to data organization can enhance the quality and usability of data.
- Articulate the importance of documentation in promoting reproducible research.

In this chapter, the groundwork is laid for deriving insights from text analysis by focusing on content and structure of data and information. The concepts of populations and samples are introduced, highlighting their similarities and key differences. Connecting these topics to text analysis, language samples, or corpora, are explored, discussing their types, sources, formats, and ethical considerations. Subsequently, key concepts in creating information from corpus data, such as organization and transformation, are introduced. Documentation in quantitative research is emphasized addressing the importance of data origin files and data dictionaries.

➤_ Lessons

What: Objects, Packages and functions^a

How: In the R Console pane load `swirl`, run `swirl()`, and follow prompts to select the lesson.

Why: To introduce you to the main types of objects in R and to understand the role and use of functions and packages in R programming.

^a<https://github.com/qtalr/lessons>

2.1 Data

Data is data, right? The term ‘data’ is so common in popular vernacular it is easy to assume we know what we mean when we say ‘data’. But as in most things in science, where there are common assumptions there are important details that require more careful consideration.

Let's turn to the first key distinction that we need to make to start to break down the term 'data': the difference between populations and samples.

2.1.1 Populations and samples

The first thing that comes to many people's mind when the term population is used is human populations (derived from Latin 'populus'). Say for example we pose the question –What's the population of Milwaukee? When we speak of a population in these terms we are talking about the total sum of individuals living within the geographical boundaries of Milwaukee. In concrete terms, a **population** is an idealized set of objects or events in reality which share a common characteristic or belong to a specific category. The term to highlight here is idealized. Although we can look up the US Census report for Milwaukee and retrieve a figure for the population, this cannot truly be the population. Why is that? Well, whatever method that was used to derive this numerical figure was surely incomplete. If not incomplete, by the time someone recorded the figure some number of residents of Milwaukee moved out, moved in, were born, or passed away. In either case, this example serves to point out that populations are not fixed and are subject to change over time.

Likewise when we talk about populations in terms of language we are dealing with an idealized aspect of linguistic reality. Let's take the words of the English language as an analog to our previous example population. In this case the words are the people and English is the grouping characteristic. Just as people, words move out, move in, are born, and pass away. Any compendium of the words of English at any moment is almost instantaneously incomplete. This is true for all populations, save those relatively rare cases in which the grouping characteristics select a narrow slice of reality which is objectively measurable and whose membership is fixed (the complete works of Shakespeare, for example).

Therefore, (most) populations are amorphous moving targets. We subjectively hold them to exist, but in practical terms we often cannot nail down the specifics of populations. So how do researchers go about studying populations if they are theoretically impossible to access directly? The strategy employed is called sampling.

A **sample** is the product of a subjective process of selecting a finite set of observations from an idealized population with the goal of capturing the relevant characteristics of this population. When we talk about data in data science, we are talking about samples.

Whether selecting a sample for your research or evaluating a sample used in someone else's research, there are two key characteristics to consider: the sampling frame and the representativeness. The **sampling frame** is the set of characteristics that define the population of interest. The **representativeness** is the degree to which the sample reflects the characteristics of the population. Both of these concern bias, albeit in different ways. By defining the population, a sampling frame sets the boundaries of the population and therefore the scope of research based on the sample. This bias is not a bad thing, in fact, the more clearly defined the sampling frame the better. Low representativeness, on the other hand, is a type of bias we

would like to avoid. Given the nature of samples, perfect representativeness is not achievable. That said, there are a series of sampling strategies that tend to increase the representativeness of a sample, seen in Table 2.1.

Table 2.1: Sampling strategies to increase representativeness

Strategy	Description
Size	Larger samples increase the likelihood of representing the population
Randomized	Avoid inadvertently including bias in selection
Stratified	Divide the population into sub-populations, ‘strata’, and sample from each
Balanced	Ensure that the relative size of the strata is reflected in the sample

Together, large randomly selected and balanced stratified samples set the benchmark for sampling. However, hitting this ideal is not always feasible. There are situations where sizeable samples are not accessible. Alternatively, there may be instances where the population or its strata are not well understood. In such scenarios, researchers have to work with the most suitable sample they can obtain given the limitations of their research project.

2.1.2 Corpora

A sample, as just defined, of a language population is called a **corpus** (*pl. corpora*). Corpora are often classified into various types. These types reflect general characteristics of the scope of the corpus sampling frame. The most common types of corpora appear in Table 2.2.

Table 2.2: Types of corpora

Type	Sampling scope
Reference	General characteristics of a language population
Specialized	Specific populations, <i>e.g.</i> spoken language, academic writing, <i>etc.</i>
Parallel	Directly comparable texts in different languages (<i>i.e.</i> translations)
Comparable	Indirectly comparable texts in different languages or language varieties (<i>i.e.</i> similar sampling frames)

Of the corpus types, **reference corpora** are the least common and most ambitious. These resources aim to model the characteristics of a language population. **Specialized corpora** aim to represent more specific populations. What specialized corpora lack in breadth of coverage, they make up for in depth of coverage by providing a more targeted representation of specific language populations. **Parallel** and **comparable corpora** are both types of specialized corpora which aim to model different languages or different language varieties for direct or indirect comparison, respectively.

💡 Consider this

The ‘Standard Sample of Present-Day American English’ (known commonly as the Brown Corpus) is widely recognized as one of the first large, machine-readable corpora. Compiled by Kucera and Francis (1967), the corpus is comprised of 1,014,312 words from edited English prose published in the United States in 1961.

Given the sampling frame and the strata and balance for this corpus visualized in Figure 2.1, can you determine what language population this corpus aims to represent? What types of research might this corpus support or not support?

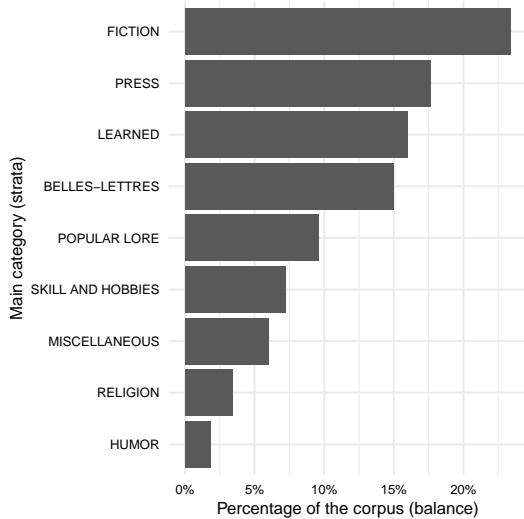


Figure 2.1: Overview of the sampling characteristics of the Brown Corpus.

In text analysis, corpora are the raw materials of research. The aim of the quantitative text researcher is to select the corpus, or corpora, which best align with the purpose of the research. For example, a reference corpus such as the American National Corpus may be better suited to address a question dealing with the way American English works, but this general resource may lack detail in certain areas, such as medical language, that may be vital for a research project aimed at understanding changes in medical terminology. Furthermore, a researcher studying spoken language might collect a corpus of transcribed conversations from a particular community or region, such as the Santa Barbara Corpus of Spoken American English. While this would not include every possible spoken utterance produced by members of that group, it could be considered a representative sample of the population of speech in that context.

2.1.3 Other considerations

In preparing and conducting research using corpora, the most primary concerns is aligning research goals with the corpus resource. However, there are other, more practical, considerations to keep in mind.

2.1.3.1 Access

Ensuring access both in terms of physical access to the data and legal access to the data should not be overlooked in the design and execution of a project. Simply put, without access to the data, research cannot proceed. It is better to consider access early in the research process to avoid delays and complications later on.

The medium to acquire corpus data most used in contemporary quantitative research is the internet. Although a general search query can lead you to corpus data, there are a few primary sources of corpora you should be aware of, summarized in Table 2.3.

Table 2.3: Sources of corpus data

Source	Description	Examples
Language repositories	Repositories that specialize in language data	Language Data Consortium ¹ , TalkBank ²
Data sharing platforms	Platforms that enable researchers to securely store, manage, and share data	GitHub ³ , Zenodo ⁴ , OSF ⁵
Developed corpora	Corpora prepared by researchers for research purposes	APIs, web scraping

It is always advisable to start looking for data in a **language repository**. The advantage of beginning your data search in repositories is that a repository, especially those geared towards the linguistic community, will make identifying language corpora faster than through a general web search. Furthermore, repositories often require certain standards for corpus format and documentation for publication.

💡 Consider this

Explore some of the resources listed on the qtalrkit companion site^a and consider their sampling frames. Can you think of a research question or questions that this resource may be well-suited to support research into? What types of questions would be less-than-adequate for a given resource?

^a<https://qtalr.github.io/qtalrkit/articles/guide-4.html>

As part of a general movement towards reproducibility, more corpora are available on **data sharing platforms**. These platforms enable researchers to securely store, manage, and share data with others. Support is provided for various types of data, including documents and code,

¹<https://www.ldc.upenn.edu/>

²<http://talkbank.org/>

³<https://github.com>

⁴<https://zenodo.org>

⁵<https://osf.io/>

and as such they are a good place to look as they often include reproducible research projects as well.

Finally, if satisfactory data cannot be found in a repository or data sharing platform, researchers may need to develop their own corpus. There are two primary ways to attain language data from the web. The first is through an **Application Programming Interface** (API). APIs are, as the title suggests, programming interfaces which allow access, under certain conditions, to information that a website or database accessible via the web contains.

Dive deeper

The process of corpus development is a topic in and of itself. For a more in-depth discussion of the process, see Ädel (2020).

The second, more involved, way to acquire data from the web is through the process of web scraping. **Web scraping** is the process of harvesting data from the public-facing web. Language texts may be found on sites as uploaded files, such as pdf or doc (Word) documents, or found displayed as the primary text of a site. Given the wide variety of documents uploaded and language behavior recorded daily on news sites, blogs and the like, compiling a corpus has never been easier. Having said that, how the data is structured and how much data needs to be retrieved can pose practical obstacles to collecting data from the web, particularly if the approach is to acquire the data by manually instead of automating the task.

Beyond physical access to the data, legal access is also a consideration. Just because data is available on the web does not mean it is free to use. Repositories, APIs, and individual data resources often have licensing agreements and terms of use, ranging from public domain to proprietary licenses. Respecting intellectual property rights is crucial when working with corpus data. Violating these rights can lead to legal and ethical issues, including lawsuits, fines, and damage to one's professional reputation. To avoid these problems, researchers must ensure they have the necessary permissions to use copyrighted works in their research.

2.1.3.2 Formats

Whether you are using a published corpus or developing your own, it is important to understand how the data you want to work with is formatted so you can ensure that you are prepared to conduct the subsequent processing steps. When referring to the format of a corpus, this includes the folder and file structure, the file types, and how file content is encoded electronically. Yet, the most important characteristic, especially for language-based data, is the internal structure of the files themselves. With this in mind less discuss the difference between unstructured, semi-structured, and structured data.

A corpus may include various types of linguistic (*e.g.* part of speech, syntactic structure, named entities, *etc.*) or non-linguistic (*e.g.* source, dates, speaker information, *etc.*) attributes. These attributes are known as **metadata**, or data about data. As a general rule, files which include

more metadata tend to be more internally structured. Internal file structure refers to the degree to which the content is easy to query and analyze by a computer. Let's review characteristics of the three main types of file structure types and associate common file extensions that files in each have.

Unstructured data is data which does not have a machine-readable internal structure. This is the case for plain text files (*.txt*), which are simply a sequence of characters. For example, in Example 2.1 we see a snippet of a plain text file from the the Manually Annotated Sub-Corpus of American English (MASC) (Ide et al. 2008):

Example 2.1. MASC plain text

```
Sound is a vibration. Sound travels as a mechanical wave through a medium, and
↳ in space, there is no
medium. So when my shuttle malfunctioned and the airlocks didn't keep the air
↳ in, I heard nothing. After the
first whoosh of the air being sucked away, there was lightning, but no thunder.
↳ Eyes bulging in
panic, but no screams. Quiet and peaceful, right? Such a relief to never again
↳ hear my crewmate Jesse natter
about his girl back on Earth and that all-expenses-paid vacation-for-two she won
↳ last time he was on leave. I
swore, if I ever had to see a photo of him in a skimpy bathing suit again,
↳ giving the camera a cheesy thumbs-up
from a lounge chair on one of those white sandy beaches, I'd kiss a monkey.
↳ Metaphorically, of course.
```

Other examples of files which often contain unstructured data include *.pdf* and *.docx* files. While these file types may contain data which appears structured to the human eye, the structure is not designed to be machine-readable. As such the data would typically be read into R as a vector of **character strings**. It is possible to perform only the most rudimentary queries on this type of data, such as string matches. For anything more informative, it is necessary to further process this data, as we will see in Section 2.2.1 and Section 2.2.2.

On the other end of the spectrum, **structured data** is data which conforms to a tabular format in which elements in tables and relationships between tables are defined. This makes querying and analyzing easy and efficient. Relational databases (*e.g.* MySQL, PostgreSQL, *etc.*) are designed to store and query structured data. The data frame object in R is also a structured data format. In each case, the data is stored in a tabular format in which each row represents a single observation and each column represents a single attribute whose values are of the same type.

In Example 2.2 we see an example of an R data frame object which overlaps with the language in the plain text file in Example 2.1:

Example 2.2. MASC data frame

title	date	modality	domain	ref_num	word	lemma	pos
<chr>	<dbl>	<fct>	<chr>	<int>	<chr>	<chr>	
1	Hotel California	2008	Writing	General	Fiction	1	Sound
2	Hotel California	2008	Writing	General	Fiction	2	is
3	Hotel California	2008	Writing	General	Fiction	3	a
4	Hotel California	2008	Writing	General	Fiction	4	vibration
5	Hotel California	2008	Writing	General	Fiction	5	.
6	Hotel California	2008	Writing	General	Fiction	6	Sound
7	Hotel California	2008	Writing	General	Fiction	7	travels
8	Hotel California	2008	Writing	General	Fiction	8	as
9	Hotel California	2008	Writing	General	Fiction	9	a
10	Hotel California	2008	Writing	General	Fiction	10	mechanical
	JJ						mechanical

Here we see that the data is stored in a tabular format with each row representing a single observation (word) and each column representing a single attribute. This tabular structure supports the increased number of metadata attributes. Internally, R applies a schema to ensure the values in each column are of the same type (e.g. <chr>, <dbl>, <fct>, etc.). This structured format is designed to be easy to query and analyze and as such is the primary format for data analysis in R.

Semi-structured data falls between unstructured and structured data. This covers a wide range of file structuring approaches. For example, a otherwise plain text file with part-of-speech tags appended to each word is minimally structured (Example 2.3).

Example 2.3. MASC plain text with part-of-speech tags

```
Sound/NNP is/VBZ a/DT vibration/NN ./. Sound/NNP travels/VBZ as/IN a/DT
← mechanical/JJ wave/NN through/IN a/DT medium/NN ,/, and/CC in/IN space/NN
← ,/, there/EX is/VBZ no/DT medium/NN ./. So/RB when/WRB my/PRP$ shuttle/NN
← malfunctioned/JJ and/CC the/DT airlocks/NNS did/VBD n't/RB keep/VB the/DT
← air/NN in/IN ,/, I/PRP heard/VBD nothing/NN ./. After/IN the/DT
```

Towards the more structured end of semi-structured data, many file formats including *.xml* and *.json* contain highly structured, hierarchical data. For example, in Example 2.4 shows a snippet from a *.xml* file from the MASC corpus.

Example 2.4. MASC XML

```
<a xml:id="penn-N264215" label="tok" ref="penn-n7345" as="anc">
  <fs>
    <f name="base" value="sound"/>
    <f name="msd" value="NNP"/>
    <f name="string" value="Sound"/>
  </fs>
</a>
<node xml:id="penn-n7346">
  <link targets="seg-r13152"/>
</node>
<a xml:id="penn-N264243" label="tok" ref="penn-n7346" as="anc">
  <fs>
    <f name="string" value="is"/>
    <f name="msd" value="VBZ"/>
    <f name="base" value="be"/>
  </fs>
</a>
<node xml:id="penn-n7347">
  <link targets="seg-r13154"/>
</node>
```

The format of semi-structured data is often influenced by characteristics of the data or reflect an author's individual preferences. It is sometimes the case that data will be semi-structured in a less-standard format. For example, the SWDA corpus includes a *.utt* file extension for files which contain utterances annotated with dialogue act tags.

Example 2.5. SWDA *.utt* file

```
o          A.1 utt1: Okay. /
qw         A.1 utt2: {D So, }

qy^d       B.2 utt1: [ [ I guess, +
                     A.3 utt1: What kind of experience [ do you, + do you ] have, then with
                     ↵ child care? /
```

+ B.4 utt1: I think,] + {F uh, } I wonder] if that worked. /

qy A.5 utt1: Does it say something? /

Whether standard or not, semi-structured data is often designed to be machine-readable. As with unstructured data, the ultimate goal is to convert the data into a structured format and augment the data where necessary to prepare it for a particular research analysis.

2.2 Information

Identifying an adequate corpus resource, in terms of content, access, and formatting, for the target research question is the first step in moving a quantitative text research project forward. The next step is to select the components or characteristics of this resource that are relevant for the research and then move to organize the attributes of this data into a more informative format. This is the process of converting corpus data into a **dataset** –a tabular representation of particular attributes of the data as the basis for generating information. Once the data represented as dataset, it is often manipulated and transformed adjusting and augmenting the data such that it better aligns with the research question and the target analytical approach.

2.2.1 Organization

Data alone is not informative. Only through explicit organization of the data in a way that makes relationships and meaning explicit does data become information. In this form, our data is called a dataset. This is a particularly salient hurdle in text analysis research. Many textual sources are unstructured or semi-structured. This means relationships that will be used in the analysis have yet to be purposefully drawn and organized as a dataset.

2.2.1.1 Tidy Data

The selection of the attributes from a corpus and the juxtaposition of these attributes in a relational format, or dataset, that converts data into information is known as **data curation**. The process of data curation minimally involves deriving a base dataset, or *curated dataset*, which establishes the main informational associations according to philosophical approach outlined by Wickham (2014).

In this work, a **tidy dataset** refers both to the structural (physical) and informational (semantic) organization of the dataset. Physically, a tidy dataset is a tabular data structure, illustrated in Figure 2.2, where each *row* is an observation and each *column* is a variable that

contains measures of a feature or attribute of each observation. Each cell where a given row-column intersect contains a *value* which is a particular attribute of a particular observation for the particular observation-feature pair also known as a *data point*.

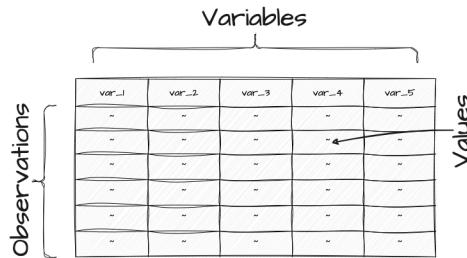


Figure 2.2: Visual summary of the tidy format.

In terms of semantics, columns and rows both contribute to the informational value of the dataset. Let's start with columns. In a tidy dataset, each column is a variable, an attribute that can take on a number of values. Although variables vary in terms of values, they do not in type. A variable is of one and only one informational type. Statistically speaking, informational types are defined as **levels of measurement**, a classification system used to semantically distinguish between types of variables. There are four levels (or types) in this system: nominal, ordinal, interval, and ratio.

In practice, however, text analysis researchers often group these levels into three main informational types: categorical, ordinal, and numeric (S. T. Gries 2021). What do these informational types represent? **Categorical data** is for labeled data or classes that answer the question “what?” **Ordinal data** is categorical data with rank order that answers the question “what order?” **Numeric data** is ordinal data with equal intervals between values that answers the question “how much or how many?”

Let's look at an example of a tidy dataset. Using the criteria just described, let's see if we can identify the informational values (categorical, ordinal, or numeric) of the variables that appear in a snippet from the MASC corpus in dataset form in Table 2.4.

Table 2.4: MASC dataset variables.

title	modality	date	ref_num	word	pos	num_letters
Hotel California	Writing	2008	1	Sound	NNP	5
Hotel California	Writing	2008	2	is	VBZ	2
Hotel California	Writing	2008	3	a	DT	1
Hotel California	Writing	2008	4	vibration	NN	9
Hotel California	Writing	2008	5	.	.	1
Hotel California	Writing	2008	6	Sound	NNP	5
Hotel California	Writing	2008	7	travels	VBZ	7

Table 2.4: MASC dataset variables.

title	modality	date	ref_num	word	pos	num_letters
Hotel California	Writing	2008	8	as	IN	2
Hotel California	Writing	2008	9	a	DT	1
Hotel California	Writing	2008	10	mechanical	JJ	10

We have seven variables listed as headers for each of the columns. We could go one-by-one left-to-right but let's take another tack. Instead, let's identify all those variables that cannot be numeric –these are all the non-numeral variables: `title`, `modality`, `word`, and `pos`. The question to ask of these variables is whether they represent an order or rank. Since titles, modalities, words, and parts-of-speech are not ordered values, they are all categorical.

Now in relation to `date`, `ref_num`, and `num_letters`. All three are numerals, so they could be numeric. But they could also be numeral representations of ordinal data. Before we can move forward, we need to make sure we understand what each variable means and how it is measured, or **operationalized**. The variable name and the values can be helpful in this respect. `date` is what it sounds like, a date, and is operationalized as a year in the Gregorian calendar. And `num_letters` seems quite descriptive as well, number of letters, appearing as a letter count. But in some cases it may be opaque as to what is being measured by the variable name alone, for example `ref_num`, and one will have to refer to the dataset documentation. In this case `ref_num` is a reference number operationalized as a unique identifier for each word per document in the corpus.

With this in mind, let's return to the question of whether `date`, `ref_num`, and `num_letters` are numeric or ordinal. Starting with the trickiest one, `date`, we can ask the question to identify numeric data: “how much or how many?”. In the case of `date`, the answer is neither. A date is a point in time, not a quantity. So `date` is not numeric. But it does provide information about order. Hence, `date` is ordinal. `ref_num` is also ordinal because the question “what order?” can be asked of it. Finally, `num_letters` is numeric because it answers the question “how many?”.

Let's turn to the second semantic value of a tidy dataset. In a tidy dataset, each row is an observation. But an observation of what? This depends on what the unit of observation is. That sounds circular, but it's not. The **unit of observation** is simply the primary entity that is being observed or measured (Sedgwick 2015). Even without context, it can often be identified in a dataset by looking at the level of specificity of the variable values and asking what each variable describes. When one variable appears to be the most individualized and other variables appear to describe that variable, then the most individualized variable is likely the unit of observation of the dataset, *i.e.* the meaning of each observation.

Applying these strategies to the Table in 2.4, we can see that each observation at its core is a word. We see that the values of each observation are the attributes of each word. `word` is

the most individualized variable and the `pos` (part-of-speech), `num_letters`, and `ref_num` all describe the word.

The other variables `title`, `modality`, and `date` are not direct attributes of the word. Instead, they are attributes of the document in which the word appears. Together, however, they all provide information about the word.

💡 Consider this

Data can be organized in many ways. It is important to make clear that data in tabular format in itself does not constitute a dataset, in the tidy sense we will be using. Can you think of examples of tabular information that would not be in a tidy format? What would be the implications of this for data analysis?

As we round out this section on data organization, it is important to stress that the purpose of curation is to represent the corpus data in an informative, tidy format. A curated dataset serves as a reference point making relationships explicit, enabling more efficient querying, and paving the way for further processing before analysis. In the subsequent section, we will highlight common approaches to modifying the curated dataset, either row-wise or column-wise, to make it more amenable to the particular aims of a given analysis leading to one or more *transformed datasets*.

2.2.2 Transformation

At this point have introduced the first step towards creating a dataset ready for analysis, data curation. However, a curated dataset is rarely the final organizational step before proceeding to statistical analysis. Many times, if not always, the curated dataset requires **transformation** to derive or generate new data for the dataset. This process may incur row-wise (observation) or column-wise (variable) level changes, as illustrated in Figure 2.3.

var_1	var_2	var_3	var_4	var_5	var_6
~	~	~	~	~	~
~	~	~	~	~	~
~	~	~	~	~	~
~	~	~	~	~	~
~	~	~	~	~	~
~	~	~	~	~	~
~	~	~	~	~	~

Figure 2.3: Visualization of row-wise and column-wise transformation operations on a dataset.

The results build on and manipulate the curated dataset to produce a *transformed dataset*. While there is typically one curated dataset that serves as the base organizational dataset,

there may be multiple transformed datasets, each aligning with the informational needs of specific analyses in the research project.

In what follows, we will group common transformation processes into two purpose-based groupings: preparation and enrichment. The purpose of preparation transformations is to clean, standardize, and derive the key attributes of the dataset on which further processing will depend. Enrichment transformations, on the other hand, are designed to add new attributes to the dataset. These attributes may be derived from the existing attributes or may be integrated from other datasets. Together, the goal of these transformations is to make the dataset more informative and more amenable to the particular aims of a given analysis.

2.2.2.1 Preparation

Common preparation transformations include text normalization and text tokenization. **Text normalization** is the process of standardizing text to convert the text into a uniform format and reduce unwanted variation and noise. It is often a preliminary step in data transformation processes which include variables with text.

Let's take a toy dataset, in Table 2.5, as an example starting point. In this dataset, we have three variables, `text_id`, `sent_id`, and `sentence`. It has five observations.

Table 2.5: A toy dataset with three variables, `text_id`, `sent_id`, and `sentence`.

text_id	sent_id	sentence
1	1	It's a beautiful day in the US, and our group decided to visit the famous Grand Canyon.
1	2	As we reached the destination, Jane said, "I can't believe we're finally here!"
1	3	The breathtaking view left us speechless; indeed, it was a sight to behold.
1	4	During our trip, we encountered tourists from different countries, sharing stories and laughter.
1	5	For all of us, this experience will be cherished forever.

The types of transformations we apply will depend on the specific needs of the project, but can include those found in Table 2.6.

Table 2.6: Common text normalization tasks

Task name	Relevant example	Typical purpose
Lowercasing	"Text" to "text"	Minimizing case sensitivity in subsequent analysis
Removal of Punctuation and Special Characters	"Hello, World!" to "Hello World"	Removing non-alphanumeric characters that may not carry semantic value
Adjustment of Forms	"colour" to "color", "it's" to "it is", "1" to "one"	Standardizing variations in spelling, contractions, and numeric forms to a common format

These transformations are column-wise operations, meaning they preserve the number of rows in the dataset. They also preserve the number of columns, but *do* change the values of the variables. These tasks should be applied with an understanding of how the changes will impact the analysis. For example, lowercasing can be useful for reducing differences between words that are otherwise identical, yet differ in case due to word position in a sentence ("The" versus "the"). However, lowercasing can also be problematic if the case of the word carries semantic value, such as in the case of "US" (United States) and "us" (first person plural pronoun).

Text tokenization involves adapting the text such that it reflects the target linguistic unit that will be used in the analysis. This is a row-wise operation expanding the number of rows, if the linguistic unit is smaller than the original variable, or reducing the number of rows, if the linguistic unit is larger than the original variable.

Text variables can be tokenized at any linguistic level, to the extent we can operationalize the linguistic unit. For example, a text variable can be tokenized into characters, words, sentences, *etc*. The choice of tokenization level often reflects the unit of observation of the dataset. For example, if the unit of observation is a word, then the text variable will be tokenized into words. If the unit of observation is a sentence, then the text variable will be tokenized into sentences.

Sequential groupings of characters and words are also common tokenization units. These are known as **n-grams**, where n is the number of words or characters in the grouping. For example, a word bigram is a sequence of two words, and a character trigram is a sequence of three characters.

In Table 2.7, we see examples of tokenization at word and character levels.

At its core, tokenization is the process which enables the quantitative analysis of text. Choosing the right tokenization level is crucial for the success of the analysis.

Table 2.7: Examples of tokenization at word and character levels.

(a) Word tokenization			(b) Word bigram tokenization			(c) Character trigram tokenization		
text_id	sent_id	word	text_id	sent_id	bigram	text_id	sent_id	trigram
1	1	it's	1	1	it's a	1	1	its
1	1	a	1	1	a beautiful	1	1	tsa
1	1	beautiful	1	1	beautiful day	1	1	sab
1	1	day	1	1	day in	1	1	abe
1	1	in	1	1	in the	1	1	bea
1	1	the	1	1	the us	1	1	eau
1	1	us	1	1	us and	1	1	aut
1	1	and	1	1	and our	1	1	uti
1	1	our	1	1	our group	1	1	tif
1	1	group	1	1	group decided	1	1	ifu

2.2.2.2 Enrichment

Let's now turn to transformations that augment the variables of the dataset. Common enrichment transformations include recoding, generation, and integration of observations and/ or variables.

Recoding is the process of transforming the values of one or more variables into new values which are more amenable to analysis. This is a column-wise operation which can be applied to categorical or numeric variables alike.

The aim is to simplify complex variables, making it easier to identify patterns and trends relevant for the research question. Say for example, we have a variable in our dataset that represents the part-of-speech (POS) of each word token in the text. The measure is a POS tag from the Penn Treebank tagset (Marcus, Santorini, and Marcinkiewicz 1993). This tagset makes twelve major and 45 minor grammatical class distinctions. In an analysis that aims to explore only major class distinctions, it would be useful to recode the POS variable into major classes only (*i.e.* noun, pronoun, adjective, verb, adverb, *etc.*) to facilitate queries, summaries, and visualizations.

Along these lines, the surface forms of words can be recoded to their lemmatized or stemmed forms. **Stemming** is the process of reducing inflected words to their word stem, base, or root form. **Lemmatization** is the process of reducing inflected words to their dictionary form, or lemma.

In Table 2.8, we see an example of recoding surface forms of words to their lemmatized forms.

Table 2.8: A toy dataset illustrating recoding of surface forms of words to their lemmatized forms.

text_id	sent_id	word	lemma
1	2	as	as
1	2	we	we
1	2	reached	reach
1	2	the	the
1	2	destination	destination
1	2	jane	jane
1	2	said	say
1	2	i	i
1	2	can	can
1	2	not	not
1	2	believe	believe
1	2	we	we
1	2	are	be
1	2	finally	finally
1	2	here	here

Case study

Inflectional family size is the number of inflectional forms for a given word and can be calculated from a corpus by counting the number of surface forms for each lemma in the corpus (Kostić, Marković, and Baucal 2003). R. Harald Baayen, Feldman, and Schreuder (2006) found that words with larger inflectional family size are associated with faster word recognition times in lexical processing tasks.

Recoding transformations can be useful for simplifying complex variables, making it easier to identify patterns, as we see in Table 2.8. However, it is important to note that recoding can also lead to loss of information. For example, recoding a variable with many levels into a binary variable can lead to loss of information about the original levels. It is important to consider the trade-offs of recoding and to ensure that the recoding aligns with the research question.

Furthermore, it is important to note recoding can be used to create more nuanced variables instead of more simplified. This draws on the combination of level information from multiple variables creating a variable that reflects a more complex relationship that was previously implicit in the dataset.

Generation is the process of creating new variables from existing variables, and as such it is a column-wise operation. Generation can include applying calculations or extracting relevant

information from existing variables or enhancing text variables with linguistic annotation. Simplifying a bit, generation helps make implicit attributes explicit.

Let's highlight a some common calculation and extraction examples that generate variables. First, let's look at the calculation of measures. In text analysis, measures are often used to describe the properties of a document or linguistic unit. For example, the number of words in a corpus document, the lengths of sentences, the number of clauses in a sentence, *etc..* In turn, these measures can be used to calculate other measures, such as lexical diversity or syntactic complexity measures.

In terms of extraction, the goal is to distill relevant information from existing variables. For example, extracting the year from a date variable, or extracting the first name from a full name variable. In text analysis, extraction is often used to extract information from text variables. Say we have a dataset with a variable containing conversation utterances. We may want to extract some characteristic from those utterances and capture their occurrence in a new variable.

But what if we want to extract linguistic information from a text variable that is not explicitly present in the text? This is where linguistic annotation comes in. Linguistic annotation is the process of enriching text with linguistic information, such as part-of-speech tags, morphological features, syntactic structure, *etc..* This can be done manually by linguist coders and/ or done using natural language processing (NLP) tools, such as part-of-speech taggers, parsers, *etc..*

To illustrate the process of linguistic annotation, we will start with the dataset from Table 2.5. Applying a pre-trained model from the Universal Dependencies (UD)⁶⁷ project, we can generate linguistic annotation for each word in the `sentence` variable.

Table 2.9: Automatic linguistic annotation for grammatical category and syntactic structure for an example English sentence from the MASC.

token_id	token	pos	features	syn_relation
1	It	PRP	Case=Nom Gender=Neut Number=Sing Person=3 PronType=Prs	
2	's	VBZ	Mood=Ind Number=Sing Person=3 Tense=Pres VerbForm=Fin	
3	a	DT	Definite=Ind PronType=Art	det
4	beautiful	JJ	Degree=Pos	amod
5	day	NN	Number=Sing	root
6	in	IN	NA	case
7	the	DT	Definite=Def PronType=Art	det
8	US	NNP	Number=Sing	nmod
9	,	,	NA	punct

⁶<https://universaldependencies.org/>

⁷The Universal Dependency project is an effort to develop cross-linguistically consistent treebank annotation for many languages. The project has developed a set of annotation guidelines and a set of tools for generating linguistic annotation. The project has also developed a set of pre-trained models for many languages.

Table 2.9: Automatic linguistic annotation for grammatical category and syntactic structure for an example English sentence from the MASC.

token_idoken	pos	features	syn_relation
10	and	CC NA	cc
11	our	PRP\$ Number=Plur Person=1 Poss=Yes PronType=Prs	nmod:poss
12	group	NN Number=Sing	nsubj
13	decided	VBD Mood=Ind Tense=Past VerbForm=Fin	conj
14	to	TO NA	mark
15	visit	VB VerbForm=Inf	xcomp
16	the	DT Definite=Def PronType=Art	det
17	famous	JJ Degree=Pos	amod
18	Grand	NNP Number=Sing	compound
19	Canyon	NNP Number=Sing	obj
20	.	NA	punct

The annotated dataset now includes the key variables `pos` (Penn treebank tags), `features` (morphological features), and `syn_relation`. The results of this process can then be further transformed as need be to fit the needs of the analysis. The results of this process enables more direct access during analysis to features that were hidden or otherwise difficult to access.

A word of caution: automated linguistic annotation offers rapid access to abundant and highly dependable linguistic data for numerous languages. However, linguistic annotation tools are not infallible. They are tools developed by training computational algorithms to identify patterns in previously annotated and verified datasets, resulting in a language model. This model is then employed to predict linguistic annotations for new language data (as seen in Table 2.9). The accuracy of the linguistic annotation heavily relies on the congruence between the language sampling frame of the trained data and that of the dataset to be automatically annotated.

Integration is a transformation step which can be row-wise or column-wise. Row-wise integration is the process of combining datasets by appending observations from one dataset to another. Column-wise integration is the process of combining datasets by appending variables from one dataset to another.

To integrate in row-wise manner the datasets involved in the process must have the same variables and variable types. This process is often referred to as **concatenating datasets**. It can be thought of as stacking datasets on top of each other to create a larger dataset. Remember, having the same variables and variable types is not the same as having the same values.

Take, for example, a case when a corpus resource contains data for two populations. In the course of curating and transforming the datasets, it may make more sense to work with

the datasets separately. However, when it comes time to analyze the data, it may be more convenient to work with the datasets as a single dataset. In this case, the datasets can be concatenated to create a single dataset.

To illustrate, consider the toy datasets in Table 2.10 and Table 2.11.

Table 2.10: Toy dataset of written text data.

participant_id	text_id	modality	text
P1	T1	Written	Technology has revolutionized our lives in many ways. It has made communication easier, faster, and more efficient.
P3	T3	Written	Climate change is a pressing issue that affects everyone on Earth. We must take immediate action to reduce our carbon footprint.
P5	T5	Written	Education is the key to personal and societal growth. Investing in quality education will lead to a brighter future for all.

Table 2.11: Toy dataset of spoken text data.

participant_id	text_id	modality	text
P2	T2	Spoken	Hello, my name is X. I am a software engineer working at XYZ company.
P4	T4	Spoken	Hi, I'm X, and I work as a project manager. My main responsibility is to ensure that projects are completed on time and within budget.
P6	T6	Spoken	Hi, my name is X, and I'm a teacher. I teach English at a local high school.

These datasets, in Table 2.10 and Table 2.11, contain the same variables and variable types, but different observations –one in which the sample contains written language and the other spoken. Conveniently, they can be concatenated to create a single dataset that contains all of the observations, as seen in Table 2.12.

Table 2.12: Toy dataset of written and spoken text data concatenated.

participant_id	text_id	modality	text
P1	T1	Written	Technology has revolutionized our lives in many ways. It has made communication easier, faster, and more efficient.
P3	T3	Written	Climate change is a pressing issue that affects everyone on Earth. We must take immediate action to reduce our carbon footprint.
P5	T5	Written	Education is the key to personal and societal growth. Investing in quality education will lead to a brighter future for all.
P2	T2	Spoken	Hello, my name is X. I am a software engineer working at XYZ company.
P4	T4	Spoken	Hi, I'm X, and I work as a project manager. My main responsibility is to ensure that projects are completed on time and within budget.
P6	T6	Spoken	Hi, my name is X, and I'm a teacher. I teach English at a local high school.

Integrating datasets can be performed in a column-wise manner as well. In this process, the datasets need not have the exact same variables and variable types, rather it is required that the datasets share a common variable of the same informational type that can be used to index the datasets. This process is often referred to as **joining datasets**.

Corpus resources often include metadata in stand-off annotation format. That is, the metadata is not embedded in the corpus files, but rather is stored in a separate file. The metadata and corpus files will share a common variable which is used to join the metadata with the corpus files.

To exemplify, here's another toy dataset that shares the `participant_id` index with the previous dataset in Table 2.12 and includes the variables `eng_native`, `age`, and `gender`:

Table 2.13: Toy dataset of participant data with a shared variable `participant_id` to index the datasets.

participant_id	eng_native	age	gender
P1	Yes	28	M
P2	No	35	M
P3	Yes	42	F
P4	No	26	F

Table 2.13: Toy dataset of participant data with a shared variable `participant_id` to index the datasets.

participant_id	eng_native	age	gender
P5	Yes	31	M
P6	No	39	F

This dataset provides additional information about each participant, such as their English native speaker status, age, and gender.

Since the two datasets share the `participant_id` variable, we can merge them to create a new dataset that combines the information from both datasets, as we see in Table 2.14.

Table 2.14: Joining variables from two datasets based on a shared index variable.

participant_id	text_id	modality	text	eng_native	age	gender
P1	T1	Written	Technology has revolutionized our lives in many ways. It has made communication easier, faster, and more efficient.	Yes	28	M
P3	T3	Written	Climate change is a pressing issue that affects everyone on Earth. We must take immediate action to reduce our carbon footprint.	Yes	42	F
P5	T5	Written	Education is the key to personal and societal growth. Investing in quality education will lead to a brighter future for all.	Yes	31	M
P2	T2	Spoken	Hello, my name is X. I am a software engineer working at XYZ company.	No	35	M
P4	T4	Spoken	Hi, I'm X, and I work as a project manager. My main responsibility is to ensure that projects are completed on time and within budget.	No	26	F
P6	T6	Spoken	Hi, my name is X, and I'm a teacher. I teach English at a local high school.	No	39	F

Joining datasets is a powerful tool for enriching a dataset with additional column-wise information. It is important to note that integrating datasets can also remove information in a row-wise manner. For example, when merging two datasets with a shared variable, it is possible to remove observations that do not have a match one of the two datasets. This process

effectively filters out observations not shared between the two datasets. On the other hand, an anti-join explicitly removes observations that are shared between the two datasets.

Dive deeper

In some analyses, it may be useful to remove words with little semantic value, such as articles, prepositions, and conjunctions or words that are very common in the language. These are known as stopwords. There are various predefined lists of stopwords for different languages available on the web and through R in the `stopwords` package (Benoit, Muhr, and Watanabe 2021). Anti-joining a stopword list with a dataset of word tokens is often used to remove stopwords from the dataset.

However, it is important to note the criteria used to determine which words are considered stopwords in a particular resource may not fit a researcher's needs or the characteristics of the data. Learn more about approaches to identifying stopwords in Kaur and Buttar (2018).

In sum, the transformation steps described here collectively aim to produce higher quality datasets that are relevant in content and structure to submit to analysis. The process may include one or more of the previous transformations but is rarely linear and is most often iterative. It is typical to do some normalization then generation, then recoding, and then return to normalizing, and so forth. This process is highly idiosyncratic given the characteristics of the curated dataset and the ultimate goal for the transformed dataset(s).

2.3 Documentation

As we have seen in this chapter, acquiring corpus data and converting that data into information involves a number of conscious decisions and implementation steps. As a favor to ourselves, as researchers, and to the research community, it is crucial to document these decisions and steps. This makes it both possible to retrace our own steps and also provides a guide for future researchers that want to reproduce and/ or build on your research. A programmatic approach to quantitative research helps ensure that the implementation steps are documented and reproducible but it is also vital that the decisions that are made are documented as well. This includes data origin information for the acquired corpus data and data dictionaries for the curated and transformed datasets.

2.3.1 Data origin

Data acquired from corpus resources should be accompanied by information about the **data origin**. Table 2.15 provides a list of the types of information that should be included in the data origin information.

Table 2.15: Data origin information.

Information	Description
Resource name	Name of the corpus resource.
Data source	URL, DOI, <i>etc.</i>
Data sampling frame	Language, language variety, modality, genre, <i>etc.</i>
Data collection date(s)	The date or date range of the data collection.
Data format	Plain text, XML, HTML, <i>etc.</i>
Data schema	Relationships between data elements: files, folders, <i>etc.</i>
License	CC BY, CC BY-NC, <i>etc.</i>
Attribution	Citation information for the data source.

For many corpus resources, the corpus documentation will include all or most of this information as part of the resource download or documented online. If this information is not present in the corpus resource or you compile your own, it is important to document this information yourself. This information can be documented in file, such as a plain text file or spreadsheet, that is included with the corpus resource.

2.3.2 Data dictionaries

The process of organizing the data into a dataset, curation, and modifications to the dataset in preparation for analysis, transformation, each include a number of project-specific decisions. These decisions should be documented.

On the one hand, each dataset that is created should have a **data dictionary** file. A data dictionary is a document, usually in a spreadsheet format, that describes the variables in a dataset. The key information that should be included in a data dictionary is provided in Table 2.16.

Table 2.16: Data dictionary information.

Information	Description
Variable name	The name of the variable as it appears in the dataset, <i>e.g.</i> <code>participant_id</code> , <code>modality</code> , <i>etc.</i>

Table 2.16: Data dictionary information.

Information	Description
Readable variable name	A human-readable name for the variable, <i>e.g.</i> ‘Participant ID’, ‘Language modality’, <i>etc.</i>
Variable type	The type of information that the variable contains, <i>e.g.</i> ‘categorical’, ‘ordinal’, <i>etc.</i>
Variable description	A prose description expanding on the readable name and can include measurement units, allowed values, <i>etc.</i>

Organizing this information in a tabular format, such as a spreadsheet, can make it easy for others to read and understand your data dictionary.

 **Tip**

It is conventional to work with variable names for datasets in R using the same conventions that are used for naming objects. It is a matter of taste which convention is used, but I have adopted snake case^a as my personal preference (*e.g.* `ref_num`). There are also alternatives^b. Regardless of the convention you choose, it is good practice to be consistent.

It is also of note that the variable names should be balanced for meaningfulness and brevity. This brevity is of practical concern but can be somewhat opaque. For questions into the meaning of the variable and its values consult the resource’s dataset documentation.

^ahttps://bookdown.org/content/d1e53ac9-28ce-472f-bc2c-f499f18264a3/names.html#snake_case

^b<https://bookdown.org/content/d1e53ac9-28ce-472f-bc2c-f499f18264a3/names.html>

On the other hand, the data curation and transformation steps should be documented in the code that is used to create the dataset. This is one of the valuable features of a programmatic approach to quantitative research. The transparency of this documentation is enhanced by using **literate programming** strategies to intermingling prose descriptions and code the steps in the same, reproducible document.

By providing a comprehensive data dictionary and using a programmatic approach to data curation and transformation, you ensure that others can easily understand and work with your dataset, facilitating collaboration and reproducibility.

Activities

In the following activities, we will be tackle a common scenario in data analysis: to read, to inspect, and to write datasets. The recipe will discuss the necessary packages and functions

to accomplish these tasks including `readr` and `dplyr`. The recipe will also refresh and expand on the elements of code blocks in Quarto documents such as the `label`, `echo`, `message`, and `include` options.

_recipe

What: Reading, inspecting, and writing datasets^a

How: Read Recipe 2, complete comprehension check, and prepare for Lab 2.

Why: To use literate programming in Quarto to work with R coding strategies for reading, inspecting, and writing datasets.

^a<https://qtalr.github.io/qtalrkit/articles/recipe-2.html>

Lab

What: Dive into datasets^a

How: Clone, fork, and complete the steps in Lab 2.

Why: To read datasets from packages and from plain-text files, inspect and report characteristics of datasets, and write datasets to plain-text files.

^a<https://github.com/qtalr/lab-02>

Summary

In this chapter we have focused on data and information –the first two components of DIKI Hierarchy. This process is visualized in Figure 2.4.

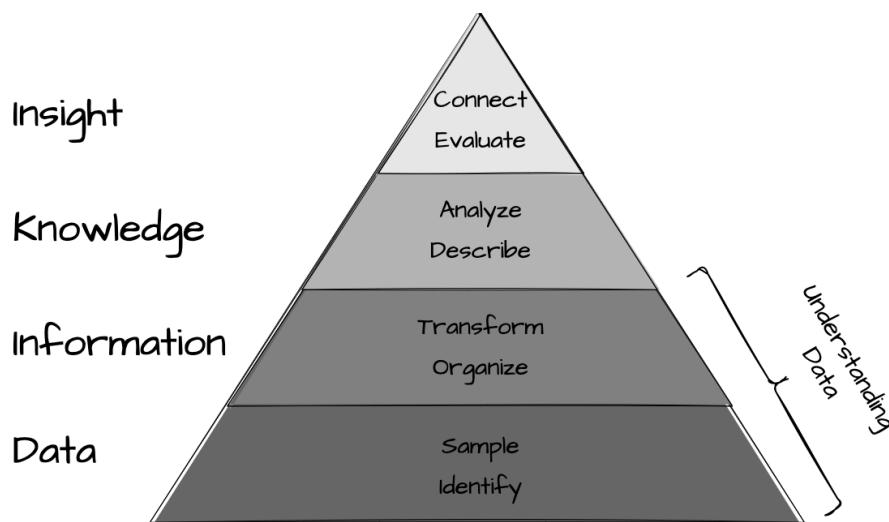


Figure 2.4: Understanding data: visual summary

First a distinction is made between populations and samples, the latter being a intentional and subjective selection of observations from the world which attempt to represent the population of interest. The result of this process is known as a corpus. Whether developing a corpus or selecting an existing a corpus it is important to vet the sampling frame for its applicability and viability as a resource for a given research project.

Once a viable corpus is identified, then that corpus is converted into a curated dataset which adopts the tidy dataset format where each column is a variable, each row is an observation, and the intersection of columns and rows contain values. This curated dataset serves to establish the base informational relationships from which your research will stem.

The curated dataset will most likely require transformations which may include normalization, tokenization, recoding, generation, and/ or integration to enhance the usefulness of the information to analysis. A transformed dataset or set of datasets will be the result from this process.

Finally, documentation should be implemented at the acquisition, curation, and transformation stages of the analysis project process. The combination of data origin, data dictionary, and literate programming files establishes documentation of the data and implementation steps to ensure transparent and reproducible research.

3 Analysis

Statistical thinking will one day be as necessary for efficient citizenship as the ability to read and write.

— H.G. Wells

▀ Outcomes

- Recall the fundamental concepts and principles of statistics in data analysis.
- Articulate the roles of diagnostic, analytic, and interpretive statistics in quantitative analysis.
- Compare the similarities and differences between analytic approaches to data analysis.

The aim of analysis is to derive knowledge from information, the next step in the DIKI Hierarchy. Where the creation of information from data involves human intervention and conscious decisions, as we have seen, deriving knowledge from information involves another level of intervention. The goal is to break down complex information into simpler components which are more readily interpretable.

In what follows, we will cover the main steps in the process of analysis. The first is to inspect the data to ensure its quality and understand its characteristics. The second is to interrogate the data to uncover patterns and relationships and interpret the findings. To conclude this chapter, I will outline methods to and the importance of communicating the analysis results and procedure in a transparent and reproducible manner.

➤ Lessons

What: Summarizing data, Visual summaries^a

How: In the R Console pane load `swirl`, run `swirl()`, and follow prompts to select the lesson.

Why: To showcase methods for statistical summaries of vectors and data frames and to create informative graphics that enhance data interpretation and analysis.

^a<https://github.com/qtalr/lessons>

3.1 Describe

The goal of descriptive statistics is to summarize the data in order to understand and prepare the data for the analysis approach to be performed. This is accomplished through a combination of statistic measures and/ or tabular or graphic summaries. The choice of descriptive statistics is guided by the type of data, as well as the question(s) being asked of the data.

In descriptive statistics, there are four basic questions that are asked of each of the variables in the dataset. Each correspond to a different type of descriptive measure.

1. **Central Tendency:** Where do the data points tend to be located?
2. **Dispersion:** How spread out are the data points?
3. **Distribution:** What is the overall shape of of the data points?
4. **Association:** How are these data points related to other data points?

To ground this discussion I will introduce a new dataset. This dataset is drawn from the Barcelona English Language Corpus (BELC) (Muñoz 2006), which is found in the TalkBank repository. I've selected the "Written composition" task from this corpus which contains 80 writing samples from 36 second language learners of English at different ages. Participants were given the task of writing for 15 minutes on the topic of "Me: my past, present and future". Data was collected for participants from one to three times over the course of seven years (at 10, 12, 16, and 17 years of age).

In Table 3.1 we see the data dictionary for the BELC dataset which reflects structural and transformational steps I've done so we start with a tidy dataset with `essay_id` as the unit of observation.

Table 3.1: Data dictionary for the BELC dataset.

variable	name	variable_type	description
essay_id	Essay ID	categorical	Unique identifier for each essay
part_id	Participant ID	categorical	Identifier for each participant learner
sex	Sex	categorical	Sex of the participant
group	Group	ordinal	Time group of the essay, ordered from T1 to T4 (10, 12, 16, and 17 years old)
tokens	Tokens	numeric	Number of word tokens in the essay
types	Types	numeric	Number of unique word types in the essay
ttr	TTR	numeric	Type-Token Ratio (TTR) of the essay
prop_l2	Proportion of L2	numeric	Proportion of words in the essay identified as second (target) language (L2)

The data dictionary provides a easily accessible overview of the dataset. This includes a human-readable mapping from variable names to variable descriptions. Further, it provides

information about the type of variable (e.g., categorical, ordinal, numeric). As we will see the informational type of variables is key to descriptive measures, as well as all other components of analysis.

Now, let's take a look at the first few observations of the BELC dataset to get another perspective on the dataset as we view the values of the dataset.

Table 3.2: First 5 observations of the BELC dataset.

essay_id	part_id	sex	group	tokens	types	ttr	prop_l2
E1	L01	female	T2	79	46	0.582	0.987
E2	L02	female	T1	18	18	1.000	0.667
E3	L02	female	T3	101	53	0.525	1.000
E4	L05	female	T1	20	17	0.850	0.900
E5	L05	female	T3	158	80	0.506	0.987

In Table 3.2, each of the variables are attributes or measures of the `essay_id` variable. `tokens` is the number of total words, `types` is the number of unique words, `ttr` is the ratio of unique words to total words. This is known as the Type-Token Ratio and it is a standard metric for measuring lexical diversity. Finally, the proportion of L2 words (English) to the total words (`tokens`) is provided in `prop_l2`.

Case study

Type-Token Ratio is a standard metric for measuring lexical diversity, but it is not without its flaws. Most importantly, TTR is highly sensitive to the word length of the text. Duran (2004) discuss this limitation, and the limitations of other lexical diversity measures and propose a new measure D which shows a stronger correlation with language proficiency in their comparative studies.

Let's now turn our attention to exploring descriptive measures using the BELC dataset.

3.1.1 Central tendency

The central tendency is a measure which aims to summarize the data points in a variable as the most representative, middle or most typical value. There are three common measures of central tendency: the mode, mean and median. Each differ in how they summarize the data points.

The **mode** is the value, or values, that appears most frequently in a set of values. If there are multiple values with the highest frequency, then the variable is said to be multimodal. The most versatile of the central tendency measures as it can be applied to all levels of measurement,

although the mode is not often used for numeric variables as it is not as informative as other measures.

💡 Consider this

Grieve, Nini, and Guo (2018) compiled a 8.9 billion-word corpus of geotagged posts from Twitter between 2013-2014 in the United States. The authors provide a search interface^a to explore relationship between lexical usage and geographic location. Explore this corpus searching for terms related to slang (“hella”, “wicked”), geographical (“mountain”, “river”), meteorological (“snow”, “rain”), and/ or any other term types. What types of patterns do you find? What are the benefits and/ or limitations of this type of data, data summarization, and/ or interface?

^a<https://isogloss.shinyapps.io/isogloss/>

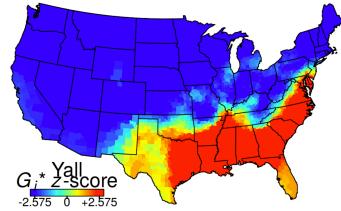


Figure 3.1: Example distribution of the term ‘Ya’ll’ the Word Mapper project.

The more common measures for numeric variables are the mean and the median. The **mean** is a summary statistic calculated by summing all the values and dividing by the number of values. The **median** is calculated by sorting all the values in the variable and then selecting the middle value. Given that the mean and median are calculated differently, they will not always yield the same result. Differences that appear between the mean and median will be of interest to us later in this chapter.

3.1.2 Dispersion

The mean, median, and mode provide summary information where data points tend to be located. However, they do not provide us with any understanding as to how representative this value is. To provide this context, the spread of the values around the central tendency, or **dispersion**, is calculated.

For categorical variables, the spread is framed in terms of how balanced the values are across the levels. One way to do this is to calculate the (normalized) entropy. **Entropy** is a measure of uncertainty. The more balanced the values are across the levels, the closer entropy is 1. In practice, however, proportions are often used to assess the balance of the values across the levels. The **proportion** of each level is the frequency of the level divided by the total number of values.

The most common measure of dispersion for numeric variables is the **standard deviation**. The standard deviation is calculated by taking the square root of the variance. The **variance**

is the average of the squared differences from the mean. So, more succinctly, the standard deviation is a measure of the spread of the values around the mean. Where the standard deviation is anchored to the mean, the **interquartile range** (IQR) is tied to the median. The median represents the sorted middle of the values, in other words the 50th percentile. The IQR is the difference between the 75th percentile and the 25th percentile. Again, just as the mean and the median, the standard deviation and the IQR are calculated in different ways, they are not always the same.

Let's now consider the relevant central tendency and dispersion of the variables in the BELC dataset. In Table 3.3, we see the categorical measures.

Table 3.3: Central tendency and dispersion of the categorical variables

variable	top_counts	norm_entropy
essay_id	E1: 1, E10: 1, E11: 1, E12: 1	1.00
part_id	L05: 3, L10: 3, L11: 3, L12: 3	0.98
sex	fem: 48, mal: 32	0.97
group	T1: 25, T3: 24, T2: 16, T4: 15	0.98

In Table 3.3, the `top_counts` measure gives us a short list of the most frequent levels of the variable. From `top_count` we can gather whether the variable has one mode or is multimodal. Both `essay_id` and `part_id` have the same most frequent value for the levels listed. On the other hand, `sex` and `group` have a single mode. We can also appreciate the dispersion of these variables based on the `norm_entropy` of each variable. `essay_id` is completely balanced across the levels, so it has a normalized entropy of 1. the other variables are not as balanced, but still quite balanced as the normalized entropy is close to 1.

In Table 3.4, we see the numeric measures.

Table 3.4: Central tendency and dispersion for numeric variables.

variable	mean	sd	median	iqr
tokens	67.62	44.20	56.50	61.250
types	41.85	23.03	38.50	31.500
ttr	0.68	0.13	0.66	0.149
prop_l2	0.96	0.10	0.99	0.027

In Table 3.4, we have measures for the mean, median, standard deviation, and IQR for each variable. The variable `tokens` has a larger difference between the mean and median than the other variables and the standard deviation is relatively large suggesting that the values are more spread out around the mean. In the case of `ttr` the mean and median are quite close and

the standard deviation is relatively small suggesting that the values are more tightly clustered around the mean.

When interpreting these numeric summary values, it is important to only directly compare column-wise. That is, focusing only on a single variable, not across variables. Each variable, as is, is measured on a different scale and only relative to itself can we make sense of the values.

Dive deeper

The inability to compare summary statistics across variables is a key reason why **standardization** is often applied before submitting a dataset for analysis (Johnson 2008; R. Harald Baayen 2008).

Standardization is a scale-based transformation that changes the scale of the values to a common scale, or *z-scores*. The result of this transformation puts data points of each variable on the same scale and allows for direct comparison. Furthermore, standardization also mitigates the influence of variables with large values relative to other variables. This is particularly important in multivariate analysis where the influence of variables with large values can be magnified.

The caveat is that standardization masks the original meaning of the data. That is, if we consider token frequency, before standardization, we can say that a value of 1000 tokens is 1000 tokens. After standardization, we can only say that a value of 1 is 1 standard deviation from the mean. This is why standardization is often applied after the descriptive phase of analysis.

Another thing to note in Table 3.4 is that the mean and median are not the same. They are both measures of central tendency, but the mean is more sensitive to extreme values than the median. The difference between the mean and median is a numeric representation that gives us a first glimpse of the distribution of the data. With this in mind, let's turn to the distribution of the variables.

3.1.3 Distributions

Summary statistics of the central tendency and dispersion of a variable provide a sense of the most representative value and how spread out the data is around this value. However, to gain a more comprehensive understanding of the variable, it is key to consider the frequencies of all the data points. The **distribution** of a variable is the pattern or shape of the data that emerges when the frequencies of all data points are considered. This can reveal patterns that might not be immediately apparent from summary statistics alone.

When assessing the distribution of categorical variables, we can use a frequency table or bar plot. A **frequency table** is a useful method to display the frequency and proportion of each level in a categorical variable in a clear and concise manner. In Table 3.5 we see the frequency table for the variable `sex`.

Table 3.5: Frequency table for the variable `sex`.

sex	frequency	proportion
female	48	0.6
male	32	0.4

A **bar plot** is a type of plot where the x-axis is a categorical variable and the y-axis is the frequency of the values. The frequency is represented by the height of the bar. The variables can be ordered by frequency, alphabetically, or some other order. Figure 3.2 is a bar chart for the variables `sex` and `group` ordered alphabetically.

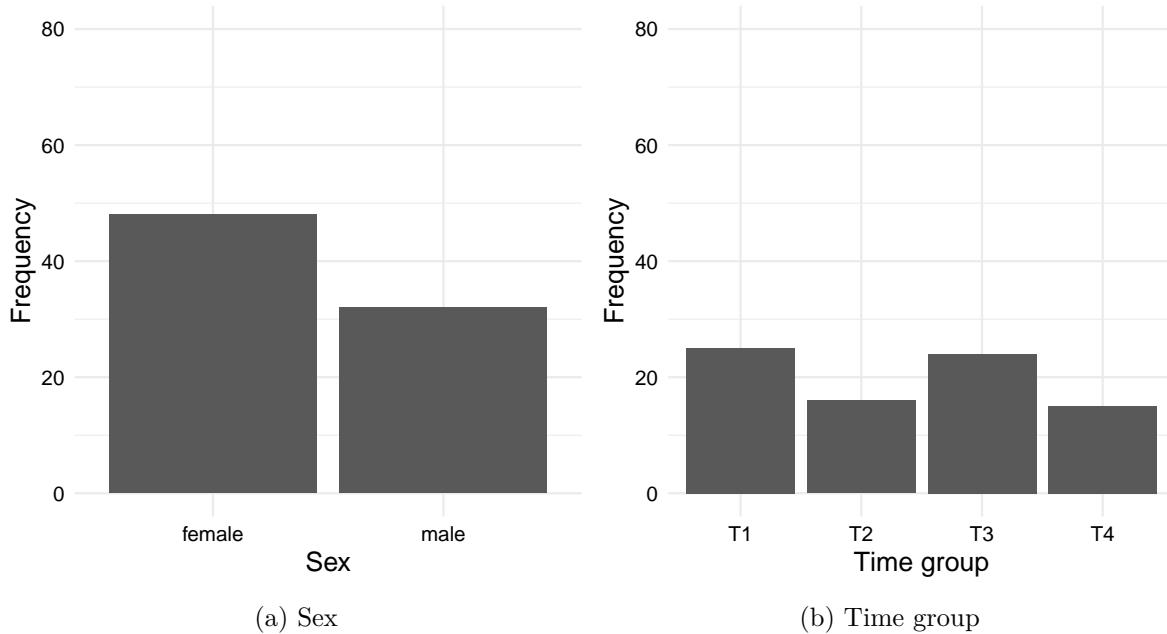


Figure 3.2: Bar plots for categorical variables `sex` and `group`.

So for a frequency table or barplot, we can see the frequency of each level of a categorical variable. This gives us some knowledge about the BELC dataset: there are more girls in the dataset and more essays appear in first and third time groups. If we were to see any clearly loopsided categories, this would be a sign of imbalance in the data and we would need to consider how this might impact our analysis.

💡 Consider this

The goal of descriptive statistics is to summarize the data in a way that is meaningful and interpretable. With this in mind, compare the frequency table in 3.5 and bar plot

in 3.2a. Does one provide a more interpretable summary of the data? Why or why not? Are there any other ways you might communicate this distribution more effectively?

For numeric variables, a frequency table, as in Table 3.5, does not summarize a distribution well. Instead, the distribution of a numeric variable is best understood visually. Furthermore, we aim to assess the distribution of the variable in terms of the shape of the distribution and the presence of outliers.

The most common visualizations of the distribution of a numeric variable are histograms and density plots. **Histograms** are a type of bar plot where the x-axis is a numeric variable and the y-axis is the frequency of the values falling within a determined range of values, or bins. The frequency of values within each bin is represented by the height of the bars.

Density plots are a smoothed version of histograms. The y-axis of a density plot is the probability of the values. When frequent values appear closely together, the plot line is higher. When the frequency of values is lower or more spread out, the plot line is lower.

An example of these plots is show in Figure 3.3 for the variable `tokens`.

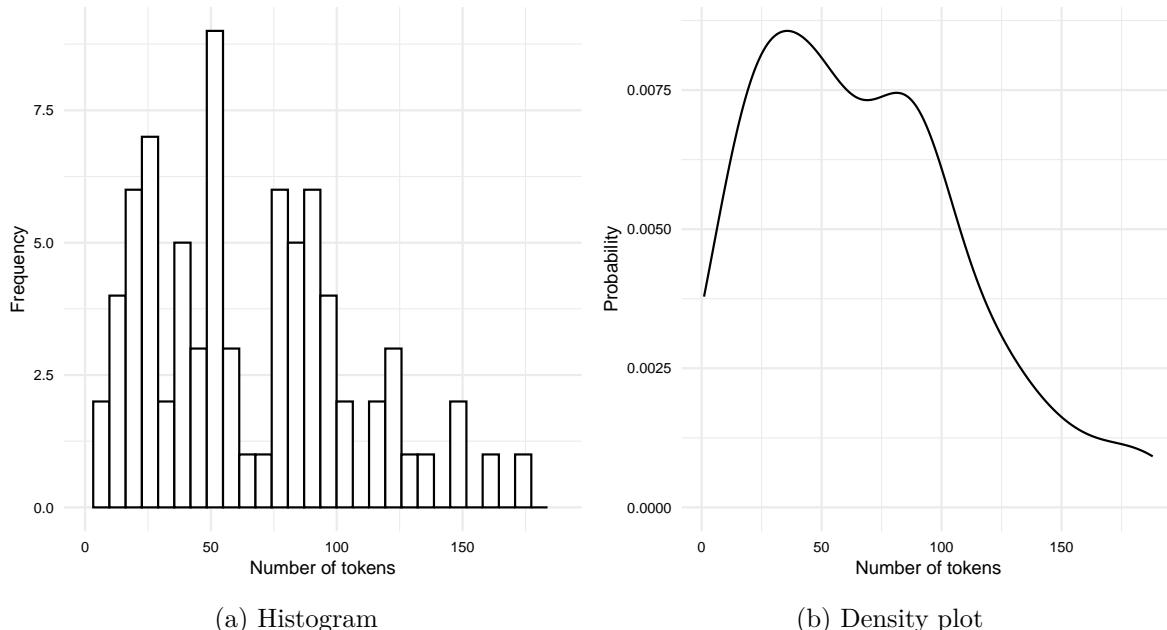


Figure 3.3: Distribution plots for the variable `tokens`.

Both the histogram in Figure 3.3a and the density plot in Figure 3.3b show the distribution of the variable `tokens` in slightly different ways which translate into trade-offs in terms of interpretability.

The histogram shows the frequency of the values in bins. The number of bins and/ or binwidth can be changed for more or less granularity. A rough grain histogram shows the general shape of the distribution, but it is difficult to see the details of the distribution. A fine grain histogram shows the details of the distribution, but it is difficult to see the general shape of the distribution. The density plot shows the general shape of the distribution, but it hides the details of the distribution. Given this trade-off, it is often useful explore outliers with histograms and the overall shape of the distribution with density plots.

In Figure 3.4 we see both histograms and density plots combined for the variables `tokens`, `types`, and `ttr`.

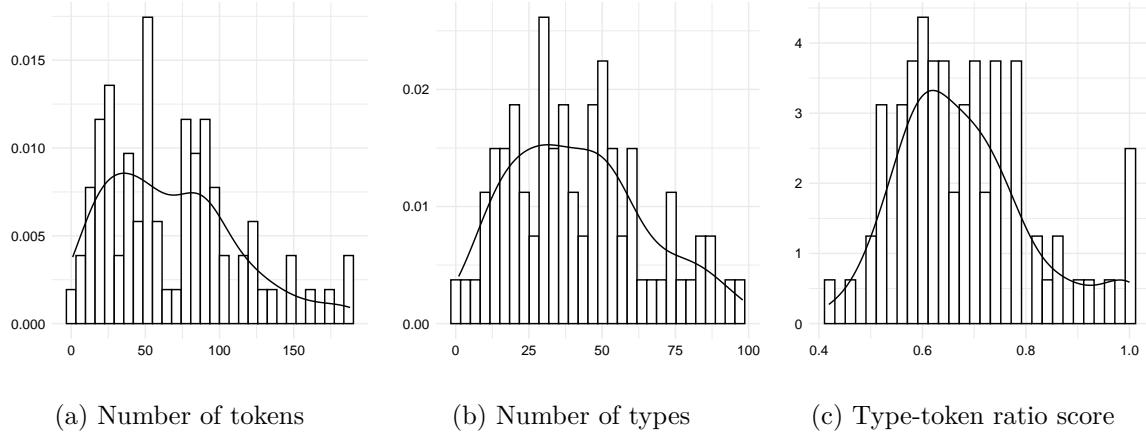
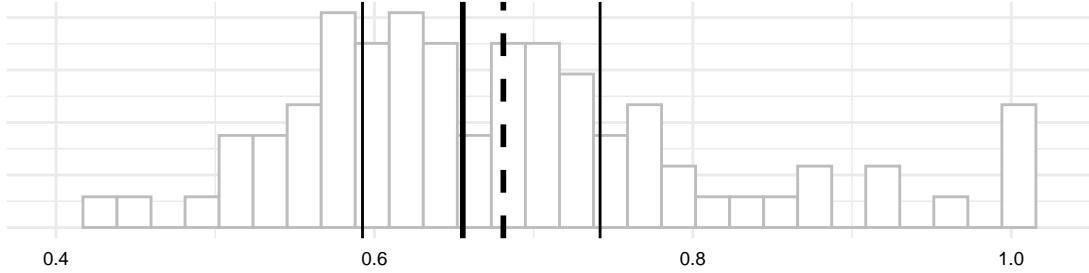


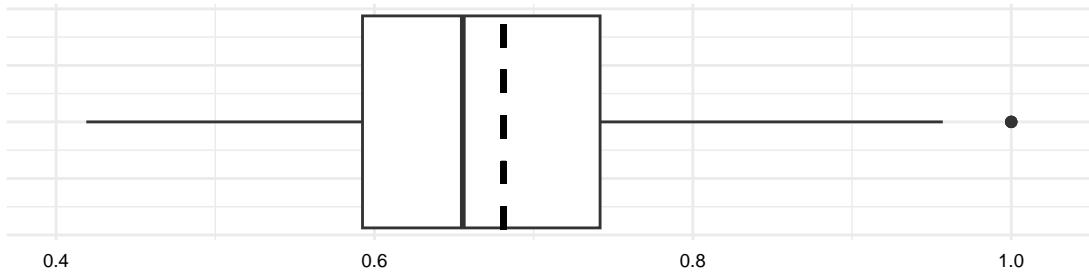
Figure 3.4: Histograms for numeric variables `tokens`, `types`, and `ttr`.

Focusing on the details captured in the histogram we are better able to detect potential outliers. Outliers can reflect valid values that are simply extreme or they can reflect something erroneous in the data. To distinguish between these two possibilities, it is important to know the context of the data. Take, for example, Figure 3.4c. We see that there is a bin near the value 1.0. Given that the type-token ratio is a ratio of the number of types to the number of tokens, it is unlikely that the type-token ratio would be exactly 1.0 as this would mean that every word in an essay is unique. Another, less dramatic, example is the bin to the far right of Figure 3.4a. In this case, the bin represents the number of tokens in an essay. An uptick in the number of essays with a large number of tokens is not surprising and would not typically be considered an outlier. On the other hand, consider the bin near the value 0 in the same plot. It is unlikely that a true essay would have 0, or near 0, words and therefore a closer look at the data is warranted.

It is important to recognize that outliers contribute undue influence to overall measures of central tendency and dispersion. To appreciate this, let's consider another helpful visualization called a **boxplot**. A boxplot is a visual representation which aims to represent the central tendency, dispersion, and distribution of a numeric variable in one plot.



(a) Histogram



(b) Boxplot

Figure 3.5: Understanding boxplots

In Figure 3.5b we see a boxplot for `ttr` variable. The box in the middle of the plot represents the interquartile range (IQR) which is the range of values between the first quartile and the third quartile. The solid line in the middle of the box represents the median. The lines extending from the box are called ‘whiskers’ and provide the range of values which are within 1.5 times the IQR. Values outside of this range are plotted as individual points.

Now let’s consider boxplots from another angle. Just above in Figure 3.5a I’ve plotted a histogram. In this view, we can see that a boxplot is a simplified histogram augmented with central tendency and dispersion statistics. While histograms focus on the frequency distribution of data points, boxplots focus on the data’s quartiles and potential outliers.

I’ve added a dashed line in Figure 3.5a and Figure 3.5b to signal the mean in this set of plots, but it is not typically included. I include the dashed line to make a point: the mean is more sensitive to outliers than the median. As I pointed out in Section 3.1.1, the mean is the sum of all values divided by the number of values. If there are extreme values, the mean will be pulled in the direction of the extreme values. The median, however, is the middle value and a few extreme values have less effect. So, when central tendency is reported, if there is a sizeable difference between the mean and the median, measures of dispersion will be larger and the direction of the difference can be used to infer the presence of outliers.

Returning to outliers, it is important to address them to safeguard the accuracy of the analysis. There are two main ways to address outliers: 1) transform the data and 2) eliminate observations with outliers (**trimming**). Trimming is more extreme as it removes data but can be the best approach for true outliers. Transforming the data is an approach to mitigating the influence of extreme but valid values. **Transformation** involves applying a mathematical function to the data which changes the scale and/ or shape of the distribution, but does not remove data nor does it change the relative order of the values.

In Figure 3.6, we see two boxplots. Figure 3.6a is the original `ttr` data and Figure 3.6b reflects the data trimmed to remove outliers. In this case, we have removed essays with a type-token ratio of 1.

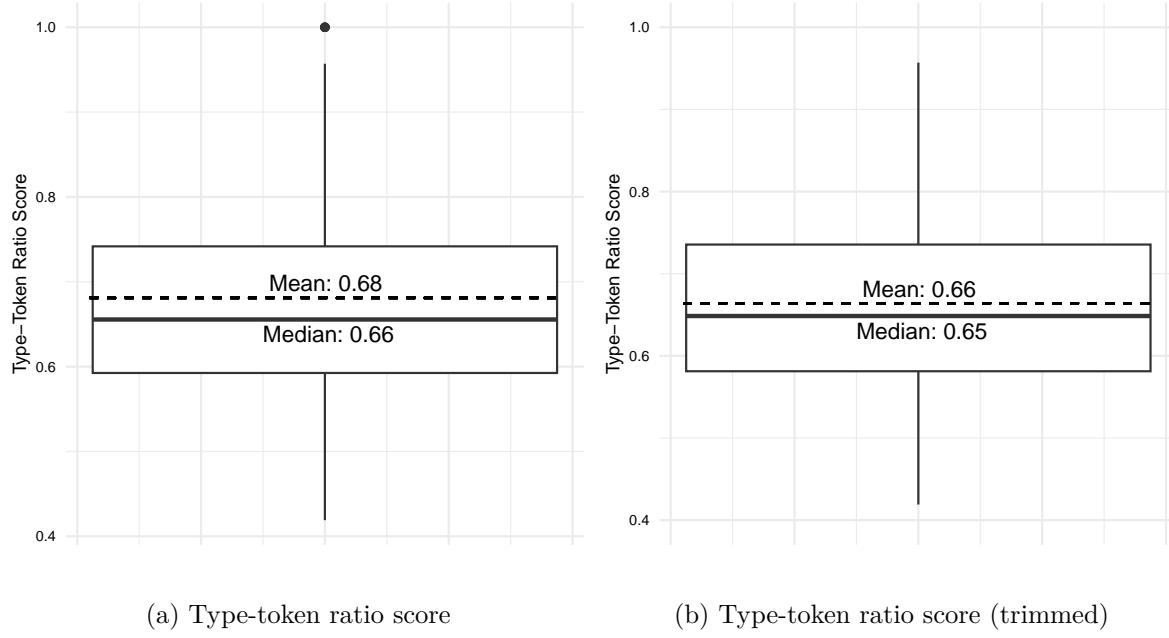


Figure 3.6: Boxplots for `ttr` before and after trimming.

We can now appreciate the relatively larger effect that the outliers had on the mean value of the `ttr` variable. As outliers are removed as the difference between the mean and median will become smaller.

The exploration the data points with histograms and boxplots has helped us to identify outliers. Now we turn to the question of the overall shape of the distribution. The key question is whether the observed distribution of each variable groups around a central tendency in a symmetrical manner or if the distribution is skewed in one direction or another.

When values are symmetrically dispersed around the central tendency, the distribution is said to be normal. The **Normal Distribution** is characterized by a distribution where the mean

and median are the same. The Normal Distribution has a key role in theoretical statistics and is the foundation for many statistical tests. This distribution is also known as the Gaussian Distribution or the Bell Curve for the hallmark bell shape of the distribution. In a normal distribution, extreme values are less likely than values near the center.

When values are not symmetrically dispersed around the central tendency, the distribution is said to be skewed. A distribution in which values tend to disperse to the left of the central tendency is **left skewed** and a distribution in which values tend to disperse to the right of the central tendency is **right skewed**.

Stepping away from our BELC dataset, I've created simulated data that fit normal and non-normal, or skewed, distributions. I present each of these distributions as density plots with mean and median line overlays in Figure 3.7.

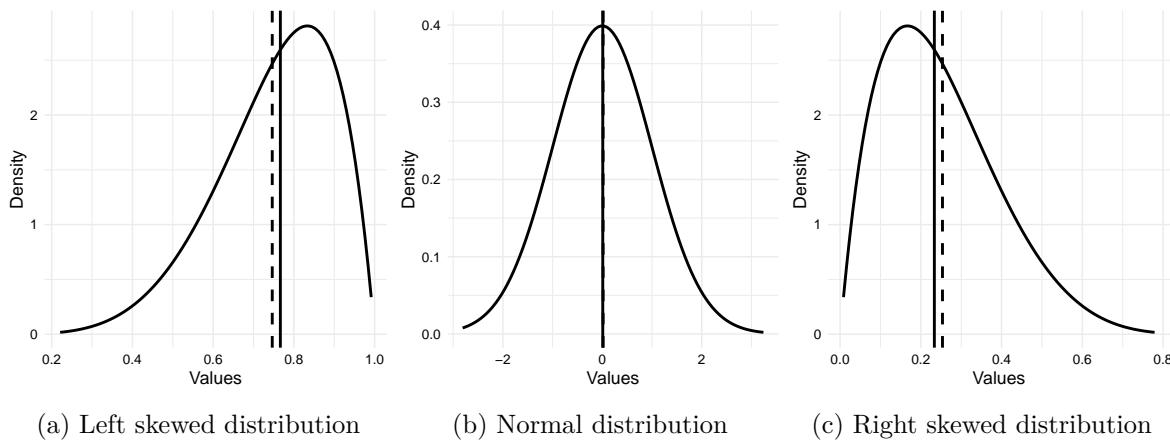


Figure 3.7: Mean and median for normal and skewed distributions.

Assessing the distribution of a variable is important for two reasons. First, the distribution of a variable can inform the choice of statistical test in theory-based hypothesis testing. Data that are normally, or near-normally distributed are often analyzed using parametric tests while data that exhibit a skewed distribution are often analyzed using non-parametric tests. Second, highly skewed distributions have the effect of compressing the range of values. This can lead to a loss of information and can make it difficult to detect patterns in the data.

Interestingly, a key feature of the distribution of linguistic units (phonemes, words, morphemes, *etc*) is that they tend to be highly skewed. This is due to the fact that a small number of linguistic units are used frequently and a large number of linguistic units are used infrequently. This is known as Zipf's Law (Zipf 1949). **Zipf's Law** is a statistical principle that states that the frequency of a word (other other linguistic units) is inversely proportional to its rank in the frequency table. In other words, the most frequent units will appear twice as often as the second most frequent unit, three times as often as the third most frequent unit, and so on.

The plot in Figure 3.8a is simulated data that fits a Zipfian distribution.

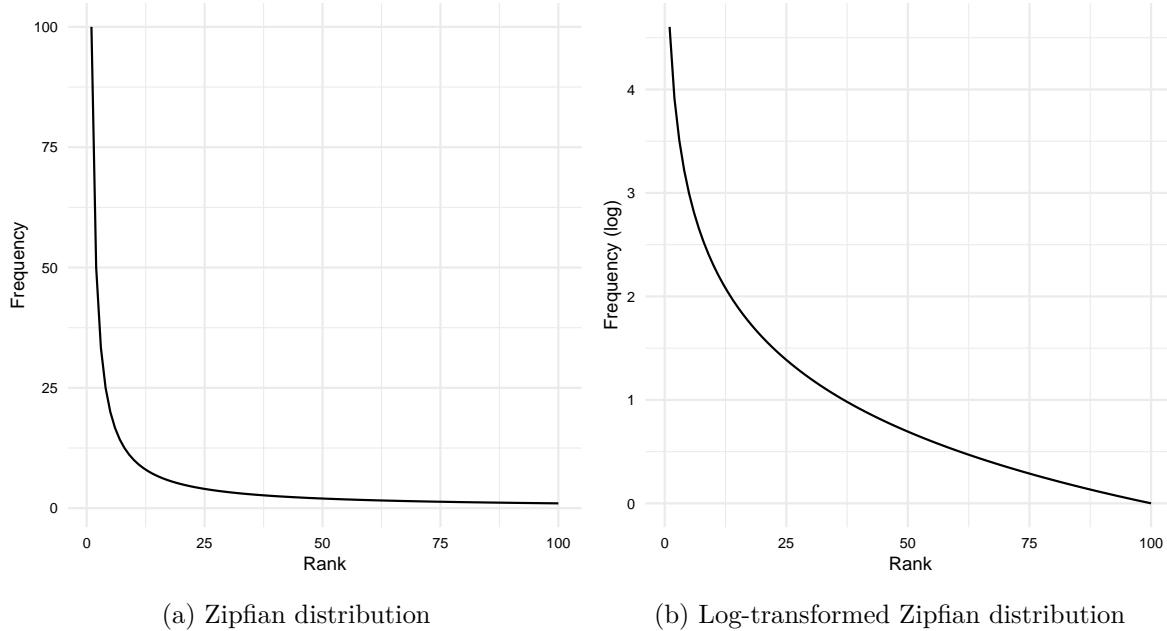


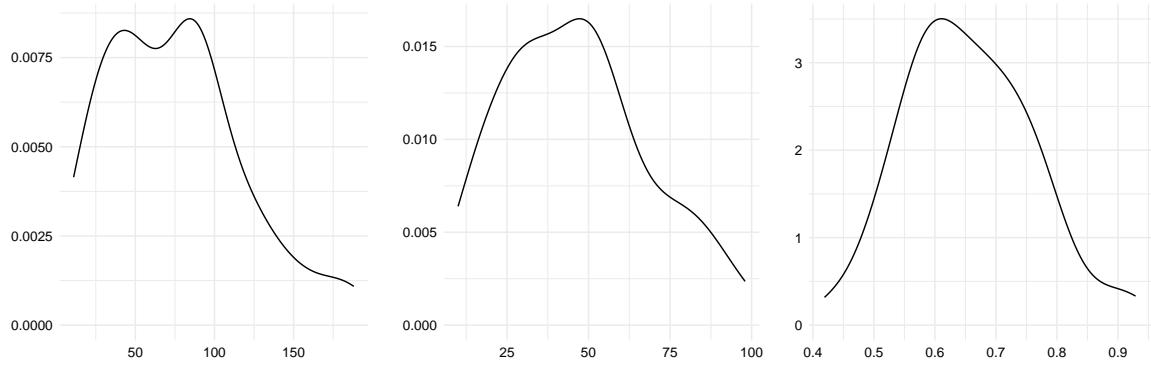
Figure 3.8: Zipfian distribution

Zipf's law describes a theoretical distribution, and the actual distribution of units in a corpus is affected by various sampling factors, including the size of the corpus. The larger the corpus, the closer the distribution will be to the Zipf distribution.

➊ Dive deeper

As stated above, Zipfian distributions are typical of natural language and are observed at various linguistic levels. This is because natural language is a complex system, and complex systems tend to exhibit Zipfian distributions. Other examples of complex systems that exhibit Zipfian distributions include the size of cities, the frequency of species in ecological communities, the frequency of links in the World Wide Web, *etc.*

Let's return to the BELC dataset and assess the distribution of the variables `tokens`, `types` and `ttr` in Figure 3.9 to the three distributions in Figure 3.7, we see that all three numeric variables in the BELC dataset are skewed to some degree, but not as extreme as the simulated data.



(a) Number of tokens

(b) Number of types

(c) Type-token ratio score

Figure 3.9: Histogram/ Density plots for numeric variables in the BELC dataset.

Figure 3.9a and 3.9b for `tokens` and `types` has a bit more right skewing than `ttr` seen in Figure 3.9c. This is consistent with the summary statistics for the central tendency in Table 3.4. The mean and median for `tokens` and `types` are not the same and the mean is larger than the median. For `ttr`, the mean and median is much closer.

In the case that a variable is highly skewed, it is often useful to attempt transform the variable to reduce the skewness. In contrast to scale-based transformations (*e.g.* centering and scaling), shape-based transformations change the scale and the shape of the distribution. The most common shape-based transformation is the logarithmic transformation. The **logarithmic transformation** (log-transformation) takes the log (typically base 10) of each value in a variable. The log-transformation is useful for reducing the skewness of a variable as it compresses large values and expands small values. If the skewness is due to these factors, the log-transformation can help, as in the case of the Zipfian distribution in Figure 3.8b.

It is important to note, however, that if scale-based transformations are to be applied to a variable, they should be applied after the log-transformation as the log of negative values is undefined.

3.1.4 Association

We have covered the first three of the four questions we are interested in asking in a descriptive analysis. The fourth, and last, question is whether there is an association between variables. If so, what is the directionality and what is the apparent magnitude of the dependence? Knowing the answers to these questions will help frame our approach to analysis.

To assess association, the number and information types of the variables under consideration are important. Let's start by considering two variables. If we are working with two variables, we are dealing with a **bivariate** relationship. Given there are three informational types

Table 3.7: Contingency tables for categorical variable `sex` and ordinal variable `group` in the BELC dataset.

(a) Counts				(b) Percentages			
group	female	male	Total	group	female	male	Total
T1	7	9	16	T1	43.75%	56.25%	100.00%
T2	11	4	15	T2	73.33%	26.67%	100.00%
T3	13	10	23	T3	56.52%	43.48%	100.00%
T4	9	5	14	T4	64.29%	35.71%	100.00%
Total	40	28	68	Total	58.82%	41.18%	100.00%

(categorical, ordinal, and numeric), there are six logical bivariate combinations: categorical-categorical, categorical-ordinal, categorical-numeric, ordinal-ordinal, ordinal-numeric, and numeric-numeric.

The directionality of a relationship will take the form of a tabular or graphic summary depending on the informational value of the variables involved. In Table 3.6, we see the appropriate summary types for each of the six bivariate combinations.

Table 3.6: Appropriate summary types for different combinations of variable types.

	Categorical	Ordinal	Numeric
Categorical	Contingency table	Contingency table/ Bar plot	Pivot table/ Boxplot
Ordinal	-	Contingency table/ Bar plot	Pivot table/ Boxplot
Numeric	-	-	Scatterplot

Let's first start with the combinations that include a categorical or ordinal variable. Categorical and ordinal variables reflect measures of class-type information, with add meaningful ranks to ordinal variables. To assess a relationship with these variable types, a table is always a good place to start. When combined together, a contingency table is the appropriate table. A **contingency table** is a cross-tabulation of two class-type variables, basically a two-way frequency table. This means that three of the six bivariate combinations are assessed with a contingency table: categorical-categorical, categorical-ordinal, and ordinal-ordinal.

In Table 3.7 we see contingency tables for the categorical variable `sex` and ordinal variable `group` in the BELC dataset.

A contingency table may include only counts, as in Table 3.7a, or may include proportions or percentages in an effort to normalize the counts and make them more comparable, as in Table 3.7b.

It is sometimes helpful to visualize a contingency table as a bar plot when there are a larger number of levels in either or both of the variables. Again, looking at the relationship between `sex` and `group`, we see that we can plot the counts or the proportions. In Figure 3.10, we see both.

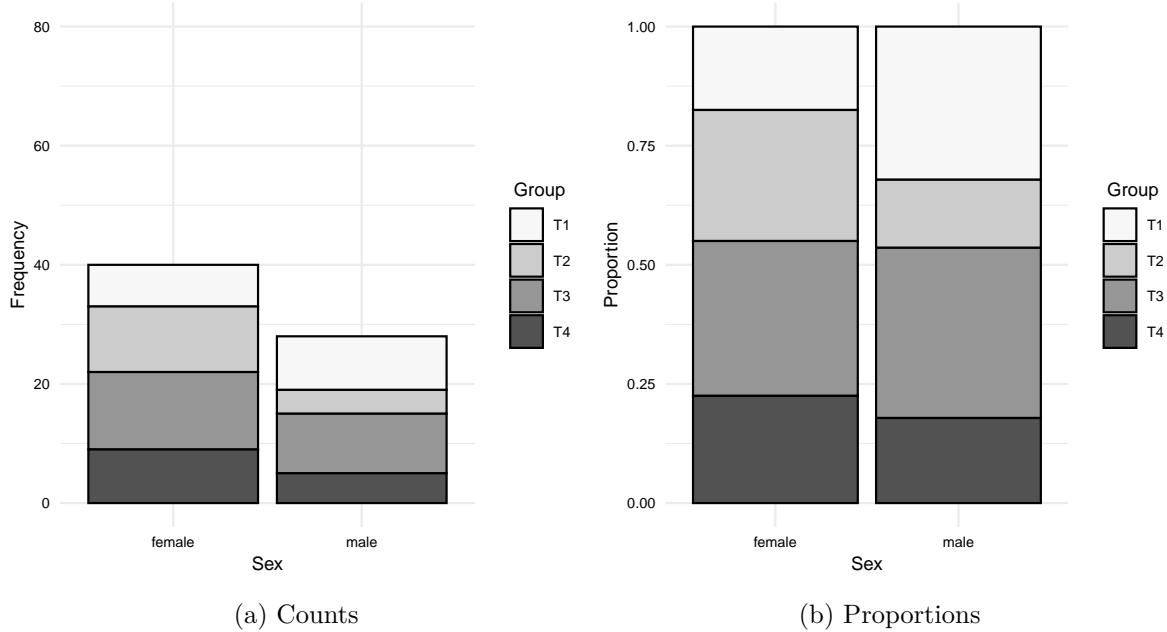


Figure 3.10: Bar plots for the relationship between `sex` and `group` in the BELC dataset.

To summarize and assess the relationship between a categorical or an ordinal variable and a numeric variable, we cannot use a contingency table. Instead, this type of relationship is best summarized in a table using a summary statistic in a **pivot table**. A pivot table is a table in which a class-type variable is used to group a numeric variable by some summary statistic appropriate for numeric variables, *e.g.* mean, median, standard deviation, *etc.*

In Table 3.8, we see a pivot table for the relationship between `group` and `tokens` in the BELC dataset. Specifically, we see the mean number of tokens by group.

Table 3.8: Pivot table for the relationship between `group` and `tokens` in the BELC dataset.

group	mean_tokens
T1	35.4
T2	62.5
T3	85.0
T4	118.9

We see that the mean number of tokens increases from Group T1 to T4, which is consistent with the idea that the students in the higher groups are writing longer essays.

Although a pivot table may be appropriate for targeted numeric summaries, a visualization is often more informative for assessing the dispersion and distribution of a numeric variable by a categorical or ordinal variable. There are two main types of visualizations for this type of relationship: a boxplot and a **violin plot**. A violin plot is a visualization that summarizes the distribution of a numeric variable by a categorical or ordinal variable, adding the overall shape of the distribution, much as a density plot does for histograms.

In Figure 3.11, we see both a boxplot and a violin plot for the relationship between `group` and `tokens` in the BELC dataset.

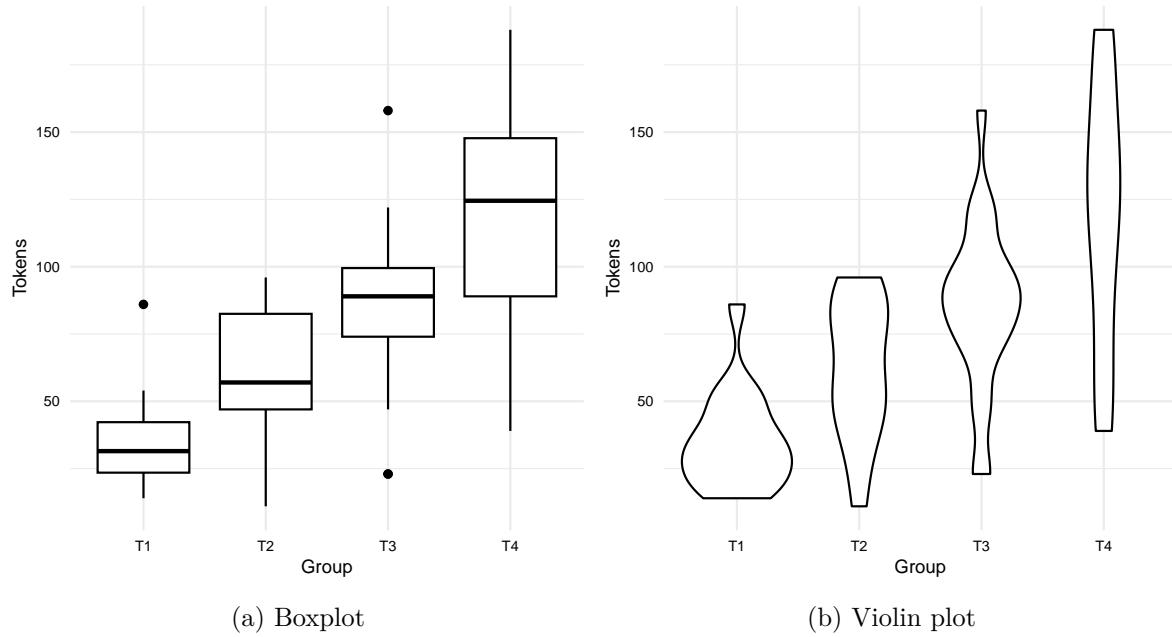


Figure 3.11: Boxplot and violin plot for the relationship between `group` and `tokens` in the BELC dataset.

From the boxplot in Figure 3.11a, we see that the general trend towards more tokens used by students in higher groups. But we can also appreciate the dispersion of the data within each group looking at the boxes and whiskers. On the surface it appears that the data for groups T1 and T3 are closer to each other than groups T2 and T4, in which there is more variability within these groups. Furthermore, we can see outliers in groups T1 and T3, but not in groups T2 and T4. From the violin plot in Figure 3.11b, we can see the same information, but we can also see the overall shape of the distribution of tokens within each group. In this plot, it is very clear that group T4 includes a wide range of token counts.

The last bivariate combination is numeric-numeric. To summarize this type of relationship a scatterplot is used. A **scatterplot** is a visualization that plots each data point as a point in a two-dimensional space, with one numeric variable on the x-axis and the other numeric variable on the y-axis. Depending on the type of relationship you are trying to assess, you may want to add a trend line to the scatterplot. A trend line is a line that summarizes the overall trend in the relationship between the two numeric variables. To assess the extent to which the relationship is linear, a straight line is drawn which minimizes the distance between the line and the points.

In Figure 3.12, we see a scatterplot and a scatterplot with a trend line for the relationship between `ttr` and `types` in the BELC dataset.

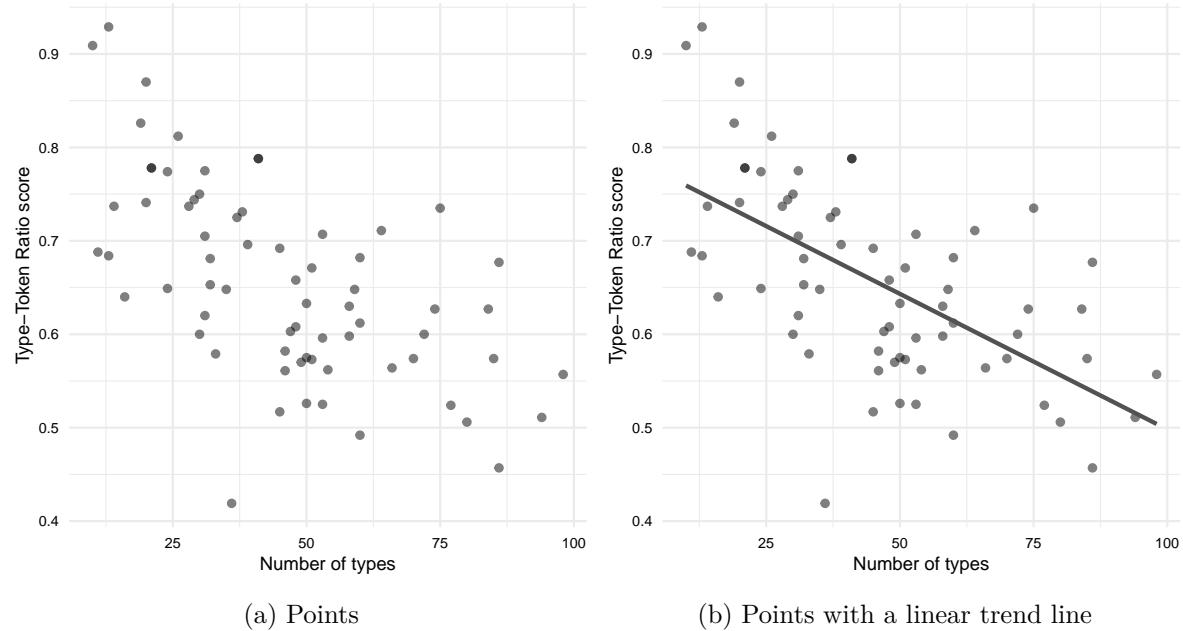


Figure 3.12: Scatter plot for the relationship between `ttr` and `types` in the BELC dataset.

We see that there is an apparent positive relationship between these two variables, which is consistent with the idea that as the number of types increases, the type-token ratio increases. In other words, as the number of unique words increases, so does the lexical diversity of the text. Since we are evaluating a linear relationship, we are assessing the extent to which there is a **correlation** between `ttr` and `types`. A correlation simply means that as the values of one variable change, the values of the other variable change in a consistent manner.

Before moving on to the next section, it is important to remember that through the process of descriptive measures, we gain a thorough understanding of our data's characteristics and quality, preparing us for the analysis. The decisions we make at this stage, from estimating central tendency to understanding the possible association between our variables, can have

significant implications on our approach and interpretation in the subsequent analysis. So, this initial step of data analysis deserves our careful attention and scrutiny.

3.2 Analyze

The goal of analysis, generally, is to generate knowledge from information. The type of knowledge generated and the process by which it is generated, however, differ and can be broadly grouped into three analysis types: exploratory, predictive, and inferential.

Table 3.9: Overview of analysis types.

Type	Aims	Approach	Methods	Evaluation
Exploratory	Explore: gain insight	Inductive, data-driven, and iterative	Descriptive, pattern detection with machine learning (unsupervised)	Associative
Predictive	Examine: validate associations	Semi-deductive, data-/ theory-driven, and iterative	Predictive modeling with machine learning (supervised)	Model performance, feature importance, and associative
Inferential	Explain: test hypotheses	Deductive, theory-driven, and non-iterative	Hypothesis testing with statistical tests	Causal

In this section, I will elaborate briefly on the distinctions between analysis types seen in Table 3.9. I will structure the discussion moving from the least structured (inductive) to most structured (deductive) approach to deriving knowledge from information with the aim to provide enough information for you to identify these research approaches in the literature and to make appropriate decisions as to which approach your research should adopt.

3.2.1 Explore

In **Exploratory Data Analysis (EDA)**, we use a variety of methods to identify patterns, trends, and relations within and between variables. The goal of EDA is uncover insights in

an inductive, data-driven manner. That is to say, that we do not enter into EDA with a fixed hypothesis in mind, but rather we explore intuition, probe anecdote, and follow hunches to identify patterns and relationships and to evaluate whether and why they are meaningful. We are admittedly treading new or unfamiliar terrain letting the data guide our analysis. This means that we can use and reuse the same data to explore different angles and approaches adjusting our methods and measures as we go. In this way, EDA is an iterative, meaning generating process.

In line with the investigative nature of EDA, the identification of variables of interest is a discovery process. We most likely have a intuition about the variables we would like to explore, but we are able to adjust our variables as need be to suit our research aims. When the identification and selection of variables is open, the process is known as **feature engineering**. A process that is much an art as a science, feature engineering leverages a mixture of relevant domain knowledge, intuition, and trial and error to identify features that serve to best represent the data and to best serve the research aims. Furthermore, the roles of features in EDA are fluid –no variable has a special status, as seen in Figure 3.13. We will see that in other types of analysis, some or all the roles of the variables are fixed.

Features					
feat_1	feat_2	feat_3	feat_4	feat_5	→
~	~	~	~	~	...
~	~	~	~	~	...
~	~	~	~	~	...
~	~	~	~	~	...
~	~	~	~	~	...
~	~	~	~	~	...
~	~	~	~	~	...
↓

Figure 3.13: Roles of variables in EDA.

Any given dataset could serve as a starting point to explore many different types of research questions. In order to maintain research coherence so our efforts to not careen into a free-for-all, we need to tether our feature engineering to a unit of analysis that is relevant to the research question. A **unit of analysis** is the entity that we are interested in studying. Not to be confused with the unit of observation, which is the entity that we are able to observe and measure (Sedgwick 2015). Depending on the perspective we are interested in investigating, the choice of how to approach engineering features to gain insight will vary.

By the same token, approaches for interrogating the dataset can differ significantly, between research projects and within the same project, but for instructive purposes, let's draw a distinction between descriptive methods and unsupervised learning methods, as seen in Table 3.10.

Table 3.10: Some common EDA methods

Descriptive methods	Unsupervised learning methods
Frequency analysis	Cluster analysis
Co-occurrence analysis	Principal component analysis
Keyness analysis	Topic Modeling Vector space models

The first group, **descriptive methods** can be seen as an extension of the descriptive statistics covered earlier in this chapter including statistic, tabular, and visual techniques. The second group, **unsupervised learning**, is a subtype of machine learning in which an algorithm is used to find patterns within and between variables in the data without any guidance (supervision). In this way, the algorithm, or machine learner, is left to make connections and associations wherever they may appear in the input data.

Either through descriptive, unsupervised learning methods, or a combination of both, EDA employs quantitative methods to summarize, reduce, and sort complex datasets in order to provide the researcher novel perspective to be qualitatively assessed. Exploratory methods produce results that require associative thinking and pattern detection. Speculative as they are, the results from exploratory methods can be highly informative and lead to new insight and inspire further study in directions that may not have been expected.

3.2.2 Predict

Predictive Data Analysis (PDA) employs a variety of techniques to examine and evaluate the association strength between a variable or set of variables, with a specific focus on predicting a target variable. The aim of PDA is to construct models that can accurately forecast future outcomes, using either data-driven or theory-driven approaches. In this process, **supervised learning** methods, where the machine learning algorithm is guided (supervised) by a target outcome variable, are used. This means we don't begin PDA with a completely open-ended exploration, but rather with an objective - accurate predictions. However, the path to achieving this objective can be flexible, allowing us freedom to adjust our models and methods. Unlike EDA, where the entire dataset can be reused for different approaches, PDA requires a portion of the data to be reserved for evaluation, enhancing the validity of our predictive models. Thus, PDA is an iterative process that combines the flexibility of exploratory analysis with the rigor of confirmatory analysis.

There are two types of variables in PDA: the outcome variable and the predictor variables, or features. The **outcome variable** is the variable that the researcher is trying to predict. It is the only variable that is necessarily fixed as part of the research question. The features are the variables that are used to predict the outcome variable. An overview of the roles of these variables in PDA is shown in Figure 3.14.

Outcome		Features			
Outcome	feat_1	feat_2	feat_3	feat_4	→
~	~	~	~	~	...
~	~	~	~	~	...
~	~	~	~	~	...
~	~	~	~	~	...
~	~	~	~	~	...
~	~	~	~	~	...
↓

Figure 3.14: Roles of variables in PDA.

Feature selection can be either data-driven or theory-driven. Data-driven features are those that are engineered to enhance predictive power, while theory-driven features are those that are selected based on theoretical relevance.

The approach to interrogating the dataset includes three main steps: feature engineering, model selection, and model evaluation. We've discussed feature engineering, so what is model selection and model evaluation? And how do we go about performing these steps?

Model selection is the process of choosing a machine learning algorithm and set of features that produces the best prediction accuracy for the outcome variable. To refine our approach such that we arrive at the best combination of algorithm and features, we need to train our machine learner on a variety of combinations and evaluate the accuracy of each. We don't want to train and evaluate on the same data, as this would be cheating, and likely would not produce a model that generalizes well to new data. Instead, we split our data into two sets: a training set and a test set. The **training set** is used to train the machine learner, while the **test set** is used to evaluate the accuracy of the model¹. The larger portion of the data, from 60% to 80%, is used for training, while the remaining portion is used for testing.

¹Depending on the application and the amount of available data, a third *development set* is sometimes created as a pseudo test set to facilitate the testing of multiple approaches on data outside the training set before the final evaluation on the test set is performed.

The elephant in the room is, what type of machine learning algorithm do I use? Well, there are many different types of machine learning algorithms, each with their own strengths and weaknesses. The first rough cut is to decide what type of outcome variable we are predicting: categorical or numeric. If the outcome variable is categorical, we are performing a **classification** task, and if the outcome variable is numeric, we are performing a **regression** task. As we see in Table 3.11, there are various algorithms that can be used for each task.

Table 3.11: Some common supervised learning algorithms used in PDA.

Classification	Regression
Logistic Regression	Linear Regression
Random Forest Classifier	Random Forest Regressor
Support Vector Machine	Support Vector Regression
Neural Network Classifier	Neural Network Regressor

There are a number of algorithm-specific strengths and weaknesses to be considered in the process of model selection. These hinge on characteristics of the data, such as the size of the dataset, the number of features, the type of features, and the expected type of relationships between features or on computing resources, such as the amount of time available to train the model or the amount of memory available to store the model.

Model evaluation is the process of assessing the accuracy of the model on the test set, which is a proxy for how well the model will generalize to new data. Model evaluation is performed quantitatively by calculating the accuracy of the model on the training, to develop the model, and ultimately, the test set. It is important to note that whether the accuracy metrics are good is to some degree qualitative judgment.

In the end, PDA offers a versatile path to discover data-driven insights, to probe theory-driven associations, or even simply to perform tasks that are too complex or time-consuming for humans to perform.

3.2.3 Infer

The most commonly recognized of the three data analysis approaches, **Inferential data analysis (IDA)** is the bread-and-butter of science. IDA is a deductive, theory-driven approach in which all aspects of analysis stem from a pre-determined premise, or hypothesis, about the nature of a relationship in the world and then aims to test whether this relationship is statistically supported given the evidence. Since the goal is to infer conclusions about a certain relationship in the population based on a statistical evaluation of a (corpus) sample, the representativeness of the sample is of utmost importance. Furthermore, the use of the data is limited to the scope of the hypothesis –that is, the data cannot be used iteratively for exploratory purposes.

The selection of variables and the roles they play in the analysis are determined by the hypothesis. In a nutshell, a **hypothesis** is a formal statement about the state of the world. This statement is theory-driven meaning that it is predicated on previous research. We are not exploring or examining relationships, rather we are testing a specific relationship. In practice, however, we are in fact proposing two mutually exclusive hypotheses. The first is the **Alternative Hypothesis**, or H_1 . This is the hypothesis I just described –the statement grounded in the previous literature outlining a predicted relationship. The second is the **Null Hypothesis**, or H_0 . This is the flip-side of the hypothesis testing coin and states that there is no difference or relationship. Together H_1 and H_0 cover all logical outcomes.

Now, in standard IDA one variable is the response variable and one or more variables are explanatory variables. The **response variable**, sometimes referred to as the outcome or dependent variable, is the variable which contains the information which is hypothesized to depend on the information in the explanatory variable(s). It is the variable whose variation a research study seeks to explain. An **explanatory variable**, sometimes referred to as a independent or predictor variable, is a variable whose variation is hypothesized to explain the variation in the response variable.

Explanatory variables add to the complexity of a study because they are part of our research focus, specifically our hypothesis. It is, however, common to include other variables which are not of central focus, but are commonly assumed to contribute to the explanation of the variation of the response variable. These are known as **control variables**. Control variables are included in the analysis to account for the influence of other variables on the relationship between the response and explanatory variables, but will not be included in the hypothesis nor interpreted in our results.

We can now see in Figure 3.15 the variables roles assigned to variables in a hypothesis-driven study.

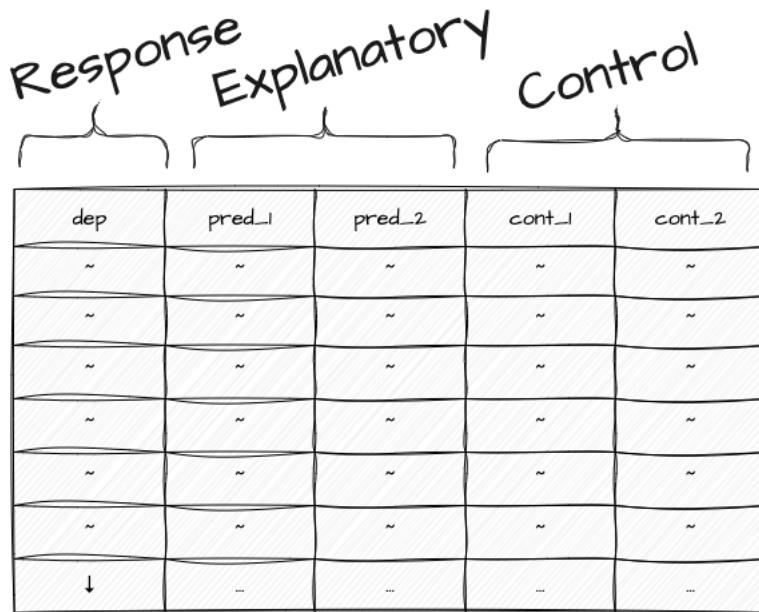


Figure 3.15: Roles of variables in IDA.

At this point let's look at the main characteristics that need to be taken into account to statistically interrogate the variables we have chosen to test our hypothesis. The type of statistical test that one chooses is based on (1) the informational value of the dependent variable and (2) the number of predictor variables included in the analysis. Together these two characteristics go a long way in determining the appropriate class of statistical test (see S. Th. Gries (2013) and Paquot and Gries (2020) for a more exhaustive description).

IDA relies heavily on quantitative evaluation methods to draw conclusions that can be generalized to the target population. It is key to understand that our goal in hypothesis testing is not to find evidence in support of H_1 , but rather to assess the likelihood that we can reliably reject H_0 .

The metric used to determine if there is sufficient evidence is based on the probability that given the nature of the relationship and the characteristics of the data, the likelihood of there being no difference or relationship is low. The threshold for likelihood has traditionally been summarized in the *p*-value statistic. In the Social Sciences, a *p*-value lower than .05 is considered *statistically significant* which when interpreted correctly means that there is more than a 95% chance that the observed relationship would not be predicted by H_0 .

Note that we are working in the realm of probability, not in absolutes, therefore an analysis that produces a significant result does not prove H_1 is correct or that H_0 is incorrect, for that matter. A margin of error is always present. For this reason, other metrics such as effect size and confidence intervals are also used to interpret the results of statistical tests.

3.3 Communicate

Conducting research should be enjoyable and personally rewarding but the effort you have invested and knowledge you have generated should be shared with others. Whether part of a blog, presentation, journal article, or for your own purposes it is important to document your analysis results and process in a way that is informative and interpretable. This enhances the value of your work, allowing others to learn from your experience and build on your findings.

3.3.1 Report

The most widely recognized form of communicating research is through a report. A report is a narrative of your analysis, including the research question, the data you used, the methods you applied, and the results you obtained. We are both reporting our findings and documenting our process to inform others of what we did and why we did it but also to invite readers to evaluate our findings for themselves. The scientific process is a collaborative one and evaluation by peers is a key component of the process.

The audience for your report will determine the level of detail and the type of information you will need to include in your report but there are some common elements to reference in any report. First, the research question and/ or hypothesis should be clearly stated and the motivation for the question should be explained. This will help the reader understand the context of the analysis and the importance of the results. Second, diagnostic procedures to verify or describe the data should be explained. This may include anomaly correction, missing data, data transformation, etc. and/ or descriptive summaries of the data including assessments of individual variables (central tendency, dispersion, distribution) and/ or relationships between variables (association strength). Third, a blueprint of the methods used will describe the variable selection process, how the variables are operationalized, what analysis methods are employed, and how the variables are used in the statistical analysis. Fourth, the results from the analysis are reported. Reporting details will depend on the type of analysis and the particular method(s) employed. Finally, the results are interpreted in light of the research question and/ or hypothesis. This will include a discussion of the limitations of the analysis and a discussion of the implications of the results for future research.

3.3.2 Document

While a good report will include the most vital information to understand the procedures, results, and findings of an analysis, there is much more information generated in the course of an analysis which does not traditionally appear in prose. If a research project is conducted programmatically, however, data, code, and documentation can be made available to others as part of the communication process. Increasingly, researchers are sharing their data and code

as part of the publication process. This allows others to reproduce the analysis and verify the results contributing to the collaborative nature of the scientific process.

Together, data, code, and documentation form a **research compendium**. As you can imagine the research process can quickly become complex and unwieldy as the number of files and folders grows. If not organized properly, it can be difficult to find the information you need. Furthermore, if not documented, decisions made in the course of the analysis can be difficult or impossible to trace. For this reason, it is recommendable to follow a set of best practices for organizing and documenting your research compendium. We will cover this in more detail in subsequent chapters.

Activities

In the following activities, we will build on our understanding of how to summarize data using statistics, tables, and plots. We will dive deeper into the use of the `skimr` package (Waring et al. 2022) to summarize data and the `ggplot2` package (Wickham, Chang, et al. 2023) to create plots. We also introduce producing Quarto tables and figures with appropriate code block options. We will reinforce our understanding of the `readr` package (Wickham, Hester, and Bryan 2024) to read in data and the `dplyr` package (Wickham, François, et al. 2023) to manipulate data.

_recipe

What: Descriptive assessment of datasets^a

How: Read Recipe 3, complete comprehension check, and prepare for Lab 3.

Why: To explore appropriate methods for summarizing variables in datasets given the number and informational values of the variable(s).

^a<https://qtalr.github.io/qtalrkit/articles/recipe-3.html>

_lab

What: Trace the datascape^a

How: Clone, fork, and complete the steps in Lab 3.

Why: To identify and apply the appropriate descriptive methods for a vector's informational value and to assess both single variables and multiple variables with the appropriate statistical, tabular, and/ or graphical summaries.

^a<https://github.com/qtalr/lab-03>

Summary

In this chapter we have focused on description and analysis –the third component of DIKI Hierarchy. This process is visually summarized in Figure 3.16.

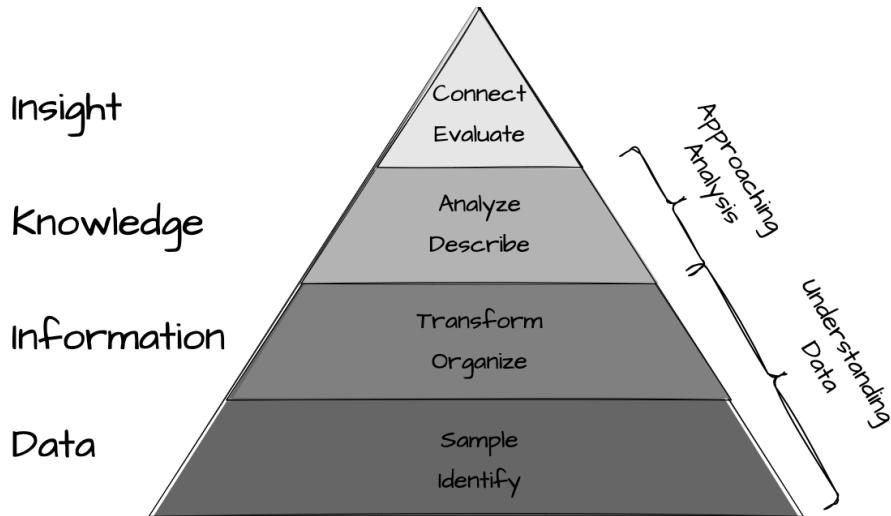


Figure 3.16: Approaching analysis: visual summary

The first key step in any analysis is to perform a diagnostic assessment of the individual variables and relationships between variables. To select the appropriate descriptive measures we covered the various informational values that a variable can take. In addition to providing key information for reporting purposes, descriptive measures are important to explore so the researcher can get a better feel for the dataset before conducting an analysis.

We outlined three data analysis types in this chapter: exploratory, predictive, and inferential. Each of these embodies distinct approaches to deriving knowledge from data. Ultimately the choice of analysis type is highly dependent on the goals of the research. Inferential analysis is centered around the goal of testing a hypothesis, and for this reason it is the most highly structured approach to analysis. This structure is aimed at providing the mechanisms to draw conclusions from the results that can be generalized to the target population. Predictive analysis has a less-ambitious but at times more relevant goal of examining the extent to which a given relationship can be established from the data to provide a model of language that can accurately predict an outcome using new data. This methodology is highly effective for applying different algorithmic approaches and examining relationships between an outcome variable and various configurations of variables. The ability to explore the data in multiple ways, is also a key strength of employing an exploratory analysis. The least structured and most variable of the analysis types, exploratory analyses are a powerful approach to generating knowledge from data in an area where clear predictions cannot be made.

I rounded out this chapter with a short description of the importance of communicating the analysis process and results. Reporting, in its traditional form, is documented in prose in an article. This reporting aims to provide the key information that a reader will need to understand what was done, how it was done, and why it was done. This information also provides the necessary information for reader's with a critical eye to understand the analysis in more detail. Yet even the most detailed reporting in a write-up still leaves many practical, but key, points of the analysis obscured. A programming approach provides the procedural steps taken that when shared provide the exact methods applied. Together with the write-up, a research compendium which provides the scripts to run the analysis and documentation on how to run the analysis forms an integral part of creating reproducible research.

4 Research

Thus, the task is, not so much to see what no one has seen yet; but to think what nobody has thought yet, about that what everybody sees.

— Erwin Schrödinger

▀ Outcomes

- Identify a research area and problem by listing key strategies and describing their contribution towards research identification.
- Explain the significance of a well-framed research question in guiding the overall research project.
- Comprehend how the conceptual and practical steps involved in developing a research blueprint aid not only the researcher but also the broader scientific community.

In this chapter, we discuss how to frame research, that is how to position your research project's findings to contribute insight to understanding of the world. We will cover how to connect with the literature, selecting a research area and identifying a research problem, and how to design research best positioned to return relevant findings that will connect with this literature, establishing a research aim and research question. We will round out this chapter with a guide on developing a research blueprint –a working plan to organize the conceptual and practical steps to implement the research effectively and in a way that supports communicating the research findings and the process by which the findings were obtained.

➤ Lessons

What: Project Environment^a

How: In the R Console pane load `swirl`, run `swirl()`, and follow prompts to select the lesson.

Why: To highlight the importance of the computing environment in R for project management and reproducibility.

^a<https://github.com/qtalr/lessons>

4.1 Frame

Together a research area, problem, aim and question and the research blueprint that forms the conceptual and practical scaffolding of the project ensure from the outset that the project is solidly grounded in the main characteristics of good research. These characteristics, summarized by Cross (2006), are found in Table 4.1.

Table 4.1: Characteristics of research (Cross, 2006).

Characteristic	Description
Purposive	Based on identification of an issue or problem worthy and capable of investigation
Inquisitive	Seeking to acquire new knowledge
Informed	Conducted from an awareness of previous, related research
Methodical	Planned and carried out in a disciplined manner
Communicable	Generating and reporting results which are feasible and accessible by others

With these characteristics in mind, let's get started with the first component to address – connecting with the literature.

4.2 Connect

4.2.1 Research area

The first decision to make in the research process is to identify a research area. A **research area** is a general area of interest where a researcher wants to derive insight and make a contribution to understanding. For those with an established research trajectory in language, the area of research to address through text analysis will likely be an extension of their prior work. For others, which include new researchers or researchers that want to explore new areas of language research or approach an area through a language-based lens, the choice of area may be less obvious. In either case, the choice of a research area should be guided by a desire to contribute something relevant to a theoretical, applied, and/ or practical matter of personal interest. Personal relevance goes a long way to developing and carrying out *purposive* and *inquisitive* research.

So how do we get started? Consider your interests in a language or set of languages, a discipline, a methodology, or some applied area. Language is at the heart of the human experience and therefore found in some fashion anywhere one seeks to find it. But it is a big world and more often than not the general question about what area to explore language use is sometimes the most difficult. To get the ball rolling, it is helpful to peruse disciplinary encyclopedias

or handbooks of linguistics and language-related an academic fields (*e.g.* Encyclopedia of Language and Linguistics (Brown 2005), A Practical Guide to Electronic Resources in the Humanities (Dubnjakovic and Tomlin 2010), Routledge encyclopedia of translation technology (Chan 2014))

A more personal, less academic, approach is to consult online forums, blogs, *etc.* that one already frequents or can be accessed via an online search. Through social media you may find particular people that maintain a blog worth browsing. Perusing these resources can help spark ideas and highlight the kinds of questions that interest you.

Regardless of whether your inquiry stems from academic, professional, or personal interest, try to connect these findings to academic areas of research. Academic research is highly structured and well-documented and making associations with this network will aid in subsequent steps in developing a research project.

4.2.2 Research problem

Once you've made a rough-cut decision about the area of research, it is now time to take a deeper dive into the subject area and jump into the literature. This is where the rich structure of disciplinary research will provide aid to traverse the vast world of academic knowledge and identify a research problem. A **research problem** highlights a particular topic of debate or uncertainty in existing knowledge which is worthy of study.

Surveying the relevant literature is key to ensuring that your research is *informed*, that is, connected to previous work. Identifying relevant research to consult can be a bit of a 'chicken or the egg' problem –some knowledge of the area is necessary to find relevant topics, some knowledge of the topics is necessary to narrow the area of research. Many times the only way forward is to jump into conducting searches. These can be world-accessible resources (*e.g.* Google Scholar) or limited-access resources that are provided through an academic institution (*e.g.* Linguistics and Language Behavior Abstracts, ERIC, PsycINFO, *etc.*). Some organizations and academic institutions provide research guides to help researcher's access the primary literature. There are even a new breed of search engines that are designed to help researchers aggregate and search academic literature (*e.g.* Scite, Elicit, *etc.*).

Another avenue to explore are journals and conference proceedings dedicated to linguistics and language-related research. Text analysis is a rapidly expanding methodology which is being applied to a wide range of research areas.

To explore research related to text analysis it is helpful to start with the (sub)discipline name(s) you identified in when selecting your research area, more specific terms that occur to you or key terms from the literature, and terms such as 'corpus study' or 'corpus-based'. The results from first searches may not turn out to be sources that end up figuring explicitly in your research, but it is important to skim these results and the publications themselves to mine information that can be useful to formulate better and more targeted searches.

Relevant information for honing your searches can be found throughout an academic publication. However, pay particular attention to the abstract, in articles, and the table of contents, in books, and the cited references. Abstracts and tables of contents often include discipline-specific jargon that is commonly used in the field. In some articles, there is even a short list of key terms listed below the abstract which can be extremely useful to seed better and more precise search results. The references section will contain relevant and influential research. Scan these references for publications which appear to narrow in on topic of interest and treat it like a search in its own right.

Once your searches begin to show promising results it is time to keep track and organize these references. Whether you plan to collect thousands of references over a lifetime of academic research or your aim is centered around one project, software such as Zotero¹², Mendeley⁴, or BibDesk⁵ provide powerful, flexible, and easy-to-use tools to collect, organize, annotate, search, and export references. Citation management software is indispensable for modern research –and often free!

As your list of relevant references grows, you will want to start the investigation process in earnest. Begin skimming (not reading) the contents of each of these publications, starting with the most relevant first⁶. Annotate these publications using highlighting features of the citation management software to identify: (1) the stated goal(s) of the research, (2) the data source(s) used, (3) the information drawn from the data source(s), (4) the analysis approach employed, and (5) the main finding(s) of the research as they pertain to the stated goal(s).

Next, in your own words, summarize these five key areas in prose adding your summary to the notes feature of the citation management software. This process will allow you to efficiently gather and document references with the relevant information to guide the identification of a research problem, to guide the formation of your problem statement, and ultimately, to support the literature review that will figure in your project write-up.

From your preliminary annotated summaries you will undoubtedly start to recognize overlapping and contrasting aspects in the research literature. These aspects may be topical, theoretical, methodological, or appear along other lines. Note these aspects and continue to conduct more refined searches, annotate new references, and monitor for any emerging patterns of uncertainty or debate (gaps) which align with your research interest(s). When a promising pattern takes shape, it is time to engage with a more detailed reading of those references which appear most relevant highlighting the potential gap(s) in the literature.

At this point you can focus energy on more nuanced aspects of a particular gap in the literature with the goal to formulate a problem statement. A **problem statement** directly acknowledges a gap in the literature and puts a finer point on the nature and relevance of this gap for

¹<https://www.zotero.org/>

²Zotero Guide³

⁴<https://www.mendeley.com/reference-management/reference-manager>

⁵<https://bibdesk.sourceforge.io/>

⁶Or what appears to be most relevant. This may change as you start to take a closer look.

understanding. This statement reflects your first deliberate attempt to establish a line of inquiry. It will be a targeted, but still somewhat general, statement framing the gap in the literature that will guide subsequent research design decisions.

4.3 Define

4.3.1 Research aim

With a problem statement in hand, it is now time to consider the goal(s) of the research. A **research aim** frames the type of inquiry to be conducted. Will the research aim to explore, examine, or explain? As you can appreciate, the research aim is directly related to the analysis methods we touched upon in Chapter 3.

To gauge how to frame your research aim, reflect on the literature that led you to your problem statement and the nature of the problem statement itself. If the gap at the center of the problem statement is a lack of knowledge, your research aim may be exploratory. If the gap concerns a conjecture about a relationship, then your research may take a predictive approach. When the gap points to the validation of a relationship, then your research will likely be inferential in nature. Before selecting your research aim it is also helpful to consult the research aims of the primary literature that led you to your research statement.

Typically, a problem statement addressing a subtle, specific issue tends to adopt research objectives similar to prior studies. In contrast, a statement focusing on a broader, more distinct issue is likely to have unique research goals. Yet, this is more of a guideline than a strict rule.

It's crucial to understand both the existing literature and the nature of various types of analyses. Being clear about your research goals is important to ensure that your study is well-placed to produce results that add value to the current understanding in an informed manner.

4.3.2 Research question

The next step in research design is to craft the research question. A **research question** is clearly defined statement which identifies an aspect of uncertainty and the particular relationships that this uncertainty concerns. The research question extends and narrows the line of inquiry established in the research statement and research aim. To craft a research question, we can use the research statement for the content and the research aim for the form.

4.3.2.1 Form

The form of a research question will vary based on the research aim, which as I mentioned, is intimately connected to the analysis approach. For inferential-based research, the research question will actually be a statement, not a question. This statement makes a testable claim about the nature of a particular relationship –*i.e.* asserts a hypothesis.

For illustration, let's posit a hypothesis (H_1), leaving aside the implicit null hypothesis (H_0), seen in Example 4.1.

Example 4.1. Women use more questions than men in spontaneous conversations.

For predictive- and exploratory-based research, the research question is in fact a question. A reframing of the example hypothesis for a predictive-based research question might take the form seen in Example 4.2.

Example 4.2. Can the number of questions used in spontaneous conversations predict if a speaker is male or female?

And a similar exploratory-based research question might take the form seen in Example 4.3.

Example 4.3. Do men and women differ in terms of the number of questions they use in spontaneous conversations?

The central research interest behind these hypothetical research questions is, admittedly, quite basic. But from these simplified examples, we are able to appreciate the similarities and differences between the forms of research statements that correspond to distinct research aims.

4.3.2.2 Content

In terms of content, the research question will make reference to two key components. First, is the unit of analysis. The **unit of analysis** is the entity which the research aims to investigate. For our three example research aims, the unit of analysis is the same, namely *speakers*. Note, however, that the current unit of analysis is somewhat vague in the example research questions. A more precise unit of analysis would include more information about the population from which the speakers are drawn (*i.e.* English speakers, American English speakers, American English speakers of the Southeast, *etc.*).

The second key component is the unit of observation. The **unit of observation** is the primary element on which the insight into the unit of analysis is derived and in this way constitutes the essential organizational unit of the dataset to be analyzed. In our examples, the unit of observation, again, is unchanged and is *spontaneous conversations*. Note that while the unit of

observation is key to identify as it forms the organizational backbone of the research, it is very common for the research to derive variables from this unit to provide evidence to investigate the research question.

In examples 4.1, 4.2, and 4.3, we identified the number of conversations as part of the research question. Later in the research process it will be key to operationalize this variable. For example, will the number of conversations be the total number of conversations in the dataset or will it be the average number of conversations per speaker? These are important questions to consider as they will influence variable selection, statistical choices, and ultimately the interpretation of the results.

4.4 Blueprint

The efforts to develop a research question will produce a clear and focused line of inquiry with the necessary background literature and a well-defined problem statement that forms the basis of *purposeful*, *inquisitive*, and *informed* research (returning to Cross's characteristics of research in Table 4.1).

Moving beyond the research question in the project means developing and laying out the research design in a way such that the research is *methodical* and *communicable*. In this textbook, the method to achieve these goals is through the development of a research blueprint. The blueprint includes two components: (1) the conceptual plan and (2) the organizational scaffolding that will support the implementation of the research.

As Ignatow and Mihalcea (2017) point out:

Research design is essentially concerned with the basic architecture of research projects, with designing projects as systems that allow theory, data, and research methods to interface in such a way as to maximize a project's ability to achieve its goals [...]. Research design involves a sequence of decisions that have to be taken in a project's early stages, when one oversight or poor decision can lead to results that are ultimately trivial or untrustworthy. Thus, it is critically important to think carefully and systematically about research design before committing time and resources to acquiring texts or mastering software packages or programming languages for your text mining project.

In what follows, I will cover the main aspects of developing a research blueprint. I will start with the conceptual plan and then move on to the organizational scaffolding.

4.4.1 Plan

Importance of establishing a feasible research design from the outset and documenting the key aspects required to conduct the research cannot be understated. On the one hand, this process links a conceptual plan to a tangible implementation. In doing so, a researcher is better-positioned to conduct research with a clear view of what will be entailed. On the other hand, a promising research question may present unexpected challenges once a researcher sets about to implement the research. This is not uncommon to encounter issues that require modification or reevaluation of the viability of the project. However, a well-documented research plan will help a researcher to identify and address many of these challenges at the conceptual level before expending unnecessary effort during implementation.

Let's now consider the subsequent steps to develop a research plan, outlined in Table 4.2.

Table 4.2: Research plan checklist

Step	Stage	Activity
1	Research Question or Hypothesis	Formulate a research question or hypothesis based on a thorough review of existing literature including references. This will guide every subsequent step from data selection to interpretation of results.
2	Data Source(s)	Identify viable data source(s) and vet the sample data in light of the research question. Consider to what extent the goal is to generalize findings to a target population, and ensure that the corpus aligns as much as feasible with this target.
3	Key Variables	Determine the key variables needed for the research, define how they will be operationalized, and ensure they can be derived from the corpus data. Additionally, identify any features that need to be extracted, recoded, generated, or integrated from other data sources.
4	Analysis Method	Choose an appropriate method of analysis to interrogate the dataset. This choice should be in line with your research aim (<i>e.g.</i> , exploratory, predictive, or inferential). Be aware of what each method can offer and how it addresses your research question.
5	Interpretation & Evaluation	Establish criteria to interpret and evaluate the results. This will be a function of the relationship between the research question and the analysis method.

First, identify a viable data source. Viability includes the accessibility of the data, availability of the data, and the content of the data. If a purported data source is not accessible and/ or it has stringent restrictions on its use, then it is not a viable data source. If a data source is accessible and available, but does not contain the building blocks needed to address the

research question, then it is not a viable data source. A corpus resource should represent, to the extent feasible, with the target population(s).

The second step is to identify the key variables needed to conduct the research and then ensure that this information can be derived from the corpus data. The research question will reference the unit of analysis and the unit of observation, but it is important to pinpoint what the key variables will be. We want to envision what needs to be done to derive these variables. There may be features that need to be extracted, recoded, generated, and/ or integrated from other sources to address the research question, as discussed in Chapter 2.

The third step is to identify a method of analysis to interrogate the dataset. The selection of the analysis approach that was part of the research aim (*i.e.* explore, predict, or infer) and then the research question goes a long way to narrowing the methods that a researcher must consider. But there are a number of factors which will make some methods more appropriate than others.

Exploratory research is the least restricted of the three types of analysis approaches. Although it may be the case that a research will not be able to specify from the outset of a project what the exact analysis methods will be, an attempt to consider what types of analysis methods will be most promising to provide results to address the research question goes a long way to steering a project in the right direction and grounding the research. As with the other analysis approaches, it is important to be aware of what the analysis methods available and what type of information they produce in light of the research question.

For predictive-based research, the informational value of the outcome variable is key to deciding whether the prediction will be a classification task or a regression task. This has downstream effects when it comes time to evaluate and interpret the results. Although the feature engineering process in predictive analyses means that the features do not need to be specified from the outset and can be tweaked and changed as needed during an analysis, it is a good idea to start with a basic sense of what features most likely will be helpful in developing a robust predictive model.

In inferential research, the number and information values of the variables to be analyzed will be of key importance (S. Th. Gries 2013). The informational value of the response variable will again narrow the search for the appropriate method. The number of explanatory variables also plays an important role. These details need not be nailed down at this point, but it is helpful to have them on your radar to ensure that when the time comes to analyze the data, the appropriate steps are taken to apply the correct test.

The last of the main components of the research plan concerns the interpretation and evaluation of the results. This step brings the research plan full circle connecting the research question to the methods employed. It is important to establish from the outset what the criteria will be to evaluate the results. This is in large part a function of the relationship between the research question and the analysis method. For example, in exploratory research, the results will be evaluated qualitatively in terms of the associative patterns that emerge. Predictive and inferential research leans more heavily on quantitative metrics in particular the accuracy

of the prediction or the strength of the relationship between the response and explanatory variable(s), respectively. However, these quantitative metrics require qualitative interpretation to determine whether the results are meaningful in light of the research question.

In addition to addressing the steps outlined in Table 4.2, it is also important to document the strengths and shortcomings of the research plan including the data source(s), the information to be extracted from the data, and the analysis methods. If there are potential shortcomings, which there most often are, sketch out contingency plans to address these shortcomings. This will help buttress your research and ensure that your time and effort is well-spent.

The research plan together with the information collected to develop the research question is known as a **prospectus**. A **prospectus** is a document that outlines the key aspects of the research plan and is used to guide the research process. It is a living document that will be updated as the research progresses and as new information is collected.

Dive deeper

You may consider pre-registering your prospectus to ensure that your plans are well-documented and to provide a timestamp for your research. Pre-registration can also be a helpful way to get feedback on your research from colleagues and experts in the field. Popular pre-registration platforms include Open Science Framework^a and Center for Open Science^b.

^a<https://osf.io/>

^b<https://www.cos.io/initiatives/prereg>

4.4.2 Scaffold

The next step in developing a research blueprint is to consider how to physically implement your project. This includes how to organize files and directories in a fashion that both provides the researcher a logical and predictable structure to work with but also ensures that the research is *Communicable*. On the one hand, communicable research includes a strong write-up of the research, but, on the other hand, it is also important that the research is reproducible.

Reproducibility strategies are a benefit to the researcher (in the moment and in the future) as it leads to better work habits and to better teamwork and it makes changes to the project easier. Reproducibility is also of benefit to the scientific community as shared reproducible research enhances replicability and encourages cumulative knowledge development (Gandrud 2015).

In Table 4.3, I outline a set of guiding principles that characterize reproducible research (Gentleman and Temple Lang 2007; Marwick, Boettiger, and Mullen 2018).

Table 4.3: Reproducible Research Principles

No.	Principle	Description
1	Plain text	All files should be plain text which means they contain no formatting information other than whitespace.
2	Clear separation	There should be a clear separation between the inputs, process steps, and outputs of research. This should be apparent from the directory structure.
3	Original data	A separation between original data and data created as part of the research process should be made. Original data should be treated as ‘read-only’. Any changes to the original data should be justified, generated by the code, and documented (see point 7).
4	Modular scripts	Each computing file (script) should represent a particular, well-defined step in the research process.
5	Modular files	Each script should be modular –that is, each file should correspond to a specific goal in the analysis procedure with input and output only corresponding to this step.
6	Main script	The project should be tied together by a ‘main’ script that is used to coordinate the execution of all the project steps.
7	Document everything	Everything should be documented. This includes data collection, data preprocessing, processing steps, script code comments, data description in data dictionaries, information about the computing environment and packages used to conduct the analysis, and detailed instructions on how to reproduce the research.

These seven principles in Table 4.3 can be physically implemented in numerous ways. In recent years, there has been a growing number of efforts to create R packages and templates to quickly generate the scaffolding and tools to facilitate reproducible research. Some notable R packages include `workflowr`⁷ (J. Blischak, Carbonetto, and Stephens 2023), `ProjectTemplate`⁸ (White 2023), and `targets`⁹ (Landau 2024), but there are many other resources for R included on the CRAN Task View for Reproducible Research¹⁰.

There are many advantages to working with pre-existing frameworks for the savvy R programmer including the ability to quickly generate a project scaffold, to efficiently manage changes to the project, and to buy in to a common framework that is supported by a community of developers.

⁷<https://jdblischak.github.io/workflowr/>

⁸<http://projecttemplate.net/>

⁹<https://github.com/ropensci/targets>

¹⁰<https://cran.r-project.org/web/views/ReproducibleResearch.html>

On the other hand, these frameworks can be a bit daunting for the novice R programmer. At the most basic level, a project can implement the seven principles outlined above with a directory structure and a set of key files seen in Example 4.4.

Example 4.4. Minimal Project Framework

```
project/
├── input/
│   └── ...
├── code/
│   └── ...
├── output/
│   └── ...
├── DESCRIPTION
└── Makefile
└── README
```

The *project/* directory is composed of three main sections: *input/*, *code/*, and *output/* making the distinction between each transparent in the directory structure. The *input/* will house the data used and created in the project, ensuring that the original data is kept separate from the data created in the research process. The *code/* section will house the scripts that will conduct the project steps including acquiring, curating, transforming, and analyzing the data. These scripts will read and write data and generate output including figures, reports, results, and tables. Lastly, the *output/* section will house the resulting output from the project steps.

At the root of the project directory are three files which describe, document, and execute the project. The *Makefile* is used to automate the execution of the project steps. In effect, it is a script that runs scripts. In addition to coordinating the execution of the project steps, a Makefile will often include commands to set up the computing environment and packages. The *README* and *DESCRIPTION* files provide an overview of the project from both a conceptual and technical perspective. The *README* file includes a description of the project rationale, aims, and findings and instructions on how to reproduce the research. The *DESCRIPTION* file includes technical information about the computing environment and packages used to conduct the analysis.

The project structure in Example 4.4 meets the minimal structural requirements for reproducible research and is a good starting point for a project scaffold. However, aspects of this structure can be adjusted in minimal or more sophisticated ways to meet the needs of a particular project while still conforming to the principles outlined in Table 4.3, when we return to this topic in Chapter 11.

Activities

The following activities will build on your experience with R and cloning a GitHub repository, and recent experience with understanding the computing environment. The goal will be to bring you up to speed such that you can begin to work on your own research projects and understand how to use the tools and resources available to you to manage your project.

❖ Recipe

What: Understanding the computing environment^a

How: Read Recipe 4, complete comprehension check, and prepare for Lab 4.

Why: To introduce components of the computing environment and how to manage a reproducible research project structure.

^a<https://qtalr.github.io/qtalrkit/articles/recipe-4.html>

█ Lab

What: Scaffolding reproducible research^a

How: Clone, fork, and complete the steps in Lab 4.

Why: To establish a repository and project structure for reproducible research and apply new Git and Github skills to fork, clone, commit, and push changes.

^a<https://github.com/qtalr/lab-04>

Summary

The aim of this chapter is to provide the key conceptual and practical points to guide the development of a viable research project. Good research is purposive, inquisitive, informed, methodological, and communicable. It is not, however, always a linear process. Exploring your area(s) of interest and connecting with existing work will help couch and refine your research. But practical considerations, such as the existence of viable data, technical skills, and/ or time constraints, sometimes pose challenges and require a researcher to rethink and/ or redirect the research in sometimes small and other times more significant ways. The process of formulating a research question and developing a viable research plan is key to supporting viable, successful, and insightful research. To ensure that the effort to derive insight from data is of most value to the researcher and the research community, the research should strive to be methodological and communicable adopting best practices for reproducible research.

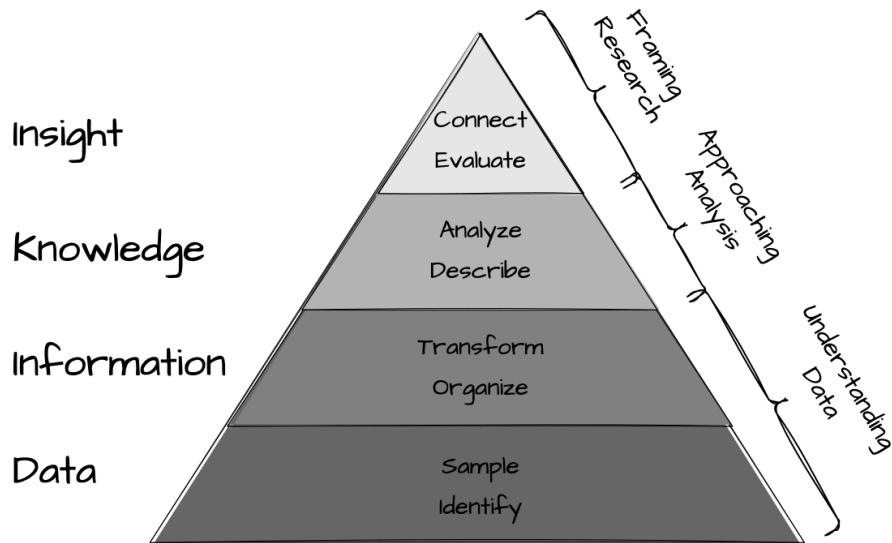


Figure 4.1: Framing research: visual summary

This chapter concludes the Foundations part of this textbook. At this stage our overview of fundamental characteristics of research are in place to move a project towards implementation, as seen in Figure 4.1. From this point forward we will integrate your conceptual knowledge and emerging R programming skills as we cover common scenarios encountered when conducting reproducible research with real-world data.

The next part, Preparation, aims to cover R coding strategies to acquire, curate, and transform data in preparation for analysis. These are the first steps in putting a research blueprint into action and by no coincidence the first components in the Data to Insight Hierarchy. Without further ado, let's get started!

Part III

Preparation

At this point we begin our journey to implement the research blueprint. As such, the content will be more focused on the practical steps to bring a plan to fruition integrating our conceptual understanding of the research process from the previous chapters with our emerging programming skills developed in lessons, recipes, and labs.

This part, Preparation, will address data acquisition, curation, and transformation steps. The goal of data preparation is to create a dataset which is ready for analysis. In each of these three upcoming chapters, I will outline some of the main characteristics to consider in each of these research steps and provide authentic examples of working with R to implement these steps. In Chapter 5 this includes the most common strategies for acquiring data: downloads and APIs. In Chapter 6 we turn to organize data into rectangular, or ‘tidy’, format. Depending on the data or dataset acquired for the research project, the steps necessary to shape our data into a base dataset will vary, as we will see. In Chapter 7 we will work to manipulate curated datasets to create datasets which are aligned with the research aim and research question. This often includes normalizing values, recoding variables, and generating new variables as well as and sourcing and merging information from other datasets with the dataset to be submitted for analysis.

Each of these chapters will cover the necessary documentation to trace our steps and provide a record of the data preparation process. Documentation serves to inform the analysis and interpretation of the results and also forms the cornerstone of reproducible research.

5 Acquire

The scariest moment is always just before you start.

— Stephen King

▀ Outcomes

- Identify common strategies for acquiring corpus data.
- Describe how to organize and document data acquisition to support reproducibility.
- Recall R programming concepts and strategies relevant to acquiring data.

As we start down the path to executing our research blueprint, our first step is to acquire the primary data that will be employed in the project. This chapter covers two commonly-used strategies for acquiring corpus data: downloads and APIs. We will encounter various file formats and folder structures in the process and we will address how to effectively organize our data for subsequent processing. Crucial to our efforts is the process of documenting our data. We will learn to provide data origin information to ensure key characteristics of the data and its source are documented.

Along the way, we will explore R coding concepts including control statements and custom functions relevant to the task of acquiring data. By the end of this chapter, you will not only be adept at acquiring data from diverse sources but also capable of documenting it comprehensively, enabling you to replicate the process in the future.

➤_ Lessons

What: Control Statements, Custom Functions^a

How: In the R Console pane load `swirl`, run `swirl()`, and follow prompts to select the lesson.

Why: To recognize the logic behind code that can make dynamic choices and to recall how functions serve to produce efficient, reusable, and more legible code.

^a<https://github.com/qtalr/lessons>

5.1 Downloads

The most common and straightforward method for acquiring corpus data is through direct downloads. In a nutshell, this method involves navigating to a website, locating the data, and downloading it to your computing environment. In some cases access to the data requires manual intervention and in others the process can be implemented programmatically. The data may be contained in a single file or multiple files. The files may be compressed or uncompressed. The data may be hierarchically organized or not. Each resource will have its own unique characteristics that will influence the process of acquiring the data. In this section we will work through a few examples to demonstrate the general process of acquiring data through downloads.

5.1.1 Manual

In contrast to the other data acquisition methods we will cover in this chapter, **manual downloads** require human intervention. This means that manual downloads are non-reproducible in a strict sense and require that we keep track of and document our procedure. It is a very common for research projects to acquire data through manual downloads as many data resources require some legwork before they are accessible for downloading. These can be resources that require institutional or private licensing and fees, require authorization/ registration, and/ or are only accessible via resource search interfaces.

The resource we will use for this demonstration is the Corpus Escrito del Español como L2 (CEDEL2)¹ (Lozano 2009), a corpus of Spanish learner writing. It includes L2 writing from students with a variety of L1 backgrounds. For comparative purposes it also includes native writing for Spanish, English, and several other languages.

The CEDEL2 corpus is a freely available resource, but to access the data you must first use a search interface to select the relevant characteristics of the data of interest. Following the search/ download link you can find a search interface that allows the user to select the subcorpus and filter the results by a set of attributes, seen in Figure 5.1.

¹<http://cedel2.learnercorpora.com/>

Figure 5.1: Search and download interface for the CEDEL2 Corpus

For this example let's assume that we want to acquire data to use in a study comparing the use of the Spanish preterite and imperfect past tense aspect in written texts by English L1 learners of Spanish to native Spanish speakers. To acquire data for such a project, we will first select the subcorpus "Learners of L2 Spanish". We will set the results to provide full texts and filter the results to "L1 English - L2 Spanish". Additionally, we will set the medium to "Written". This will provide us with a set of texts for the L2 learners that we can use for our study. The search parameters and results are shown in Figure 5.2.

The screenshot shows the CEDEL2 search interface. At the top, there are navigation links (Home, Search, Download, User guide, Statistics, About, Contact) and a version notice (v2.0, Sept. 2020). The main area is titled 'CEDEL2: Corpus Escrito del Español L2 (versión 2)'. On the left, a sidebar titled 'Corpus to search' shows a subcorpus selection for 'Learners of L2 Spanish'. Below this is a 'Sensitivity' section with checkboxes for 'Case' and 'Accents'. The main search area is titled 'Result (Output)' and includes a 'Sorting' section with dropdowns for 'L1' (selected), 'Placement test score (%)', 'Age', and 'Filename', and a 'Page size' dropdown set to 50. A 'Filters' section contains dropdowns for 'L1' (selected 'L1 English - L2 Spanish'), 'Task title' (Any), 'Medium' (Written), 'Filename' (Any), 'Sex' (Any), 'Age' (Any), 'Proficiency level' (Any), 'Placement test score (%)' (Any), 'Years studying Spanish' (Any), 'Proficiency (self-assessment)' (Any), and 'Stay abroad (months)' (Any). Below the filters is a table titled 'Results 1 to 50 of 1.906' showing three rows of data. The table columns are: Filename, L1, Age, Placement test score (%), Proficiency, Proficiency (self-assessment), Age of exposure to Spanish, Years studying Spanish, Stay abroad (months), Task title, and Medium. The data rows are:

Filename	L1	Age	Placement test score (%)	Proficiency	Proficiency (self-assessment)	Age of exposure to Spanish	Years studying Spanish	Stay abroad (months)	Task title	Medium
1 EN_WR_6_20_3_1.CJB	English	20	14	Lower beginner	2.25	17	3	0	1. Region where you live	Written
2 EN_WR_7_16_2_6.RM	English	16	16.3	Lower beginner	2.5	15	2	0	6. Recent trip	Written
3 EN_WR_7_26_2_2.TB	English	26	16.3	Lower beginner	2	18	2	0	2. Famous person	Written

At the bottom of the search results are buttons for 'Search' and 'Clean', and a 'Download' button.

Figure 5.2: Search results for the CEDEL2 Corpus

The ‘Download’ link now appears for this search criteria. Following this link will provide the user a form to fill out. This particular resource allows for access to different formats to download (Texts only, Texts with metadata, CSV (Excel), CSV (Others)). I will select the ‘CSV (Others)’ option so that the data is structured for easier processing downstream in subsequent processing steps. Then I save the CSV in the *data/original/* directory of my project and create a sub-directory named *cedel2/*, as seen in Example 5.1.

Example 5.1. Download CEDEL2 L2 Spanish Learners data

```
data/
└── analysis/
└── derived/
└── original/
    └── cedel2/
        └── cedel2-l1-english-learners.csv
```

Note that the file is named *cedel2-l1-english-learners.csv* to reflect the search criteria used to acquire the data. In combination with other data documentation, this will help us to maintain transparency.

Now, after downloading the L2 learner and the native speaker data into the appropriate directory, we move on to the next processing step, right? Not so fast! Imagine we are working on a project with a collaborator. How will they know where the data came from? What if we need to come back to this data in the future? How will we know what characteristics we used to filter the data? The directory and filenames may not be enough. To address these questions we need to document the origin of the data, and in the case of data acquired through manual downloads, we need to document the procedures we took to acquire the data to the best of our ability.

As discussed in Section 2.3.1, all acquired data should be accompanied by a data origin file. The majority of this information can typically be identified on the resource's website and/or the resource's documentation. In the case of the CEDEL2 corpus, the corpus homepage provides most of the information we need.

Structurally, data documentation files should be stored close to the data they describe. So for our data origin file this means adding it to the *data/original/* directory. Naming the file in a transparent way is also important. I've named the file *cedel2_do.csv* to reflect the name of the corpus, the meaning of the file as data origin with a suffixed **_do*, and the file extension *.csv** to reflect the file format. CSV files reflect tabular content. It is not required that data origin files are tabular, but it makes it easier to read and display them in literate programming documents.

Tip

There are many ways to create and edit CSV files. You can use a spreadsheet program like MS Excel or Google Sheets, a text editor like Notepad or TextEdit, or a code editor like RStudio or VS Code. The `qtaLRkit` package provides a convenient function, `create_data_origin()` to create a CSV file with the data origin boilerplate structure. This CSV file then can be edited to add the relevant information in any of the above mentioned programs.

Using a spreadsheet program is the easiest method for editing tabular data. The key is to save the file as a CSV file, and not as an Excel file, to maintain our adherence to the principle of using open formats for reproducible research.

In Table 5.1, I've created a data origin file for the CEDEL2 corpus.

Table 5.1: Data origin file for the CEDEL2 corpus

attribute	description
Resource name	CEDEL2: Corpus Escrito del Español como L2.
Data source	http://cedel2.learnercorpora.com/ , https://doi.org/10.1177/02676583211050522

Table 5.1: Data origin file for the CEDEL2 corpus

attribute	description
Data sampling frame	Corpus that contains samples of the language produced from learners of Spanish as a second language. For comparative purposes, it also contains a native control subcorpus of the language produced by native speakers of Spanish from different varieties (peninsular Spanish and all varieties of Latin American Spanish), so it can be used as a native corpus in its own right.
Data collection date(s)	2006-2020.
Data format	CSV file. Each row corresponds to a writing sample. Each column is an attribute of the writing sample.
Data schema	A CSV file for L2 learners and a CSV file for native speakers.
License	CC BY-NC-ND 3.0 ES
Attribution	Lozano, C. (2022). CEDEL2: Design, compilation and web interface of an online corpus for L2 Spanish acquisition research. <i>Second Language Research</i> , 38(4), 965-983. https://doi.org/10.1177/02676583211050522 .

Given this is a manual download we also need to document the procedure used to retrieve the data in prose. The script in the `code/` directory that is typically used to acquire the data is not used to programmatically retrieve data in this case. However, to keep things predictable we will use this file to document the download procedure. I've created a Quarto file named `1_acquire_data.qmd` in the `code/` directory of my project.

A glimpse at the directory structure of the project at this point is seen in Example 5.2.

Example 5.2. Project structure for the CEDEL2 corpus data acquisition

```
project/
  └── process/
    └── 1_acquire_data.qmd
  └── ...
  └── data/
    └── analysis/
    └── derived/
    └── original/
      └── cedel2_do.csv
      └── cedel2/
        └── cedel2-l1-english-learners.csv
        └── cedel2-native-spanish-speakers.csv
```

```
└── reports/
    └── DESCRIPTION
    └── Makefile
    └── README
```

Even though the *1_acquire_data.qmd* file is not used to programmatically retrieve the data, it is still a useful place to document the download procedure. This includes the URL of the resource, the search criteria used to filter the data, and the file format and location of the data. It is also good to include and display your data origin file in this file as a formatted table.

Manually downloading other resources will inevitably include unique processes for obtaining the data, but in the end the data should be archived in the project structure in the *data/original/* directory and documented in the appropriate places. Note that acquired data is always treated as ‘read-only’, meaning it is not modified in any way. This gives us a fixed starting point for subsequent steps in the data preparation process.

5.1.2 Programmatic

There are many resources that provide corpus data that is directly accessible for which programmatic downloads can be applied. A **programmatic download** is a download in which the process can be automated through code. Thus, this is a reproducible process. The data can be acquired by anyone with access to the necessary code.

In this case, and subsequent data acquisition procedures in this chapter, we use the *1_acquire_data.qmd* Quarto file to its full potential intermingling prose, code, and code comments to execute and document the download procedure.

To illustrate how this works to conduct a programmatic download, we will work with the Switchboard Dialog Act Corpus (SWDA) (University of Colorado Boulder 2008). The version that we will use is found on the Linguistic Data Consortium under the Switchboard-1 Release 2 Corpus². The corpus and related documentation are linked on the catalog page <https://catalog.ldc.upenn.edu/docs/LDC97S62/>.

From the documentation we learn that the corpus contains transcripts for 1155 5-minute two-way telephone conversations among English speakers for all areas of the United States. The speakers were given a topic to discuss and the conversations were recorded. The corpus metadata and annotations for sociolinguistic and discourse features.

This corpus, as you can image, could support a wide range of interesting research questions. Let’s assume we are following research conducted by Tottie (2011) to explore the use of filled pauses such as “um” and “uh” and traditional sociolinguistic variables such as sex, age, and education in spontaneous speech by American English speakers.

²<https://catalog.ldc.upenn.edu/LDC97S62>

With this goal in mind, let's get started writing the code to download and organize the data in our project directory. First, we need to identify the URL (Uniform Resource Locator) for the data that we want to download. More often than not this file will be some type of compressed archive file with an extension such as *.zip* (Zipped file), *.tar* (Tarball file), or *.tar.gz* (Gzipped tarball file), which is the case for the SWDA corpus. Compressed files make downloading multiple files easy by grouping files and directories into one file.

Consider this

You may be wondering what the difference between *.zip*, *.tar*, and *.tar.gz* files are. The *.zip* file format is the most common. It groups files and directories into one file (an archive) and compresses it to reduce the size of the file in one step when the file is created.

The *.tar* file format is used for archive files and folders, it does not perform compression. Gzipping performs the compression to the *.tar* file resulting in a file with the *.tar.gz* extension. Notably the *.gz* compression is highly efficient for large files. Take the *swda.tar.gz* file for example. It has a compressed file size of 4.6 MB, but when uncompressed it is 16.9 MB. This is a 73% reduction in file size.

In R, we can use the `download.file()` function from base R. The `download.file()` function minimally requires two arguments: `url` and `destfile`. These correspond to the file to download and the location where it is to be saved to disk. To break out the process a bit, I will assign the URL and destination file path to variables and then use the `download.file()` function to download the file.

Example 5.3.

```
# URL to SWDA corpus compressed file
file_url <-
  "https://catalog.ldc.upenn.edu/docs/LDC97S62/swb1_dialogact_annot.tar.gz"

# Relative path to project/data/original directory
file_path <- "../data/original/swda.tar.gz"

# Download SWDA corpus compressed file
download.file(url = file_url, destfile = file_path)
```

Warning

Note that the `file_path` variable in Example 5.3 is a relative path to the *data/original/* directory. This is because the *l_acquire_data.qmd* file that we are using for this code is located in the *code/* directory and the *data/* directory is a sibling directory to the *code/* directory.

It is also possible to use an absolute path to the *data/original/* directory. I will have more to say about the advantages and disadvantages of relative and absolute paths in reproducible research in Chapter 11.

As we can see looking at the directory structure, in Example 5.4, the *swda.tar.zip* file has been added to the *data/original/* directory.

Example 5.4. Downloaded SWDA corpus compressed file

```
data/
└── analysis/
└── derived/
└── original/
    └── swda.tar.zip
```

Once a compressed file is downloaded, however, the file needs to be ‘decompressed’ to reveal the directory structure and files. To decompress this *.tar.gz* file we use the `untar()` function with the arguments `tarfile` pointing to the *.tar.gz* file and `extract_to` specifying the directory where we want the files to be extracted to. Again, I will assign the arguments to variables. Then we can decompress the file using the `untar()` function.

Example 5.5.

```
# Relative path to the compressed file
tar_file <- "../data/original/swda.tar.gz"

# Relative path to the directory to extract to
extract_to_dir <- "../data/original/swda/"

# Decompress .zip file and extract to our target directory
untar(tar_file, extract_to_dir)
```

The directory structure of *data/* in Example 5.6 now shows the *swda.tar.gz* file and the *swda* directory that contains the decompressed directories and files.

Example 5.6.

```
data/
└── analysis/
└── derived/
```

```

└── original/
    ├── swda/
    |   ├── README
    |   ├── doc/
    |   ├── sw00utt/
    |   ├── sw01utt/
    |   ├── sw02utt/
    |   ├── sw03utt/
    |   ├── sw04utt/
    |   ├── sw05utt/
    |   ├── sw06utt/
    |   ├── sw07utt/
    |   ├── sw08utt/
    |   ├── sw09utt/
    |   ├── sw10utt/
    |   ├── sw11utt/
    |   ├── sw12utt/
    |   └── sw13utt/
    └── swda.tar.gz

```

At this point we have acquired the data programmatically and with this code as part of our workflow anyone could run this code and reproduce the same results.

The code as it is, however, is not ideally efficient. First, the *swda.tar.gz* file is not strictly needed after we decompress it and it occupies disk space, if we keep it. And second, each time we run this code the file will be downloaded from the remote server and overwrite the existing data. This leads to unnecessary data transfer and server traffic and will overwrite the data if it already exists in our project directory which could be problematic if the data changes on the remote server. Let's tackle each of these issues in turn.

To avoid writing the *swda.tar.gz* file to disk (long-term) we can use the `tempfile()` function to open a temporary holding space for the file in the computing environment. This space can then be used to store the file, decompress it, and then the temporary file will automatically be deleted. We assign the temporary space to an R object we will name `temp_file` with the `tempfile()` function. This object can now be used as the value of the argument `destfile` in the `download.file()` function.

Example 5.7.

```

# URL to SWDA corpus compressed file
file_url <-
  "https://catalog.ldc.upenn.edu/docs/LDC97S62/swb1_dialogact_annot.tar.gz"

```

```
# Create a temporary file space for our .tar.gz file
temp_file <- tempfile()

# Download SWDA corpus compressed file
download.file(file_url, temp_file)
```

👉 Tip

In Example 5.7, I've used the values stored in the objects `file_url` and `temp_file` in the `download.file()` function without specifying the argument names –only providing the names of the objects. R will assume that values of a function map to the ordering of the arguments. If your values do not map to ordering of the arguments you are required to specify the argument name and the value. To view the ordering of objects hit `tab` after entering the function name or consult the function documentation by prefixing the function name with `?` and hitting `enter`.

At this point our downloaded file is stored temporarily on disk and can be accessed and decompressed to our target directory using `temp_file` as the value for the argument `tarfile` from the `untar()` function. I've assigned our target directory path to `extract_to_dir` and used it as the value for the argument `exdir`.

Example 5.8.

```
# Assign our target directory to `extract_to_dir'
extract_to_dir <- "../data/original/swda/"

# Decompress .tar.gz file and extract to our target directory
untar(tarfile = temp_file, exdir = target_dir)
```

Our directory structure in Example 5.8 is the same as in Example 5.6, minus the `swda.tar.gz` file.

The second issue I raised concerns the fact that running this code as part of our project will repeat the download each time our script is run. Since we would like to be good citizens and avoid unnecessary traffic on the web and avoid potential issues in overwriting data, it would be nice if our code checked to see if we already have the data on disk and if it exists, then skip the download, if not then download it.

The desired functionality we've described can be implemented using the `if()` function. The `if()` function is one of a class of functions known as control statements. **Control statements**

allow us to control the flow of our code by evaluating logical statements and processing subsequent code based on the logical value it is passed as an argument.

So in this case we want to evaluate whether the data directory exists on disk. If it does then skip the download, if not, proceed with the download. In combination with `else` which provides the ‘if not’ part of the statement, we have the following logical flow in Example 5.9.

Example 5.9.

```
if (DIRECTORY_EXISTS) {  
  # Do nothing  
} else {  
  # Download data  
}
```

We can simplify this statement by using the `!` operator which negates the logical value of the statement it precedes. So if the directory exists, `!DIRECTORY_EXISTS` will return `FALSE` and if the directory does not exist, `!DIRECTORY_EXISTS` will return `TRUE`. In other words, if the directory does not exist, download the data. This is shown in Example 5.10.

Example 5.10.

```
if (!DIRECTORY_EXISTS) {  
  # Download data  
}
```

Now, to determine if a directory exists in our project directory we will turn to the `fs` package (Hester, Wickham, and Csárdi 2023). The `fs` package provides a set of functions for interacting with the file system, including `dir_exists()`. `dir_exists()` takes a path to a directory as an argument and returns the logical value, `TRUE`, if that directory exists, and `FALSE` if it does not.

We can use this function to evaluate whether the directory exists and then use the `if()` function to process the subsequent code based on the logical flow we set out in Example 5.10. Applied to our project, the code will look like Example 5.11.

Example 5.11.

```
# Load the `fs` package  
library(fs)
```

```

# URL to SWDA corpus compressed file
file_url <-
  "https://catalog.ldc.upenn.edu/docs/LDC97S62/swb1_dialogact_annot.tar.gz"

# Create a temporary file space for our .tar.gz file
temp_file <- tempfile()

# Assign our target directory to `extract_to_dir`
extract_to_dir <- "../data/original/swda/"

# Check if our target directory exists
# If it does not exist, download the file and extract it
if (!dir_exists(extract_to_dir)) {
  # Download SWDA corpus compressed file
  download.file(file_url, temp_file)

  # Decompress .tar.gz file and extract to our target directory
  untar(tarfile = temp_file, exdir = extract_to_dir)
}

```

The code in Example 5.11 is added to the *1_acquire_data.qmd* file. When this file is run, the SWDA corpus data will be downloaded and extracted to our project directory. If the data already exists, the download will be skipped, just as we wanted.

Now, before we move on, we need to make sure to document the process. Now that our Quarto document includes code we can review, explain, and comment this process. And, as always, create a data origin file as with the relevant information. The data origin file will be stored in the *data/original/* directory and the Quarto file will be stored in the *code/* directory.

We've leveraged R to automate the download and extraction of the data, depending on the existence of the data in our project directory. But you may be asking yourself, “Can’t I just navigate to the corpus page and download the data manually myself?” The simple answer is, “Yes, you can.” The more nuanced answer is, “Yes, but consider the trade-offs.”

The following scenarios highlight the some advantages to automating the process. If you are acquiring data from multiple files, it can become tedious to document the manual process for each file such that it is reproducible. It’s possible, but it’s error prone.

Now, if you are collaborating with others, you will want to share this data with them. It is very common to find data that has limited restrictions for use in academic projects, but the most common limitation is redistribution. This means that you can use the data for your own research, but you cannot share it with others. If you plan on publishing your project to a code repository to share the data as part of your reproducible project, you would be violating the

terms of use for the data. By including the programmatic download in your project, you can ensure that your collaborators can easily and effectively acquire the data themselves and that you are not violating the terms of use.

5.2 APIs

A convenient alternative method for acquiring data in R is through package interfaces to web services. These interfaces are built using R code to make connections with resources on the web through **Application Programming Interfaces** (APIs). Websites such as Project Gutenberg, Twitter, Reddit, and many others provide APIs to allow access to their data under certain conditions, some more limiting for data collection than others. Programmers (like you!) in the R community take up the task of wrapping calls to an API with R code to make accessing that data from R convenient, and of course reproducible.

Dive deeper

Many, many web services provide API access. These APIs span all kinds of data, from text to images to video to audio. Visit the Public APIs website^a to explore the diversity of APIs available.

ROpenSci maintains a curated list of R packages that provide access to data from web services. Visit the ROpenSci website^b to explore the packages available.

^a<https://publicapis.io/>

^b<https://ropensci.org/packages/data-access/>

In addition to popular public APIs, there are also APIs that provide access to repositories and databases which are of particular interest to linguists. For example, Wordbank³ provides access to a large collection of child language corpora through the `wordbankr` package (Braginsky 2023), and Glottolog⁴, World Atlas of Language Structures⁵ (WALS), and PHOIBLE⁶ provide access to large collections of language metadata that can be accessed through the `lingtypology` package (Moroz 2024).

Let's work with an R package that provides access to the TalkBank⁷ database. The TalkBank project (Macwhinney 2003) contains a large collection of spoken language corpora from various contexts: conversation, child language, multilinguals, *etc.* Resource information, web interfaces, and links to download data in various formats can be found by perusing individual resources linked from the main page. However, the `TBDBr` package (Kowalski and Cavanaugh 2022) provides convenient access to corpora using R once a corpus resource is identified.

³<http://wordbank.stanford.edu/>

⁴<https://glottolog.org/>

⁵<https://wals.info/>

⁶<https://phoible.org/>

⁷<https://talkbank.org/>

The CABNC (Albert, de Ruiter, and de Ruiter 2015) contains the demographically sampled portion⁸ of the spoken portion of the British National Corpus (BNC) (Leech 1992).

Useful for a study aiming to research spoken British English, either in isolation or in comparison to American English (SWDA).

First, we need to install and load the `TBDBr` package. Example 5.12.

Example 5.12.

```
# Load the TBDBr package
library(TBDBr)
```

The `TBDBr` package provides a set of common `get*()` functions for acquiring data from the TalkBank corpus resources. These include:

- `getParticipants()`
- `getTranscripts()`
- `getTokens()`
- `getTokenTypes()`
- `getUtterances()`

👉 Tip List functions and arguments

For any package loaded in your R session, you can list all of its functions and datasets using the `ls()` function. For example, `ls("package:TBDBr")` will list all of the functions and datasets in the `TBDBr` package.

To view all of the arguments for a function, use the `args()` function. For example, `args(getUtterances)` will list all of the arguments for the `getUtterances()` function.

For each of these function the first argument is `corpusName`, which is the name of the corpus resource as it appears in the TalkBank database. The second argument is `corpora`, which takes a character vector describing the path to the data. For the CABNC, these arguments are "ca" and `c("ca", "CABNC")` respectively. To determine these values, `TBDBr` provides the `getLegalValues()` interactive function which allows you to interactively select the repository name, corpus name, and transcript name (if necessary).

Another important aspect of these function is that they return data frame objects. Since we are accessing data that is in a structured database, this makes sense. However, we should always check the documentation for the object type that is returned by function to be aware of how to work with the data.

Let's start by retrieving the utterance data for the CABNC and preview the data frame it returns using `glimpse()`.

⁸http://www.natcorp.ox.ac.uk/docs/URG/BNCdes.html#body.1_div.1_div.5_div.1

Example 5.13.

```
# Set corpus_name and corpus_path
corpus_name <- "ca"
corpus_path <- c("ca", "CABNC")

# Get utterance data
utterances <-
  getUtterances(
    corpusName = corpus_name,
    corpora = corpus_path
  )
```

```
> [1] "Fetching data, please wait..."
> [1] "Success!"
```

```
# Preview the data
glimpse(utterances)
```

```
> Rows: 235,901
> Columns: 10
> $ filename <list> "KB0RE000", "KB0RE000", "KB0RE000", "KB0RE000", "KB0RE000", ~
> $ path      <list> "ca/CABNC/KB0/KB0RE000", "ca/CABNC/KB0/KB0RE000", "ca/CABNC~
> $ utt_num   <list> 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 1~
> $ who       <list> "PS002", "PS006", "PS002", "PS006", "PS002", "PS006", "PS00~
> $ role      <list> "Unidentified", "Unidentified", "Unidentified", "Unidentifi~
> $ postcodes <list> <NULL>, <NULL>, <NULL>, <NULL>, <NULL>, <NULL>, <NU~
> $ gems      <list> <NULL>, <NULL>, <NULL>, <NULL>, <NULL>, <NULL>, <NU~
> $ utterance  <list> "You enjoyed yourself in America", "Eh", "did you", "Oh I c~
> $ startTime <list> "0.208", "2.656", "2.896", "3.328", "5.088", "6.208", "8.32~
> $ endTime   <list> "2.672", "2.896", "3.328", "5.264", "6.016", "8.496", "9.31~
```

Inspecting the output from Example 5.13, we see that the data frame contains 235,901 observations and 10 variables.

The summary provided by `glimpse()` also provides other useful information. First, we see the data type of each variable. Interestingly, the data type for each variable in the data frame is a list object. Being that a list is two-dimensional data type, like a data frame, we have two-dimensional data inside two-dimensional data. This is known as a **nested structure**. We will work with nested structures in more depth later, but for now it will suffice to say that we

would like to ‘unnest’ these lists and reveal the list-contained vector types at the data frame level.

To do this we will pass the `utterances` data frame to the, appropriately named, `unnest()` function from the `tidyr` package (Wickham, Vaughan, and Girlich 2024). `unnest()` takes a data frame and a vector of variable names to unnest, `cols = c()`. To unnest all variables, we will use the `everything()` function from `dplyr` to select all variables at once. We will use the result to overwrite the `utterances` object with the unnested data frame.

Example 5.14.

```
# Unnest the data frame
utterances <-
  utterances |>
  unnest(cols = everything())

# Preview the data
glimpse(utterances)
```

```
> Rows: 235,901
> Columns: 10
> $ filename <chr> "KB0RE000", "KB0RE000", "KB0RE000", "KB0RE000", "KB0RE000", ~
> $ path      <chr> "ca/CABNC/KB0/KB0RE000", "ca/CABNC/KB0/KB0RE000", "ca/CABNC/~
> $ utt_num   <dbl> 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17~
> $ who       <chr> "PS002", "PS006", "PS002", "PS006", "PS002", "PS006", "PS002~
> $ role      <chr> "Unidentified", "Unidentified", "Unidentified", "Unidentifie~
> $ postcodes <lgl> NA, ~
> $ gems      <lgl> NA, ~
> $ utterance  <chr> "You enjoyed yourself in America", "Eh", "did you", "Oh I co~
> $ startTime <chr> "0.208", "2.656", "2.896", "3.328", "5.088", "6.208", "8.32"~
> $ endTime   <chr> "2.672", "2.896", "3.328", "5.264", "6.016", "8.496", "9.312~
```

The output from Example 5.14 shows that the variables are now one-dimensional vector types.

Returning to the information about our data frame from `glimpse()`, the second thing to notice is we get a short preview of the values for each variable. There are a couple things we can gleen from this. One is that we can confirm or clarify the meaning of the variable names by looking at the values. The other thing to consider is whether the values show any patterns that may be worthy of more scrutiny. For example, various variables appear to contain the same values for each observation. For a variable like `filename`, this is expected as the first values likely correspond to the same file. However, for the variables `postcodes` and `gems` the

values are ‘NA’. This suggests that these variables may not contain any useful information and we may want to remove them later.

For now, however, we want to acquire and store the data in its original form (or as closely as possible). So now, we have acquired the utterances data and have it in our R session as a data frame. To store this data in a file, we will first need to consider the file format. Data frames are tabular, so that gives us a few options.

Since we are working in R, we could store this data as an R object, in the form of an RDS file. An RDS file is a binary file that can be read back into R as an R object. This is a good option if we want to store the data for use in R, but not if we want to share the data with others or use it in other software. Another option is to store the data as a spreadsheet file, such as XSLX (MS Excel). This may make viewing and editing the contents more convenient, but it depends on the software available to you and others. A third, more viable option, is to store the data as a CSV file. CSV files are plain text files that can be read and written by most software. This makes CSV files one of the most popular for sharing tabular data. For this reason, we will store the data as a CSV file.

The `readr` package provides the `write_csv()` function for writing data frames to CSV files. The first argument is the data frame to write, and the second argument is the path to the file to write. Note, however, that the directories in the path we specify need to exist. If they do not, we will get an error.

In this case, I would like to write the file `utterances.csv` to the `../data/original/cabnc/` directory. The original project structure does not contain a `cabnc/` directory, so I need to create one. To do this, I will use `dir_create()` from the `fs` package.

Example 5.15.

```
# Create the target directory
dir_create("../data/original/cabnc/")

# Write the data frame to a CSV file
write_csv(utterances, "../data/original/cabnc/utterances.csv")
```

Chaining the steps covered in Examples 5.13, 5.14, and 5.15, we have a succinct and legible code to acquire, adjust, and write utterances from the CABNC in Example 5.16.

Example 5.16.

```
# Set corpus_name and corpus_path
corpus_name <- "ca"
corpus_path <- c("ca", "CABNC")
```

```

# Create the target directory
dir_create("../data/original/cabnc/")

# Get utterance data
getUtterances(
  corpusName = corpus_name,
  corpora = corpus_path
) |>
  unnest(cols = everything()) |>
  write_csv("../data/original/cabnc/utterances.csv")

```

If our goal is just to acquire utterances, then we are done acquiring data and we move on to the next step. However, if we want to acquire other datasets from the CABNC, say participants, tokens, *etc.*, then we can either repeat the steps in Example 5.16 for each data type, or we can write a function to do this for us!

A function serves us to make our code more legible and reusable for the CABNC, and since the TalkBank data is structured similarly across corpora, we can also use the function to acquire data from other corpora, if need be.

To write a function, we need to consider the following:

1. What is the name of the function?
2. What arguments does the function take?
3. What functionality does the function provide?
4. Does the function have optional arguments?
5. How does the function return the results?

Taking each in turn, the name of the function should be descriptive of what the function does. In this case, we are acquiring and writing data from Talkbank corpora. A possible name is `get_talkbank_data()`. The required arguments of the `get*()` functions will definitely figure in our function. In addition, we will need to specify the path to the directory to write the data. With these considerations, we can write the function signature in Example 5.17.

Example 5.17.

```

get_talkbank_data <- function(corpus_name, corpus_path, target_dir) {
  # ...
}

```

The next thing to consider is what functionality the function provides. In this case, we want to acquire and write data from Talkbank corpora. We can start by leveraging the code steps in Example 5.16, making some adjustments to the code replacing the hard-coded values with the function arguments and adding code to create the target file name based on the `target_dir` argument.

Example 5.18.

```
get_talkbank_data <- function(corpus_name, corpus_path, target_dir) {  
  
  # Create the target directory  
  dir_create(target_dir)  
  
  # Set up file path name  
  utterances_file <- path(target_dir, "utterances.csv")  
  
  # Acquire data and write to file  
  getUtterances(corpusName = corpus_name, corpora = corpus_path) |>  
    unnest(cols = everything()) |>  
    write_csv(utterances_file)  
}
```

Before we address the obvious feature missing, which is the fact that this function in Example 5.18 only acquires and writes data for utterances, let's consider some functionality which would make this function more user-friendly.

What if the data is already acquired? Do we want to overwrite it, or should the function skip the process for files that already exist? By skipping the process, we can save time and computing resources. If the files are periodically updated, then we might want to overwrite existing files.

To achieve this functionality we will use an `if()` statement to check if the file exists. If it does, then we will skip the process. If it does not, then we will acquire and write the data.

Example 5.19.

```
get_talkbank_data <- function(corpus_name, corpus_path, target_dir) {  
  
  # Create the target directory  
  dir_create(target_dir)  
  
  # Set up file path name
```

```

utterances_file <- path(target_dir, "utterances.csv")

# If the file does not exist, then...
# Acquire data and write to file
if(!file_exists(utterances_file)) {
  getUtterances(corpusName = corpus_name, corpora = corpus_path) |>
    unnest(cols = everything()) |>
    write_csv(utterances_file)
}
}

```

We can also add functionality to Example 5.19 to force overwrite existing files, if need be. To do this, we will add an optional argument to the function, `force`, which will be a logical value. We will set the default to `force = FALSE` to preserve the existing functionality. If `force = TRUE`, then we will overwrite existing files. Then we add another condition to the `if()` statement to check if `force = TRUE`. If it is, then we will overwrite existing files.

Example 5.20.

```

get_talkbank_data <- function(corpus_name, corpus_path, target_dir, force =
  FALSE) {

  # Create the target directory
  dir_create(target_dir)

  # Set up file path name
  utterances_file <- path(target_dir, "utterances.csv")

  # If the file does not exist, then...
  # Acquire data and write to file
  if(!file_exists(utterances_file) | force) {
    getUtterances(corpusName = corpus_name, corpora = corpus_path) |>
      unnest(cols = everything()) |>
      write_csv(utterances_file)
  }
}

```

From this point, we add the functionality to acquire and write the other data available from Talkbank corpora, such as participants, tokens, *etc.* This involves adding additional file path names and `if()` statements to check if the files exist surrounding the processing steps to Example 5.20. It may be helpful to perform other input checks, print messages, *etc.* for

functions that we plan to share with others. I will leave these enhancements as an exercise for the reader.

Before we leave the topic of functions, let's consider where to put functions after we write them. Here are a few options:

1. In the same script as the code that uses the function.
2. In a separate script, such as *functions.R*.
3. In a package, which is loaded by the script that uses the function.

The general heuristic for choosing where to put functions is to put them in the same script as the code that uses them if the function is only used in that script. If the function is used in multiple scripts or the function or number of functions clutters the readability of the code, then put it in a separate script. If the function is used in multiple projects, then put it in an R package.

💡 Dive deeper

If you are interested in learning more about writing functions, check out the Writing Functions chapter^a in the R for Data Science^b book.

If you find yourself writing functions that are useful for multiple projects, you may want to consider creating an R package. R packages are a great way to share your code with others. If you are interested in learning more about creating R packages, check out the R Packages book^c by Hadley Wickham and Jenny Bryan.

^a<https://r4ds.had.co.nz/functions.html>

^b<https://r4ds.had.co.nz/>

^c<https://r-pkgs.org/>

In this case, we will put the function in a separate file, *functions.R*, in the same directory as the other code files as in Example 5.23.

Example 5.21.

```
code/
|   └── 1_acquire_data.qmd
|   └── ...
|   └── functions.R
```

👉 Tip

Note that that the *functions.R* file is an R script, not a Quarto document. Therefore code blocks that are used in *.qmd* files are not used, only the R code and code comments.

To include this, or other functions in in the R session of the code file that uses them, use the `source()` function, as seen in Example 5.22.

Example 5.22.

```
# Source functions
source("functions.R")
```

It is common to source functions at the top of the code file as part of the package setup.

Given the utility of this function to my projects and potentially others', I've included the `get_talkbank_data()` function in the `qtalrkit` package. You can view the source code by calling the function without parentheses `()`, or on the `qtalrkit` GitHub repository.

After running the `get_talkbank_data()` function, we can see that the data has been acquired and written to the `data/original/cabnc/` directory.

Example 5.23.

```
data/
└── analysis
└── derived
└── original
    └── cabnc
        ├── participants.csv
        ├── token_types.csv
        ├── tokens.csv
        ├── transcripts.csv
        └── utterances.csv
```

Add comments to your code in `1-acquire-data.qmd` and create and complete the data origin documentation file for this resource, and the acquisition is complete.

Activities

Building on the activities in the previous chapter, these activities will focus on the implementation of the data acquisition process. Key programming concepts include writing custom functions, control statements, and applying functions iteratively will be covered in addition to packages and functions which provide access to data from the web.

❖ Recipe

What: Collecting and documenting data^a

How: Read Recipe 5, complete comprehension check, and prepare for Lab 5.

Why: To refine programming strategies introduced in the lesson for controlling program flow and making code more reusable in the service of programmatically acquiring and documenting data.

^a<https://qtalr.github.io/qtalrkit/articles/recipe-5.html>

❖ Lab

What: Harvesting research data^a

How: Fork, clone, and complete the steps in Lab 5.

Why: To investigate data sources, plan data collection strategies, and apply skills and knowledge to use R to collect and document data.

^a<https://github.com/qtalr/lab-05>

Summary

In this chapter, we have covered a lot of ground. On the surface we have discussed a few methods for acquiring corpus data for use in text analysis. In the process we have delved into various aspects of the R programming language. Some key concepts include writing control statements and custom functions. We have also considered topics that are more general in nature and concern interacting with data found on the internet.

Each of these methods should be approached in a way that is transparent to the researcher and to would-be collaborators and the general research community. For this reason the documentation of the steps taken to acquire data are key both in the code and in human-facing documentation.

At this point you have both a bird's eye view of the data available on the web and strategies on how to access a great majority of it. It is now time to turn to the next step in our data analysis project: data curation. In the next chapter, I will cover how to wrangle your raw data into a tidy dataset.

6 Curate

The hardest bit of information to extract is the first piece.

— Robert Ferrigno

▀ Outcomes

- Describe the importance of data curation in text analysis
- Recognize the different types of data formats
- Associate the types data formats with the appropriate R programming techniques to curate the data

In this chapter, we will now look at the next step in a text analysis project: data curation. That is, the process of converting the original data we acquire to a tidy dataset. Acquired data can come in a wide variety of formats. These formats tend to signal the richness of the metadata that is included in the file content. We will consider three general types of content formats: (1) unstructured data, (2) structured data, and (3) semi-structured data. Regardless of the file type and the structure of the data, it will be necessary to consider how to curate a dataset that such that the structure reflects the basic the unit of analysis that we wish to investigate. The resulting dataset will form the base from which we will work to further transform the dataset such that it aligns with the unit(s) of observation required for the analysis method that we will implement. Once the dataset is curated, we will create a data dictionary that describes the dataset and the variables that are included in the dataset for transparency and reproducibility.

➤ Lessons

What: Pattern Matching, Tidy Datasets^a

How: In the R Console pane load `swirl`, run `swirl()`, and follow prompts to select the lesson.

Why: To familiarize yourself with the basics of using the pattern matching syntax Regular Expressions and the `dplyr` package to manipulate data into Tidy datasets.

^a<https://github.com/qtalr/lessons>

6.1 Unstructured

The bulk of text ever created is of the unstructured variety. Unstructured data is data that has not been organized to make the information contained within machine-readable. Remember that text in itself is not information. Only when given explicit context does text become informative. The explicit contextual information that is included with data is called metadata. Metadata can be linguistic or non-linguistic in nature. So for unstructured data there is little to no metadata directly associated with the data. This information needs to be added or derived for the purposes of the research, either through manual inspection or (semi-)automatic processes. For now, however, our job is just to get the unstructured data into a structured format with as much metadata as we can derive from the resource.

6.1.1 Reading data

Some of the common file formats which contain unstructured data include TXT, PDF, and DOCX. Although these formats are unstructured, they are not all the same. Reading these files into R requires different techniques and tools.

Many times TXT files have the *.txt* extension, but it is not required. There are many ways to read TXT files into R and many packages that can be used to do so. For example, using the `readr` package, we can choose to read the entire file into a single vector of character strings with `read_file()` or read the file by lines with `read_lines()` in which each line is a character string in a vector.

Less commonly used in prepared data resources, PDF and DOCX files are more complex than TXT files as they contain formatting and embedded metadata. However, these attributes are primarily for visual presentation and not for machine-readability. Needless to say, we need an alternate strategy to extract the text content from these files and potentially some of the metadata. For example, using the `readtext` package (Benoit and Obeng 2023), we can read the text content from PDF and DOCX files into a single vector of character strings with `readtext()`.

Whether in TXT, PDF, or DOCX format, the resulting data structure will require further processing to convert the data into a tidy dataset. For example, we may need to split the data into multiple columns or rows, or extract metadata from the text content.

6.1.2 Orientation

As an example of curating an unstructured source of corpus data, let's take a look at the Europarl Parallel Corpus¹ (Koehn 2005). This corpus contains parallel texts (source and

¹<https://www.statmt.org/europarl/>

translated documents) from the European Parliamentary proceedings between 1996-2011 for some 21 European languages.

Let's assume we selected this corpus because we are interested in researching Spanish to English translations. After consulting the corpus website, downloading the compressed file, and inspecting the decompressed structure, we have the the file structure seen in Example 6.1.

Example 6.1.

```
project/
└── process/
    ├── 1-acquire-data.qmd
    ├── 2-curate-data.qmd
    └── ...
└── data/
    ├── analysis/
    ├── derived/
    └── original/
        ├── europarl_do.csv
        └── europarl/
            ├── europarl-v7.es-en.en
            └── europarl-v7.es-en.es
└── reports/
└── DESCRIPTION
└── Makefile
└── README
```

The *europarl_do.csv* file contains the data origin information documented as part of the acquisition process. The contents are seen in Table 6.1.

Table 6.1: Data origin: Europarl Corpus

attribute	description
Resource name	Europarl Parallel Corpus
Data source	https://www.statmt.org/europarl/
Data sampling frame	Spanish transcripts from the European Parliament proceedings
Data collection date(s)	1996-2011
Data format	TXT files with 'es' for source (Spanish) and 'en' for target (English) files.
Data schema	Line-by-line unannotated parallel text
License	See: https://www.europarl.europa.eu/legal-notice/en/

Table 6.1: Data origin: Europarl Corpus

attribute	description
Attribution	Please cite the paper: Koehn, P. 2005. 'Europarl: A Parallel Corpus for Statistical Machine Translation.' MT Summit X, 12-16.

Now let's get familiar with the corpus directory structure and the files. In Example 6.1, we see that there are two corpus files, *europarl-v7.es-en.es* and *europarl-v7.es-en.en*, that contain the source and target language texts, respectively. The file names indicate that the files contain Spanish-English parallel texts. The *.es* and *.en* extensions indicate the language of the text.

Looking at the beginning of the *.es* and *.en* files, in File 6.1 and File 6.2, we see that the files contain a series of lines in either the source or target language.

File 6.1 Spanish source text

```

Reanudación del período de sesiones
Declaro reanudado el período de sesiones del Parlamento Europeo, interrumpido el
↳ viernes 17 de diciembre pasado, y reitero a Sus Señorías mi deseo de que
↳ hayan tenido unas buenas vacaciones.
Como todos han podido comprobar, el gran "efecto del año 2000" no se ha
↳ producido. En cambio, los ciudadanos de varios de nuestros países han sido
↳ víctimas de catástrofes naturales verdaderamente terribles.
Sus Señorías han solicitado un debate sobre el tema para los próximos días, en
↳ el curso de este período de sesiones.
A la espera de que se produzca, de acuerdo con muchos colegas que me lo han
↳ pedido, pido que hagamos un minuto de silencio en memoria de todas las
↳ víctimas de las tormentas, en los distintos países de la Unión Europea
↳ afectados.

```

We can clearly appreciate that the data is unstructured. That is, there is no explicit metadata associated with the data. The data is just a series of character strings separated by lines. The only information that we can surmise from structure of the data is that the texts are line-aligned and that the data in each file corresponds to source and target languages.

Now, before embarking on a data curation process, it is recommendable to define the structure of the data that we want to create. I call this the “idealized structure” of the data. For a curated dataset, we want to maintain the original structure of the data as much as possible to maintain the integrity of the data and create a transparent and reproducible dataset.

Given what we know about the data, we can define the idealized structure of the data as seen in Table 6.2.

File 6.2 English target text

Resumption of the session

I declare resumed the session of the European Parliament adjourned on Friday 17

↪ December 1999, and I would like once again to wish you a happy new year in

↪ the hope that you enjoyed a pleasant festive period.

Although, as you will have seen, the dreaded 'millennium bug' failed to

↪ materialise, still the people in a number of countries suffered a series of

↪ natural disasters that truly were dreadful.

You have requested a debate on this subject in the course of the next few days,

↪ during this part-session.

In the meantime, I should like to observe a minute's silence, as a number of

↪ Members have requested, on behalf of all the victims concerned, particularly

↪ those of the terrible storms, in the various countries of the European Union.

Table 6.2: Idealized structure for the curated Europarl Corpus datasets.

variable	name	variable_type	description
type	Document	character	Contains the type of document, either 'Source' or 'Target'
line	Line	character	Contains the text of each line in the document

Our task now is to develop code that will read the original data and render the idealized structure as a curated dataset for each corpus file. We will then write the datasets to the *data/derived/* directory. The code we develop will be added to the *2-curate-data.qmd* file. And finally, the datasets will be documented with a data dictionary file.

6.1.3 Tidy the data

To create the idealized dataset structure in Table 6.2, let's start by reading the files by lines into R. We will use the `read_lines()` function from the `readr` package.

Example 6.2.

```
# Load package
library(readr)
```

```
# Read Europarl files .es and .en
europarl_es_chr <-
  read_lines("../data/original/europarl-v7.es-en.es")

europarl_en_chr <-
  read_lines("../data/original/europarl-v7.es-en.en")
```

Using the `read_lines()` function, we read each line of the files into a character vector. Since the Europarl corpus is a parallel corpus, the lines in the source and target files are aligned. This means that the first line in the source file corresponds to the first line in the target file, the second line in the source file corresponds to the second line in the target file, and so on. This alignment is important for the analysis of parallel corpora, as it allows us to compare the source and target texts line by line.

Let's inspect our character vectors to ensure that they are of the length and appear to be structured as we expect. We can use the `length()` function to get the number of lines in each file and the `head()` function to preview the first few lines of each file.

Example 6.3.

```
# Inspect Spanish character vector
length(europarl_es_chr)
head(europarl_es_chr, 5)

# Inspect English character vector
length(europarl_en_chr)
head(europarl_en_chr, 5)
```

```
> [1] 1965734
> [1] "Reanudación del período de sesiones"
> [2] "Declaro reanudado el período de sesiones del Parlamento Europeo, interrumpido el viernes 17 de diciembre de 1999. Como todos han podido comprobar, el gran \'efecto del año 2000\' no se ha producido. En cambio, los diputados han solicitado un debate sobre el tema para los próximos días, en el curso de este período de sesiones. A la espera de que se produzca, de acuerdo con muchos colegas que me lo han pedido, pido que hagamos lo que podamos para que se produzca."
> [5] "In the meantime, I should like to observe a minute's silence, as a number of Members have requested, in memory of the victims of the terrorist attacks in New York and Washington on 11 September 2001."
```

The output of Example 6.3 shows that the number of lines in each file is the same. This is good. If the number of lines in each file was different, we would need to figure out why and fix it. We also see that the content of the files is aligned as expected.

Let's now create a dataset for each of the character vectors. We will use the `tibble()` function from the `tibble` package to create a data frame object with the character vectors as the `line` column and add a `type` column with the value 'Source' for the Spanish file and 'Target' for the English file. We will assign the output two new objects `europarl_source_df` and `europarl_target_df`, respectively, as seen in Example 6.4.

Example 6.4.

```
# Create source data frame
europarl_source_df <-
  tibble(
    type = "Source",
    lines = europarl_es_chr
  )
# Create target data frame
europarl_target_df <-
  tibble(
    type = "Target",
    lines = europarl_en_chr
  )
```

Inspecting these data frames with `glimpse()` in Example 6.5, we can see if the data frames have the structure we expect.

Example 6.5.

```
# Preview source
glimpse(europarl_source_df)
```



```
> Rows: 1,965,734
> Columns: 2
> $ type <chr> "Source", "Source", "Source", "Source", "Source", "Source", "Sou~
> $ lines <chr> "Reanudación del período de sesiones", "Declaro reanudado el per~
```

```
# Preview target
glimpse(europarl_target_df)
```

```
> Rows: 1,965,734
> Columns: 2
> $ type <chr> "Target", "Target", "Target", "Target", "Target", "Target", "Tar-
> $ lines <chr> "Resumption of the session", "I declare resumed the session of t~
```

We now have our `type` and `lines` columns and the associated observations for our idealized dataset, in Table 6.2. We can now write these datasets to the `data/derived/` directory using `write_csv()` and create corresponding data dictionary files.

6.2 Structured

Structured data already reflects the physical and semantic structure of a tidy dataset. This means that the data is already in a tabular format and the relationships between columns and rows are already well-defined. Therefore the heavy lifting of curating the data is already done. There are two remaining questions, however, that need to be taken into account. One, logistical question, is what file format the dataset is in and how to read it into R. And the second, more research-based, is whether the data may benefit from some additional curation and documentation to make it more amenable to analysis and more understandable to others.

6.2.1 Reading datasets

Let's consider some common formats for structured data, *i.e.* datasets, and how to read them into R. First, we will consider R-native formats, such as package datasets and RDS files. Then we will consider non-native formats, such as relational databases and datasets produced by other software. Finally, we will consider software agnostic formats, such as CSV.

R and some R packages provide structured datasets that are available for use directly within R. For example, the `languageR` package (R. H. Baayen and Shafaei-Bajestan 2019) provides the `dative` dataset, which is a dataset containing the realization of the dative as NP or PP in the Switchboard corpus and the Treebank Wall Street Journal collection. The `janeaustenr` package (Silge 2022) provides the `austen_books` dataset, which is a dataset of Jane Austen's novels. Package datasets are loaded into an R session using either the `data()` function, if the package is loaded, or the `::` operator, if the package is not loaded. For example, `data(dative)` or `languageR::dative`.

Dive deeper

To explore the available datasets in a package, you can use the `data(package = "package_name")` function. For example, `data(package = "languageR")` will list the datasets available in the `languageR` package. You can also explore all the datasets avail-

able in the loaded packages with the `data()` function using no arguments. For example, `data()`.

R also provides a native file format for storing R objects, the RDS file. Any R object, including data frames, can be written from an R session to disk by using the `write_rds()` function from `readr`. The `.rds` files will be written to disk in a binary format that is not human-readable, which is not ideal for transparent data sharing. However, the files and the R objects can be read back into an R session using the `read_rds()` function with all the attributes intact, such as vector types, factor levels, *etc.*.

R provides a suite of tools for importing data from non-native structured sources such as databases and datasets from software such as SPSS, SAS, and Stata. For instance, if you are working with data stored in a relational database such as MySQL, PostgreSQL, or SQLite, you can use the `DBI` package (R Special Interest Group on Databases (R-SIG-DB), Wickham, and Müller 2024) to connect to the database and the `dbplyr` package (Wickham, Girlich, and Ruiz 2023) to query the database using the SQL language. Files from SPSS (`.sav`), SAS (`.sas7bdat`), and Stata (`.dta`) can be read into R using the `haven` package (Wickham, Miller, and Smith 2023).

Software agnostic file formats include delimited files, such as CSV, TSV, *etc.*. These file formats lack the robust structural attributes of the other formats, but balance this shortcoming by storing structured data in more accessible, human-readable format. Delimited files are plain text files which use a delimiter, such as a comma (,), tab (\t), or pipe (|), to separate the columns and rows. For example, a CSV file is a delimited file where the columns and rows are separated by commas, as seen in Example 6.6.

Example 6.6.

```
column_1,column_2,column_3
row 1 value 1,row 1 value 2,row 1 value 3
row 2 value 1,row 2 value 2,row 2 value 3
```

Given the accessibility of delimited files, they are a common format for sharing structured data in reproducible research. It is not surprising, then, that this is the format which we have chosen for the derived datasets in this book.

6.2.2 Orientation

With an understanding of the various structured formats, we can now turn to considerations about how the original dataset is structured and how that structure is to be used for a given research project. As an example, we will work with the CABNC datasets acquired in Chapter 5. The structure of the original dataset is shown in Example 6.7.

Example 6.7.

```
data/
└── analysis/
└── derived/
└── original/
    ├── cabnc_do.csv
    └── cabnc/
        ├── participants.csv
        ├── token_types.csv
        ├── tokens.csv
        ├── transcripts.csv
        └── utterances.csv
```

In addition to other important information, the data origin file *cabnc_do.csv* shown in Table 6.3 informs us the the datasets are related by a common variable.

Table 6.3: Data origin: CABNC datasets

attribute	description
Resource	CABNC.
name	
Data source	https://ca.talkbank.org/access/CABNC.html , doi:10.21415/T55Q5R
Data sampling frame	Over 400 British English Speakers from across the UK stratified age, gender, social group, and region, and recording their language output over a set period of time.
Data collection date(s)	1992.
Data format	CSV Files
Data schema	The recordings are linked by <code>filename</code> and the participants are linked by <code>who</code> .
License	CC BY NC SA 3.0
Attribution	Saul Albert, Laura E. de Ruiter, and J.P. de Ruiter (2015) CABNC: the Jeffersonian transcription of the Spoken British National Corpus. https://saualbert.github.io/CABNC/ .

The CABNC datasets are structured in a relational format, which means that the data is stored in multiple tables that are related to each other. The tables are related by a common

column or set of columns, which are called a keys. A key is used to join the tables together to create a single dataset. There are two keys in the CABNC datasets, `filename` and `who`. Each variable corresponds to recording- and/ or participant-oriented datasets.

Now, let's envision a scenario in which we are preparing our data for a study that aims to investigate the relationship between speaker demographics and utterances. In their original format, the CABNC datasets separate information about utterances and speakers in separate datasets, `cabnc_utterances` and `cabnc_participants`, respectively. Ideally, we would like to curate these datasets such that the information about the utterances and the speakers are ready to be joined as part of the dataset transformation process, while still retaining the relevant original structure. This usually involves removing redundant and/ or uninformative variables and/ or adjusting variable names and writing these datasets and their documentation files to disk.

6.2.3 Tidy the dataset

With these goals in mind, let's start the process of curation by reading the relevant datasets into an R session. Since we are working with CSV files will will use the `read_csv()` function, as seen in Example 6.8.

Example 6.8.

```
# Read the relevant datasets
cabnc_utterances <-
  read_csv("data/cabnc/original/utterances.csv")
cabnc_participants <-
  read_csv("data/cabnc/original/participants.csv")
```

The next step is to inspect the structure of the datasets. We can use the `glimpse()` function for this task.

Example 6.9.

```
# Preview the structure of the datasets
glimpse(cabnc_utterances)
```

```
> Rows: 235,901
> Columns: 10
> $ filename  <chr> "KB0RE000", "KB0RE000", "KB0RE000", "KB0RE000", "KB0RE000", ~
> $ path      <chr> "ca/CABNC/KB0/KB0RE000", "ca/CABNC/KB0/KB0RE000", "ca/CABNC/~
```

```

> $ utt_num    <dbl> 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17~
> $ who        <chr> "PS002", "PS006", "PS002", "PS006", "PS002", "PS006", "PS002~
> $ role       <chr> "Unidentified", "Unidentified", "Unidentified", "Unidentifie~
> $ postcodes <lgl> NA, ~
> $ gems       <lgl> NA, ~
> $ utterance  <chr> "You enjoyed yourself in America", "Eh", "did you", "Oh I co~
> $ startTime  <dbl> 0.208, 2.656, 2.896, 3.328, 5.088, 6.208, 8.320, 8.480, 10.2~
> $ endTime   <dbl> 2.67, 2.90, 3.33, 5.26, 6.02, 8.50, 9.31, 11.23, 14.34, 15.9~
```

```
glimpse(cabnc_participants)
```

```

> Rows: 6,190
> Columns: 13
> $ filename <chr> "KB0RE004", "KB0RE004", "KB0RE004", "KB0RE006", "KB0RE006", ~
> $ path      <chr> "ca/CABNC/0missing/KB0RE004", "ca/CABNC/0missing/KB0RE004", ~
> $ who       <chr> "PS008", "PS009", "KB0PSUN", "PS007", "PS008", "PS009", "KB0~
> $ name      <chr> "John", "Gethyn", "Unknown_speaker", "Alan", "John", "Gethyn~
> $ role       <chr> "Unidentified", "Unidentified", "Unidentified", "Unidentifie~
> $ language   <chr> "eng", "eng", "eng", "eng", "eng", "eng", "eng", "eng~
> $ monthage  <dbl> 481, 481, 13, 949, 481, 481, 13, 637, 565, 13, 637, 565, 13, ~
> $ age        <chr> "40;01.01", "40;01.01", "1;01.01", "79;01.01", "40;01.01", "~~
> $ sex        <chr> "male", "male", "male", "male", "male", "male", "male", "mal~
> $ numwords   <dbl> 28, 360, 156, 1610, 791, 184, 294, 93, 3, 0, 128, 24, 0, 150~
> $ numutts   <dbl> 1, 9, 27, 7, 5, 7, 6, 5, 1, 0, 11, 6, 0, 110, 74, 96, 12, 1, ~
> $ avgutt    <dbl> 28.00, 40.00, 5.78, 230.00, 158.20, 26.29, 49.00, 18.60, 3.0~
> $ medianutt <dbl> 28, 39, 5, 84, 64, 9, 3, 15, 3, 0, 9, 3, 0, 7, 6, 4, 3, 12, ~
```

From visual inspection of the output of Example 6.9 we can see that there are common variables in both datasets. In particular, we see the `filename` and `who` variables mentioned in the data origin file `cabnc_do.csv`.

The next step is to consider the variables that will be useful for future analysis. Since we are creating a curated dataset, the goal will be to retain as much information as possible from the original datasets. There are cases, however, in which there may be variables that are not informative and thus, will not prove useful for any analysis. These removable variables tend to be of one of two types: variables which show no variation across observations and variables where the information is redundant.

As an example case, let's look at the `cabnc_participants` data frame. We can use the `skim()` function from the `skimr` package to get a summary of the variables in the dataset. We can add the `yank()` function to look at variable types one at a time. We will start with the character variables, as seen in Example 6.10.

Example 6.10.

```
# Load package
library(skimr)

# Summarize character variables
cabnc_participants |>
  skim() |>
  yank("character")

>
> -- Variable type: character -----
>   skim_variable n_missing complete_rate min max empty n_unique whitespace
> 1 filename          0             1   8   8   0    2020          0
> 2 path              0             1  21  26   0    2020          0
> 3 who               0             1   4   7   0    581          0
> 4 name              0             1   3  25   0    269          0
> 5 role              0             1  12  12   0      1          0
> 6 language          0             1   3   3   0      1          0
> 7 age               0             1   7   8   0    83          0
> 8 sex               0             1   4   6   0      2          0
```

We see from the output in Example 6.10, that the variables `role` and `language` have a single unique value. This means that these variables do not show any variation across observations. We will remove these variables from the dataset.

Continuing on, let's look for redundant variables. We see that the variables `filename` and `path` have the same number unique values. And if we combine this with the visual summary in Example 6.9, we can see that the `path` variable is redundant. We will remove this variable from the dataset.

Another potentially redundant set of variables are `who` and `name` – both of which are speaker identifiers. The `who` variable is a unique identifier, but there may be some redundancy with the `name` variable, that is there may be two speakers with the same name. We can check this by looking at the number of unique values in the `who` and `name` variables from the `skim()` output in Example 6.10. `who` has 568 unique values and `name` has 269 unique values. This suggests that there are multiple speakers with the same name.

Another way to explore this is to look at the number of unique values in the `who` variable for each unique value in the `name` variable. We can do this using the `group_by()` and `summarize()` functions from the `dplyr` package. For each value of `name`, we will count the number of unique values in `who` and then sort the results in descending order.

Example 6.11.

```
cabnc_participants |>
  group_by(name) |>
  summarize(n = unique(who) |> length()) |>
  arrange(desc(n))

> # A tibble: 269 x 2
>   name                  n
>   <chr>                <int>
> 1 None                  59
> 2 Unknown_speaker       59
> 3 Group_of_unknown_speakers 21
> 4 Chris                 9
> 5 David                 9
> 6 Margaret               8
> 7 Ann                   7
> 8 John                  7
> 9 Alan                  6
> 10 Jackie                5
> # i 259 more rows
```

It is good that we performed the check in Example 6.11 beforehand. In addition to speakers with the same name, such as ‘Chris’ and ‘David’, we also have multiple speakers with generic codes, such as ‘None’ and ‘Unknown_speaker’. It is clear that `name` is redundant and we can safely remove it from the dataset.

With this in mind, we can then safely remove the following variables from the dataset: `role`, `language`, `name`, and `path`. To drop variables from a data frame we can use the `select()` function in combination with the `-` operator. The `-` operator tells the `select()` function to drop the variables that follow it.

Example 6.12.

```
# Drop variables
cabnc_participants <-
  cabnc_participants |>
  select(-role, -language, -name, -path)

# Preview the dataset
glimpse(cabnc_participants)
```

```

> Rows: 6,190
> Columns: 9
> $ filename <chr> "KB0RE004", "KB0RE004", "KB0RE004", "KB0RE006", "KB0RE006", ~
> $ who <chr> "PS008", "PS009", "KB0PSUN", "PS007", "PS008", "PS009", "KB0~
> $ monthage <dbl> 481, 481, 13, 949, 481, 481, 13, 637, 565, 13, 637, 565, 13, ~
> $ age <chr> "40;01.01", "40;01.01", "1;01.01", "79;01.01", "40;01.01", "4~
> $ sex <chr> "male", "male", "male", "male", "male", "male", "male", "mal~
> $ numwords <dbl> 28, 360, 156, 1610, 791, 184, 294, 93, 3, 0, 128, 24, 0, 150~
> $ numutts <dbl> 1, 9, 27, 7, 5, 7, 6, 5, 1, 0, 11, 6, 0, 110, 74, 96, 12, 1, ~
> $ avgutt <dbl> 28.00, 40.00, 5.78, 230.00, 158.20, 26.29, 49.00, 18.60, 3.0~
> $ medianutt <dbl> 28, 39, 5, 84, 64, 9, 3, 15, 3, 0, 9, 3, 0, 7, 6, 4, 3, 12, ~

```

Now we have a frame with 9 more informative variables which describe the participants. We would then repeat this process for the `cabnc_utterances` dataset to remove redundant and uninformative variables.

Another, optional step, is to rename and/ or organize the order the variables to make the dataset more understandable. Let's organize the columns to read left to right from most general to most specific. Again, we turn to the `select()` function, this time including the variables in the order we want them to appear in the dataset. We will take this opportunity to rename some of the variable names so that they are more informative.

Example 6.13.

```

# Rename variables
cabnc_participants <-
  cabnc_participants |>
  select(
    doc_id = filename,
    part_id = who,
    part_age = monthage,
    part_sex = sex,
    num_words = numwords,
    num_utts = numutts,
    avg_utt_len = avgutt,
    median_utt_len = medianutt
  )

# Preview the dataset
glimpse(cabnc_participants)

```

```
> Rows: 6,190
```

```

> Columns: 8
> $ doc_id      <chr> "KB0RE004", "KB0RE004", "KB0RE004", "KB0RE006", "KB0RE0~
> $ part_id     <chr> "PS008", "PS009", "KB0PSUN", "PS007", "PS008", "PS009", ~
> $ part_age    <dbl> 481, 481, 13, 949, 481, 481, 13, 637, 565, 13, 637, 565~
> $ part_sex    <chr> "male", "male", "male", "male", "male", "male", "male", ~
> $ num_words   <dbl> 28, 360, 156, 1610, 791, 184, 294, 93, 3, 0, 128, 24, 0~
> $ num_utts    <dbl> 1, 9, 27, 7, 5, 7, 6, 5, 1, 0, 11, 6, 0, 110, 74, 96, 1~
> $ avg_utt_len <dbl> 28.00, 40.00, 5.78, 230.00, 158.20, 26.29, 49.00, 18.60~
> $ median_utt_len <dbl> 28, 39, 5, 84, 64, 9, 3, 15, 3, 0, 9, 3, 0, 7, 6, 4, 3, ~

```

The variable order is organized after running Example 6.13. Now let's sort the rows by `doc_id` and `part_id` so that the dataset is sensibly organized. The `arrange()` function takes a data frame and a list of variables to sort by, in the order they are listed.

Example 6.14.

```

# Sort rows
cabnc_participants <-
  cabnc_participants |>
  arrange(doc_id, part_id)

# Preview the dataset
cabnc_participants |>
  slice_head(n = 10)

```

```

> # A tibble: 10 x 8
>   doc_id  part_id part_age part_sex num_words num_utts avg_utt_len
>   <chr>    <chr>    <dbl>   <chr>    <dbl>    <dbl>    <dbl>
> 1 KB0RE000 KB0PSUN      13 male        2        2        1
> 2 KB0RE000 PS002        721 female     759      74      10.3
> 3 KB0RE000 PS006        601 male       399      64      6.23
> 4 KB0RE001 KB0PSUN      13 male        7        3      2.33
> 5 KB0RE001 PS005        481 female     257      32      8.03
> 6 KB0RE001 PS007        949 male       284      29      9.79
> 7 KB0RE002 KB0PSUN      13 male        0        0        0
> 8 KB0RE002 PS003        601 female     379      30      12.6
> 9 KB0RE002 PS007        949 male       98      29      3.38
> 10 KB0RE003 KB0PSUN     13 male       0        0        0
> # i 1 more variable: median_utt_len <dbl>

```

Applying the sorting in Example 6.14, we can see that the utterances are now our desired order, a dataset that reads left to right from document to participant-oriented attributes and top to bottom by document and participant.

6.3 Semi-structured

Between unstructured and structured data falls semi-structured data. And as the name suggests, it is a hybrid data format. This means that there will be important structured metadata included with unstructured elements. The file formats and approaches to encoding the structured aspects of the data vary widely from resource to resource and therefore often requires more detailed attention to the structure of the data and often includes more sophisticated programming strategies to curate the data to produce a tidy dataset.

6.3.1 Reading data

The file formats associated with semi-structured data include a wide range. These include file formats conducive to more structured-leaning data, such as XML, HTML, and JSON, and file formats with more unstructured-leaning data, such as annotated TXT files. Annotated TXT files may in fact appear with the `.txt` extension, but may also appear with other, sometimes resource-specific, extensions, such as `.utt` for the Switchboard Dialogue Act Corpus or `.cha` for the CHILDES corpus annotation files, for example.

The more structured file formats use standard conventions and therefore can be read into an R session with format-specific functions. Say, for example, we are working with data in a JSON file format. We can read the data into an R session with the `read_json()` function from the `jsonlite` package (Ooms 2023). For XML and HTML files, the `rvest` package (Wickham 2024) provides the `read_xml()` and `read_html()` functions.

Semi-structured data in TXT files can be read either as a file or by lines. The choice of which approach to take depends on the structure of the data. If the data structure is line-based, then `read_lines()` often makes more sense than `read_file()`. However, in some cases, the data may be structured in a way that requires the entire file to be read into an R session and then subsequently parsed.

6.3.2 Orientation

To provide an example of the curation process using semi-structured data, we will work with the ENNTT corpus. The ENNTT corpus contains native and translated English drawn from European Parliament proceedings. Let's look at the directory structure for the ENNTT corpus in Example 6.15.

Example 6.15.

```
data/
└── analysis/
└── derived/
└── original/
    ├── enntt_do.csv
    └── enntt/
        ├── natives.dat
        ├── natives.tok
        ├── nonnatives.dat
        ├── nonnatives.tok
        ├── translations.dat
        └── translations.tok
```

We now inspect the data origin file for the ENNTT corpus, *enntt_do.csv*, in Table 6.4.

Table 6.4: Data origin file for the ENNTT corpus.

attribute	description
Resource name	Europarl corpus of Native, Non-native and Translated Texts - ENNTT
Data source	https://github.com/senisioi/enntt-release
Data sampling frame	English, European Parliament texts, transcribed discourse, political genre
Data collection date(s)	Not specified in the repository
Data format	.tok, .dat
Data schema	.tok files contain the actual text; .dat files contain the annotations corresponding to each line in the *.tok files.
License	Not specified. Contact the authors for more information.
Attribution	Nisioi, S., Rabinovich, E., Dinu, L. P., & Wintner, S. (2016). A corpus of native, non-native and translated texts. Proceedings of the Tenth International Conference on Language Resources and Evaluation (LREC 2016).

According to the data origin file, there are two important file types, *.dat* and *.tok*. The *.dat* files contain annotations and the *.tok* files contain the actual text. Let's inspect the first couple of lines in the *.dat* file for the native speakers, *nonnatives.dat*, in File 6.3.

We see that the *.dat* file contains annotations for various session and speaker attributes. The format of the annotations is XML-like. XML is a form of markup language, such as YAML,

File 6.3 Example *.dat* file for the non-native speakers.

```
<LINE STATE="Poland" MEPID="96779" LANGUAGE="EN" NAME="Danuta Hübner,"  
  ↵ SEQ_SPEAKER_ID="184" SESSION_ID="ep-05-11-17"/>  
<LINE STATE="Poland" MEPID="96779" LANGUAGE="EN" NAME="Danuta Hübner,"  
  ↵ SEQ_SPEAKER_ID="184" SESSION_ID="ep-05-11-17"/>
```

JSON, *etc.* **Markup languages** are used to annotate text with additional information about the structure, meaning, and/ or presentation of text. In XML, structure is built up by nesting of nodes. The nodes are named with tags, which are enclosed in angle brackets, `<` and `>`. Nodes are opened with `<TAG>` and closed with `</TAG>`. In Example 6.16 we see an example of a simple XML file structure.

Example 6.16.

```
<?xml version="1.0" encoding="UTF-8"?>  
<book category="fiction">  
  <title lang="en">The Catcher in the Rye</title>  
  <author>J. D. Salinger</author>  
  <year>1951</year>  
</book>
```

In Example 6.16 there are four nodes, three of which are nested inside of the `<book>` node. The `<book>` node in this example is the root node. XML files require a root node. Nodes can also have attributes, such as the `category` attribute in the `<book>` node, but they are not required. Furthermore, XML files also require a declaration, which is the first line in Example 6.16. The declaration specifies the version of XML used and the encoding.

So the *.dat* file is not strict XML, but is similar in that it contains nodes and attributes. An XML variant you are likely familiar with, HTML, has more relaxed rules than XML. HTML is a markup language used to annotate text with information about the organization and presentation of text on the web that does not require a root node or a declaration –much like our *.dat* file. So suffice it to say that the *.dat* file can safely be treated as HTML.

And the *.tok* file for the native speakers, *nonnatives.tok*, in File 6.4, shows the actual text for each line in the corpus.

In a study in which we are interested in contrasting the language of natives and non-natives, we will want to combine the *.dat* and *.tok* files for these groups of speakers.

The question is what attributes we want to include in the curated dataset. Given the research focus, we will not need the `LANGUAGE` or `NAME` attributes. We may want to modify the attribute names so they are a bit more descriptive.

File 6.4 Example *.tok* file for the non-native speakers.

```
The Commission is following with interest the planned construction of a nuclear
↳ power plant in Akkuyu , Turkey and recognises the importance of ensuring
↳ that the construction of the new plant follows the highest internationally
↳ accepted nuclear safety standards .

According to our information , the decision on the selection of a bidder has not
↳ been taken yet .
```

An idealized version of the curated dataset based on this criteria is shown in Table 6.5.

Table 6.5: Idealized structure for the curated ENNTT Corpus datasets.

variable	variable_name	variable_type	description
session_id	Session ID	character	Unique identifier for each session.
speaker_id	Speaker ID	integer	Unique identifier for each speaker.
state	State	character	The political state of the speaker.
type	Type	character	Indicates whether the text is native or non-native
session_seq	Session Sequence	integer	The sequence of the text in the session.
text	Text	character	Contains the text of the line, and maintains the structure of the original data.

6.3.3 Tidy the data

Now that we have a better understanding of the corpus data and our target curated dataset structure, let's work to extract and organize the data from the native and non-native files.

The general approach we will take is, for native and then non-natives, to read in the *.dat* file as an HTML file and then extract the line nodes and their attributes combining them into a data frame. Then we'll read in the *.tok* file as a text file and then combine the two into a single data frame.

Starting with the natives, we read in the *.dat* file as an XML file with the `read_html()` function and then extract the line nodes with the `html_elements()` function as in Example 6.17.

Example 6.17.

```

# Load packages
library(rvest)

# Read in *.dat* file as HTML
ns_dat_lines <-
  read_html("../data/original/enntt/natives.dat") |>
  html_elements("line")

# Inspect
class(ns_dat_lines)
typeof(ns_dat_lines)
length(ns_dat_lines)

```

```

> [1] "xml_nodeset"
> [1] "list"
> [1] 116341

```

When can see that the `ns_dat_lines` object is a special type of list, `xml_nodeset` which contains 116,341 line nodes. Let's now jump out of sequence and read in the `.tok` file as a text file, in Example 6.18, again by lines using `read_lines()`, and compare the two to make sure that our approach will work.

Example 6.18.

```

# Read in *.tok* file by lines
ns_tok_lines <-
  read_lines("../data/enntt/original/natives.tok")

# Inspect
class(ns_tok_lines)
typeof(ns_tok_lines)
length(ns_tok_lines)

> [1] "character"
> [1] "character"
> [1] 116341

```

We do, in fact, have the same number of lines in the `.dat` and `.tok` files. So we can proceed with extracting the attributes from the line nodes and combining them with the text from the `.tok` file.

Let's start by listing the attributes of the first line node in the `ns_dat_lines` object. To do this we will draw on the `pluck()` function from the `purrr` package (Wickham and Henry 2023) to extract the first line node. Then we use the `html_attrs()` function to get the attribute names and the values, as in Example 6.19.

Example 6.19.

```
# Load package
library(purrr)

# List attributes line node 1
ns_dat_lines |>
  pluck(1) |>
  html_attrs()
```

```
>      state      mepid      language      name
> "United Kingdom" "2099" "EN" "Evans, Robert J"
> seq Speaker_id session_id
> "2"      "ep-00-01-17"
```

No surprise here, these are the same attributes we saw in the `.dat` file preview in File 6.3. At this point, it's good to make a plan on how to associate the attribute names with the column names in our curated dataset.

- `session_id` = `session_id`
- `speaker_id` = `MEPID`
- `state` = `state`
- `session_seq` = `seq_speaker_id`

We can do this one attribute at a time using the `html_attr()` function and then combine them into a data frame with the `tibble()` function as in Example 6.20.

Example 6.20.

```
# Extract attributes from first line node
session_id <- ns_dat_lines |> pluck(1) |> html_attr("session_id")
speaker_id <- ns_dat_lines |> pluck(1) |> html_attr("mepid")
state <- ns_dat_lines |> pluck(1) |> html_attr("state")
session_seq <- ns_dat_lines |> pluck(1) |> html_attr("seq_speaker_id")
```

```
# Combine into data frame
tibble(session_id, speaker_id, state, session_seq)
```

```
> # A tibble: 1 x 4
>   session_id   speaker_id state      session_seq
>   <chr>        <chr>      <chr>      <chr>
> 1 ep-00-01-17  2099       United Kingdom 2
```

The results from Example 6.20 show that the attributes have been extracted and mapped to our idealized column names, but this would be tedious to do for each line node. A function to extract attributes and values from a line and add them to a data frame would help simplify this process. The function in Example 6.21 does just that.

Example 6.21.

```
# Function to extract attributes from line node
extract_datAttrs <- function(line_node) {
  session_id <- line_node |> html_attr("session_id")
  speaker_id <- line_node |> html_attr("mepid")
  state <- line_node |> html_attr("state")
  session_seq <- line_node |> html_attr("seq_speaker_id")

  tibble(session_id, speaker_id, state, session_seq)
}
```

It's a good idea to test out the function to verify that it works as expected. We can do this by passing the various indices to the `ns_dat_lines` object to the function as in Example 6.22.

Example 6.22.

```
# Test function
ns_dat_lines |> pluck(1) |> extract_datAttrs()

> # A tibble: 1 x 4
>   session_id   speaker_id state      session_seq
>   <chr>        <chr>      <chr>      <chr>
> 1 ep-00-01-17  2099       United Kingdom 2
```

```
ns_dat_lines |> pluck(20) |> extract_dat_attrs()
```

```
> # A tibble: 1 x 4
>   session_id speaker_id state      session_seq
>   <chr>       <chr>      <chr>      <chr>
> 1 ep-00-01-17 1309      United Kingdom 40
```

```
ns_dat_lines |> pluck(100) |> extract_dat_attrs()
```

```
> # A tibble: 1 x 4
>   session_id speaker_id state      session_seq
>   <chr>       <chr>      <chr>      <chr>
> 1 ep-00-01-18 4549      United Kingdom 28
```

Looks like the `extract_dat_attrs()` function is ready for prime-time. Let's now apply it to all of the line nodes in the `ns_dat_lines` object using the `map_dfr()` function from the `purrr` package as in Example 6.23.

Example 6.23.

```
# Extract attributes from all line nodes
ns_dat_attrs <-
  ns_dat_lines |>
  map_dfr(extract_dat_attrs)

# Inspect
glimpse(ns_dat_attrs)
```

```
> Rows: 116,341
> Columns: 4
> $ session_id <chr> "ep-00-01-17", "ep-00-01-17", "ep-00-01-17", "ep-00-01-17"~
> $ speaker_id  <chr> "2099", "2099", "2099", "4548", "4548", "4541", "4541", "4~
> $ state        <chr> "United Kingdom", "United Kingdom", "United Kingdom", "Uni~
> $ session_seq <chr> "2", "2", "2", "4", "4", "12", "12", "12", "12", "12", "12~
```

 Dive deeper

The `map*`() functions from the `purrr` package are a family of functions that apply a function to each element of a vector, list, or data frame. The `map_dfr()` function is a variant of the `map()` function that returns a data frame that is the result of row-binding the results, hence `_dfr`.

We can see that the `ns_datAttrs` object is a data frame with 116,341 rows and 4 columns, just as we expected. We can now combine the `ns_datAttrs` data frame with the `ns_tok_lines` vector to create a single data frame with the attributes and the text. This is done with the `mutate()` function assigning the `ns_tok_lines` vector to a new column named `text` as in Example 6.24.

Example 6.24.

```
# Combine attributes and text
ns_dat <-
  ns_datAttrs |>
  mutate(text = ns_tok_lines)

# Inspect
glimpse(ns_dat)

> Rows: 116,341
> Columns: 5
> $ session_id <chr> "ep-00-01-17", "ep-00-01-17", "ep-00-01-17", "ep-00-01-17"~
> $ speaker_id <chr> "2099", "2099", "2099", "4548", "4548", "4541", "4541", "4~
> $ state       <chr> "United Kingdom", "United Kingdom", "United Kingdom", "Uni~
> $ session_seq <chr> "2", "2", "2", "4", "4", "12", "12", "12", "12", "12", "12~
> $ text         <chr> "You will be aware from the press and television that ther~
```

This is the data for the native speakers. We can now repeat this process for the non-native speakers, *or* we can create a function to do it for us. Let's explore the later option.

I will name this function `combine_dat_tok()` and it will take two arguments: `dat_file` and `tok_file`. The `dat_file` argument will be the path to the `.dat` file and the `tok_file` argument will be the path to the `.tok` file. The function first reads both the files into R as lines. Then it extracts the attributes from the `.dat` file using the `extract_datAttrs()` function we created earlier. Finally, it combines the attributes with the text from the `.tok` file and returns a data frame.

Note that there is at least one tweak we need to make to our existing code base to generate our idealized curated structure. We will need to add a column `type` to which we will indicate what type of data it is (native or non-native).

There are multiple ways to do this. We could add a column to the data frame in the function before we return it, or we could add a column to the data frame after we return it. I will opt for the former and embed it inside of our function `combine_dat_tok()`, as seen in Example 6.25.

Example 6.25.

```
# Load packages
library(dplyr) # for data manipulation
library(rvest) # for reading/parsing HTML
library(purrr) # for mapping functions
library(fs) # for working with files

# Function to combine *.dat* and *.tok* files
combine_dat_tok <- function(dat_file, tok_file) {
  # Read in files by lines
  dat <-
    read_html(dat_file) |>
    html_nodes("line")
  tok <- read_lines(tok_file)

  # Create function to extract attributes
  extract_datAttrs <- function(line_node) {
    session_id <- line_node |> html_attr("session_id")
    speaker_id <- line_node |> html_attr("mepid")
    state <- line_node |> html_attr("state")
    session_seq <- line_node |> html_attr("seq_speaker_id")

    tibble(session_id, speaker_id, state, session_seq)
  }

  # Apply function to all line nodes
  datAttrs <-
    dat |>
    map_dfr(extract_datAttrs)

  # Combine attrs and text into data frame
  dataset <-
    datAttrs |>
    mutate(text = tok)

  # Add type column with value of file name (w/o extension)
  type_name <- path_file(dat_file) |> path_ext_remove()
}
```

```

dataset <-
  dataset |>
  mutate(type = type_name)

# Return data frame
return(dataset)
}

```

Apply the `combine_dat Tok()` function to read in the data for the native speakers and the non-native speakers in a few lines of code, as in Example 6.26.

Example 6.26.

```

# Native speakers
enntt_ns_df <-
  combine_dat Tok(
    dat_file = "../data/original/enntt/natives.dat",
    tok_file = "../data/original/enntt/natives.tok"
  )
# Preview
glimpse(enntt_ns_df)

# Non-native speakers
enntt_nns_df <-
  combine_dat Tok(
    dat_file = "../data/original/enntt/nonnatives.dat",
    tok_file = "../data/original/enntt/nonnatives.tok"
  )
# Preview
glimpse(enntt_nns_df)

```

```

> Rows: 116,341
> Columns: 6
> $ session_id  <chr> "ep-00-01-17", "ep-00-01-17", "ep-00-01-17", "ep-00-01-17"~
> $ speaker_id   <chr> "2099", "2099", "2099", "4548", "4548", "4541", "4541", "4~
> $ state        <chr> "United Kingdom", "United Kingdom", "United Kingdom", "Uni~
> $ session_seq  <chr> "2", "2", "2", "4", "4", "12", "12", "12", "12", "12", "12~
> $ text         <chr> "You will be aware from the press and television that ther~
> $ type         <chr> "natives", "natives", "natives", "natives", "natives", "na~

```

We now have met the idealized structure for the curated ENNTT Corpus datasets, as shown in Table 6.5. The `enntt_ns_df` and `enntt_mns_df` data frames are ready to be written to disk and documented.

6.4 Documentation

After applying the curation steps to our data, we will now want to write the dataset to disk and to do our best to document the process and the resulting dataset.

Since data frames are a tabular, we will have various options for the file type to write. Many of these formats are software-specific, such as `*.xlsx` for Microsoft Excel, `*.sav` for SPSS, `*.dta` for Stata, and `*.rds` for R. We will use the `*.csv` format since it is a common format that can be read by many software packages. We will use the `write_csv()` function from the `readr` package to write the dataset to disk.

Now the question is where to save our CSV file. Since our dataset is derived by our work, we will add it to the `derived/` directory. If you are working with multiple data sources within the same project, it is a good idea to create a subdirectory for each dataset. This will help keep the project organized and make it easier to find and access the datasets.

The final step, as always, is to document the dataset. For datasets the documentation is a data dictionary, as discussed in Section 2.3.2. As with data origin files, you can use spreadsheet software to create and/ or edit the data dictionary.

In the `qtalrkit` package we have a function, `create_data_dictionary()` that will generate the scaffolding for a data dictionary. The function takes two arguments, `data` and `file_path`. It reads the dataset columns and provides a template for the data dictionary.

★ Dive deeper

The `create_data_dictionary()` function provides a rudimentary data dictionary template by default. However, you can take advantage of OpenAI's text generation models to generate a more detailed data dictionary for you to edit. To do this create an OpenAI account^a and an API key^b and add this key to your R environment (`Sys.setenv(OPENAI_API_KEY =`

"sk..."). Then you can specify the model you would like to use in the function with the `model` = argument. For example, `model = "gpt-3.5-turbo"` will use the GPT-3.5 Turbo model.

^a<https://platform.openai.com/signup>

^b<https://platform.openai.com/account/api-keys>

An example of a data dictionary, a data dictionary for the `enntt_ns_df` dataset is shown in Table 6.6.

Table 6.6: Data dictionary for the `enntt_ns_df` dataset.

variable	name	variable_type	description
session_id	Session ID	categorical	Unique identifier for each session
speaker_id	Speaker ID	categorical	Unique identifier for each speaker
state	State	categorical	Name of the state or country the session is linked to
session_seq	Session Sequence	ordinal	Sequence number in the session
text	Text	categorical	Text transcript of the session
type	Type	categorical	The type of the speaker, whether native or nonnative

Activities

The following activities build on your skills and knowledge to use R to read, inspect, and write data and datasets in R. In these activities you will have an opportunity to learn and apply your skills and knowledge to the task of curating datasets. This is a vital component of text analysis research that uses unstructured and semi-structured data.

Recipe

What: Organizing and documenting datasets^a

How: Read Recipe 6, complete comprehension check, and prepare for Lab 6.

Why: To rehearse methods for deriving tidy datasets to use as the base for further project-specific purposes. We will explore how regular expressions are helpful in developing strategies for matching, extracting, and/or replacing patterns in character sequences and how to organize datasets in rows and columns. We will also explore how to document datasets in a data dictionary.

^a<https://qtalr.github.io/qtalrkit/articles/recipe-6.html>

¶ Lab

What: Taming data^a

How: Fork, clone, and complete the steps in Lab 6.

Why: To gain experience working with coding strategies to manipulate data using tidyverse functions and regular expressions, to practice reading/ writing data from/ to disk, and to implement organizational strategies for organizing and documenting a dataset in reproducible fashion.

^a<https://github.com/qtalr/lab-06>

Summary

In this chapter we looked at the process of structuring data into a dataset. This included a discussion on three main types of data –unstructured, structured, and semi-structured. The level of structure of the original data(set) will vary from resource to resource and by the same token so will the file format used to support the level of metadata included. The results from data curation results in a dataset that is saved separate from the original data to maintain modularity between what the data(set) looked like before we intervene and afterwards. Since there can be multiple analysis approaches applied the original data in a research project, this curated dataset serves as the point of departure for each of the subsequent datasets derived from the transformational steps. In addition to the code we use to derive the curated dataset’s structure, we also include a data dictionary which documents the curated dataset.

7 Transform

Nothing is lost. Everything is transformed.

— Michael Ende, *The Neverending Story*

▀ Outcomes

- Understand the role of data transformation in a text analysis project.
- Identify the main types of transformations used to prepare datasets for analysis.
- Recognize the importance of planning and documenting the transformation process.

In this chapter, we will focus on transforming curated datasets to refine and possibly expand their relational characteristics to align with our research. I will approach the transformation process by breaking it down into two sub-processes: preparation and enrichment. The preparation process involves normalizing and tokenizing text. The enrichment process involves recoding, generating, and integrating variables. These processes are not sequential but may occur in any order based on the researcher's evaluation of the dataset characteristics and the desired outcome.

➤_ Lessons

What: Reshape Datasets by Rows, Reshape datasets by Columns^a

How: In the R Console pane load `swirl`, run `swirl()`, and follow prompts to select the lesson.

Why: Explore data preprocessing skills to manipulate rows and columns using powerful packages like `dplyr` and `tidytext` to normalization, tokenize, and integrate datasets equipping you with the essential techniques to structure datasets for analysis.

^a<https://github.com/qtalr/lessons>

7.1 Preparation

In this section we will cover the processes of normalization and tokenization. These processes are particularly relevant for text analysis, as text conventions can introduce unwanted variability in the data and the unit of observation may need to be adjusted to align with the research question.

To illustrate these processes, we will use a curated version of the Europarl Corpus (Koehn 2005). This dataset contains transcribed source language (Spanish) and translated target language (English) from the proceedings of the European Parliament. The unit of observation is the `lines` variable whose values are lines of dialog. We will use this dataset to explore the normalization and tokenization processes.

The contents of the data dictionary for this dataset appears in Table 7.1.

Table 7.1: Data dictionary for the curated Europarl Corpus.

variable	name	variable_type	description
doc_id	Document ID	numeric	Unique identification number for each document
type	Document Type	categorical	Type of document; either ‘Source’ (Spanish) or ‘Target’ (English)
line_id	Line ID	numeric	Unique identification number for each line in each document type
lines	Lines	categorical	Content of the lines in the document

Let’s read in the dataset CSV file with `read_csv()` and inspect the first lines of the dataset with `slice_head()` in Example 7.1.

Example 7.1.

```
# Read in the dataset
europarl_tbl <-
  read_csv(file = "../data/derived/europarl_curated.csv")

# Preview the first 10 lines
europarl_tbl |>
  slice_head(n = 10)

> # A tibble: 10 x 4
>   doc_id type  line_id lines
>   <dbl> <chr> <dbl> <chr>
> 1 1965735 Source     1 "Reanudación del periodo de sesiones"
> 2     1 Target      1 "Resumption of the session"
> 3 1965736 Source     2 "Declaro reanudado el periodo de sesiones del Parlame~"
> 4     2 Target      2 "I declare resumed the session of the European Parlia~"
> 5 1965737 Source     3 "Como todos han podido comprobar, el gran \'efecto de~"
> 6     3 Target      3 "Although, as you will have seen, the dreaded 'millen~"
```

```

> 7 1965738 Source      4 "Sus Señorías han solicitado un debate sobre el tema ~
> 8          4 Target      4 "You have requested a debate on this subject in the c~
> 9 1965739 Source      5 "A la espera de que se produzca, de acuerdo con mucho~
> 10         5 Target      5 "In the meantime, I should like to observe a minute' ~

```

This dataset includes 3,931,468 observations and four variables. The key variable for our purposes is the `lines` variable. This variable contains the text we will be working with. The other variables are metadata that may be of interest for our analyses.

7.1.1 Normalization

The process of normalizing datasets in essence is to sanitize the values of variable or set of variables such that there are no artifacts that will contaminate subsequent processing. It may be the case that non-linguistic metadata may require normalization but more often than not linguistic information is the most common target for normalization as text often includes artifacts from the acquisition process which will not be desired in the analysis.

Simply looking at the first 10 lines of the dataset from Example 7.1 gives us a clearer sense of the dataset structure, but, in terms of normalization procedures we might apply, it is likely not sufficient. We want to get a sense of any potential inconsistencies in the dataset, in particular in the `lines` variable. Since this is a large dataset with 3,931,468 observations, we will need to explore the dataset in more detail using procedures for summarizing and filtering data.

After exploring variations in the `lines` variable, I identified a number of artifacts in this dataset that we will want to consider addressing. These are included in Table 7.2.

Table 7.2: Characteristics of the Europarl Corpus dataset that may require normalization.

Description	Examples
Non-speech annotations	(Abucheos), (A4-0247/98), (The sitting was opened at 09:00)
Inconsistent whitespace	5 % , , , Palacio' s
Non-sentence punctuation	-
Abbreviations	Mr., Sr., Mme., Mr, Sr, Mme, Mister, Señor, Madam
Text case	The, the, White, white

These artifacts either may not be of interest or may introduce unwanted variability in the that could prove problematic for subsequent processing (*e.g* tokenization, calculating frequencies, *etc.*).

Identifying our normalization goals is an important first step. In this case, let's just focus on removing parliamentary session descriptions for demonstration purposes. The next step is to identify the procedures that will accomplish this goal.

The majority of text normalization procedures incorporate the `stringr` package (Wickham 2023a). This package provides a number of functions for manipulating text strings. The workhorse functions we will use for our tasks are the `str_remove()` and `str_replace()` functions. As these functions give us the ability to remove or replace text based on literal strings and Regular Expressions.

Our first step, however, is to identify the patterns we want to remove or replace. For this, we can call on either the `str_view()` function or the `str_detect()` function inside a `filter()` function to identify the lines that contain the patterns we want to remove. We can also use the `str_extract()` and/or `str_extract_all()` functions inside a `mutate()` function to extract the text that matches the pattern. In any of these cases, it can be helpful to use the `slice_sample()` function work with a small sample of the dataset to get a sense of the patterns we are working with as we develop a search pattern that does not over- or under-generalize the text we want to remove or replace. If we are too general, we may end up removing or replacing text that we want to keep. If we are too specific, we may not remove or replace all the text we want to remove or replace.

Let's start by identifying non-parliamentary speech. In Example 7.2, we use `str_detect()` which detects a pattern in a character vector and returns a logical vector, `TRUE` if the pattern is detected and `FALSE` if it is not. In combination with `filter()` we can identify a variable with rows that match a pattern.

From the examples above, we can see that these instances are wrapped with parentheses (and). The text within the parentheses can vary, so we need a Regular Expression to do the heavy lifting. To start out we can match any one or multiple characters with `.+`. But it is important to recognize the `+` (and also the `*`) operators are 'greedy', meaning that if there are multiple matches, the longest match will be returned. In this case, we want to match the shortest match. To do this we can use the `?` operator to make the `+` operator 'lazy'. This will match the shortest match.

Example 7.2.

```
# Load package
library(stringr)

# Identify non-speech lines
europarl_tbl |>
  filter(str_detect(lines, "\\\(.+?\\\)")) |>
  slice_sample(n = 10)
```

```

> # A tibble: 10 x 4
>   doc_id type  line_id lines
>   <dbl> <chr>  <dbl> <chr>
> 1 3225772 Source 1260038 (PT) Señor Presidente, quisiera plantear dos pregunta-
> 2 3715842 Source 1750108 (El Parlamento decide la devolución a la Comisión)
> 3 1961715 Target 1961715 (Parliament adopted the resolution)
> 4 1429470 Target 1429470 27, originally Greens/EFA amendment in FEMM); binding-
> 5 51632 Target 51632 Question No 8 by (H-0376/00):
> 6 2482671 Source 516937 La Comisión propone proporcionar a las Agencias nacio-
> 7 1059628 Target 1059628 (The President cut off the speaker)
> 8 1507254 Target 1507254 in writing. - (LT) I welcomed this document, because ~
> 9 2765325 Source 799591 (Aplausos)
> 10 2668536 Source 702802 Las preguntas que, por falta de tiempo, no han rec-

```

The results from Example 7.2 show that we have identified the lines that contain at least one of the parliamentary session description annotations. A more targeted search to identify specific instances of the parliamentary session descriptions can be accomplished adding the `str_extract_all()` function as seen in Example 7.3.

Example 7.3.

```

# Extract non-speech fragments
europarl_tbl |>
  filter(str_detect(lines, "\\(.+?\\)")) |>
  mutate(non_speech = str_extract_all(lines, "\\(.+?\\)")) |>
  slice_sample(n = 10)

> # A tibble: 10 x 5
>   doc_id type  line_id lines          non_speech
>   <dbl> <chr>  <dbl> <chr>        <list>
> 1 3225772 Source 1260038 (PT) Señor Presidente, quisiera plantear d~ <chr [1]>
> 2 3715842 Source 1750108 (El Parlamento decide la devolución a la C~ <chr [1]>
> 3 1961715 Target 1961715 (Parliament adopted the resolution)      <chr [1]>
> 4 1429470 Target 1429470 27, originally Greens/EFA amendment in FEM~ <chr [1]>
> 5 51632 Target 51632 Question No 8 by (H-0376/00):                 <chr [1]>
> 6 2482671 Source 516937 La Comisión propone proporcionar a las Age~ <chr [2]>
> 7 1059628 Target 1059628 (The President cut off the speaker)       <chr [1]>
> 8 1507254 Target 1507254 in writing. - (LT) I welcomed this documen~ <chr [1]>
> 9 2765325 Source 799591 (Aplausos)                                <chr [1]>
> 10 2668536 Source 702802 Las preguntas que, por falta de tiempo,~ <chr [1]>

```

OK, that might not be what you expected. The `str_extract_all()` function returns a list of character vectors. This is because for any given line in `lines` there may be a different number of matches. To maintain the data frame as rectangular, a list is returned for each value of `non_speech`. We could expand the list into a data frame with the `unnest()` function from the `tidyverse` package if our goal were to work with these matches. But that is not our aim. Rather, we want to know if we have multiple matches per line. Note that the information provided for the `non_speech` column by the tibble object tells us that we have some lines with multiple matches, as we can see in line 6 of our small sample. So good thing we checked!

Let's now remove these parliamentary session description annotations from each line in the `lines` column. We turn to `str_remove_all()`, a variant of `str_remove()`, that, as you expect, will remove multiple matches in a single line. We will use the `mutate()` function to overwrite the `lines` column with the modified text. The code is seen in Example 7.4.

Example 7.4.

```
# Remove non-speech fragments
europarl_tbl <-
  europarl_tbl |>
  mutate(lines = str_remove_all(lines, "\\\(.+?\\)"))
```

I recommend spot checking the results of this normalization step by running the code in Example 7.2 again, if nothing appears we've done our job.

When you are content with the results, drop the observations that have no text in the `lines` column given the entire line was non-speech. This can be done with the `is.na()` function and the `filter()` function as seen in Example 7.5.

Example 7.5.

```
# Drop empty lines
europarl_tbl <-
  europarl_tbl |>
  filter(!is.na(lines))
```

Normalization goals will vary from dataset to dataset but the procedures often follow a similar line of attack to those outlined in this section. There are cases, however, in which normalization procedures are more easily accomplished after subsequent transformation steps or need to be post-pended to further the goals of other transformation steps. For example, standardizing abbreviated forms may be more easily accomplished after tokenization when each token is a word. Another example is the case of case conversion. Even if we are not directly interested in the case differences between words, certain generation procedures, Named Entity Recognition

(NER) for example, may use case information to identify the names of people, locations, organizations, *etc.*. In these cases, it may be better to leave the case as is until after the generation step.

7.1.2 Tokenization

Another common transformation process that is particularly relevant for preparing text for analysis is tokenization. Tokenization is the process of segmenting units of language into components relevant for the research question. This includes breaking text in curated datasets into smaller units, such as words, *n*-grams, sentences, *etc.* or combining text into larger units relative to the original text.

The process of tokenization is fundamentally row-wise. By scaling the text units up or down, we change the unit of observation. It is important both for the research and the text processing to operationalize our language units. For example, while it may appear obvious to you what ‘word’ or ‘sentence’ means, a computer, and your reproducible research, needs a definition. This can prove trickier than it seems. For example, in English, we can segment text into words by splitting on whitespace. This works fairly well but there are some cases where this is not ideal. For example, in the case of contractions, such as `don't`, `won't`, `can't`, *etc.* the apostrophe is not a whitespace character. If we want to consider these contractions as separate words, then we need to consider a different tokenization strategy.

💡 Consider this

Consider the following paragraph:

“As the sun dipped below the horizon, the sky was set ablaze with shades of orange-red, illuminating the landscape. It’s a sight Mr. Johnson, a long-time observer, never tired of. On the lakeside, he’d watch with friends, enjoying the ever-changing hues—especially those around 6:30 p.m.—and reflecting on nature’s grand display. Even in the half-light, the water’s glimmer, coupled with the echo of distant laughter, created a timeless scene. The so-called ‘magic hour’ was indeed magical, yet fleeting, like a well-crafted poem; it was the essence of life itself.”

What text conventions would pose issues for word tokenization based on a whitespace criterion?

Furthermore, tokenization strategies can vary between languages. For German words are often compounded together, meaning many ‘words’ will not be captured by the whitespace convention. Whitespace may not even be relevant for word tokenization in logographic writing systems such as Chinese. The take home message is there is no one-size-fits-all tokenization strategy.

❖ Dive deeper

For processing Chinese text, including tokenization, see the `jiebaR` package (Wenfeng and Yanyi 2019) and the `gibasa` package (Kato, Ichinose, and Kudo 2023).

Let's say we continue to work with the Europarl Corpus dataset. We have already removed non-speech annotations from the `lines` variable. Now we want to tokenize the text. We will start by tokenizing the text into words. If we envision what this should look like, we might imagine something like Table 7.3.

Table 7.3: Example of tokenizing the `lines` variable into word tokens.

doc_id	type	line_id	token
1	Target	2	I
1	Target	2	declare
1	Target	2	resumed
1	Target	2	the
1	Target	2	session

Comparing Table 7.3 to the fourth row of the output of Example 7.1, we can see that we want to segment the words in `lines` and then have each segment appear as a separate observation, retaining the relevant metadata variables.

This is a very common strategy in text analysis. So common, in fact, that the `tidytext` package (Robinson and Silge 2023) includes a function, `unnest_tokens()` that tokenizes text in just such a way. Various tokenization types can be specified including ‘characters’, ‘words’, ‘ngrams’, ‘sentences’ among others. We will use the ‘word’ tokenization type to recreate the structure we envisioned in Table 7.3.

In Example 7.6, we see set our output variable to `token` and our input variable to `lines`.

Example 7.6.

```
# Load package
library(tidytext)

# Tokenize the lines into words
europarl_unigrams_tbl <-
  europarl_tbl |>
  unnest_tokens(
    output = token,
    input = lines,
```

```
    token = "words"  
)
```

Let's preview the very same lines we modeled in Table 7.3 to see the results of our tokenization.

```
# Preview  
europarl_unigrams_tbl |>  
  filter(type == "Target", line_id == 2) |>  
  slice_head(n = 10)  
  
> # A tibble: 10 x 4  
>   doc_id type  line_id token  
>   <dbl> <chr>  <dbl> <chr>  
> 1     2 Target    2 i  
> 2     2 Target    2 declare  
> 3     2 Target    2 resumed  
> 4     2 Target    2 the  
> 5     2 Target    2 session  
> 6     2 Target    2 of  
> 7     2 Target    2 the  
> 8     2 Target    2 european  
> 9     2 Target    2 parliament  
> 10    2 Target    2 adjourned
```

The `token` column now contains our word tokens. One thing to note, however, is that text is lowercased by default. If we want to retain the original case, keep the original variable, or change the tokenization strategy, we can update the `to_lower`, `drop`, and `token` parameters, respectively.

💡 Dive deeper

`unnest_tokens()` approaches tokenization from a segmentation point of view. That is, the context separating our tokens is targeted and is removed. In some cases, it may be more feasible to turn the approach around and instead target the tokens to extract. The `str_extract_all()` can be used for this purpose. Note, however, the former approach is often more effective and efficient. The latter requires a regular expression, or set of, which can be tricky to develop for some tokenization tasks.

As we derive datasets to explore, let's also create bigram tokens. We can do this by changing the `token` parameter to `"ngrams"` and specifying the value for `n` with the `n` parameter. I

will assign the result to `europarl_bigrams_tbl` as we will have two-word tokens, as seen in Example 7.7.

Example 7.7.

```
# Tokenize the lines into bigrams
europarl_bigrams_tbl <-
  europarl_tbl |>
  unnest_tokens(
    output = token,
    input = lines,
    token = "ngrams",
    n = 2
  )
# Preview
europarl_bigrams_tbl |>
  filter(type == "Target", line_id == 2) |>
  slice_head(n = 10)

> # A tibble: 10 x 4
>   doc_id type   line_id token
>   <dbl> <chr>   <dbl> <chr>
> 1     2 Target     2 i declare
> 2     2 Target     2 declare resumed
> 3     2 Target     2 resumed the
> 4     2 Target     2 the session
> 5     2 Target     2 session of
> 6     2 Target     2 of the
> 7     2 Target     2 the european
> 8     2 Target     2 european parliament
> 9     2 Target     2 parliament adjourned
> 10    2 Target     2 adjourned on
```

The two-word token sequences for lines appear as observations in the `europarl_bigrams_tbl` dataset.

Dive deeper

The `tidytext` package is one of a number of packages that provide tokenization functions. Some other notable packages include `tokenizers` (Mullen 2022) and `textrecipes` (Hvitfeldt 2023). In fact, the functions from the `tokenizers` package are used under the hood in the `tidytext` package. The `textrecipes` package is part of the `tidymodels` framework

and is designed to work with the `tidymodels` suite of packages. It is particularly useful for integrating tokenization with other preprocessing steps and machine learning models, as we will see in Chapter 9.

The most common tokenization strategy is to segment text into smaller units, often words. However, there are times when we may want text segments to be larger than the existing token unit, effectively collapsing over rows. For example, if we are working with a curated dataset which is tokenized by words, we may want to group the words into sentences. A couple considerations are in order, however. First, we need to be clear about what we mean by ‘sentence’ and how we will group the words into sentences. In some cases key cues for sentence boundaries, such as sentential punctuation have been stripped from the text, making a simple definition of a sentence difficult or impossible to be performed computationally. Second, we also need to be clear how we will handle the metadata variables. In other words, when we collapse over rows, we need to be aware and intentional about how we group these new units of observation.

7.2 Enrichment

Where preparation steps are focused on sanitizing and segmenting the text, enrichment steps are aimed towards augmenting the dataset either through recoding, generating, or integrating variables. These processes can prove invaluable for aligning the dataset with the research question and facilitating the analysis.

As a practical example of these types of transformations, we’ll posit that we are conducting translation research. Specifically, we will set up an investigation into the effect of translation on the syntactic simplification of text. The basic notion is that when translators translate text from one language to another, they subconsciously simplify the text, relative to native texts (Liu and Afzaal 2021).

To address this research question, we will use the ENNTT corpus, introduced in Section 6.3.2. This data contains European Parliament proceedings and the type of text (native, non-native, or translation) from which the text was extracted. There is one curated dataset for each of the text types.

The data dictionary for the curated native dataset appears in Table 7.4.

Table 7.4: Data dictionary for the curated native ENNTT dataset.

variable	name	variable_type	description
session_id	Session ID	categorical	Unique identifier for each session
speaker_id	Speaker ID	categorical	Unique identifier for each speaker
state	State	categorical	The country or region the speaker is from

Table 7.4: Data dictionary for the curated native ENNTT dataset.

variable	name	variable_type	description
session_seq	Session Sequence	ordinal	The order in which the session occurred
text	Text	categorical	The spoken text during the session
type	Type	categorical	The type of speaker. Natives in this dataset.

All three curated datasets have the same variables. The unit of observation for each dataset is the `text` variable.

Before we get started, let's consider what the transformed dataset might look like and what its variables mean. First, we will need to operationalize what we mean by syntactic simplification. There are many measures of syntactic complexity (Szmrecsanyi 2004). For our purposes, we will focus on two measures of syntactic complexity: number of T-units and sentence length (in words). A T-unit is a main clause and all of its subordinate clauses. To calculate the number of T-units, we will need to identify the main clauses and their subordinate clauses. The sentence length is straightforward to calculate after word tokenization.

The next step is to operationalize what we mean by syntactic simplification. For our purposes, let's focus on two: number of T-units and sentence length (in words). Length is straightforward to calculate after word tokenization but a T-unit is a bit more involved. A T-unit is a main clause and all of its subordinate clauses. To calculate the number of T-units, we will need to identify the main clauses and their subordinate clauses.

An idealized transformed dataset dictionary for this investigation should look something like Table 7.5.

Table 7.5: Idealized transformed dataset for the syntactic simplification investigation.

variable	variable_name	variable_type	description
doc_id	Document ID	integer	Unique identifier for each document.
type	Type	character	Type of text (native or translated).
t_units	T-units	integer	Number of T-units in the text.
word_len	Word Length	integer	Number of words in the text.

We will be using the the native and translated datasets for our purposes so let's go ahead and read in these datasets.

```
# Read in curated natives
enntt_natives_tbl <-
```

```
read_csv("data/enntt_natives_curated.csv")

# Read in curated translations
enntt_translations_tbl <-
  read_csv("data/enntt_translations_curated.csv")
```

7.2.1 Generation

The process of generation involves the addition of information to a dataset. This differs from other transformation procedures in that instead of manipulating, classifying, and/ or deriving information based on characteristics explicit in a dataset, generation involves deriving new information based on characteristics implicit in a dataset.

The most common type of operation involved in the generation process is the addition of linguistic annotation. This process can be accomplished manually by a researcher or research team or automatically through the use of pre-trained linguistic resources and/ or software. Ideally the annotation of linguistic information can be conducted automatically. It is important to note, however, that the quality of the annotations is contingent on the quality of the pre-trained resources, their alignment with the language variety and register to be annotated, and the quality of the text to be annotated. To be clear, no annotation method, whether manual or automatic is guaranteed to be perfectly accurate, but we must be aware of the limitations of the annotation method we choose.

To identify the main clauses and their subordinate clauses in our datasets, we will need to derive syntactic annotation information from the ENNTT `text` variable.

As fun as it would be to hand-annotate the ENNTT corpus, we will instead turn to automatic linguistic annotation. Specifically, we will use the `udpipe` package (Wijffels 2023) which provides an interface for annotating text using pre-trained models from the Universal Dependencies¹ (UD) project (Nivre et al. 2020). The UD project is an effort to develop cross-linguistically consistent treebank annotation for a variety of languages.

Our first step, then, is to peruse the available pre-trained models for the languages we are interested in and selected the most register-aligned models. The models, model names, and licensing information are documented in the `udpipe` package and can be accessed by running `?udpipe::udpipe_download_model()` in the R console. For illustrative purposes, the `english` treebank model from the <https://github.com/bnosac/udpipe.models.ud> repository which is released under the CC-BY-SA license². This model is trained on various sources including news, Wikipedia, and web data of various genres.

Let's set the stage by providing an overview of the annotation process.

¹<https://universaldependencies.org/>

²<https://creativecommons.org/licenses/by-sa/4.0/>

1. Load the `udpipe` package.
2. Select the pre-trained model to use and the directory where the model will be stored in your local environment.
3. Prepare the dataset to be annotated (if necessary). This includes ensuring that the dataset has a column of text to be annotated and a grouping column. By default, the names of these columns are expected to be `text` and `doc_id`, respectively. The `text` column needs to be a character vector and the `doc_id` column needs to be a unique index for each text to be annotated.
4. Annotate the dataset. The result returns a data frame.

Steps 3 and 4 are repeated for the `enntt_natives_tbl` and the `enntt_translations_tbl` datasets. For brevity, I will only show the code for the dataset for the natives. Additionally, I will subset the dataset to 10,000 randomly selected lines for both datasets, as in Example 7.8 for the natives. Syntactic annotation is a computationally expensive operation and the natives and translations datasets contain 116,341 and 738,597 observations, respectively.

Example 7.8.

💡 Dive deeper Computational Performance

In your own research computationally expensive cannot be avoided, but it can be managed. One strategy is to work with a subset of the data until your code is working as expected. Once you are confident that your code is working as expected, then you can scale up to the full dataset.

If you are using Quarto, you can use the `cache: true` metadata field in your code blocks to cache the results of computationally expensive code blocks. This will allow you to run your code once and then use the cached results for subsequent runs.

Parallel processing is another strategy for managing computationally expensive code. Some packages, such as `udpipe`, have built-in support for parallel processing. Other packages, such as `tidytext`, do not. In these cases, you can use the `future` package (Bengtsson 2023) to parallelize your code.

With the subsetted `enntt_natives_tbl` object, let's execute steps 1-4, as seen in Example 7.9.

Example 7.9.

```
# Load package
library(udpipe)

# Model and directory
model <- "english"
model_dir <- "../data/"
```

```

# Prepare the dataset to be annotated
enntt_natives_prep_tbl <-
  enntt_natives_tbl |>
  mutate(doc_id = row_number()) |>
  select(doc_id, text)

# Annotate the dataset
enntt_natives_ann_tbl <-
  udpipe(
    x = enntt_natives_prep_tbl,
    object = model,
    model_dir = model_dir
  ) |>
  tibble()

# Preview
glimpse(enntt_natives_ann_tbl)

```

There is quite a bit of information which is returned from `udpipe()`. Note that the input lines have been tokenized by word. Each token includes the `token`, `lemma`, part of speech (`upos` and `xpos`), morphological features (`feats`), and syntactic relationships (`head` `token id` and `dep` `rel`).

The `token_id` keeps track of the token's position in the sentence and the `sentence_id` keeps track of the sentence's position in the original text. Finally, the `doc_id` column and its values correspond to the `doc_id` in the `enntt_natives_tbl` dataset.

The number of variables in the `udpipe()` annotation output is quite overwhelming. However, these attributes come in handy for manipulating, extracting, and plotting information based on lexical and syntactic patterns. See the dependency tree in Figure 7.1 for an example of the syntactic information that can be extracted from the `udpipe()` annotation output.

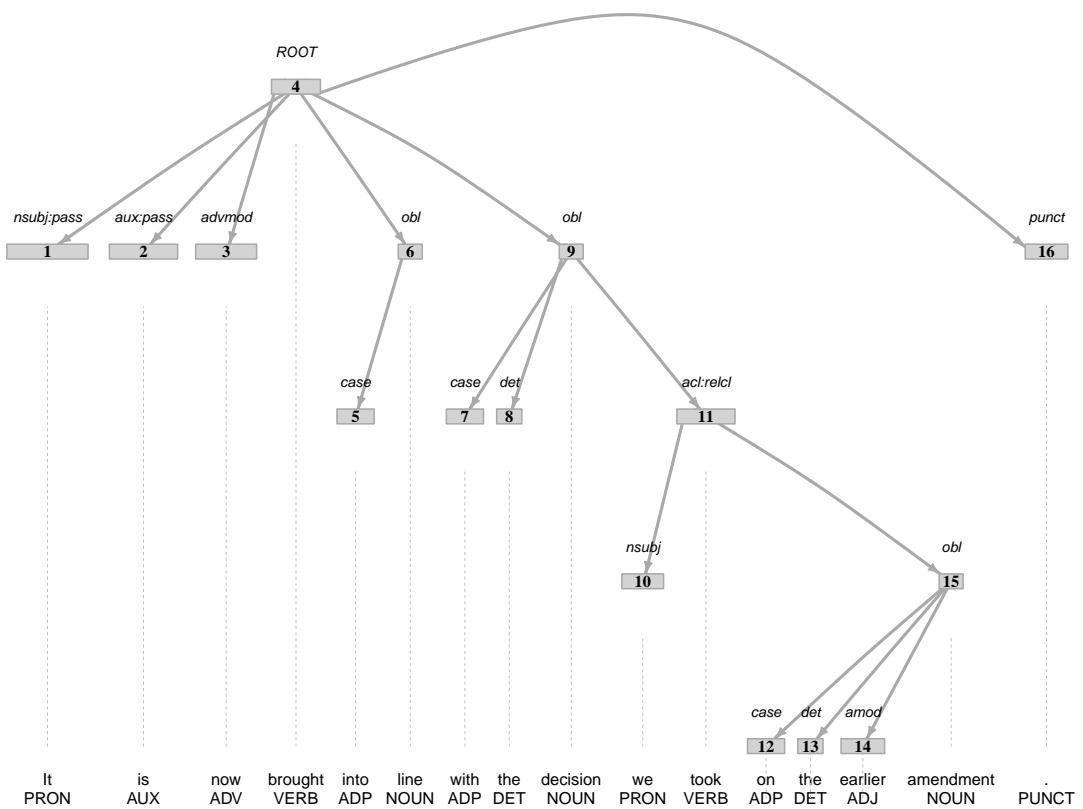


Figure 7.1: Plot of the syntactic tree for a sentence in the ENNTT natives dataset.

➊ Dive deeper

The plot in Figure 7.1 was created using the `rsyntax` package (Welbers and van Atteveldt 2022). In addition to creating dependency tree plots, the `rsyntax` package can be used to extract syntactic patterns from the `udpipe()` annotation output. See the documentation for more information^a.

^a<https://github.com/vanatteveldt/rsyntax>

In Figure 7.1 we see the syntactic tree for a sentence in the ENNTT natives dataset. Each node is labeled with the `token_id` which provides the linear ordering of the sentence. Above the nodes the `dep_relation`, or dependency relationship label is provided. These labels are based on the UD project’s dependency relations³. We can see that the ‘ROOT’ relation is at the top of the tree and corresponds to the verb ‘brought’. ‘ROOT’ relations mark predicates in the sentence. Not seen in the example tree, ‘cop’ relation is a copular, or non-verbal predicate and should be included. These are the key syntactic pattern we will use to identify main clauses for T-units.

7.2.2 Recoding

Recoding processes can be characterized by the creation of structural changes which are derived from values in variables effectively recasting values as new variables to enable more direct access in our analyses.

Specifically, we will need to identify and count the main clauses and their subordinate clauses to create a variable `t_units` from our natives and translations annotations objects. In the UD project’s listings, the relations ‘ccomp’ (clausal complement), ‘xcomp’ (open clausal complement), and ‘acl:relcl’ (relative clause), as seen in Figure 7.1 are subordinate clauses. Furthermore, we will also need to count the number of words in each sentence to create a variable `word_len`.

To calculate T-units and words per sentence we turn to the `dplyr` package. We will use the `group_by()` function to group the dataset by `doc_id` and `sentence_id` and then use the `summarize()` function to calculate the number of T-units and words per sentence, where a T-unit is the combination of the sum of main clauses and sum of subordinate clauses. The code is seen in Example 7.10.

Example 7.10.

```
# Calculate the number of T-units and words per sentence
enntt_natives_syn_comp_tbl <-
  enntt_natives_ann_tbl |>
  group_by(doc_id, sentence_id) |>
  summarize(
    main_clauses = sum(dep_rel %in% c("ROOT", "cop")),
    subord_clauses = sum(dep_rel %in% c("ccomp", "xcomp", "acl:relcl")),
    t_units = main_clauses + subord_clauses,
```

³<https://universaldependencies.org/u/dep/index.html>

```

  word_len = n()
) |>
ungroup()

# Preview
glimpse(enntt_natives_syn_comp_tbl)

```

```

> Rows: 10,199
> Columns: 6
> $ doc_id      <chr> "1", "10", "100", "1000", "10000", "1001", "1002", "100~
> $ sentence_id <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1~
> $ main_clauses <int> 1, 0, 0, 0, 2, 0, 0, 1, 1, 0, 1, 1, 1, 0, 2, 0, 1, 1, 1~
> $ subord_clauses <int> 3, 2, 1, 0, 1, 2, 1, 1, 0, 2, 1, 0, 3, 2, 0, 4, 2, 1, 1~
> $ t_units      <int> 4, 2, 1, 0, 3, 2, 1, 2, 1, 2, 2, 1, 4, 2, 2, 4, 3, 2, 2~
> $ word_len     <int> 21, 25, 27, 15, 40, 43, 29, 23, 13, 30, 33, 9, 68, 35, ~

```

A quick spot check of some sentences calculations `enntt_natives_syn_comp_tbl` dataset against the `enntt_natives_ann_tbl` is good to ensure that the calculation is working as expected. In Figure 7.2 we see a sentence that has a word length of 13 and a T-unit value of 5.

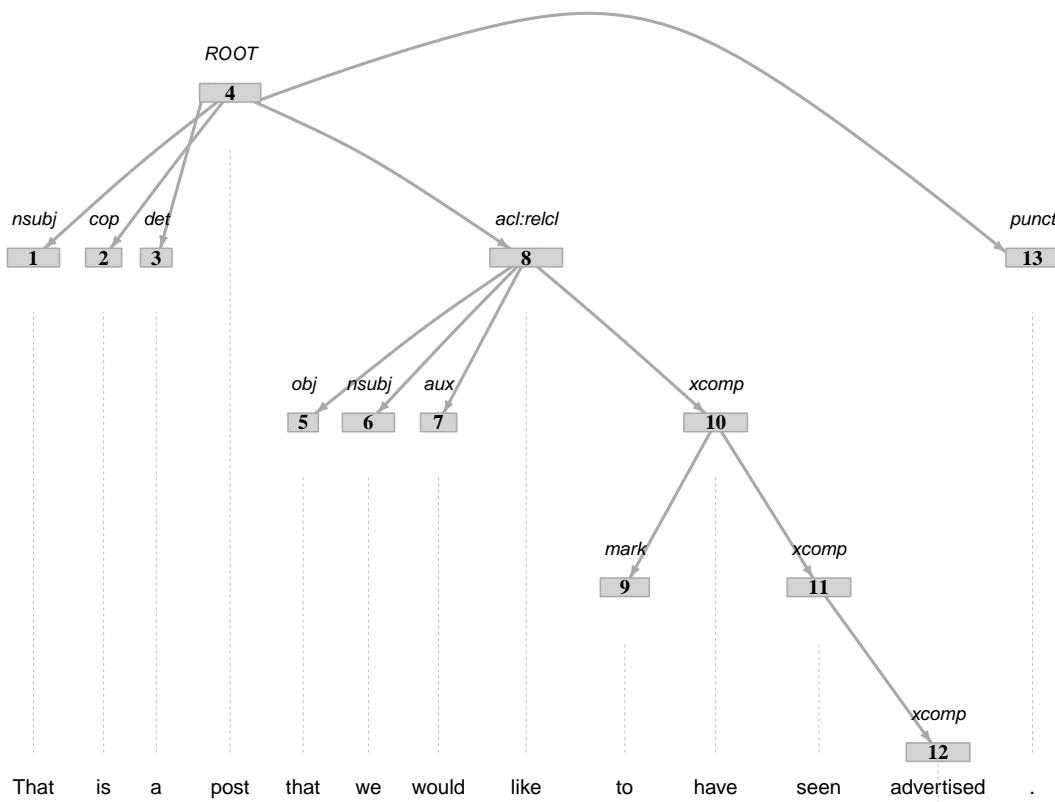


Figure 7.2: Sentence with a word length of 13 and a T-unit value of 5.

Now we can drop the intermediate columns we created to calculate our key syntactic complexity measures using `select()` to indicate those that we do want to keep, as seen in Example 7.11.

💡 Consider this

As confident as we may be in our recoding process, it is always a good idea to perform some data checks to ensure that the recoding process was successful. In the process, we can also gain some insight into the data. Considering the structure in the transformed ENNTT Corpus dataset, what are some data checks we might want to perform? What are some insights we might gain from these data checks?

Example 7.11.

```
# Select columns
enntt_natives_syn_comp_tbl <-
  enntt_natives_syn_comp_tbl |>
  select(doc_id, sentence_id, t_units, word_len)
```

Now we can repeat the process for the ENNTT translated dataset. I will assign the result to `enntt_translations_syn_comp_tbl`. The next step is to join the `sentences` from the annotated data frames into our datasets so that we have the information we set out to generate for both datasets. Then we will combine the native and translations datasets into a single dataset. These steps are part of the transformation process and will be covered in the next section.

7.2.3 Integration

One final class of transformations that can be applied to curated datasets to enhance their informativeness for a research project is the process of integrating two or more datasets. There are two primary types of integrations: joins and concatenation. **Joins** can be row- or column-wise operations that combine datasets based on a common attribute or set of attributes. **Concatenation** is exclusively a row-wise operation that combines datasets that share the same attributes.

Of the two types, joins are the most powerful and sometimes more difficult to understand. When two datasets are joined at least one common variable must be shared between the two datasets. The common variable(s) are referred to as **keys**. The keys are used to match observations in one dataset with observations in another dataset by serving as an index.

There are a number of join types. The most common are left, full, semi, and anti. The type of join determines which observations are retained in the resulting dataset. Let's see this in practice. First, let's create two datasets to join with a common variable `key`, as seen in Example 7.12.

Example 7.12.

```

a_tbl <-
  tibble(
    key = c(1, 2, 3, 5, 8),
    a = letters[1:5]
  )

a_tbl
b_tbl <-
  tibble(
    key = c(1, 2, 4, 6, 8),
    b = letters[6:10]
  )

b_tbl

```

> # A tibble: 5 x 2					> # A tibble: 5 x 2
> key a					> key b
> <dbl> <chr>					> <dbl> <chr>
> 1 1 a					> 1 1 f
> 2 2 b					> 2 2 g
> 3 3 c					> 3 4 h
> 4 5 d					> 4 6 i
> 5 8 e					> 5 8 j

The `a_tbl` and the `b_tbl` datasets share the `key` variable, but the values in the `key` variable are not identical. The two datasets share values 1, 2, and 8. The `a_tbl` dataset has values 3 and 5 in the `key` variable and the `b_tbl` dataset has values 4 and 6 in the `key` variable.

If we apply a left join to the `a_tbl` and `b_tbl` datasets, the result will be a dataset that retains all of the observations in the `a_tbl` dataset and only those observations in the `b_tbl` dataset that have a match in the `a_tbl` dataset. The result is seen in Example 7.13.

Example 7.13.

```
left_join(x = a_tbl, y = b_tbl, by = "key")
```

> # A tibble: 5 x 3				
> key a b				
> <dbl> <chr> <chr>				
> 1 1 a f				
> 2 2 b g				

```
> 3      3 c      <NA>
> 4      5 d      <NA>
> 5      8 e      j
```

Now, if the key variable has the same name, R will recognize and assume that this is the variable to join on and we don't need the `by =` argument, but if there are multiple potential key variables, we use `by =` to specify which one to use.

A full join retains all observations in both datasets, as seen in Example 7.14.

Example 7.14.

```
full_join(x = a_tbl, y = b_tbl)
```

```
> # A tibble: 7 x 3
>   key a     b
>   <dbl> <chr> <chr>
> 1     1 a     f
> 2     2 b     g
> 3     3 c     <NA>
> 4     5 d     <NA>
> 5     8 e     j
> 6     4 <NA>  h
> 7     6 <NA>  i
```

Left and full joins maintain or increase the number of observations. On the other hand, semi and anti joins aim to decrease the number of observations. A semi join retains only those observations in the left dataset that have a match in the right dataset, as seen in Example 7.15.

Example 7.15.

```
semi_join(x = a_tbl, y = b_tbl)
```

```
> # A tibble: 3 x 2
>   key a
>   <dbl> <chr>
> 1     1 a
> 2     2 b
> 3     8 e
```

And an anti join retains only those observations in the left dataset that do not have a match in the right dataset, as seen in Example 7.16.

Example 7.16.

```
anti_join(x = a_tbl, y = b_tbl)

> # A tibble: 2 × 2
>   key a
>   <dbl> <chr>
> 1     3 c
> 2     5 d
```

Of these join types, the left join and the anti join are some of the most common to encounter in research projects.

💡 Consider this

In addition to datasets that are part of an acquired resource or derived from a corpus resource, there are also a number of datasets that are included in R packages that are particularly relevant for text analysis. For example, the `tidytext` package includes `sentiments` and `stop_words` datasets. The `lexicon` package (Rinker 2019) includes large number of datasets that include sentiment lexicons, stopword lists, contractions, and more.

With this in mind, let's return to our syntactic simplification investigation. Recall that we started with two curated ENNTT datasets: the natives and translations. We manipulated these datasets subsetting them to 10,000 randomly selected lines, prepped them for annotation by adding a `doc_id` column and dropping all columns except `text`, and then annotated them using the `udpipe` package. We then calculated the number of T-units and words per sentence and created the variables `t_units` and `word_len` for each.

These steps produced two datasets for both the natives and for the translations. The first dataset for each is the annotated data frame. The second is the data frame with the syntactic complexity measures we calculated. The annotated data frames are named `enntt_natives_ann_tbl` and `enntt_translations_ann_tbl`. The data frames with the syntactic complexity measures are named `enntt_natives_syn_comp_tbl` and `enntt_translations_syn_comp_tbl`.

In the end, we want a dataset that looks something like Table 7.6.

Table 7.6: Idealized integrated dataset for the syntactic simplification investigation.

doc_id	type	t_units	word_len	text
1	natives	1	5	I am happy right now.
2	translation	3	11	I think that John believes that Mary is a good person.

To create this unified dataset, we will need to apply joins and concatenation. First, we will join the prepped datasets with the annotated datasets. Then, we will concatenate the two resulting datasets.

Let's start by joining the annotated datasets (`enntt_natives_ann_tbl` and `enntt_translations_ann_tbl`) with the datasets with the syntactic complexity calculations (`enntt_natives_syn_comp_tbl` and `enntt_translations_syn_comp_tbl`). In these joins, we can see that the prepped and calculated datasets share a couple variables, `doc_id` and `sentence_id`, in Example 7.17.

Example 7.17.

```
# Preview datasets to join
enntt_natives_ann_tbl |>
  slice_head(n = 3)

> # A tibble: 3 x 17
>   doc_id paragraph_id sentence_id sentence     start   end term_id token_id token
>   <chr>      <int>      <int> <chr>     <int> <int> <int> <chr>   <chr>
> 1 1           1          1 It is extr~     1     2     1 1      It
> 2 1           1          1 It is extr~     4     5     2 2      is
> 3 1           1          1 It is extr~     7    15     3 3      extr~
> # i 8 more variables: lemma <chr>, upos <chr>, xpos <chr>, feats <chr>,
> #   head_token_id <chr>, dep_rel <chr>, deps <chr>, misc <chr>

enntt_natives_syn_comp_tbl |>
  slice_head(n = 3)

> # A tibble: 3 x 4
>   doc_id sentence_id t_units word_len
>   <chr>      <int>    <int>    <int>
> 1 1           1        4      21
> 2 10          1        2      25
> 3 100         1        1      27
```

The `doc_id` and `sentence_id` variables are both keys that we will use to join the datasets. The reason being that if we only use one of the two we will not align the two datasets at the sentence level. Only the combination of `doc_id` and `sentence_id` isolates the sentences for which we have syntactic complexity measures. Beyond having common variables (or variables in our case), we must also ensure that join key variables are of the same vector type in both data frames and that we are aware of any differences in the values. From the output in Example 7.17, we can see that the `doc_id` and `sentence_id` variables aligned in terms of vector type; `doc_id` is character and `sentence_id` is integer in both data frames. If they happened not to be, there types would need to be adjusted.

Now, we need to check for differences in the values. We can do this by using the `setequal()` function. This function returns `TRUE` if the two vectors are equal and `FALSE` if they are not. If the two vectors are not equal, the function will return the values that are in one vector but not the other. So if one has `10001` and the other doesn't we will get `FALSE`. Let's see this in practice, as seen in Example 7.18.

Example 7.18.

```
# Check for differences in the values
setequal(
  enntt_natives_ann_tbl$doc_id,
  enntt_natives_syn_comp_tbl$doc_id
)
```

```
> [1] TRUE
```

```
setequal(
  enntt_natives_ann_tbl$sentence_id,
  enntt_natives_syn_comp_tbl$sentence_id
)
```

```
> [1] TRUE
```

So the values are the same. The final check is to see if the vectors are of the same length. We know the values are the same, but we don't know if the values are repeated. We do this by simply comparing the length of the vectors, as seen in Example 7.19.

Example 7.19.

```
# Check for differences in the length
length(enntt_natives_ann_tbl$doc_id) ==
  length(enntt_natives_syn_comp_tbl$doc_id)
```

```
> [1] FALSE
```

```
length(enntt_natives_ann_tbl$sentence_id) ==
  length(enntt_natives_syn_comp_tbl$sentence_id)
```

```
> [1] FALSE
```

So they are not the same length. Using the `nrow()` function, I can see that the annotated dataset has 264,124 observations and the calculated dataset has 10,199 observations. The annotation data frames will have many more observations due to the fact that the unit of observations is word tokens. The recoded syntactic complexity data frames' unit of observation is the sentence.

To appreciate the difference in the number of observations, let's look at the first 10 observations of the natives annotated frame for just the columns of interest, as seen in Example 7.20.

Example 7.20.

```
# Preview the annotated dataset
enntt_natives_ann_tbl |>
  select(doc_id, sentence_id, sentence, token) |>
  slice_head(n = 10)

> # A tibble: 10 x 4
>   doc_id sentence_id sentence                                              token
>   <chr>     <int> <chr>
> 1 1          1 It is extremely important that action is taken to e~ It
> 2 1          1 It is extremely important that action is taken to e~ is
> 3 1          1 It is extremely important that action is taken to e~ extr~
> 4 1          1 It is extremely important that action is taken to e~ impo~
> 5 1          1 It is extremely important that action is taken to e~ that
> 6 1          1 It is extremely important that action is taken to e~ acti~
> 7 1          1 It is extremely important that action is taken to e~ is
> 8 1          1 It is extremely important that action is taken to e~ taken
> 9 1          1 It is extremely important that action is taken to e~ to
> 10 1         1 It is extremely important that action is taken to e~ ensu~
```

The annotated data frames have a lot of redundancy in for the join variables and the `sentence` variable that we want to add to the calculated data frames. We can reduce the redundancy by using the `distinct()` function from the `dplyr` package. In this case we want all observations where `doc_id`, `sentence_id` and `sentence` are distinct. We then select these variables with `distinct()`, as seen in Example 7.21.

Example 7.21.

```
# Reduce annotated data frames to unique sentences
enntt_natives_ann_distinct <-
  enntt_natives_ann_tbl |>
  distinct(doc_id, sentence_id, sentence)

enntt_translations_ann_distinct <-
  enntt_translations_ann_tbl |>
  distinct(doc_id, sentence_id, sentence)
```

We now have two datasets that are ready to be joined with the recoded datasets. The next step is to join the two. We will employ a left join where the syntactic complexity data frames are on the left and the join variables will be both the `doc_id` and `sentence_id` variables. The code is seen in Example 7.22.

Example 7.22.

```
# Join the native datasets
enntt_natives_transformed_tbl <-
  left_join(
    x = enntt_natives_syn_comp_tbl,
    y = enntt_natives_ann_distinct,
    by = c("doc_id", "sentence_id")
  )

# Preview
glimpse(enntt_natives_transformed_tbl)
```

```
> Rows: 10,199
> Columns: 5
> $ doc_id      <chr> "1", "10", "100", "1000", "10000", "1001", "1002", "1003", ~
> $ sentence_id <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ~
> $ t_units     <int> 4, 2, 1, 0, 3, 2, 1, 2, 2, 1, 4, 2, 2, 4, 3, 2, 2, 1 ~
> $ word_len    <int> 21, 25, 27, 15, 40, 43, 29, 23, 13, 30, 33, 9, 68, 35, 16, ~
```

```
> $ sentence      <chr> "It is extremely important that action is taken to ensure ~
# Join the translations datasets
enntt_translations_transformed_tbl <-
  left_join(
    x = enntt_translations_syn_comp_tbl,
    y = enntt_translations_ann_distinct,
    by = c("doc_id", "sentence_id")
  )
# Preview
glimpse(enntt_translations_transformed_tbl)

> Rows: 10,392
> Columns: 5
> $ doc_id      <chr> "1", "10", "100", "1000", "10000", "1001", "1002", "1003", ~
> $ sentence_id <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ~
> $ t_units      <int> 0, 2, 0, 1, 3, 0, 3, 2, 3, 3, 2, 0, 1, 0, 3, 1, 0, 1, 2, 2, ~
> $ word_len     <int> 24, 31, 5, 39, 44, 26, 67, 23, 46, 28, 24, 68, 19, 18, 36, ~
> $ sentence     <chr> "To my great surprise , on leaving the sitting , I found t~
```

The two data frames now have the same columns and we are closer to our final dataset. The next step is to move toward concatenating the two datasets. Before we do that, we need to do some preparation. First, and most important, we need to add a `type` column to each dataset. This column will indicate whether the sentence is a native or a translation. The second is that our `doc_id` does not serve as a unique identifier for the sentences. Only in combination with `sentence_id` can we uniquely identify a sentence.

So our plan will be to add a `type` column to each dataset specifying the values for all the observations in the respective dataset. Then we will concatenate the two datasets. Note, if we combine them before, distinguishing the type will be more difficult. After we concatenate the two datasets, we will add a `doc_id` column that will serve as a unique identifier for the sentences and drop the `sentence_id` column. OK, that's the plan. Let's execute it in Example 7.23.

Example 7.23.

```
# Add a type column
enntt_natives_transformed_tbl <-
  enntt_natives_transformed_tbl |>
  mutate(type = "natives")
```

```

enntt_translations_transformed_tbl <-
  enntt_translations_transformed_tbl |>
  mutate(type = "translations")

# Concatenate the datasets
enntt_transformed_tbl <-
  bind_rows(
    enntt_natives_transformed_tbl,
    enntt_translations_transformed_tbl
  )

# Overwrite the doc_id column with a unique identifier
enntt_transformed_tbl <-
  enntt_transformed_tbl |>
  mutate(doc_id = row_number()) |>
  select(doc_id, type, t_units, word_len, text = sentence)

# Preview
glimpse(enntt_transformed_tbl)

```

```

> Rows: 20,591
> Columns: 5
> $ doc_id  <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18~
> $ type     <chr> "natives", "natives", "natives", "natives", "nativ~
> $ t_units  <int> 4, 2, 1, 0, 3, 2, 1, 2, 1, 2, 2, 1, 4, 2, 2, 4, 3, 2, 2, 1, 1~
> $ word_len <int> 21, 25, 27, 15, 40, 43, 29, 23, 13, 30, 33, 9, 68, 35, 16, 53~
> $ text     <chr> "It is extremely important that action is taken to ensure tha~

```

The output of Example 7.23 now looks like Table 7.6. We have a dataset that has the syntactic complexity measures for both the natives and the translations. We can now write this dataset to disk and document it in the data dictionary.

Activities

In the following activities, you will review the concept of transforming data to prepare it for analysis and working to implement these steps with R. This includes preparation and enrichment of curated datasets using normalization, tokenization, recoding, generation, and/or integration strategies.

_recipe

What: Transforming and documenting datasets^a

How: Read Recipe 7, complete comprehension check, and prepare for Lab 7.

Why: To work with to primary types of transformations, tokenization and joins. Tokenization is the process of recasting textual units as smaller textual units. The process of joining datasets aims to incorporate other datasets to augment or filter the dataset of interest.

^a<https://qtalr.github.io/qtalrkit/articles/recipe-7.html>

Lab

What: Dataset alchemy^a

How: Fork, clone, and complete the steps in Lab 7.

Why: To gain experience working with coding strategies for transforming datasets using tidyverse functions and regular expressions, practice reading/ writing data from/ to disk, and implement organizational strategies for organizing and documenting a dataset in reproducible fashion.

^a<https://github.com/qtalr/lab-07>

Summary

In this chapter we covered the process of transforming datasets. The goal is to manipulate the curated dataset to make it align better for analysis. We covered various types of transformation procedures from text normalization to data frame integrations. In any given research project some or all of these steps will be employed –but not necessarily in the order presented in this chapter. It is not uncommon to mix procedures as well. The etiology of the transformation is as unique as the data that you are working with.

Since you are applying techniques that have a significant factor on the shape and contents of your dataset(s) it is important to perform data checks to ensure that the transformations are working as expected. You may not catch everything, and some things may not be caught until later in the analysis process, but it is important to do as much as you can as early as you can.

In line with the reproducible research principles, it is important to write the transformed dataset to disk and to document it in the data dictionary. This is especially important if you are working with multiple datasets. Good naming conventions also come into play. Choosing descriptive names is so easily overlooked by your present self but so welcomed by your future self.

Part IV

Analysis

In this section we turn to the analysis of datasets, the evaluation of results, and the interpretation of the findings. We will outline the three main types of statistical analyses: Exploratory Data Analysis (EDA), Predictive Data Analysis (PDA), and Inferential Data Analysis (IDA). Each of these analysis types have distinct, non-overlapping aims and therefore should be determined from the outset of the research project and included as part of the research blueprint. The aim of this section is to establish a clearer picture of the goals, methods, and value of each of these approaches.

8 Explore

The data speaks for itself, but only if we are willing to listen.

— Nate Silver

▀ Outcomes

- Identify when an exploratory data analysis approach is the best fit for a given research project.
- Describe the fundamental methods of descriptive analysis and unsupervised learning, recognizing their strengths in revealing patterns and summarizing data.
- Interpret the basic insights gained from data summarization and pattern recognition, considering how these insights could guide further questions or research.

In this chapter, we examine a wide range of strategies for deriving insight from data in cases where the researcher does not start with a preconceived hypothesis or prediction, but rather the researcher aims to uncover patterns and associations from data allowing the data to guide the trajectory of the analysis. The chapter outlines two main branches of exploratory data analysis: descriptive analysis which statistically and/ or visually summarizes a dataset and unsupervised learning which is a machine learning approach that does not assume any particular relationship between variables in a dataset. Either through descriptive or unsupervised learning methods, exploratory data analysis employs quantitative methods to summarize, reduce, and sort complex datasets and statistically and visually interrogate a dataset in order to provide the researcher novel perspective to be qualitatively assessed.

➤ Lessons

What: Advanced objects^a

How: In the R Console pane load `swirl`, run `swirl()`, and follow prompts to select the lesson.

Why: To learn about advanced objects in R, including lists and matrices, and create, inspect, access, and manipulate these objects.

^a<https://github.com/qtalr/lessons>

8.1 Orientation

The aim of this section is to provide an overview of exploratory data analysis (EDA). We will delve into various descriptive methods, such as frequency analysis and co-occurrence analysis, which are fundamental tools in linguistic research. However, our exploration won't stop there. We will also integrate modern exploratory methods from unsupervised learning approaches, including clustering, dimensionality reduction, and vector space modeling. This may sound overwhelming, but I will strive to keep explanations clear and concise, ensuring their practicality and relevance to your linguistic inquiries is apparent. To this end, we will provide real-world examples to exemplify the applicability of these methodologies.

8.1.1 Goals and approach

As discussed in Section 3.2.1 and Section 4.3.1, the goal of exploratory data analysis is to discover, describe, and posit new hypotheses. This analysis approach is best-suited for research where the literature on a research question is limited, or where the researcher is interested in exploring a new research question.

Since the researcher does not start with a preconceived hypothesis, the researcher is not able to test a hypothesis and generalize to a population, but rather the researcher is able to describe the data and provide a new perspective to be qualitatively assessed. This is achieved through an iterative and inductive process of data exploration, where the researcher uses quantitative methods to summarize, reduce, and sort complex datasets and statistically and visually interrogate a dataset letting the data guide the analysis.

To reign in the analysis, however, it is important to have a research question to guide the analysis. The research question will often be broad and exploratory in nature, but it will provide a framework for the analysis including the unit of analysis and sometimes the units of observation. Yet the units of observation can be modified as needed to address the research question. Furthermore, the methods applied to the data can evolve as the research unfolds. The researcher may start with a descriptive analysis and then move to an unsupervised learning approach, or vice versa. The researcher may also pivot the approach to explore new questions and new variables.

With a research question and relevant data in hand, we can look to conduct the analysis. The general workflow for exploratory data analysis is shown in Table 8.1.

Table 8.1: Workflow for exploratory data analysis

Step	Name	Description
1	Identify	Consider the research question and identify variables of potential interest to provide insight into our question.

Step	Name	Description
2	Inspect	Check for missing data, outliers, <i>etc.</i> and check data distributions and transform if necessary.
3	Interrogate	Submit the selected variables to descriptive (frequency, keyword, co-occurrence analysis, <i>etc.</i>) or unsupervised learning (clustering, dimensionality reduction, vector spacing modeling, <i>etc.</i>) methods to provide quantitative measures to evaluate.
4	Interpret	Evaluate the results and determine if they are valid and meaningful to respond to the research question.
5	Iterate (Optional)	Repeat steps 1-4 as new questions emerge from your interpretation.

Let's now demonstrate the workflow in practice.

8.2 Analysis

To frame our discussion of exploratory data analysis, let's tackle a task. The task will be to identify relevant materials for an English Language Learner (ELL) textbook. This will involve multiple research questions and allow us to illustrate some very fundamental concepts that emerge across text analysis research in both descriptive and unsupervised learning approaches.

Since our task is geared towards English language use, we will want a data source that is representative of English language use. For this, we will use the Manually Annotated Sub-Corpus (MASC) of the American National Corpus (Ide et al. 2008).

The data dictionary for the dataset we will use as our point of departure is shown in Table 8.2.

Table 8.2: Data dictionary for the MASC dataset.

variable	name	variable_type	description
doc_id	Document ID	numeric	Unique identifier for each document
modality	Modality	categorical	The form in which the document is presented (written or spoken)
genre	Genre	categorical	The category or type of the document
term_num	Term Number	numeric	Index number term per document
term	Term	categorical	Individual word forms in the document
lemma	Lemma	categorical	Base or dictionary form of the term

Table 8.2: Data dictionary for the MASC dataset.

variable	name	variable_type	description
pos	Part of Speech	categorical	Grammatical category of the term (modified PENN Treebank tagset)

First, I'll read in and preview the dataset in Example 8.1.

Example 8.1.

```
# Read the dataset
masc_tbl <-
  read_csv("../data/masc/masc_transformed.csv")

# Preview the MASC dataset
masc_tbl |>
  slice_head(n = 5)

> # A tibble: 5 x 7
>   doc_id modality genre  term_num term      lemma      pos
>   <dbl> <chr>    <chr>    <dbl> <chr>    <chr>    <chr>
> 1     1 Written  Letters      0 December  december  NNP
> 2     1 Written  Letters      1 1998     1998     CD
> 3     1 Written  Letters      2 Your      your     PRP$
> 4     1 Written  Letters      3 contribution contribution NN
> 5     1 Written  Letters      4 to       to      T0
```

From the output in Example 8.1, we get some sense of the structure of the dataset. However, we also need to perform diagnostic and descriptive procedures. This will include checking for missing data and anomalies and assessing central tendency, dispersion, and/ or distributions of the variables. This may include using `skimr`, `dplyr`, `stringr`, `ggplot2`, *etc.* to identify the most relevant variables for our task and to identify any potential issues with the dataset.

After a descriptive and diagnostic assessment of the dataset, I identified and addressed missing data and anomalies (including many non-words). I also recoded the `doc_id` variable to a character variable. The dataset now has 486,368 observations, a reduction from the original 591,036 observations. There are 392 documents, 2 modalities, 18 genres, almost 38k unique terms (which are words), almost 26k lemmas (word base forms), and 34 distinct part of speech tags.

8.2.1 Descriptive analysis

Descriptive analysis includes common techniques such as frequency analysis to determine the most frequent words or phrases, dispersion analysis to see how terms are distributed throughout a document or corpus, keyword analysis to identify distinctive terms, and/ or co-occurrence analysis to see what terms tend to appear together.

Using the MASC dataset, we will entertain questions such as:

- What are the most common terms a beginning ELL should learn?
- Are there term differences between spoken and written discourses that should be emphasized?
- What are the most common verb particle constructions?

Along the way, we will introduce touch on frequency, dispersion, and co-occurrence measures. In addition, we will apply various descriptive analysis techniques and visualizations to explore the dataset and identify new questions and new variables of interest.

8.2.1.1 Frequency analysis

At its core, frequency analysis is a descriptive method that counts the number of times a linguistic unit occurs in a dataset. The results of frequency analysis can be used to describe the dataset and to identify terms that are linguistically distinctive or distinctive to a particular group or sub-group in the dataset.

Raw frequency

Let's consider what the most common words in the MASC dataset are as a starting point to making inroads on our task by identifying relevant vocabulary for an ELL textbook.

In the `masc_tbl` data frame we have the linguistic unit `term` which corresponds to the word-level annotation of the MASC. The `lemma` corresponds to the base form of each term, for words with inflectional morphology, the lemma is the word sans the inflection (*e.g.* is - be, are - be). For other words, the `term` and the `lemma` will be the same (*e.g.* the - the, in - in). These two variables pose a choice point for us: do we consider words to be the actual forms or the base forms? There is an argument to be made for both. In this case, I will operationalize our linguistic unit as the `lemma` variable, as this will allow us to group words with distinct inflectional morphology together.

To perform a basic word frequency analysis, we can apply `summarize()` in combination with `n()` or the convenient `count()` function from the `dplyr` package. Our sorted lemma counts appear in Example 8.2.

Example 8.2.

```
# Lemma count, sorted in descending order
masc_tbl |>
  count(lemma, sort = TRUE)

> # A tibble: 25,923 x 2
>   lemma      n
>   <chr> <int>
> 1 the     26137
> 2 be      19466
> 3 to      13548
> 4 and     12528
> 5 of      12005
> 6 a       10461
> 7 in      8374
> 8 i       7783
> 9 that    7082
> 10 you    5276
> # i 25,913 more rows
```

The output of this frequency tabulation in Example 8.2 is a data frame with two columns: `lemma` and `n`.

At this point, it is important to define the vocabulary for concepts that are fundamental to working with text. First, a **term** is a defined linguistic unit extracted from a corpus. In our dataset, the terms are words, such as ‘the’, ‘houses’, ‘are’. A lemma is an annotated recoding of words which represent the uninflected base form of a word. In either case, the term or lemma is an instance of a linguistic unit. The individual instances of a linguistic unit are called **tokens**. When we count the number of times a term or lemma occurs in a dataset, we are counting the number of tokens (`n`), such as in Example 8.2. Now, the list of unique terms is a list of **types** (`lemma`). By definition, then, there will always be at least as many tokens as types, but more often than not (many) more tokens than types.

As we discussed in Section 3.1.3, the frequency of linguistic units in a corpus tends to be highly right-skewed distribution, approximating the Zipf distribution. If we calculate the cumulative frequency of the lemmas in the `masc_tbl` data frame, we can see that the top 10 types account for around 25% of the lemmas used in the entire corpus –by 100 types that increases to near 50% and 1,000 around 75%, as seen in Example 8.3.

Example 8.3.

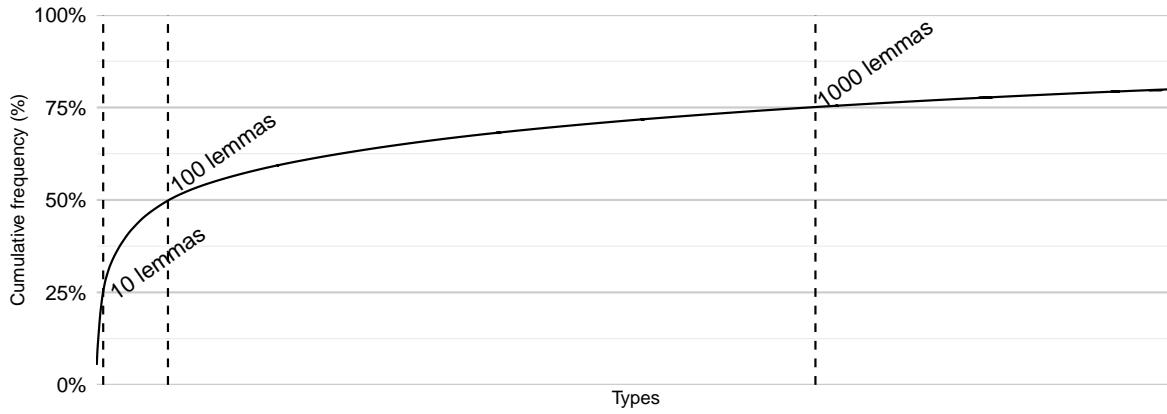


Figure 8.1: Cumulative frequency of lemmas in the MASC dataset

If we look at the types that appear within the first 50 most frequent, you can likely also appreciate another thing about language use. Let's list the top 50 types in Example 8.4.

Example 8.4.

```
# Top 50 types
lemma_cumul_freq |>
  slice_head(n = 50) |>
  pull(lemma) |>
  matrix(ncol = 10) |>
  kable(col.names = NULL)
```

Table 8.3: Top 50 lemma types in the MASC dataset.

the	a	have	with	at	will	your	his	all	know
be	in	it	we	from	my	an	if	there	get
to	i	for	as	he	or	say	's	me	make
and	that	on	this	but	n't	what	can	would	out
of	you	do	not	by	they	so	go	about	up

For the most part, the most frequent words are not content words, but rather function words (*e.g.* determiners, prepositions, pronouns, auxiliary verbs). Function words include a closed class of relatively few words that are used to express grammatical relationships between content words. It then is no surprise that they are the comprise many of the most frequent words in a corpus.

Another key observation is that among the most frequency content words (*e.g.* nouns, verbs, adjectives, adverbs) are words that are quite semantically generic –that is, they are words that are used in a wide range of contexts and take a wide range of meanings.

Take for example the adjective ‘good’. It can be used to describe a wide range of nouns, such as ‘good food’, ‘good people’, ‘good times’, *etc.* A sometimes near-synonym of ‘good’, for example ‘good student’, is the word ‘studious’. Yet, ‘studious’ is not as frequent as ‘good’ as it is used to describe a narrower range of nouns, such as ‘studious student’, ‘studious scholar’, ‘studious researcher’, *etc.* In this way, ‘studious’ is more semantically specific than ‘good’.

💡 Consider this

Based on what you now know about the expected distribution of words in a corpus, what if your were asked to predict what the most frequency English word used is in each U.S. State? What would you predict? How confident would you be in your prediction? What if you were asked to predict what the most frequency word used is in the language of a given country? What would you want to know before making your prediction?

So common across corpus samples, in some analyses these usual suspects of the most common words are considered irrelevant and are filtered out. In our ELL materials task, however, we might exclude them for this simple fact that it will be a given that we will teach these words given their grammatical importance. If we want to focus on the most common content words, we can filter out the function words.

One approach to filtering out these words is to use a pre-determined list of **stopwords**. The `tidytext` package includes a data frame `stop_words` of stopword lexicons for English. We can select a lexicon from `stop_words` and use `anti_join()` to filter out the words that appear in the `word` variable from the `lemma` variable in the `masc_tbl` data frame.

Eliminating words in this fashion, however, may not always be the best approach. Available lists of stopwords vary in their contents and are determined by other researchers for other potential uses. We may instead opt to create our own stopword list that is tailored to the task, or we may opt to use a statistical approach based on their distribution in the dataset using frequency and/ or dispersion measures.

For our case, however, we have another strategy to apply. Since our task is to identify relevant vocabulary, beyond the fundamental function words in English, we can use the part of speech tags to reduce our dataset to just the content words, that is nouns, verbs, adjectives, and adverbs. We need to consult the Penn Tagset again, to ensure we are selecting the correct tags. I will assign this data frame to `masc_content_tbl` to keep it separate from our main data frame `masc_tbl`, seen in Example 8.5.

Example 8.5.

```

# Penn Tagset for content words
# Nouns: NN, NNS,
# Verbs: VB, VBD, VBG, VBN, VBP, VBZ
# Adjectives: JJ, JJR, JJS
# Adverbs: RB, RBR, RBS

content_pos <- c("NN", "NNS", "VB", "VBD", "VBG", "VBN", "VBP", "VBZ", "JJ",
  "JJR", "JJS", "RB", "RBR", "RBS")

# Select content words
masc_content_tbl <-
  masc_tbl |>
  filter(pos %in% content_pos)

# Preview top 50
masc_content_tbl |>
  count(lemma, sort = TRUE) |>
  slice_head(n = 50) |>
  pull(lemma) |>
  matrix(ncol = 10) |>
  kable(col.names = NULL)

```

Table 8.4: Frequency of tokens in the MASC dataset after filtering out lemmas with part of speech tags that are not content words

be	say	think	other	work	look	also	new	t	man
have	go	more	see	year	then	need	find	first	ask
do	know	just	people	come	right	way	give	help	very
not	get	time	take	use	only	back	thing	day	much
n't	make	so	now	well	want	here	tell	many	even

The resulting list in Table 8.4 paints a different picture of the most frequent words in the dataset. The most frequent words are now content words, and included in most frequent words are more semantically specific words. We now have reduced the number of observations by 50% focusing on the content words. We are getting closer to identifying the vocabulary that we want to include in our ELL materials, but we will need some more tools to help us identify the most relevant vocabulary.

Dispersion

Dispersion is a measure of how evenly distributed a linguistic unit is across a dataset. This is a key concept in text analysis, as important as frequency. It is important to recognize that frequency and dispersion are measures of different characteristics. We can have two words that occur with the same frequency, but one word may be more evenly distributed across a dataset than the other. Depending on the researcher's aims, this may be an important distinction to make. For our task, it is likely the case that we want to capture words that are well-dispersed across the dataset as words that have a high frequency and a low dispersion tend to be connected to a particular context, whether that be a particular genre, a particular speaker, a particular topic, *etc.* In other research, aim may be the reverse; to identify words that are highly frequent and highly concentrated in a particular context to identify words that are distinctive to that context.

There are a variety of measures that can be used to estimate the distribution of types across a corpus. Let's focus on three measures: document frequency (df), inverse document frequency (idf), and Gries' Deviation of Proportions (dp).

The most basic measure is **document frequency** (df). This is the number of documents in which a type appears at least once. For example, if a type appears in 10 documents, then the document frequency is 10. This is a very basic measure, but it is a good starting point.

A nuanced version of document frequency is **inverse document frequency** (idf). This measure takes the total number of documents and divides it by the document frequency. This results in a measure that is inversely proportional to the document frequency. That is, the higher the document frequency, the lower the inverse document frequency. This measure is often log-transformed to spread out the values.

One thing to consider about df and idf is that neither takes into account the length of the documents in which the type appears nor the spread of the type within each document. To take these factors into account, we can use Gries' Deviation of Proportions (dp) measure (S. T. Gries 2023, 87–88). The dp measure is calculated as the difference between the proportion of a tokens in a document and tokens in the corpus. The metric can be subtracted from 1 to create a normalized measure of dispersion ranging between 0 and 1, with lower values being more dispersed.

Let's consider how these measures differ with three scenarios:

Imagine a type with a token frequency of 100 appears in each of the 10 documents in a corpus.

- A. Each of the documents is 100 words long. The type appears 10 times in each document.
- B. Each of the documents is 100 words long. But now the type appears once in 9 documents and 91 times in 1 document.
- C. Nine of the documents constitute 99% of the corpus. The type appears once in each of the 9 documents and 91 times in the 10th document.

Scenario A is the most dispersed, scenario B is less dispersed, and scenario C is the least dispersed. Yet, the type's *df* and *idf* scores will be the same. But the *dp* score will reflect increasing concentration of the type from A to B to C.

👀 Dive deeper Dispersion measures

You may wonder why we would want to use *df* or *idf* at all. The answer is some combination of the fact that they are computationally less expensive to calculate, they are widely used (especially *idf*), and/ or in many practical situations they often highly correlated with *dp*.

So for our task we will use *dp* as our measure of dispersion. The `qtalrkit` package includes the `calc_type_metrics()` function which calculates, among other metrics, the dispersion metrics *df*, *idf*, and/ or *dp*. Let's select *dp* and assign the result to `masc_lemma_disp`, as seen in Example 8.6.

Example 8.6.

```
# Load package
library(qtalrkit)

# Calculate deviance of proportions (DP)
masc_lemma_disp <-
  mascot_content_tbl |>
  calc_type_metrics(
    type = lemma,
    documents = doc_id,
    dispersion = "dp"
  ) |>
  arrange(dp)

# Preview
masc_lemma_disp |>
  slice_head(n = 10)
```

```
> # A tibble: 10 x 3
>   type     n     dp
>   <chr> <dbl> <dbl>
> 1 be     19231 0.123
> 2 have   5136  0.189
> 3 not    2279  0.240
> 4 make   1149  0.266
```

```

> 5 other 882 0.269
> 6 more 1005 0.276
> 7 take 769 0.286
> 8 only 627 0.286
> 9 time 931 0.314
> 10 see 865 0.327

```

We would like to identify lemmas that are frequent and well-dispersed. But an important question arises, what is the threshold for frequency and dispersion that we should use to identify the lemmas that we want to include in our ELL materials?

💡 Consider this

You may be wondering why the Inverse Document Frequency is, in fact, the inverse of the document counts, instead of just a count of the documents that each type appears in. The *idf* is a very common measure in machine learning that is used in combination with (term) frequency to calculate the *tf-idf* (term frequency-inverse document frequency) measure. That is, the product of the frequency of a term and the inverse document frequency of the term. This serves as a weighting measure that lowers the *tf-idf* score for terms that are frequent across documents and increases the *tf-idf* score for terms that are infrequent across documents.

Consider what types will end up with a high or a low *tf-idf* score. What use(s) could this measure have for distinguishing between types in a corpus?

Hint: consider the earlier discussion of stopword lists.

There are statistical approaches to identifying natural breakpoints, including clustering, but a visual inspection is often good enough for practical purposes. Let's create a density plot to see if there is a natural break in the distribution of our dispersion measure, as seen in Figure 8.2.

Example 8.7.

```

# Density plot of dp
masc_lemma_disp |>
  ggplot(aes(x = dp)) +
  geom_density() +
  scale_x_continuous(breaks = seq(0, 1, .1)) +
  labs(x = "Deviation of Proportions")

```

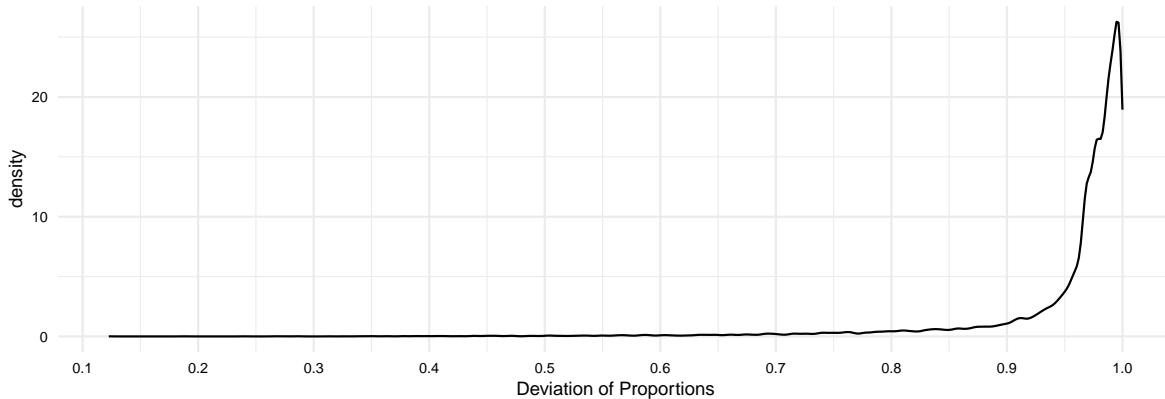


Figure 8.2: Density plot of Deviation of Proportions for lemmas in the MASC dataset

What we are looking for is an elbow in the distribution of dispersion measures. In Figure 8.2, we can see that there is distinctive bend in the distribution between .85 and .97. This bend is called an elbow, and using this approach to make informed decisions about thresholds is called the **elbow method**. We can split the difference and use this as a threshold to filter out lemmas that are less dispersed. In Example 8.8, I filter out lemmas that have a dispersion measure less than .91. Then in Table 8.5, I preview the top and bottom 50 lemmas in the dataset.

Example 8.8.

```

# Filter for lemmas with dp <= .91
masc_lemma_disp_thr <-
  masc_lemma_disp |>
  filter(dp <= .91) |>
  arrange(desc(n))

# Preview top
masc_lemma_disp_thr |>
  slice_head(n = 50) |>
  pull(type) |>
  matrix(ncol = 10) |>
  kable(col.names = NULL)
# Preview bottom
masc_lemma_disp_thr |>
  slice_tail(n = 50) |>
  pull(type) |>

```

Table 8.5: Frequency of tokens in the MASC dataset after filtering out lemmas with a Deviation of Proportions less than .91

(a) Top 50 lemmas									
be	say	think	other	work	look	also	new	t	man
have	go	more	see	year	then	way	find	first	ask
do	know	just	people	come	right	need	give	help	very
not	get	time	take	use	only	back	thing	day	much
n't	make	so	now	well	want	here	tell	many	even
(b) Bottom 50 lemmas									
dump	sting	tuition	unleash	blur	liberty	wound	nostalgic	acciden	
instrument	mainstream	awaken	prosperous	litigation	going	devote	shy	protect	
triumph	wildly	hook	buzz	resistance	awkward	alright	proximity	preside	
harsh	dismiss	fetch	presume	absurd	afterwards	evolutionary	sandy	rethink	
ignorance	liability	brave	summarize	qualify	eve	envy	interfere	strictly	

```
matrix(ncol = 10) |>
  kable(col.names = NULL)
```

We now have a good candidate list of common vocabulary that is spread well across the corpus.

Relative frequency

Gauging frequency and dispersion across the entire corpus is a good starting point for any frequency analysis, but it is often the case that we want to compare the frequency and dispersion of linguistic units across corpora or sub-corpora.

In the case of the MASC dataset, for example, we may want to compare metrics across the two modalities or the various genres. Simply comparing frequency counts across these sub-corpora is not a good approach, and can be misleading, as the sub-corpora may vary in size. For example, if one sub-corpus is twice as large as another sub-corpus, then, all else being equal, the frequency counts will be twice as large in the larger sub-corpus. This is why we use relative frequency measures, which are normalized by the size of the sub-corpus.

💡 Consider this

A variable in the MASC dataset that has yet to be used is the `pos` part of speech variable. How could we use this variable to refine our frequency and dispersion analysis of lemma types?

Hint: consider lemma forms that may be tagged with different parts-of-speech.

To normalize the frequency of linguistic units across sub-corpora, we can use the **relative frequency** measure. This is the frequency of a linguistic unit divided by the total number of linguistic units in the sub-corpus. This bakes in the size of the sub-corpus into the measure. The notion of relative frequency is key to all research working with text, as it is the basis for the statistical approach to text analysis where comparisons are made.

There are some field-specific terms that are used to refer to relative frequency measures. For example, in information retrieval and Natural Language Processing, the relative frequency measure is often referred to as the **term frequency**. In corpus linguistics, the relative frequency measure is often modified slightly to include a constant (*e.g.* $rf * 100$) which is known as the **observed relative frequency**. Although the observed relative frequency per number of tokens is not strictly necessary, it is often used to make the values more interpretable as we can now talk about an observed relative frequency of 1.5 as a linguistic unit that occurs 1.5 times per 100 linguistic units.

Let's consider how we might compare the frequency and dispersion of lemmas across the two modalities in the MASC dataset, spoken and written. To make this a bit more interesting and more relevant, let's add the **pos** variable to our analysis. The intent, then, will be to identify lemmas tagged with particular parts of speech that are particularly indicative of each of the modalities.

We can do this by collapsing the **lemma** and **pos** variables into a single variable, **lemma_pos**, with the **str_c()** function, as seen in Example 8.9.

Example 8.9.

```
# Collapse lemma and pos into type
masc_content_tbl <-
  masc_content_tbl |>
  mutate(lemma_pos = str_c(lemma, pos, sep = "_"))

# Preview
masc_content_tbl |>
  slice_head(n = 10)

> # A tibble: 10 × 8
>   doc_id modality genre  term_num term      lemma      pos  lemma_pos
>   <chr>   <chr>   <chr>     <dbl> <chr>     <chr>   <chr> <chr>
> 1 1       Written  Letters      3 contribution contribution NN contributio~
> 2 1       Written  Letters      7 mean       mean       VB mean_VB
```

> 3 1	Written	Letters	8	more	more	JJR	more_JJR
> 4 1	Written	Letters	12	know	know	VB	know_VB
> 5 1	Written	Letters	15	help	help	VB	help_VB
> 6 1	Written	Letters	17	see	see	VB	see_VB
> 7 1	Written	Letters	19	much	much	JJ	much_JJ
> 8 1	Written	Letters	21	contribution	contribution	NN	contribution
> 9 1	Written	Letters	22	means	mean	VBZ	mean_VBZ
> 10 1	Written	Letters	25	'm	be	VBP	be_VBP

Now this will increase the number of lemma types in the dataset as we are now considering lemmas where the same lemma form is tagged with different parts-of-speech.

Getting back to calculating the frequency and dispersion of lemmas in each modality, we can use the `calc_type_metrics()` function with `lemma_pos` as our type argument. We will, however, need to apply this function to each sub-corpus independently and then concatenate the two data frames. This function returns a (raw) frequency measure by default, but we can specify `thefrequency` argument to `rf` to calculate the relative frequency of the linguistic units as in Example 8.10.

Example 8.10.

```

# Calculate relative frequency
# Spoken
masc_spoken_metrics <-
  masc_content_tbl |>
  filter(modality == "Spoken") |>
  calc_type_metrics(
    type = lemma_pos,
    documents = doc_id,
    frequency = "rf",
    dispersion = "dp"
  ) |>
  mutate(modality = "Spoken") |>
  arrange(desc(n))

# Written
masc_written_metrics <-
  masc_content_tbl |>
  filter(modality == "Written") |>
  calc_type_metrics(
    type = lemma_pos,
    documents = doc_id,
  )

```

```

    frequency = "rf",
    dispersion = "dp"
) |>
mutate(modality = "Written") |>
arrange(desc(n))

# Concatenate spoken and written metrics
masc_metrics <-
bind_rows(masc_spoken_metrics, masc_written_metrics)

# Preview
masc_metrics |>
slice_head(n = 5)

```

```

> # A tibble: 5 x 5
>   type      n      rf      dp modality
>   <chr>    <dbl>  <dbl>  <dbl> <chr>
> 1 be_VBZ    2612  0.0489  0.0843 Spoken
> 2 be_VBP    1282  0.0240  0.111  Spoken
> 3 be_VBD    1020  0.0191  0.300  Spoken
> 4 n't_RB    829   0.0155  0.139  Spoken
> 5 have_VBP  766   0.0143  0.152  Spoken

```

With the `rf` measure, we are now in a position to compare ‘apples to apples’, as you might say. We can now compare the relative frequency of lemmas across the two modalities. Let’s preview the top 5 lemmas in each modality, as seen in Example 8.11.

Example 8.11.

```

# Preview top 10 lemmas in each modality
masc_metrics |>
group_by(modality) |>
slice_max(n = 10, order_by = rf) |>
ungroup()

> # A tibble: 20 x 5
>   type      n      rf      dp modality
>   <chr>    <dbl>  <dbl>  <dbl> <chr>
> 1 be_VBZ    2612  0.0489  0.0843 Spoken
> 2 be_VBP    1282  0.0240  0.111  Spoken

```

```

> 3 be_VBD    1020 0.0191  0.300  Spoken
> 4 n't_RB    829 0.0155  0.139  Spoken
> 5 have_VBP  766 0.0143  0.152  Spoken
> 6 do_VBP    728 0.0136  0.180  Spoken
> 7 be_VB     655 0.0123  0.147  Spoken
> 8 not_RB    638 0.0119  0.137  Spoken
> 9 just_RB   404 0.00757 0.267  Spoken
> 10 so_RB    387 0.00725 0.357  Spoken
> 11 be_VBZ   4745 0.0249  0.230  Written
> 12 be_VBD   3317 0.0174  0.366  Written
> 13 be_VBP   2617 0.0137  0.237  Written
> 14 be_VB    1863 0.00976 0.218  Written
> 15 not_RB   1640 0.00859 0.259  Written
> 16 have_VBP 1227 0.00643 0.291  Written
> 17 n't_RB   905 0.00474 0.540  Written
> 18 have_VBD 859 0.00450 0.446  Written
> 19 have_VBZ 777 0.00407 0.335  Written
> 20 say_VBD   710 0.00372 0.609  Written

```

We can appreciate, now, that there are similarities and a few differences between the most frequent lemmas for each modality. First, there are similar lemmas in written and spoken modalities, such as ‘be’, ‘have’, and ‘not’. Second, the top 10 include verbs and adverbs. Now we are looking at the most frequent types, so it is not surprising that we see more in common than not. However, looking close we can see that contracted forms are more frequent in the spoken modality, such as ‘isn’t’, ‘don’t’, and ‘can’t’ and that ordering of the verb tenses differs to some degree. Whether these are important distinctions for our task is something we will need to consider.

We can further cull our results by filtering out lemmas that are not well-dispersed across the sub-corpora. Although it may be tempting to use the threshold we used earlier, we should consider that the size of the sub-corpora are different and the distribution of the dispersion measure may be different. With this in mind, we need to visualize the distribution of the dispersion measure for each modality and apply the elbow method to identify a threshold for each modality.

After assessing the density plots for the dispersion of each modality via the elbow method, we update our thresholds. We maintain the .91 threshold for the written subcorpus and use a .79 threshold for the spoken subcorpus. I apply these filters as seen in Example 8.12.

Example 8.12.

```

# Filter for lemmas with
# dp <= .91 for written and

```

```

# dp <= .79 for spoken
masc_metrics_thr <-
  masc_metrics |>
  filter(
    (modality == "Written" & dp <= .91) |
    (modality == "Spoken" & dp <= .79)
  ) |>
  arrange(desc(rf))

```

Filtering the less-dispersed types reduces the dataset from 33,428 to 4,865 observations. This will provide us with a more succinct list of common and well-dispersed lemmas that are used in each modality.

As much as the frequency and dispersion measures can provide us with a good starting point, it does not provide an understanding of what types are more indicative of a particular sub-corpora, modality subcorpora in our case. We can do this by calculating the log odds ratio of each lemma in each modality.

The **log odds ratio** is a measure that quantifies the difference between the frequencies of a type in two corpora or sub-corpora. In spirit and in name, it compares the odds of a type occurring in one corpus versus the other. The values range from negative to positive infinity, with negative values indicating that the type is more frequent in the first corpus and positive values indicating that the lemma is more frequent in the second corpus. The magnitude of the value indicates the strength of the association.

The **tidylo** package provides a convenient function `bind_log_odds()` to calculate the log odds ratio, and a weighed variant, for each type in each sub-corpora. The weighted log odds ratio measure provides a more robust and interpretable measure for comparing term frequencies across corpora, especially when term frequencies are low or when corpora are of different sizes. The weighting (or standardization) also makes it easier to identify terms that are particularly distinctive or characteristic of one corpus over another. Note that the weighted measure's interpretation is slightly different than the log odds's. The larger positive values in each corpus indicate that the type is more indicative of that (sub-)corpus, and the larger negative values indicate that the type is less indicative.

Let's calculate the weighted log odds ratio for each lemma in each modality and preview the top 10 lemmas in each modality, as seen in Example 8.13.

Example 8.13.

```

# Load package
library(tidylo)

```

```

# Calculate log odds ratio
masc_metrics_thr <-
  masc_metrics_thr |>
  bind_log_odds(
    set = modality,
    feature = type,
    n = n
  )

# Preview top 10 lemmas in each modality
masc_metrics_thr |>
  group_by(modality) |>
  slice_max(n = 10, order_by = log_odds_weighted) |>
  ungroup()

```

```

> # A tibble: 20 x 6
>   type              n      rf      dp modality log_odds_weighted
>   <chr>            <dbl>  <dbl>  <dbl> <chr>            <dbl>
> 1 be_VBZ           2612  0.0489  0.0843 Spoken            14.0
> 2 n't_RB           829   0.0155  0.139  Spoken            10.4
> 3 do_VBP           728   0.0136  0.180  Spoken            10.3
> 4 be_VBP           1282  0.0240  0.111  Spoken            8.67
> 5 think_VBP        350   0.00655 0.259  Spoken            8.32
> 6 have_VBP         766   0.0143  0.152  Spoken            8.01
> 7 know_VBP         282   0.00528 0.260  Spoken            7.04
> 8 well_RB           334   0.00626 0.283  Spoken            6.91
> 9 go_VBG            285   0.00534 0.207  Spoken            6.47
> 10 understanding_NN 45    0.000843 0.649  Spoken            6.41
> 11 t_NN              475   0.00249  0.778  Written            10.6
> 12 figure_NN         140   0.000733 0.868  Written            5.75
> 13 financial_JJ      138   0.000723 0.880  Written            5.71
> 14 city_NN            137   0.000718 0.766  Written            5.69
> 15 email_NN           133   0.000697 0.866  Written            5.61
> 16 eye_NNS            129   0.000676 0.731  Written            5.52
> 17 style_NN            108   0.000566 0.829  Written            5.05
> 18 mail_NN             106   0.000555 0.876  Written            5.00
> 19 text_NN              103   0.000540 0.845  Written            4.93
> 20 gift_NN              98   0.000513 0.826  Written            4.81

```

Let's imagine we would like to extract the most indicative verbs for each modality using the weighted log odds as our measure. We can do this with a little regular expression magic. Let's

use the `str_subset()` function to filter for lemmas that contain `_V` and then use `slice_max()` to extract the top 10 most indicative verb lemmas, as seen in Example 8.14.

Example 8.14.

```
# Preview (ordered by log_odds_weighted)
masc_metrics_thr |>
  group_by(modality) |>
  filter(str_detect(type, "_V")) |>
  slice_max(n = 10, order_by = log_odds_weighted) |>
  select(-n) |>
  ungroup()

> # A tibble: 20 x 5
>   type          rf      dp modality log_odds_weighted
>   <chr>      <dbl>  <dbl> <chr>           <dbl>
> 1 be_VBZ      0.0489  0.0843 Spoken          14.0
> 2 do_VBP      0.0136  0.180  Spoken          10.3
> 3 be_VBP      0.0240  0.111  Spoken          8.67
> 4 think_VBP   0.00655 0.259  Spoken          8.32
> 5 have_VBP    0.0143  0.152  Spoken          8.01
> 6 know_VBP    0.00528 0.260  Spoken          7.04
> 7 go_VBG      0.00534 0.207  Spoken          6.47
> 8 do_VBD      0.00603 0.321  Spoken          5.97
> 9 mean_VBP    0.00247 0.543  Spoken          5.95
> 10 do_VB      0.00455 0.207  Spoken          5.61
> 11 don_VB     0.000361 0.839  Written         4.04
> 12 doe_VBZ    0.000351 0.870  Written         3.98
> 13 walk_VBD   0.000320 0.790  Written         3.79
> 14 associate_VBN 0.000304 0.777  Written         3.70
> 15 reply_VBD  0.000293 0.837  Written         3.64
> 16 develop_VBG 0.000288 0.812  Written         3.60
> 17 require_VBN 0.000272 0.793  Written         3.50
> 18 fall_VBD   0.000267 0.757  Written         3.47
> 19 meet_VB    0.000241 0.729  Written         3.30
> 20 regard_VBG 0.000225 0.823  Written         3.19
```

Note that the log odds are larger for the spoken modality than the written modality. This indicates that these types are more strongly indicative of the spoken modality than the types in the written modality are indicative of the written modality. This is not surprising, as the written modality is typically more diverse in terms of lexical usage than the spoken modality, where the terms tend to be repeated more often, including verbs.

8.2.1.2 Co-occurrence analysis

Moving forward on our task, we have a good idea of the general vocabulary that we want to include in our ELL materials and can identify lemma types that are particularly indicative of each modality. Another useful approach to complement our analysis is to identify words that co-occur with our target lemmas –in particular verbs. In English, it is common for verbs to appear with a preposition or adverb, such as ‘give up’, ‘look after’. These ‘phrasal verbs’ form a semantic unit that is distinct from the verb alone.

In cases such as this, we are aiming to do a co-occurrence analysis. Co-occurrence analysis is a set of methods that are used to identify words that appear in close proximity to a target type.

An exploratory, primarily qualitative, approach is to display the co-occurrence of words in a Keyword in Context (KWIC). This is a table that displays the target word in the center of the table and the words that appear before and after the target word. This is a useful approach for spot identifying collocations of a target word or phrase.

The `quanteda` package includes a function `kwic()` that can be used to create a KWIC table. It does require some transformation to the data, however. We need to collapse the `lemma` column into a single string for each document from the original transformed dataset, `masc_tbl`. Then we can apply the `corpus()` and then `tokens` function to create a `quanteda` `tokens` object. Then we can apply the `kwic()` function to create a KWIC table based on a search pattern.

Example 8.15.

```
# Collapse lemma, pos into a single string
masc_text_tbl <-
  masc_tbl |>
  mutate(lemma_pos = str_c(lemma, pos, sep = "_")) |>
  group_by(doc_id, modality, genre) |>
  summarize(text = str_c(lemma_pos, collapse = " ")) |>
  ungroup()

# Load package
library(quanteda)

masc_corpus <-
  masc_text_tbl |>
  corpus(
    text_field = "text",
    docid_field = "doc_id"
  )
```

```

masc_corpus |>
  tokens() |>
  kwic(
    pattern = phrase("*_V* *_IN*"),
    window = 3
  ) |>
  as_tibble() |>
  select(docname, pre, keyword, post) |>
  slice_sample(n = 10)

```

```

> # A tibble: 10 x 4
>   docname pre                 keyword          post
>   <chr>   <chr>
> 1 256    what_WDT when_WRB you_PRP
> 2 200    beer_NN rachel_NNP be_VBD
> 3 171    of_IN las_NNP vegas_NNP
> 4 384    whose_WP $ stock_NN
> 5 98     know_VB that_IN he_PRP
> 6 216    western_JJ release_NNS be_VBP
> 7 155    can_MD best_JJS be_VB
> 8 77     $ porch_NN light_NNS
> 9 254    a_DT slut_NNP and_CC
> 10 187   suffer_VBZ for_IN it_PRP

```

The output of a KWIC table, as in Example 8.15, is a useful, qualitative, way to identify collocations of a target word or phrase.

A straightforward quantitative way to explore co-occurrence is to set the unit of observation to an n -gram of terms. Then, the frequency and dispersion metrics can be calculated for each n -gram.

In general, deriving n -grams from a corpus is a straightforward process. The `tidytext` package includes a function `unnest_tokens()` that can be used to create n -grams from a corpus. The function can take a single column of untokenized text or a tokenized column in combination with a variable to use as the grouping variable. In the `masc_tbl` dataset, we have tokenized text in the `lemma` column and a grouping variable in the `doc_id` column. We can use the `unnest_tokens()` function to create a new data frame with a row for each n -gram in each document by setting `collapse = "doc_id"`, as seen in Example 8.16.

Example 8.16.

```

# Load package
library(tidytext)

# Create bigrams
masc_tbl |>
  unnest_tokens(
    output = bigrams,
    input = lemma,
    token = "ngrams",
    n = 2,
    collapse = "doc_id"
  ) |>
  slice_head(n = 10)

```

```

> # A tibble: 10 x 2
>   doc_id   bigrams
>   <chr>   <chr>
> 1 1       december your
> 2 1       your contribution
> 3 1       contribution to
> 4 1       to goodwill
> 5 1       goodwill will
> 6 1       will mean
> 7 1       mean more
> 8 1       more than
> 9 1       than you
> 10 1      you may

```

The result of this operation can be joined with the original dataset using the `doc_id` as the key variable. Then we can calculate the frequency and dispersion metrics for each n -gram in each modality. However, this approach is not ideal for our task, as we've lost access to part of speech information.

Another, more informative approach is to create a new variable that combines the lemma and part of speech for each observation before using `unnest_tokens()` to generate the bigrams. We can use the `str_c()` function from the `stringr` package to join the `lemma` and `pos` columns into a single string, so that we have a variable `lemma_pos` with the lemma and part of speech joined by an underscore.

One consideration that we need to take for our goal to identify verb particle constructions, is how we ultimately want to group our `lemma_pos` values. This is particularly important given the fact that our `pos` tags for verbs include information about the verb's tense and person.

This means that a verb in a verb particle bigram, such as ‘look after’, will be represented by multiple `lemma_pos` values, such as `look_VB`, `look_VBP`, `look_VBD`, and `look_VBG`. If we want this level of detail, we just proceed as described above. However, if we want to group the verb particle bigrams by a single verb value, we need to recode the `pos` values for verbs. We can do this with the `case_when()` function from the `dplyr` package.

In Example 8.17, I recode the `pos` values for verbs to `V` and then join the `lemma` and `pos` columns into a single string.

Example 8.17.

```
# Collapse lemma into a single string
masc_lemma_pos_tbl <-
  masc_tbl |>
  mutate(pos = case_when(
    str_detect(pos, "^V") ~ "V",
    TRUE ~ pos
  )) |>
  group_by(doc_id) |>
  mutate(lemma_pos = str_c(lemma, pos, sep = "_")) |>
  ungroup()

# Preview
masc_lemma_pos_tbl |>
  slice_head(n = 10)
```

```
> # A tibble: 10 x 8
>   doc_id modality genre  term_num term      lemma      pos lemma_pos
>   <chr>   <chr>   <chr>     <dbl> <chr>     <chr>     <chr> <chr>
> 1 1      Written  Letters      0 December  december  NNP  december_NNP
> 2 1      Written  Letters      2 Your     your      PRP$  your_PRP$
> 3 1      Written  Letters      3 contribution  contribution  NN  contribution
> 4 1      Written  Letters      4 to       to       TO  to_TO
> 5 1      Written  Letters      5 Goodwill  goodwill  NNP  goodwill_NNP
> 6 1      Written  Letters      6 will     will     MD  will_MD
> 7 1      Written  Letters      7 mean     mean     V  mean_V
> 8 1      Written  Letters      8 more     more     JJR  more_JJR
> 9 1      Written  Letters      9 than     than     IN  than_IN
> 10 1     Written  Letters     10 you     you     PRP  you_PRP
```

```

masc_lemma_pos_tbl |>
  unnest_tokens(
    output = bigrams,
    input = lemma_pos,
    token = "ngrams",
    n = 2,
    to_lower = FALSE,
    collapse = "doc_id"
  ) |>
  filter(str_detect(bigrams, "_V.*_IN")) |>
  calc_type_metrics(
    type = bigrams,
    documents = doc_id,
    frequency = "rf",
    dispersion = "dp"
  ) |>
  arrange(desc(rf))

```

```

> # A tibble: 4,513 x 4
>   type             n      rf      dp
>   <chr>        <dbl>    <dbl>    <dbl>
> 1 be_V in_IN     359  0.0259  0.366
> 2 be_V that_IN   210  0.0151  0.504
> 3 look_V at_IN   157  0.0113  0.528
> 4 say_V that_IN  134  0.00965 0.580
> 5 be_V on_IN     120  0.00865 0.523
> 6 talk_V about_IN 114  0.00821 0.622
> 7 be_V of_IN     111  0.00800 0.504
> 8 know_V that_IN  98  0.00706 0.605
> 9 think_V that_IN  90  0.00648 0.643
> 10 be_V about_IN  76  0.00548 0.608
> # i 4,503 more rows

```

We have identified and derived frequency and dispersion metrics for n -grams that include verb particle construction candidates. Yet, there is a issue with this approach. The frequency and dispersion of n -grams does not necessarily relate to whether the two words form a semantic unit.

To address this issue, we can use a statistical measures to estimate collocational strength between two words. A **collocation** is a sequence of words that co-occur more often than would be expected by chance. A common measure of collocation is the **pointwise mutual**

information (PMI) measure. The PMI measure is calculated as the log ratio of the observed frequency of two words co-occurring to the expected frequency of the two words co-occurring. The expected frequency is calculated as the product of the frequency of each word. The PMI measure is a log ratio, the direction indicates relatedness and the magnitude of the value indicates the strength of the association.

Let's calculate the PMI for all the bigrams in the MASC dataset. We can use the `calc_assoc_metrics()` function from `qtlrkit`. We need to specify the `association` argument to `pmi` and the `type` argument to `bigrams`, as seen in Example 8.18.

Example 8.18.

```

masc_lemma_pos_assoc <-
  masc_lemma_pos_tbl |>
  calc_assoc_metrics(
    doc_index = doc_id,
    token_index = term_num,
    type = lemma_pos,
    association = "pmi"
  )

# Preview
masc_lemma_pos_assoc |>
  arrange(desc(pmi)) |>
  slice_head(n = 10)

> # A tibble: 10 x 4
>   x                  y                  n     pmi
>   <chr>              <chr>              <dbl> <dbl>
> 1 #Christian_NN    bigot_NN           1    12.4
> 2 #FAIL_NN          phenomenally_RB  1    12.4
> 3 #NASCAR_NN        #indycar_NN       1    12.4
> 4 #PALM_NN          merchan_NN        1    12.4
> 5 #Twitter_NN       #growth_NN         1    12.4
> 6 #college_NN       #jobs_NN          1    12.4
> 7 #education_NN     #teaching_NN       1    12.4
> 8 #faculty_NN       #cites_NN         1    12.4
> 9 #fb_NN             siebel_NNP        1    12.4
> 10 #glitchmyass_NN  reps_NNP         1    12.4

```

One caveat to using the PMI measure is that it is sensitive to the frequency of the words. If the words in a bigram pair are infrequent, and especially if they only occur once, then the

PMI measure will be inflated. To mitigate this issue, we can apply a frequency threshold to the bigrams before calculating the PMI measure. Let's filter out bigrams that occur less than 10 times, as seen in Example 8.19.

Example 8.19.

```
# Filter for bigrams that occur >= 10 times
masc_lemma_pos_assoc_thr <-
  masc_lemma_pos_assoc |>
  filter(n >= 10) |>
  arrange(desc(pmi))

# Preview
masc_lemma_pos_assoc_thr |>
  slice_head(n = 10)
```

```
> # A tibble: 10 x 4
>   x           y           n     pmi
>   <chr>       <chr>       <dbl> <dbl>
> 1 pianista_NN irlandesa_NN  10  10.0
> 2 costa_NNP   rica_NNP    10  9.95
> 3 nanowrimo_NNP novel_NNP  12  9.87
> 4 bin_NN       laden_NNP   11  9.79
> 5 osama_NNP   bin_NN      11  9.79
> 6 bin_NNP      ladin_NNP   11  9.70
> 7 los_NNP      angeles_NNP 11  9.64
> 8 chilean_JJ   seabass_NNS 13  9.64
> 9 novel_NNP    ch_NNP      12  9.58
> 10 st_NNP      zip_NNP     10  9.52
```

Now we are in a position to identify verb particle constructions. We can filter for bigrams that include a verb and a particle and that have a PMI measure greater than 0, as seen in Example 8.20.

Example 8.20.

```
# Filter for bigrams that include a verb and a particle
# and that have a PMI measure greater than 0
masc_verb_part_assoc <-
  masc_lemma_pos_assoc_thr |>
  filter(str_detect(x, "_V")) |>
```

```

filter(str_detect(y, "_IN")) |>
filter(pmi > 0) |>
arrange(x)

# Preview
masc_verb_part_assoc |>
slice_head(n = 10)

```

```

> # A tibble: 10 x 4
>   x           y       n   pmi
>   <chr>     <chr> <dbl> <dbl>
> 1 account_V for_IN    17  3.74
> 2 acknowledge_V that_IN   13  3.62
> 3 act_V       as_IN    14  2.96
> 4 agree_V      with_IN   45  3.21
> 5 agree_V      that_IN   14  1.94
> 6 appear_V      on_IN    12  1.97
> 7 appear_V      in_IN    24  1.76
> 8 argue_V       that_IN   20  3.26
> 9 arrive_V      at_IN    18  3.39
> 10 arrive_V     in_IN    10  1.48

```

We can clean up the results a bit by removing the part of speech tags from the `x` and `y` variables, up our minimum PMI value, and create a network plot to visualize the results, as seen in Figure 8.3.

```

# Clean up results
masc_verb_part_assoc_plot <-
  masc_verb_part_assoc |>
  filter(pmi >= 2) |>
  mutate(
    x = str_remove(x, "_V.*"),
    y = str_remove(y, "_IN")
  )

# Create an association network plot
# `x` and `y` are the nodes
# `pmi` is the edge weight

library(igraph)

```

```
library(ggraph)

masc_verb_part_assoc_plot |>
  graph_from_data_frame() |>
  ggraph(layout = "nicely") +
  geom_edge_link(aes(color = pmi),
    alpha = 0.8,
    edge_width = 0.8,
    arrow = grid::arrow())
) +
  geom_node_point(color = "black") +
  geom_node_text(aes(label = name), repel = TRUE) +
  scale_edge_color_gradient(low = "grey90", high = "grey20") +
  theme_void()
```

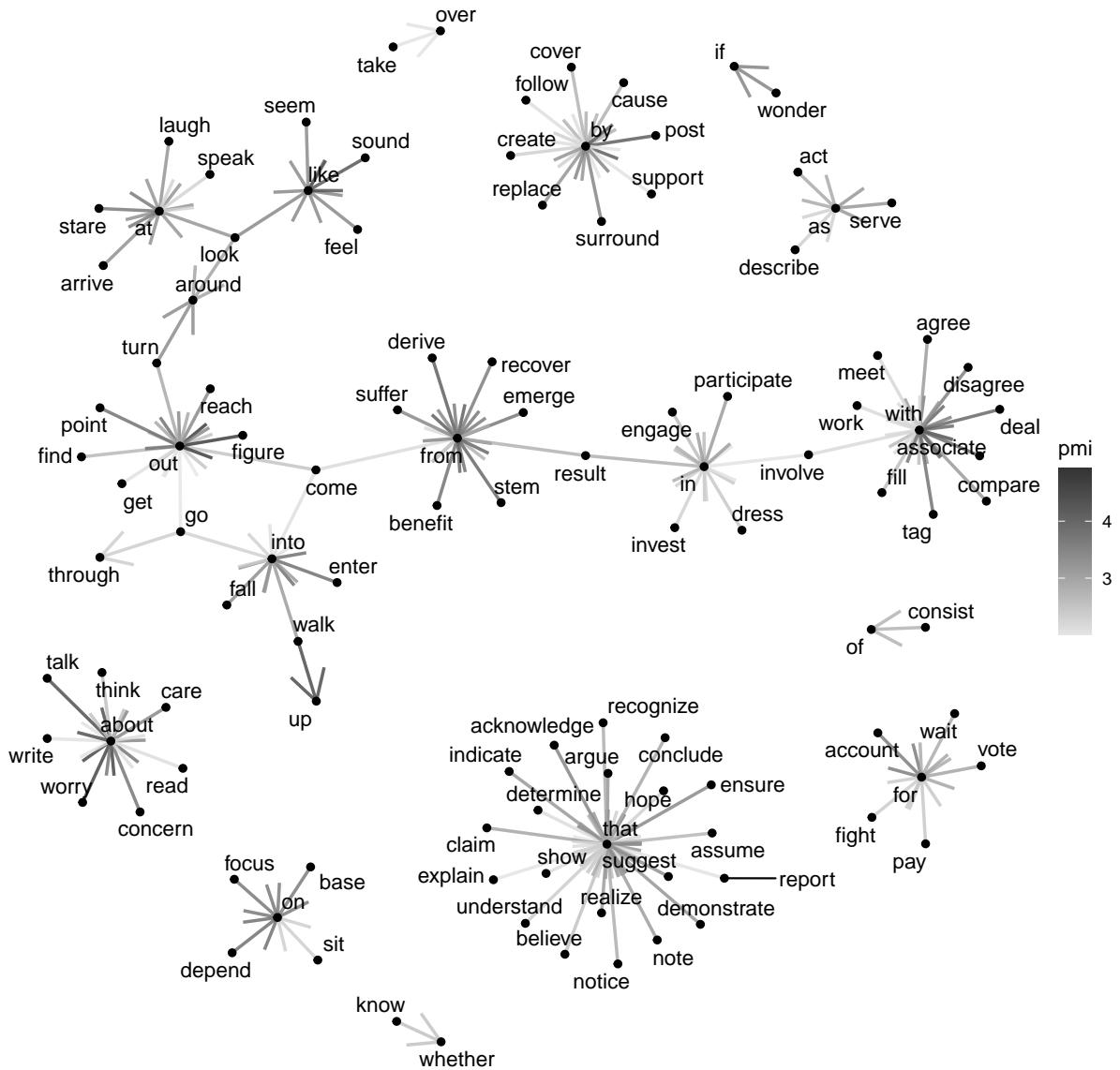


Figure 8.3: Network plot of verb particle constructions in the MASC dataset

From this plot, and from the underlying data, we can explore verb particle constructions. We could go further and apply our co-occurrence methods to each modality separately, if we wanted to identify verb particle constructions that are distinctive to each modality. We could also apply our co-occurrence methods to other parts-of-speech, such as adjectives and nouns, to identify collocations of these parts-of-speech. There is much more to explore with

co-occurrence analysis, but this should give you a good idea of the types of questions that can be addressed.

8.2.2 Unsupervised learning

Aligned in purpose with descriptive approaches, unsupervised learning approaches to exploratory data analysis are used to identify patterns in the data from an algorithmic perspective. Common methods in text analysis include principle component analysis, clustering, and vector space modeling.

We will continue to use the MASC dataset as we develop materials for our ELL textbook to illustrate unsupervised learning methods. In the process, we will explore the following questions:

- Can we identify and group documents based on linguistic features or co-occurrence patterns of the data itself?
- Do the groups of documents relate to categories in the dataset?
- Can we estimate the semantics of words based on their co-occurrence patterns?

Through these questions we will build on our knowledge of frequency, dispersion, and co-occurrence analysis and introduce concepts and methods associated with machine learning.

8.2.2.1 Clustering

Clustering is a unsupervised learning technique that can be used to group similar items in the text data, helping to organize the data into distinct categories and discover relationships between different elements in the text. The main steps in the procedure includes identifying the relevant linguistic features to use for clustering, representing the features in a way that can be used for clustering, and applying a clustering algorithm to the data. However, it is important to consider the strengths and weaknesses of the clustering algorithm for a particular task and how the results will be evaluated.

In our ELL textbook task, we may very well want to explore the similarities and/ or differences between the documents based on the distribution of linguistic features. This provides us a view to evaluate to what extent the labels in the dataset (modality and genre) map to the distribution of linguistic features. Based on this evaluation, we may want to consider re-labeling the documents, collapsing labels, or even adding new labels.

Enter clustering. Instead of relying entirely on the labels in the MASC dataset, we can let the data itself say something about how related the documents are. Yet, a pivotal question is what features should we use, otherwise known as **feature selection**. We could use terms or lemmas, but we may want to consider other features, such as parts-of-speech or some co-occurrence patterns. We are not locked into using one criterion, and we can perform clustering

multiple times with different features, but we should consider the implications of our feature selection for our interpretation of the results.

Another key question is what clustering algorithm to use. Again, we are not married to one algorithm, and we can perform clustering multiple times with different algorithms, but not all algorithms are created equal. Some algorithms are better suited for certain types of data and certain types of tasks. For example, **Hierarchical clustering** is a good choice when we are not sure how many clusters we want to identify, as it does not require us to specify the number of clusters from the outset. However, it is not a good choice when we have a large dataset, as it can be computationally expensive compared to some other algorithms. **K-means clustering**, on the other hand, is a good choice when we want to identify a pre-defined number of clusters, and the aim is to gauge how well the data fit the clusters. These two clustering techniques, therefore, complement each other with Hierarchical clustering being a good choice for initial exploration and K-means clustering being a good choice for targeted evaluation.

With these considerations in mind, let's start by identifying the linguistic features that we want to use for clustering. Imagine that among the various features that we are interested in associating documents, we consider lemma use and part of speech use. However, we need to operationalize what we mean by 'use'. In machine learning, this process is known as **feature engineering**. Since we aim to compare documents it is logical for us to use the document-normalized features. So in both lemma and part of speech tags, we will use the relative frequency. An additional operation that we can apply to the lemma feature is to weight the relative frequency by the dispersion of the lemma. This will give us a measure of the distinctiveness of the lemma in the document. A common implementation of this approach is to use the *tf-idf* measure, which is the product of the relative frequency and the inverse document frequency.

Each of these engineered feature sets represents a different aspect of the lexical nature of the documents. The relative frequency of lemmas represents the lexical diversity of the documents, the dispersion-weighted *tf-idf* of lemmas represents the distinctiveness of the lemmas in the documents, and the relative frequency of part of speech tags represents the grammatical diversity of the documents (Petrenz and Webber 2011).

The next question to address in any analysis is how to represent the features. In our case, we want to represent the features in each document. In machine learning, the most common way to represent features is in a matrix. In our case, we want to create a matrix with the documents in the rows and the features in the columns. The values in the matrix will be the operationalization of lexical use in each document for each of our three candidate measures. This configuration is known as a **document-term matrix** (DTM).

To recast a data frame into a DTM, we can use the `cast_dtm()` function from the `tidytext` package. This function takes a data frame with a document identifier, a feature identifier, and a value for each observation and casts it into a matrix. Operations such as normalization are easily and efficiently performed in R on matrices, so initially we can cast a frequency table of lemmas and part of speech tags into a matrix and then normalize the matrix by documents.

For the *tf-idf* measure we use the `bind_tf_idf()` function from the `tidytext` package. This function takes a data frame with a document, feature, and frequency column (`n`) and calculates the *tf-idf* measure for each feature in each document. This is a normalized measure, so we do not need to normalize the matrix by documents. Let's see how this works with the MASC dataset in Example 8.21.

Example 8.21.

```
# Create a document-term matrix of lemmas
masc_lemma_dtm <-
  masc_tbl |>
  count(doc_id, lemma) |>
  cast_dtm(doc_id, lemma, n) |>
  as.matrix()

# Create a document-term matrix of part of speech tags
masc_pos_dtm <-
  masc_tbl |>
  count(doc_id, pos) |>
  cast_dtm(doc_id, pos, n) |>
  as.matrix()

# Create a document-term matrix of tf-idf weighted lemmas
masc_lemma_tfidf_dtm <-
  masc_tbl |>
  count(doc_id, lemma) |>
  bind_tf_idf(doc_id, lemma, n) |>
  cast_dtm(doc_id, lemma, tf_idf) |>
  as.matrix()
```

Note preview the a subset of the contents of a matrix, such as in Example 8.21, we use bracket syntax `[]` instead of the `head()` function. Let's take a look at the first 5 rows and 5 columns of the matrices, as seen in Example 8.22.

Example 8.22.

```
# Preview
masc_lemma_dtm[1:5, 1:5]
```

```
>      Terms
> Docs 'd 's M. a account
```

```

> 1 1 1 1 15 1
> 10 0 0 0 7 0
> 100 0 0 0 0 0
> 101 0 0 0 2 0
> 102 0 0 0 1 0

```

```
masc_pos_dtm[1:5, 1:5]
```

```

>      Terms
> Docs CC DT EX IN JJ
> 1 14 35 1 44 27
> 10 11 38 0 39 18
> 100 0 2 0 2 3
> 101 3 16 0 23 7
> 102 20 29 0 34 20

```

```
masc_lemma_tfidf_dtm[1:5, 1:5]
```

```

>      Terms
> Docs 'd 's M. a account
> 1 0.0555 0.00324 0.227 0.006533 0.0413
> 10 0.0000 0.00000 0.000 0.003312 0.0000
> 100 0.0000 0.00000 0.000 0.000000 0.0000
> 101 0.0000 0.00000 0.000 0.001064 0.0000
> 102 0.0000 0.00000 0.000 0.000484 0.0000

```

Now we can normalize the lemma and pos matrices by documents. We can do this by dividing each feature count by the total count in each document. This is a row-wise transformation, so we can use the `rowSums()` function from base R to calculate the total count in each document. Then each count divided by its row's total count, as seen in Example 8.23.

Example 8.23.

```

# Normalize lemma and pos matrices by documents
masc_lemma_dtm <-
  mascot_lemma_dtm / rowSums(masc_lemma_dtm)

```

```
masc_pos_dtm <-
  masc_pos_dtm / rowSums(masc_pos_dtm)
```

There are two concerns to address before we can proceed with clustering. First, clustering algorithm performance tends to degrade with the number of features. If we consider either the relative frequency of lemmas or the dispersion-weighted *tf-idf* of lemmas, we are looking at over 25k features! Second, clustering algorithms perform better with more informative features. That is to say, features that are more distinct across the documents provide better information for deriving useful clusters.

We can address both of these concerns by reducing the number of features and increasing the informativeness of the features. To accomplish this is to use **dimensionality reduction**. Dimensionality reduction is a set of methods that are used to reduce the number of features in a dataset while retaining as much information as possible. The most common method for dimensionality reduction is **principle component analysis** (PCA). PCA is a method that transforms a set of correlated variables into a set of uncorrelated variables, known as principle components. The principle components are ordered by the amount of variance that they explain in the data. The first principle component explains the most variance, the second principle component explains the second most variance, and so on.

We can apply PCA to each of these features and assess how well the features account for the variation in the data. We can then use the features that account for the most variation in the data for clustering. The `prcomp()` function from base R can be used to perform PCA. Let's apply PCA to each of our candidate feature matrices, as seen in Example 8.24.

Example 8.24.

```
# Set seed for reproducibility
set.seed(123)

# Apply PCA to each feature matrix
masc_lemma_pca <-
  masc_lemma_dtm |>
  prcomp()

masc_pos_pca <-
  masc_pos_dtm |>
  prcomp()

masc_lemma_tfidf_pca <-
  masc_lemma_tfidf_dtm |>
  prcomp()
```

We can visualize the amount of variance explained by each principle component with a scree plot. The `fviz_eig()` function from the `factoextra` package can be used to create a scree plot. The `fviz_eig()` function takes the output of the `prcomp()` function as its argument and an argument `ncp = 10` to specify the number of principle components to include in the plot. Let's create a scree plot for each of our candidate feature matrices, as seen in Figure 8.4.

```
# Load package
library(factoextra)

# Scree plot: lemma relative frequency
fviz_eig(masc_lemma_pca, ncp = 10)

# Scree plot: lemma dispersion-weighted tf-idf
fviz_eig(masc_lemma_tfidf_pca, ncp = 10)

# Scree plot: part of speech relative frequency
fviz_eig(masc_pos_pca, ncp = 10)
```

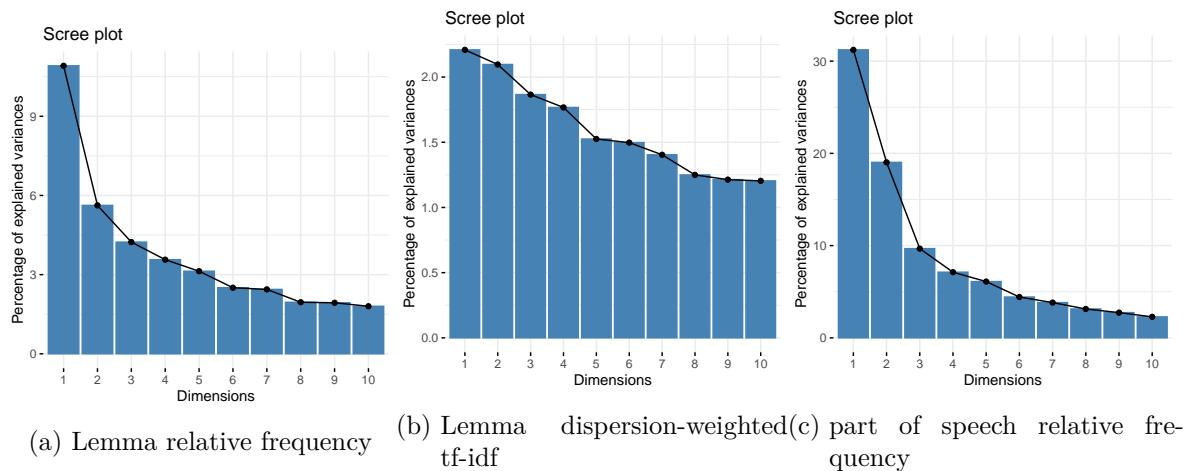


Figure 8.4: Scree plot of the principle components of the MASC dataset

From Figure 8.4, we can see the plots are different. All trend toward less variance explained as the number of dimensions increase. But for our purposes, we are interested in the largest variance explained with the fewest dimensions. To that end, the Figure 8.4c plot is the most reduced and most informative. The amount of variance explained is over 30% for the first dimension alone, however, the variance explained decreases between 4 and 5 dimensions. This is a good indication that we should use 4 dimensions for our clustering algorithm.

To calculate the amount of variance explained by each principle component we can square the standard deviations of the principle components and divide by the sum of the squared standard deviations. Let's calculate the amount of variance explained by each principle component for each of our candidate feature matrices, as seen in Example 8.25.

Example 8.25.

```
# Calculate variance explained for first 3 principle components
# lemma
masc_lemma_pca_var <-
  masc_lemma_pca$sdev^2 / sum(masc_lemma_pca$sdev^2) * 100

sum(masc_lemma_pca_var[1:4])
```

```
> [1] 24.3
```

```
# pos
masc_pos_pca_var <-
  masc_pos_pca$sdev^2 / sum(masc_pos_pca$sdev^2) * 100

sum(masc_pos_pca_var[1:4])
```

```
> [1] 67
```

```
# lemma tf-idf
masc_lemma_tfidf_pca_var <-
  masc_lemma_tfidf_pca$sdev^2 / sum(masc_lemma_tfidf_pca$sdev^2) * 100

sum(masc_lemma_tfidf_pca_var[1:4])
```

```
> [1] 7.94
```

Combining the findings in the Scree plots and the variance explained calculations, we can see that the first four principle components of the part of speech features account for a good proportion of the variance. Therefore, all else being equal, we should use the part of speech features. As with all things exploratory, however, it is important to consider the implications of our feature selection for our interpretation of the results. In this case, the part of speech features approximate grammatical diversity of the documents, more so than lexical diversity.

This means that the clusters that we identify will be based on a particular measure of grammatical diversity of the documents. If, for example, we want to identify clusters based on the lexical diversity of the documents, we may opt to use the lemma features, or some other operationalized measure of lexical diversity.

Before we leave PCA, let's also take a look at the principle components themselves. The `get_pca_var()` function from the `factoextra` package can be used to extract the principle components from the output of the `prcomp()` function. The `get_pca_var()` function takes the output of the `prcomp()` function as its argument and an argument `ncp = 10` to specify the number of principle components to include in the plot. Let's create a plot of the first five principle components for the part of speech data, as seen in Figure 8.5.

```
# Load package
library(factoextra)

# Plot principle components: pos
masc_pos_pca |>
  fviz_contrib(
    choice = "var",
    axes = 1:4,
    top = 20
  )
```

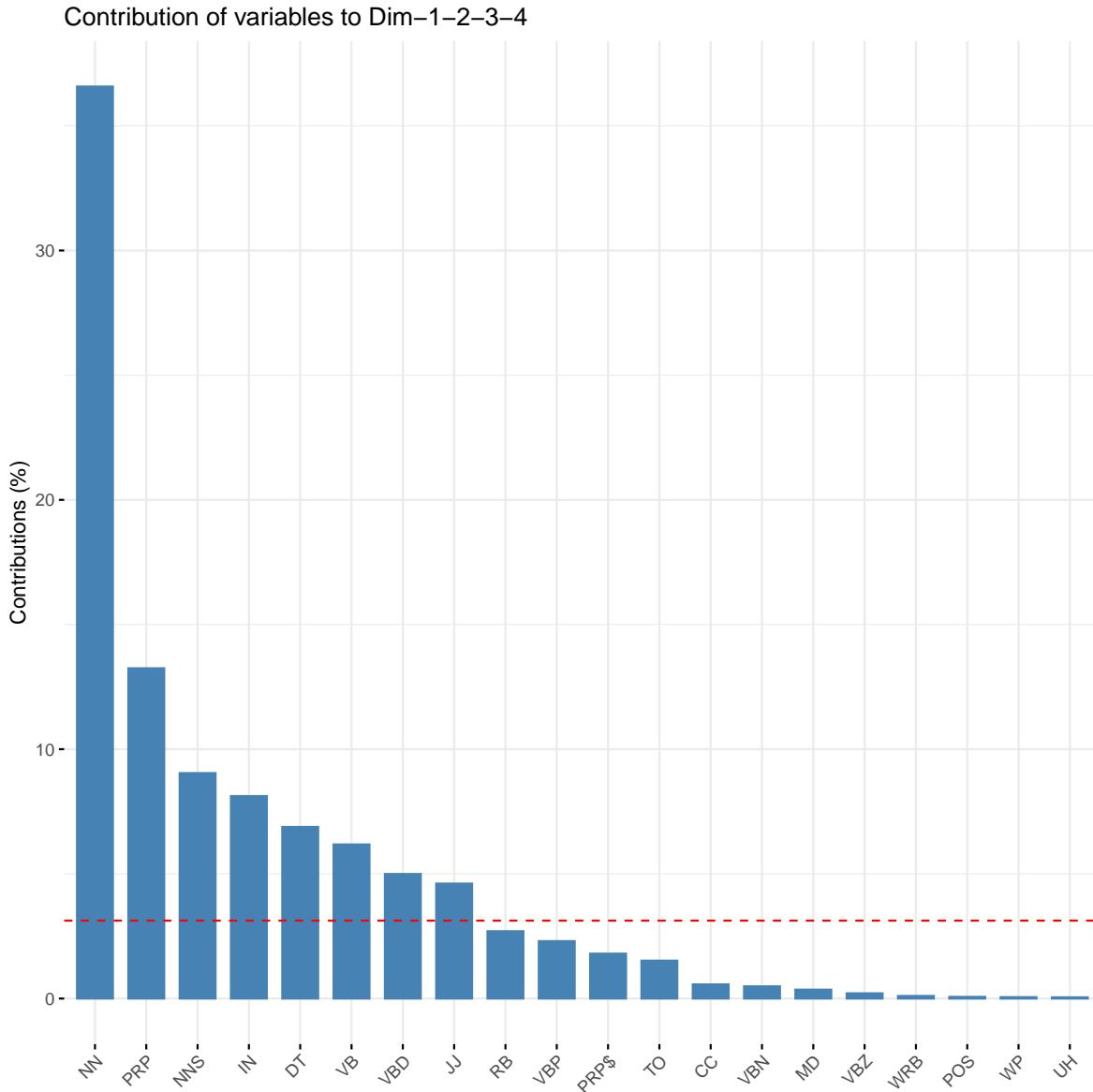


Figure 8.5: Feature contributions to the PCA of the MASC dataset

From Figure 8.5, we can see that the four principle components are dominated by the relative frequency of nouns, personal pronouns, prepositions, and determiners. This information can help us better understand the results of the clustering algorithm.

Now that we have identified the features that we want to use for clustering and we have represented the features in a way that can be used for clustering, we can apply a clustering algorithm to the data. For Hiearchical clustering, we can use the `hclust()` function from base

R. The `hclust()` function takes a distance matrix as its argument and an argument `method = "average"` to specify the average linkage method. The average linkage method takes the average of the dissimilarities between all pairs in two clusters. It is less sensitive to outliers compared to other methods. Let's apply the clustering algorithm to the part of speech features, as seen in Example 8.26.

Example 8.26.

```
# Extract first 4 principle components
masc_pos_pca_pc <-
  masc_pos_pca$x[, 1:4]

# Create distance matrix
masc_pos_dist <-
  masc_pos_pca_pc |>
  dist(method = "manhattan")

# Apply the clustering algorithm
masc_pos_hc <-
  masc_pos_dist |>
  hclust(method = "average")

# Visualize
masc_pos_hc |> fviz_dend(show_labels = FALSE)
```

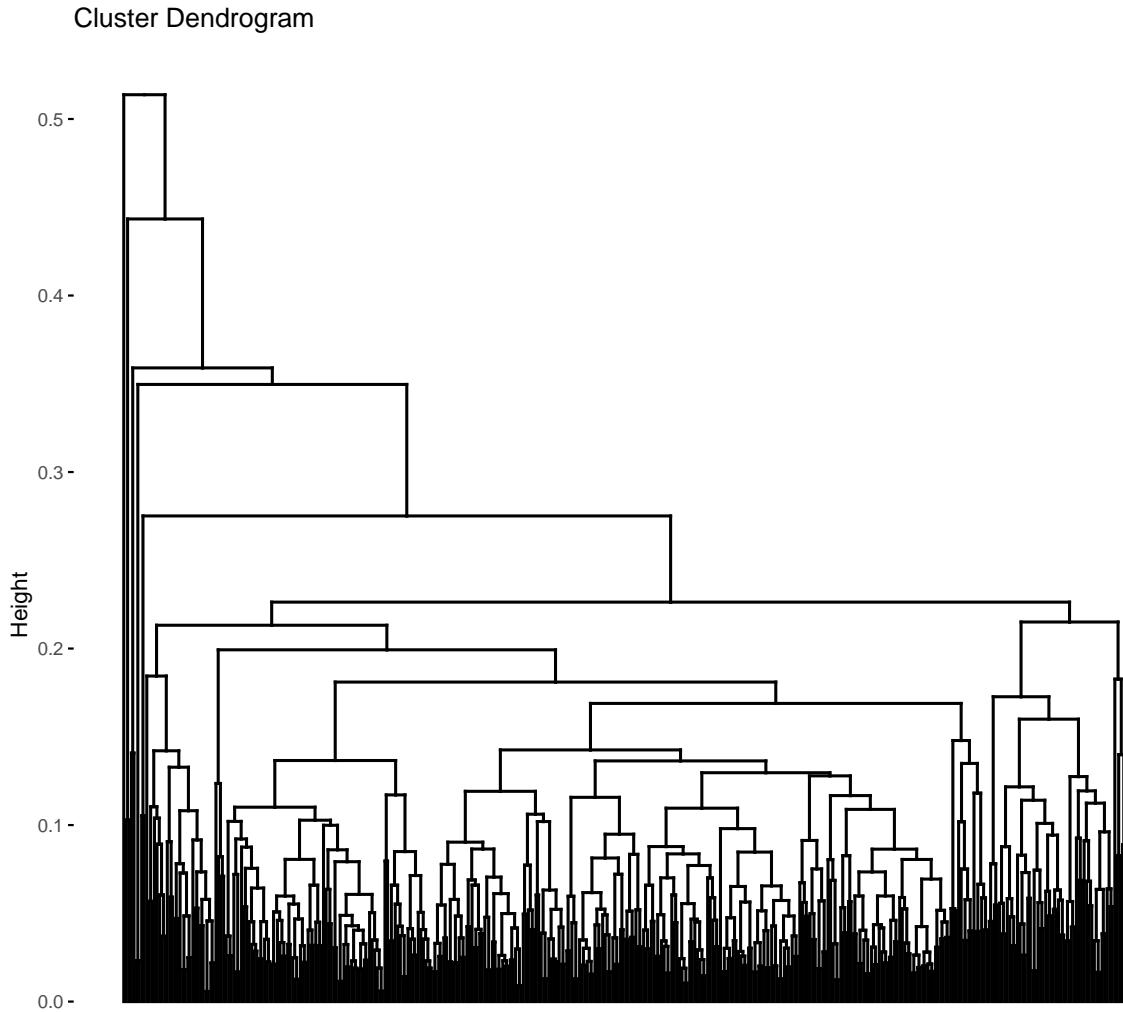


Figure 8.6: Hierarchical clustering of the MASC dataset

Since we are exploring the usefulness of the 18 genre labels used in the MASC dataset we have a good idea of how many clusters we want to start with. This is a good case to employ the K-means clustering algorithm. In K-means clustering, we specify the number of clusters that we want to identify. For each cluster number, a random center is generated. Then each observation is assigned to the cluster with the nearest center. The center of each cluster is then recalculated based on the distribution of the observations in the cluster. This process is

iterates either a pre-defined number of times, or until the centers converge (*i.e* observations stop switching clusters).

We can use the `kmeans()` function from base R to apply the K-means clustering algorithm. The `kmeans()` function takes the matrix of features as its first argument and the number of clusters as its second argument. We can specify the number of clusters with the `centers` argument. The `kmeans()` function also takes an argument `nstart` to specify the number of random starts. The K-means algorithm is sensitive to the initial starting points, so it is a good idea to run the algorithm multiple times with different starting points. The `nstart` argument specifies the number of random starts. The default value is 1, but we can increase this to 10 or 20 to increase the likelihood of finding a good solution.

Our goal, then, will be to assess how well this number of clusters fits the data. If it does not fit the data well, we can try a different number of clusters. We can then compare the results of the clustering with the genre labels to see how well the clusters map to the labels and make adjustments to the way we group the labels as necessary.

Let's start with 18 clusters, assuming the target of the number of genres in the MASC dataset. We can apply the K-means clustering algorithm to the part of speech features, as seen in Example 8.27.

Example 8.27.

```
# Extract first 4 principle components
masc_pos_pca_pc <-
  masc_pos_pca$x[, 1:4]

# K-means clustering
masc_pos_kmeans <-
  masc_pos_pca_pc |>
  kmeans(
    centers = 18,
    nstart = 25,
    iter.max = 20
  )
```

The `factoextra` package provides `fviz_cluster()` function for visualizing the results of clustering algorithms. The `fviz_cluster()` function takes the output of the `kmeans()` function as its first argument and the matrix of features as its second argument. The `fviz_cluster()` function can be used to visualize the clusters in the data, as seen in Figure 8.7.

```
# Visualize
masc_pos_kmeans |> # output of kmeans()
```

```
fviz_cluster(  
  data = masc_pos_pca_pc, # matrix of features  
  ellipse.type = "norm",  
  ellipse.level = 0.95,  
  geom = "point",  
  pointsize = 1,  
  palette = "grey",  
  ggtheme = theme_qtalr()  
)
```

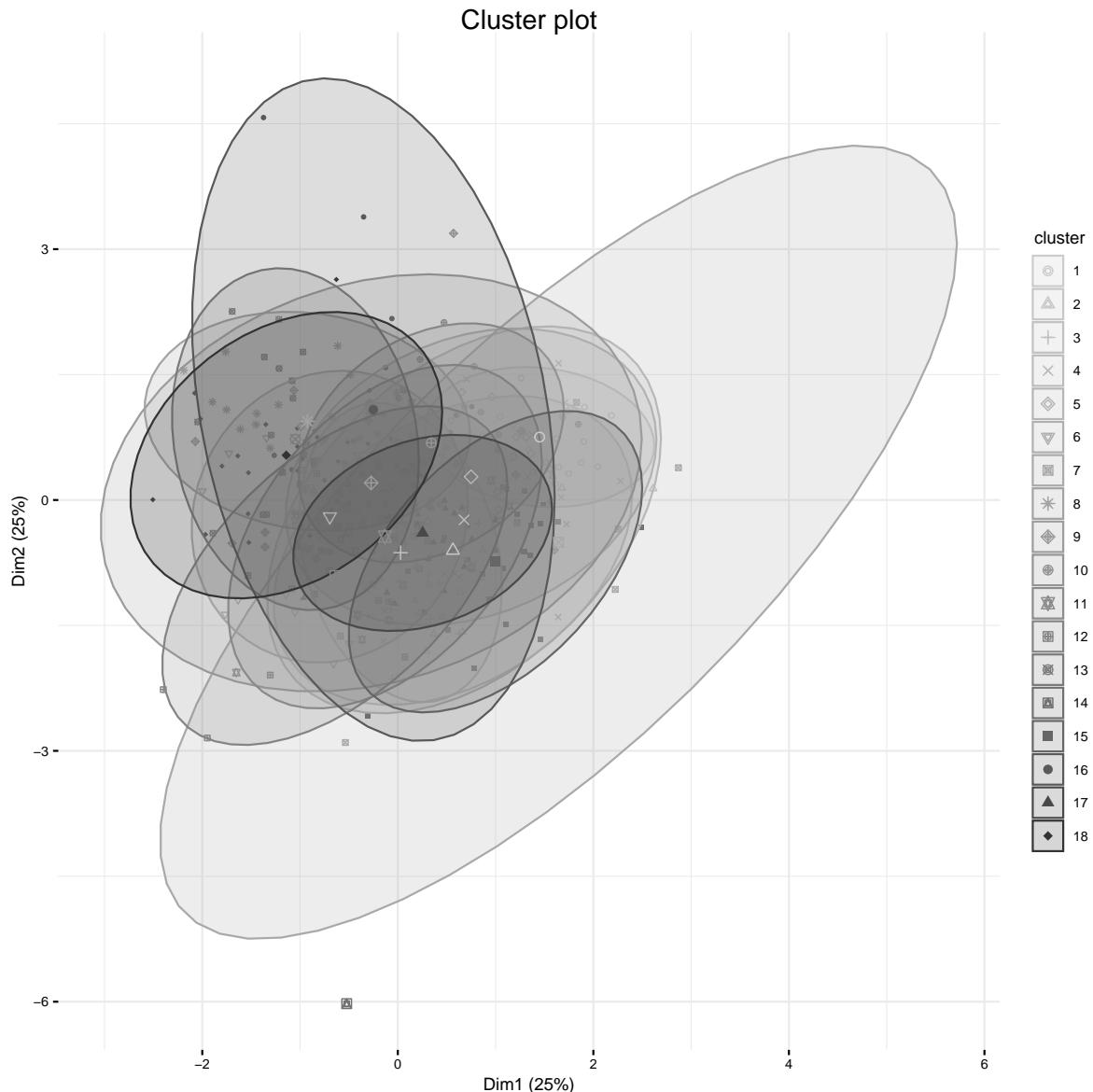


Figure 8.7: K-means clustering of the MASC dataset

The ellipses in a k-means plot represent the 95% confidence interval for each cluster. The ellipses are based on the multivariate normal distribution of the data in each cluster. The size and shape of the ellipses tell us about the variance of the data in each cluster. The larger the ellipse the greater the dispersion of values. A wide ellipse suggests high within cluster variability. The distance between the clusters also tells us about the similarity between the

clusters. The closer the clusters are to each other, the more similar they are. The further the clusters are from each other, the more dissimilar they are.

So in Figure 8.7, we see a mix of shapes and sizes. This suggests that some clusters are more homogeneous than others. We also see separation between the large wide clusters towards the top of the plot and the smaller, more circular clusters towards the center. With 18 clusters, we have a lot of clusters, so it is difficult to interpret the results as there is a large amount of overlap. In sum, 18 clusters is likely not an optimal number for this clustering approach.

We could run the code in Example 8.27 for different values for k and plot each in turn. But a more effective way to determine the optimal number of clusters is to plot the within-cluster sum of squares (WSS) for a range of values for k . The WSS is the sum of the squared distance between each observation and its cluster center. With a plot of the WSS for a range of values for k , we can identify the value for k where the WSS begins to level off, using the elbow method. It is not always clear where the elbow is, yet it is a good starting point for identifying the optimal number of clusters.

Again, the `factoextra` package has us covered. The `fviz_nbclust()` function can be used to plot the WSS for a range of values for k . The `fviz_nbclust()` function takes the `kmeans()` function as its first argument and the matrix of features as its second argument. The `fviz_nbclust()` function also takes arguments `method = "wss"` to specify the WSS method and `k.max = 20` to specify the maximum number of clusters to plot. Let's plot the WSS for a range of values for k , as seen in Figure 8.8.

```
# Determine the optimal number of clusters
masc_pos_pca_pc |>
  fviz_nbclust(
    FUNcluster = kmeans,
    method = "wss", # method
    k.max = 20,
    nstart = 25,
    iter.max = 20
  )
```

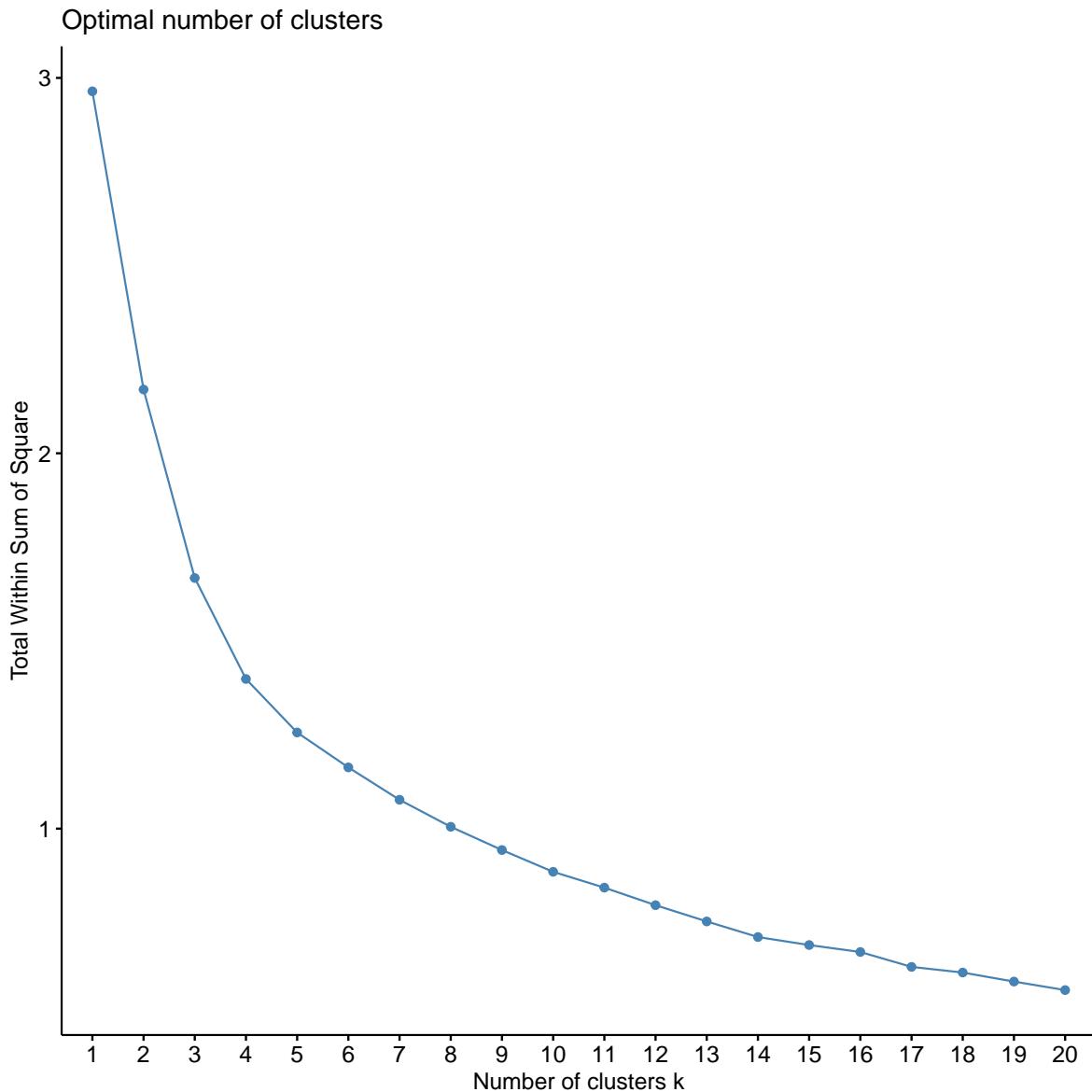


Figure 8.8: Elbow method for k-means clustering of the MASC dataset

It is clear that there is significant gains in cluster fit from 1 to 4 clusters, but the gains begin to level off after 5-7 clusters. Now we can skip ahead and try 4 clusters, as seen in Example 8.28.

Example 8.28.

```
# Set seed for reproducibility
set.seed(123)

# K-means: for 5 clusters
masc_pos_kmeans_fit <-
  masc_pos_pca_pc |>
  kmeans(
    centers = 4,
    nstart = 25,
    iter.max = 20
  )

# Visualize
masc_pos_kmeans_fit |>
  fviz_cluster(
    data = masc_pos_pca_pc,
    ellipse.type = "norm",
    ellipse.level = 0.95,
    geom = "point",
    pointsize = 1,
    palette = "grey",
    ggtheme = theme_qtalr()
  )
```

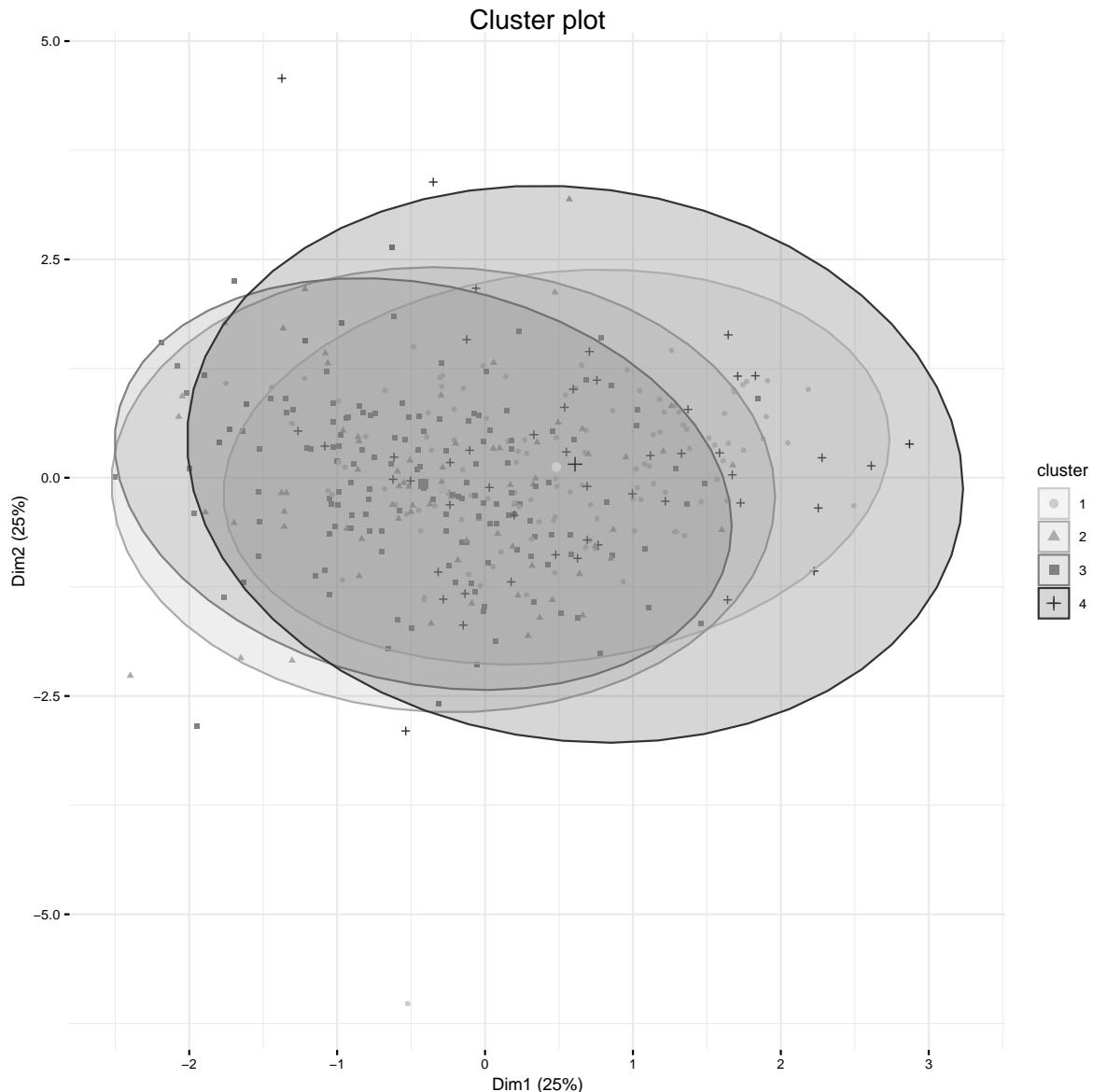


Figure 8.9: K-means clustering of the MASC dataset with 4 clusters

The results are much more interpretable with 4 clusters. We can see that the clusters are more homogeneous and more distinct from each other, in particular clusters 1 and 2, and are generally similar in shape and size. However, there is still some overlap between the clusters, in particular for clusters 3 and 4. We expect there to be noise as we have paired down the number of features from over 25k to 4, so this is a good working solution.

From this point we can join document-cluster pairings produced by the k-means algorithm with the original dataset. We can then explore the clusters in terms of the original features. We can also explore the clusters in terms of the original labels. Let's join the cluster assignments to the original dataset, as seen in Example 8.29.

Example 8.29.

```
# Organize k-means clusters into a tibble
masc_pos_cluster_tbl <-
  tibble(
    doc_id = names(masc_pos_kmeans_fit$cluster),
    cluster = masc_pos_kmeans_fit$cluster
  )

# Join cluster assignments to original dataset
masc_cluster_tbl <-
  masc_tbl |>
  left_join(
    masc_pos_cluster_tbl,
    by = "doc_id"
  )

# Preview
masc_cluster_tbl |>
  slice_head(n = 5)

> # A tibble: 5 x 8
>   doc_id modality genre  term_num term      lemma      pos  cluster
>   <chr>   <chr>   <chr>     <dbl> <chr>     <chr>     <chr>   <int>
> 1 1       Written  Letters      2 Your      your      PRP$      1
> 2 1       Written  Letters      3 contribution contribution NN      1
> 3 1       Written  Letters      4 to        to        T0        1
> 4 1       Written  Letters      6 will      will      MD        1
> 5 1       Written  Letters      7 mean      mean      VB        1
```

We now see that the cluster assignments from the k-means algorithm have been joined to the original dataset. We can now explore the clusters in terms of the original features. For example, let's look at the distribution of the clusters across modality first, as seen in Example 8.30. To do this, we first need to reduce our dataset to the distinct combinations of modality, genre, and cluster. Then, we can use the `janitor` package's `tabyl()` function to provide formatted percentages.

Example 8.30.

```
# Load package
library(janitor)

# Reduce to distinct combinations of modality, genre, and cluster
masc_meta_tbl <-
  masc_cluster_tbl |>
  distinct(modality, genre, cluster)

# Tabulate: cluster by modality
masc_meta_tbl |>
  tabyl(cluster, modality) |>
  adorn_percentages("row") |>
  adorn_pct_formatting(digits = 1)

>   cluster Spoken Written
>     1    30.8%  69.2%
>     2     0.0% 100.0%
>     3     8.3%  91.7%
>     4     0.0% 100.0%
```

From Example 8.30, we can see that the clusters are not evenly distributed across the modalities. In particular, cluster 1 is where the great majority of the spoken modality appears. We can also appreciate that there may be some written genres that are more similar to spoken genres than other written genres. This may be something we could like to explore further.

Let's dive into genres and limit our analysis to the written modality, as seen in Example 8.31. To do this, we first need to filter the dataset to the written modality. In addition to the row-wise percentages which capture the proportion of the genre that contributes to each cluster, let's also consider the column-wise percentages to consider how each genre is distributed across the clusters.

Example 8.31.

```
# Tabulate: cluster by genre for written modality
masc_meta_tbl |>
  filter(modality == "Written") |>
  tabyl(cluster, genre) |>
  adorn_percentages("row") |>
  adorn_pct_formatting(digits = 1)
```

```

> cluster Blog Email Essay Fiction Fictlets Government Jokes Journal Letters
>      1 11.1% 11.1% 11.1% 11.1% 11.1% 0.0% 11.1% 11.1% 11.1%
>      2 20.0% 20.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 20.0%
>      3 9.1% 9.1% 9.1% 9.1% 0.0% 9.1% 0.0% 9.1% 9.1%
>      4 0.0% 20.0% 20.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0%
> Newspaper Non-fiction Technical Travel Guide Twitter
>      11.1% 0.0% 0.0% 0.0% 0.0%
>      20.0% 0.0% 0.0% 0.0% 20.0%
>      9.1% 9.1% 9.1% 9.1% 0.0%
>      20.0% 20.0% 20.0% 0.0% 0.0%

```

```

# Tabulate: cluster by genre for written modality
masc_meta_tbl |>
  filter(modality == "Written") |>
  tabyl(cluster, genre) |>
  adorn_percentages("col") |>
  adorn_pct_formatting(digits = 1)

```

```

> cluster Blog Email Essay Fiction Fictlets Government Jokes Journal Letters
>      1 33.3% 25.0% 33.3% 50.0% 100.0% 0.0% 100.0% 50.0% 33.3%
>      2 33.3% 25.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 33.3%
>      3 33.3% 25.0% 33.3% 50.0% 0.0% 100.0% 0.0% 50.0% 33.3%
>      4 0.0% 25.0% 33.3% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0%
> Newspaper Non-fiction Technical Travel Guide Twitter
>      25.0% 0.0% 0.0% 0.0% 0.0%
>      25.0% 0.0% 0.0% 0.0% 100.0%
>      25.0% 50.0% 50.0% 100.0% 0.0%
>      25.0% 50.0% 50.0% 0.0% 0.0%

```

On the other hand, looking at the written genres, we see that there are some genres which are grouped entirely in cluster 1. In other words, these genres, such as ‘Fictlets’ and ‘Jokes’, align with spoken genres in terms of their grammatical diversity. This is an interesting finding that we may want to explore further. Furthermore, it may be of interest to explore individual documents in genres which have a significant proportion of documents in cluster 1. There are too many possibilities to explore here but this is a good example of how exploratory data analysis can be used to identify new questions and new variables of interest.

💡 Consider this

Given the cluster assignments derived using the distribution of part of speech tags, what other relationships between the clusters and the original features could one explore?

What are the limitations of this approach? What are the implications of this approach for the interpretation of the results?

8.2.2.2 Vector space models

In our discussion of clustering, we targeted associations between documents based on the distribution of linguistic features. We now turn to targeting associations between linguistic features based on their distribution across documents. The technique we will introduce is known as **vector space modeling**. Vector space modeling aims to represent linguistic features as numerical vectors which reflect the various linguistic contexts in which the features appear. Together these vectors form a feature-context space in which features with similar contextual distributions are closer together.

An interesting property of vector space models is that are able to capture semantic and/ or syntactic relationships between features based on their distribution. In this way, vector space modeling can be seen as an implementation of the **distributional hypothesis** –that is, words that appear in similar linguistic contexts tend to have similar meanings (Harris 1954). As Firth (1957) states “you shall know a word by the company it keeps”.

Case study

Garg et al. (2018) quantify and compare gender and ethnic stereotypes over time using word embeddings. The authors explore the temporal dynamics of stereotypes using word embeddings as a quantitative measure of bias. The data used includes word embeddings from the Google News dataset for contemporary analysis, as well as embeddings from the COHA and Google Books datasets for historical analysis. Additional validation is done using embeddings from the New York Times Annotated Corpus. Several word lists representing gender, ethnicity, and neutral words are collated for analysis. The main finding is that language reflects and perpetuates cultural stereotypes, and the analysis shows consistency in the relationships between embedding bias and external metrics across datasets over time. The results also highlight the impact of historical events, such as the women’s movement of the 1960s, on the encoding of stereotypes.

Let’s assume in our textbook project we are interested in gathering information about English’s expression of the semantic concepts of manner and motion. For learners of English, this can be an area of difficulty as languages differ in how these semantic properties are expressed. English is a good example of a “satellite-framed” language, that is that manner and motion are often encoded in the same verb with a particle encoding the motion path (“rush out”, “climb up”). Other languages such as Spanish, Turkish, and Japanese are “verb-framed” languages, that is that motion but not manner is encoded in the verb (“salir corriendo”, “koşarak çıkmak”, “ ”).

We can use vector space modeling to represent the distribution of verbs in the MASC dataset and then target the concepts of manner and motion to then explore how English encodes these concepts. The question will be what will our features be. They could be terms, lemmas, pos tags, *etc.* Or they could be some combination. Considering the task at hand which we will ultimately want to know something about verbs, it makes sense to include the part of speech information in combination with either the term or the lemma.

If we include term and pos then we have a feature for every morphological variant of the term (*e.g.* house_VB, housed_VBD, housing_VBG). This can make the model more sizeable than it needs to be. If we include lemma and pos then we have a feature for every lemma with a distinct grammatical category (*e.g.* house_NN, house_VB). Note that as the pos tags are from the Penn tagset, many morphological variants appear in the tag itself (*e.g.* house_VB, houses_VBZ, housing_VBG). This is a good example of how the choice of features can impact the size of the model. In our case, it is not clear that we need to include the morphological variants of the verbs, so we will use lemma and a simplified pos as our features.

To engineer these features we will need to simplify the tags. We will conflate Penn tagset distinctions between nouns, verbs, adjectives, and adverbs. This will give us a feature for every lemma with a distinct grammatical category (*e.g.* house_NOUN, house_VERB), and no more than that. To do this we can apply the `case_when()` function from the `dplyr` package. The `case_when()` function takes a series of logical statements and returns a value based on the first logical statement that is `TRUE`. Let's conflate the Penn tagset distinctions between nouns, verbs, adjectives, and adverbs, as seen in Example 8.32.

Example 8.32.

```
# Conflate Penn tagset into Universal-like tagset
masc_tbl <-
  masc_tbl |>
  mutate(xpos = case_when(
    pos %in% c("NN", "NNS", "NNP", "NNPS") ~ "NOUN",
    pos %in% c("VB", "VBD", "VBG", "VBN", "VBP", "VBZ") ~ "VERB",
    pos %in% c("JJ", "JJR", "JJS") ~ "ADJ",
    pos %in% c("RB", "RBR", "RBS") ~ "ADV",
    TRUE ~ pos # keep other tags
  ))

# Lemma + pos
masc_tbl <-
  masc_tbl |>
  mutate(lemma_pos = str_c(lemma, xpos, sep = "_"))
```

```
# Preview  
masc_tbl |> glimpse()
```

```
> Rows: 439,215
> Columns: 9
> $ doc_id    <chr> "1", "1", "1", "1", "1", "1", "1", "1", "1", "1", "1", "1", "1", ~
> $ modality  <chr> "Written", "Written", "Written", "Written", "Written", "Written", ~
> $ genre     <chr> "Letters", "Letters", "Letters", "Letters", "Letters", "Letters", ~
> $ term_num  <dbl> 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 18, 19, 20, ~
> $ term      <chr> "Your", "contribution", "to", "will", "mean", "more", "than", ~
> $ lemma     <chr> "your", "contribution", "to", "will", "mean", "more", "than", ~
> $ pos        <chr> "PRP$", "NN", "TO", "MD", "VB", "JJR", "IN", "PRP", "MD", "VB", ~
> $ xpos       <chr> "PRP$", "NOUN", "TO", "MD", "VERB", "ADJ", "IN", "PRP", "MD", "VB", ~
> $ lemma_pos <chr> "your_PRP$", "contribution_NOUN", "to_TO", "will_MD", "mean_IN", ~
```

When VSM is applied to words, it is known as **word embedding**. To calculate word embeddings there are various algorithms that can be used (BERT, word2vec, GloVe, *etc.*) The most common algorithm is **word2vec** (Mikolov et al. 2013). Word2vec is a neural network-based algorithm that learns word embeddings from a large corpus of text. In the word2vec algorithm the researcher can choose to learn embeddings from a Continuous Bag of Words (CBOW) or a Skip-gram model. The CBOW model predicts a target word based on the context words. The Skip-gram model predicts the context words based on the target word. The CBOW model is faster to train and is better for frequent words. The Skip-gram model is slower to train and is better for infrequent words.

Another consideration to take into account is the size of the corpus used to train the model. VSM provide more reliable results when trained on larger corpora. The MASC dataset is relatively small. We've simplified our features in order to have a smaller vocabulary in hopes to offset this limitation to a degree. But the choice of either CBOW or Skip-gram can also help to offset this limitation. CBOW can be better for smaller corpora as it aggregates context information.

To implement the word2vec algorithm on our lemma + pos features, we will use the `word2vec` package. The `word2vec()` function takes a text file and uses it to train the vector representations. To prepare the MASC dataset for training, we will need to write the lemma + pos features to a text file as a single character string. We can do this by first collapsing the `lemma_pos` variable into a single string for each document using the `str_c()` function. Then we can use the `write_lines()` function to write the string to a text file. Let's prepare the MASC dataset for training, as seen in Example 8.33.

Example 8.33.

```

# Prepare data for word2vec training
masc_tbl |>
  summarize(text = str_c(lemma_pos, collapse = " ")) |>
  pull(text) |>
  write_lines(
    file = "../data/analysis/masc_word2vec.txt"
  )

```

With our *masc_word2vec.txt* file, we read in, apply the word2vec algorithm using the `word2vec` package, and write the model to disk. By default, the `word2vec()` function applies the CBOW model, with 50 dimensions, a window size of 5, and a minimum word count of 5. We can change these parameters as needed, but let's apply the default algorithm to the text file splitting features by sentence punctuation, as seen in Example 8.34.

Example 8.34.

```

# Load package
library(word2vec)

# Training word2vec model
masc_model <-
  word2vec(
    x = "../data/analysis/masc_word2vec.txt",
    split = c(" ", ".?!")
  )

# Write model to disk
write.word2vec(
  mascot,
  file = "../data/analysis/masc_word2vec.bin"
)

```

Writing the model to disk is important as it allows us to read the model in without having to retrain it. In cases where the corpus is large, this can save a lot of computational time.

Now that we have a trained model, we can read it in with the `read.vectors()` function from the `wordVectors` package.

Example 8.35.

```

# Load package
library(wordVectors)

# Read word2vec model
masc_model <-
  read.vectors(
    filename = "../data/analysis/masc_word2vec.bin"
  )

```

The `read.vectors()` function returns a matrix where each row is a term in the model and each column is a dimension in the vector space, as seen in Example 8.36.

Example 8.36.

```

# Inspect
dim(masc_model)

> [1] 5892 50

# Preview
masc_model[1:5, 1:5]

> A VectorSpaceModel object of 5 words and 5 vectors
>           [,1]   [,2]   [,3]   [,4]   [,5]
> map_VERB      -1.487  1.510 -0.662 -1.2129 -0.6458
> KGCUBS10_NOUN -0.387  1.751 -0.603  0.6270 -0.1965
> MICKEY3_NOUN   0.675  1.035 -0.516  1.1289 -0.0784
> amenity_NOUN   -0.311  0.682 -1.225  0.0541 -0.8392
> transmission_NOUN -0.837 -0.354 -1.193 -0.5576 -0.7866
> attr(".cache")
> <environment: 0x7f9f5bf5dd98>

```

The row-wise vector in the model is the vector representation of each feature. The notion is that these values can now be compared with other terms to explore distributional relatedness. We can extract specific features from the matrix using the `[]` operator.

As an example, let's compare the vectors for noun-verb pairs for the lemmas 'run' and 'walk'. To do this we extract these features from the model. To appreciate the relatedness of these features it is best to visualize them. We can do this by first reducing the dimensionality of the

vectors using principal components analysis (PCA). We can then plot the first two principle components, as seen in Figure 8.10.

Example 8.37.

```
# Extract vectors
word_vectors <-
  masc_model[c("run_VERB", "walk_VERB", "run_NOUN", "walk_NOUN"), ] |>
  as.matrix()

pca <-
  word_vectors |>
  scale() |>
  prcomp()

pca_tbl <-
  as_tibble(pca$x[, 1:2]) |>
  mutate(word = rownames(word_vectors))

pca_tbl |>
  ggplot(aes(x = PC1, y = PC2, label = word)) +
  geom_point() +
  ggrepel::geom_text_repel()
```

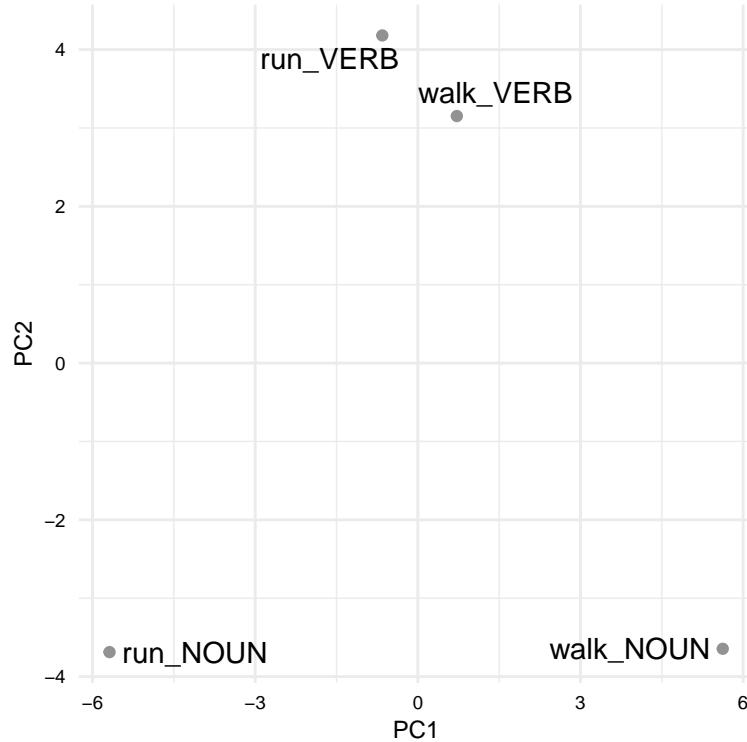


Figure 8.10: Similarity between ‘run’ and ‘walk’ in the MASC dataset

From Figure 8.10, we can see that each of these features occupies a distinct position in the reduced vector space. But on closer inspection, we can see that there is a relationship between the lemma pairs. Remember that PCA reduces the dimensionality of the data by identifying the dimensions that capture the greatest amount of variance in the data. This means that of the 50 dimensions in the model, the PC1 and PC2 correspond to orthogonal dimensions that capture the greatest amount of variance in the data. If we look along PC2, we can see that there is a distinction between part of speech. Looking along PC1, we see some pariyty between lemma meanings. Given these features, we can see that meaning and grammatical category can be approximated in the vector space.

An interesting property of vector space models is that we can build up a dimension of meaning by adding vectors that we expect to approximate that meaning. For example, we can add the vectors for typical motion verbs to create a vector for motion-similarity and one for manner-similarity. We can then compare the feature vectors for all verbs and assess their motion-similarity and manner-similarity.

To do this let’s first subset the model to only include verbs, as in Example 8.38. We will also remove the part of speech tags from the rownames of the matrix as they are no longer needed.

Example 8.38.

```
# Filter to verbs
verbs <- str_subset(rownames(masc_model), ".*_VERB")
verb_vectors <- masc_model[verbs, ]

# Remove part of speech tags
rownames(verb_vectors) <-
  verb_vectors |>
  rownames() |>
  str_replace_all("_VERB", "")

# Inspect
dim(verb_vectors)
```

```
> [1] 1115 50
```

```
# Preview
verb_vectors[1:5, 1:5]
```

```
> A VectorSpaceModel object of 5 words and 5 vectors
>      [,1] [,2] [,3] [,4] [,5]
> map     -1.4875 1.510 -0.662 -1.2129 -0.646
> whip     0.0496 0.919 -1.020  0.3087  0.350
> enroll   -0.6251 1.620 -1.878  0.0861 -0.428
> tuck     0.5610 1.054 -1.331 -0.5298  1.598
> suppress 0.3824 1.928 -1.750 -0.3229 -0.643
> attr(".cache")
> <environment: 0x7f9f3858aea0>
```

We now have `verb_vectors` which includes the vector representations for all verbs 1,115 in the MASC dataset. Next, let's seed the vectors for motion-similarity and manner-similarity and calculate the vector 'closeness' to the motion and manner seed vectors with the `closest_to()` function from the `wordVectors()` package.

Example 8.39.

```
# Add vectors for motion-similarity and manner-similarity
motion <-
```

```

c("go", "come", "leave", "arrive", "enter", "exit", "depart", "return")

motion_similarity <-
  verb_vectors |> closest_to(motion, n = Inf)

# Preview
motion_similarity |> glimpse()

```

```

> Rows: 1,115
> Columns: 2
> $ word           <chr> "tie", "approach", "enter", "step", "race", "ru-
> $ `similarity to motion` <dbl> 0.803, 0.803, 0.786, 0.784, 0.781, 0.770, 0.769-

```

```

manner <-
  c("run", "walk", "jump", "crawl", "swim", "fly", "drive", "ride")

manner_similarity <-
  verb_vectors |> closest_to(manner, n = Inf)

# Preview
manner_similarity |> glimpse()

```

```

> Rows: 1,115
> Columns: 2
> $ word           <chr> "walk", "drop", "pull", "climb", "step", "throw-
> $ `similarity to manner` <dbl> 0.885, 0.877, 0.864, 0.860, 0.859, 0.842, 0.840-

```

The `motion_similarity` and `manner_similarity` data frames each contain all the verbs with a corresponding closeness measure. We can join these two data frames by feature to create a single data frame with the motion-similarity and manner-similarity measures, as seen in Example 8.40.

Example 8.40.

```

# Join motion-similarity and manner-similarity
manner_motion_similarity <-
  manner_similarity |>
  inner_join(motion_similarity)

```

```
# Preview
manner_motion_similarity |> glimpse()
```

```
> Rows: 1,115
> Columns: 3
> $ word           <chr> "walk", "drop", "pull", "climb", "step", "throw"
> $ `similarity to manner` <dbl> 0.885, 0.877, 0.864, 0.860, 0.859, 0.842, 0.840~
> $ `similarity to motion` <dbl> 0.743, 0.751, 0.623, 0.753, 0.784, 0.582, 0.709~
```

The result of Example 8.40 is a data frame with the motion-similarity and manner-similarity measures for all verbs in the MASC dataset. We can now visualize the distribution of motion-similarity and manner-similarity measures, as seen in Figure 8.11.

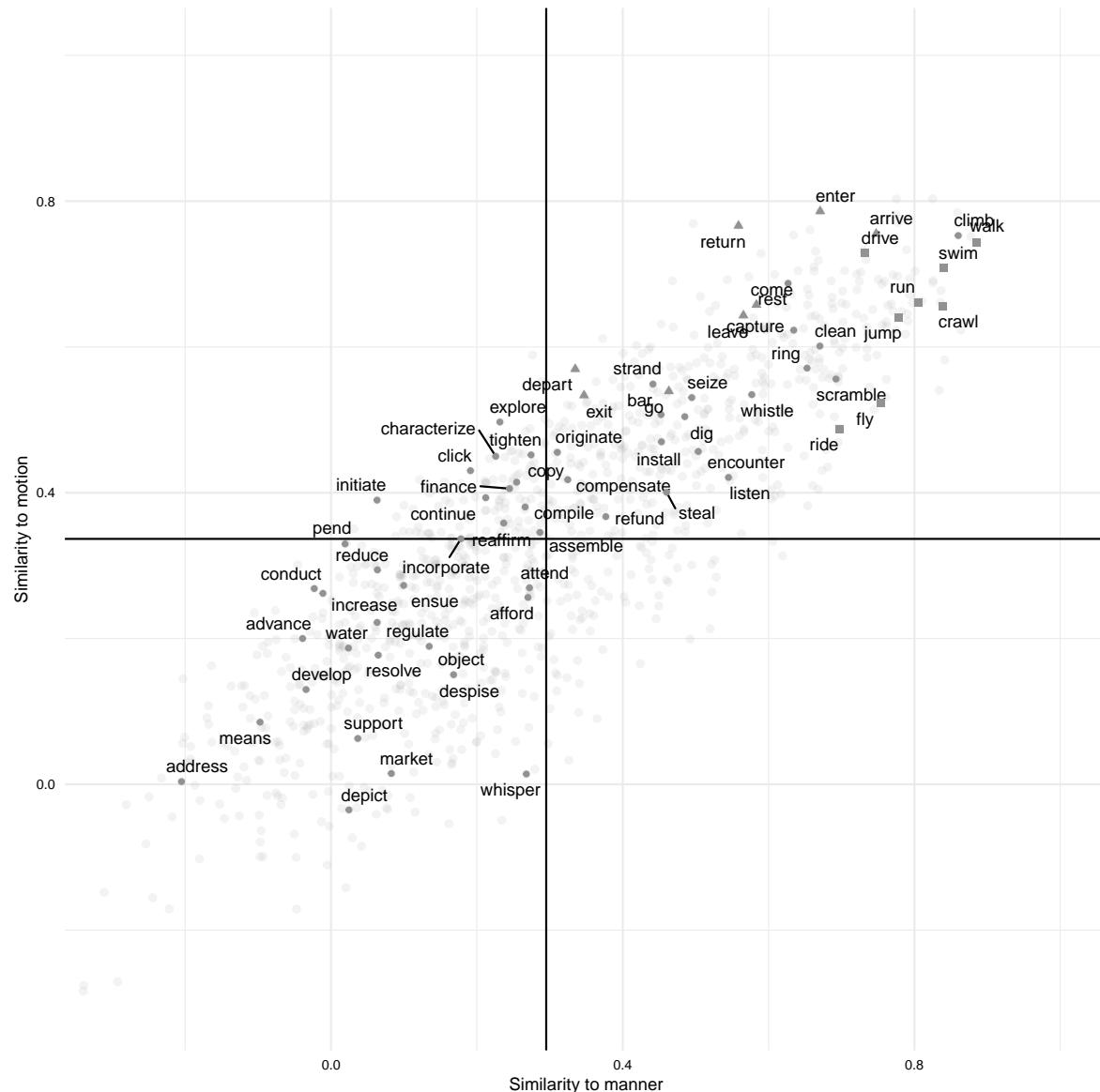


Figure 8.11: Motion-similarity and manner-similarity of verbs in the MASC dataset

From Figure 8.11, we can see that the manner-similarity is plotted on the x-axis and the motion-similarity on the y-axis. I've added horizontal and vertical lines to break the scatterplot into quadrants – the top-right corresponding to high manner- and motion-similarity and the bottom-left corresponding to low manner- and motion-similarity. This captures the majority of the verbs in the dataset. The verbs in the top-left quadrant have high motion-similarity but

lower manner similarity, and verbs in the bottom-right quadrant have high manner-similarity but lower motion-similarity.

I've randomly sampled 50 verbs from the dataset and plotted them as text labels. I've also plotted the motion and manner seed vectors as triangle and box points, respectively. We can see that motion- and manner-similarity seed verbs are found in the top-left quadrant together, showing that they are semantically related. Verbs in the other quadrants are either lower in motion- or manner-similarity, or both. From a qualitative point of view it appears that many of the verbs coincide with intuition. Some, however, less so. This is to be expected to some degree as the model is trained on a relatively small corpus. All in all, this serves as an example of how vector space modeling can be used to explore semantic relationships between linguistic features.

Activities

_recipe

What: Exploratory analysis methods^a

How: Read Recipe 8 and participate in the Hypothes.is online social annotation.

Why: To illustrate how to prepare a dataset for descriptive and unsupervised machine learning methods and evaluate the results for exploratory data analysis.

^a<https://qtalr.github.io/qtalrkit/articles/recipe-8.html>

_lab

What: Pattern discovery^a

How: Clone, fork, and complete the steps in Lab 08.

Why: To gain experience working with coding strategies to prepare, feature engineer, explore, and evaluate results from exploratory data analyses, practice transforming datasets into new object formats and visualizing relationships, and implement organizational strategies for organizing and reporting results in a reproducible fashion.

^a<https://github.com/qtalr/lab-08>

Summary

In this chapter we surveyed a range of methods for uncovering insights from data, particularly when we do not have a predetermined hypothesis. We broke the chapter discussion along the two central branches of exploratory data analysis: descriptive analysis and unsupervised learning. Descriptive analysis offers statistical or visual summaries of datasets through frequency, dispersion, and co-occurrence measures, while unsupervised learning utilizes machine learning

techniques to uncover patterns without predefining variable relationships. Here we covered a few unsupervised learning methods including clustering, dimensionality reduction, and vector space modeling. Through either descriptive or unsupervised learning methodologies, we probe questions in a data-driven fashion and apply methods to summarize, reduce, and sort complex datasets. This in turn facilitates novel, quantitative perspectives that can subsequently be evaluated qualitatively, offering us a robust approach to exploring and generating research questions.

9 Predict

All models are wrong, but some are useful.

— George E.P. Box

▀ Outcomes

- Identify the research goals of predictive data analysis
- Describe the workflow for predictive data analysis
- Recognize quantitative and qualitative methods for evaluating predictive models

In this chapter, I introduce supervised learning as an approach to data analysis, specifically focusing on its applications in text analysis. Supervised learning aims to establish a relationship between a target (or outcome) variable and a set of feature variables derived from text data. By leveraging this relationship, statistical generalizations (models) can be created to accurately predict values of the target variable based on the values of the feature variables. Throughout the chapter, we explore practical tasks and theoretical applications of statistical learning in text analysis. We also cover the standard workflow for building predictive models, testing and evaluating model performance, improving model accuracy, and interpreting and reporting findings.

➤_ Lessons

What: Advanced Visualization^a

How: In the R Console pane load `swirl`, run `swirl()`, and follow prompts to select the lesson.

Why: ... ↗

^a<https://github.com/qtalr/lessons>

9.1 Orientation

In this section, I introduce the concept of supervised learning and provide an overview of the workflow for building and evaluating predictive models for text analysis. First we will discuss the research goals that are typically addressed using supervised learning, contrasting them with the goals of exploratory and inferential analysis. Next, we will discuss the approaches that are

typically used to address these goals, including the types of data structures and algorithms that are used. Finally, we will discuss the workflow for building predictive models, including the steps for preparing data, training and testing models, and evaluating and reporting results.

9.1.1 Research goal

Predictive data analysis (PDA) is a powerful analysis method for linguists and other researchers interested in making predictions about new or future data based on patterns in existing data. As discussed in Section 3.2.2 and Section 4.4.1, PDA is a type of supervised learning, which means that it involves training a model on a labeled dataset where the input data and desired output are both provided. The model is able to make predictions or classifications based on the input data by learning the relationships between the input and output data. Supervised machine learning is an important tool for linguists studying language and communication, as it allows us to analyze language data to identify patterns or trends in language use, assess hypotheses, and prescribe actions.

In contrast to EDA, PDA does require that we have a particular goal in mind from the outset. This goal is to predict a fixed outcome variable based on a set of predictor variables. However, PDA can be applied with distinct aims in mind: exploratory-oriented or hypothesis-driven prediction. In exploratory-oriented prediction, the goal is to examine potential relationships between an outcome and a mutable set of predictor variables. The results of this type of analysis can be used to generate new insight and questions. In hypothesis-driven prediction, in contrast, the goal is to use predictive data analysis to test a hypothesis about the relationship between the outcome and a pre-defined set of predictor variables. In this case, the results of the analysis is used to explain or infer a relationship between the outcome and predictor variables.

Dive deeper

- expand description of hypothesis-driven prediction
 - MuPDAR approach (Multifactorial Prediction and Deviation Analysis with Regressions) (Deshors and Gries 2016; S. Th. Gries and Deshors 2014) and
 - Training on group
 - Testing on another group (or groups)
 - Discriminant analysis (R. Harald Baayen 2011)

It is important to establish which aim is being taken, as this will influence the approach that is taken. In this chapter we will focus on the exploratory-driven approach to predictive data analysis.

9.1.2 Approach

The approach to conducting predictive analysis shares some commonalities with exploratory data analysis ([?@sec-eda-approach](#)) (as well as inferential analysis Chapter 10), but there are also some key differences. Let's look at the workflow in Table 9.1 and then discuss these commonalities and differences.

Table 9.1: Workflow for predictive data analysis

Step	Name	Description
1	Identify	Consider the research question and aim and identify relevant variables
2		Split the data into representative training and testing sets
3		Apply variable selection and engineering procedures
4	Inspect	Inspect the data to ensure that it is in the correct format and that the training and testing sets are representative of the data
5	Interrogate	Train and evaluate the model on the training set, adjusting models or hyperparameters as needed, to produce a final model
6	(Optional) Iterate	Repeat steps 3-5 to select new variables, models, hyperparameters
7	Interpret	Interpret the results of the final model in light of the research question or hypothesis

Focusing on the overlap with other analysis methods, we can see some fundamental steps such as identifying relevant variables, inspecting the data, interrogating the data, and interpreting the results. And if our research aim is exploratory in nature, iteration may also be a part of the workflow. These steps highlight the importance conducting methodologic and communicable research, as discussed in Section 4.1.

There are two main differences, however, between the PDA and the EDA workflow we discussed in Chapter 8. The first, reflected the majority of the steps in the workflow, is that PDA requires partitioning the data into training and testing sets. As discussed in Section 3.2.2, the training set is used to develop the model, and the testing set is used to evaluate the model's performance. This strategy is used to ensure that the model is robust and generalizes well to new data. It is well known, and makes intuitive sense, that using the same data to develop and evaluate a model likely will not produce a model that generalizes well to new data. This is because the model will have potentially conflated the nuances of the data ('the noise') with any real trends ('the signal') and therefore will not be able to generalize well to new data. This is called overfitting and by holding out a portion of the data for testing, we can evaluate the model's performance on data that it has not seen before and therefore get a more accurate estimate of the generalizable trends in the data.

Another procedure to avoid the perils of overfitting, is to use resampling methods as part of the model evaluation on the training set. Resampling is the process of repeatedly drawing samples from the training set and evaluating the model on each sample. The two most common resampling methods are **bootstrapping** (resampling with replacement) and **cross-validation** (resampling without replacement). The performance of these multiple models are summarized and the error between them is assessed. The goal is to minimize the performance differences between the models while maximizing the overall performance. These measures go a long way to avoiding overfitting and therefore maximizing the chance that the training phase will produce a model which is robust at the testing phase.

The second difference, not reflected in the workflow but inherent in predictive analysis, is that PDA requires a fixed outcome variable. This means that the outcome variable must be defined from the outset and cannot be changed during the analysis. Furthermore, the informational nature of the outcome variable will dictate the what type of algorithm we choose to interrogate the data and how we will evaluate the model's performance. If the outcome is categorical in nature, we will use a **classification algorithm** (e.g. logistic regression, naive bayes, *etc.*). Classification evaluation metrics include accuracy, precision, recall, and F1 score which can be derived from and visualized in a cross-tabulation of the predicted and actual outcome values.

To understand these measures it is helpful to consider a confusion matrix, which is a table that describes the performance of a classification model on data for which the true values are known. The confusion matrix is a two-by-two matrix that shows the number of true positives (TP), false positives (FP), true negatives (TN), and false negatives (FN), as seen in Table 9.2.

Table 9.2: A labeled confusion matrix

	Actual positive	Actual negative
Predicted positive	TP	FP
Predicted negative	FN	TN

If the outcome is numeric in nature, we will use a **regression algorithm** (e.g. linear regression, support vector regression, *etc.*). Since the difference between prediction and actual values is numeric, metrics that quantify numerical differences, such as root mean square error (RMSE) or R^2 , are used to evaluate the model's performance.

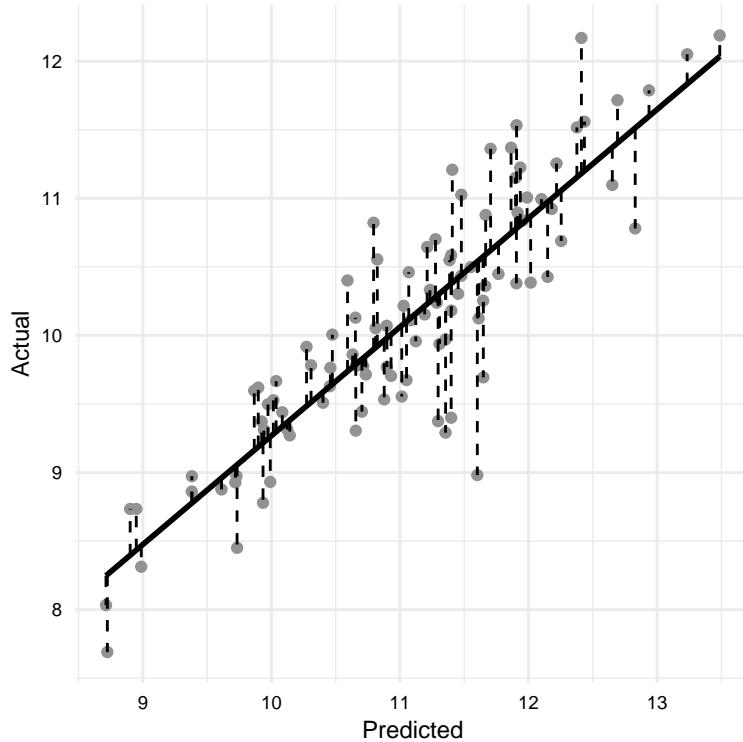


Figure 9.1: A plot of the actual and predicted values for a regression model

The evaluation of the model is quantitative on the one hand, but it is also qualitative in that we need to consider the implications of the model's performance in light of the research question or hypothesis. Furthermore, depending on our research question we may be interested in exploring the features that are most important to the model's performance. This is called **feature importance** and can be derived from the model's coefficients or weights. Notably, however, some of the most powerful models in use today, such as deep neural networks, are not easily interpretable and therefore feature importance is not easily derived. This is something to keep in mind when considering the research question and the type of model that will be used to address it.

9.2 Analysis

In this section we now turn to the practical application of predictive data analysis. The discussion will be separated into classification and regression tasks, as model selection and evaluation procedures differ between the two. For each task, we will frame a research goal and work through the process of building a predictive model to address that goal. Along the

way we will cover concepts and methods that are common to both classification and regression tasks and specific to each.

To frame our analyses, we will posit research aimed at identifying language usage patterns in second language use, one for a classification task and one for a regression task. Our first research question will be to identify potential salient differences in Spanish language use between natives and L1 English learners (categorical). Our second research question will be to gauge the extent to which the L1 English learners' Spanish language placement test scores (numeric) can be predicted based on their language use.

We will use data from the CEDEL2 corpus¹. We will include a subset of the variables from this data that are relevant to our research questions. The data dictionary for this dataset is seen in Table 9.3.

Table 9.3: Data dictionary for

variable	name	variable_type	description
doc_id	Document ID	numeric	Unique identifier for each document
subcorpus	Subcorpus	categorical	The subcorpus to which the document belongs ('Learned English', 'Native English', 'L1 English', 'L2 English')
placement_score	Placement Score	numeric	The score obtained by the document author in a placement test (0 to 100)
proficiency	Proficiency	ordinal	The level of language proficiency of the document author (1 to 5)
text	Text	character	The written text provided by the document author

We will be using the `tidymodels` framework in R to perform this analysis. `tidymodels` is a metapackage, much like `tidyverse`, that provides a consistent interface for modeling and machine learning. Some key packages unique to `tidymodels` are `recipes`, `parsnip`, `workflows`, and `tune`. `recipes` includes functions for preprocessing and engineering features. `parsnip` provides a consistent interface for specifying modeling algorithms. `workflows` allows us to combine recipes and models into a single pipeline. Finally, `tune` give us the ability to evaluate and tune hyperparameters of models.

Since we are using text data, we will also be using the `textrecipes` package which makes various functions available for preprocessing text including extracting and engineering features.

Let's go ahead and do the setup, loading the necessary packages and data. This is seen in Example 9.1.

Example 9.1.

```
# Load packages
library(tidymodels)    # modeling metapackage
library(textrecipes)    # text preprocessing
```

¹See Appendix A.3 for more information on the CEDEL2 corpus.

```

library(janitor)      # data inspection

# Set global options
tidymodels_prefer()  # prefer tidymodels functions over other functions with
# the same name

# Read in the dataset
df <- 
  read_csv("../data/cedel2/cedel2_df.csv")

# Preview
df |> glimpse()

```

```

> Rows: 2,957
> Columns: 5
> $ doc_id      <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, ~
> $ subcorpus   <chr> "Learner", "Learner", "Learner", "Learner", ~
> $ placement_score <dbl> 14.0, 16.3, 16.3, 18.6, 18.6, 18.6, 20.9, 20.9, ~
> $ proficiency <chr> "Lower beginner", "Lower beginner", "Lower beginner", ~
> $ text         <chr> "Yo vivo es Atlanta, Georgia. Atlanta es muy grande ciu~
```

The results from Example 9.1 show that we have five variables and 2957 observations. The primary variables for the classification task are the `subcorpus` variable and the `text` variable. The `placement_score` variable is the outcome variable for the regression task.

9.2.1 Text classification

The goal of this analysis is to classify texts as either native or learner based on the writing samples. This is a binary classification problem. We will approach this problem from an exploratory perspective, and therefore our aim is to identify features from the text that best distinguish between the two classes.

Let's modify the data frame to include only the variables we need for this analysis. In the process, we will rename the `subcorpus` variable to `outcome` to reflect that it is the outcome variable and convert it to a factor vector to meet requirements of the modeling functions we will use in our analysis. This is seen in Example 9.2.

Example 9.2.

```

# Select variables and factor outcome
cls_df <-
  df |>
  select(outcome = subcorpus, proficiency, text) |>
  mutate(outcome = factor(outcome))

# Preview
cls_df |> glimpse()

```

```

> Rows: 2,957
> Columns: 3
> $ outcome      <fct> Learner, Learner, Learner, Learner, Learner, Lear-
> $ proficiency <chr> "Lower beginner", "Lower beginner", "Lower beginner", "Low-
> $ text         <chr> "Yo vivo es Alanta, Georgia. Atlanta es muy grande ciudad.~"

```

To view the distribution of the outcome variable between the two levels we can use the `tabyl()` function from the `janitor` package, as seen in Example 9.3.

Example 9.3.

```

# View the distribution of the outcome variable
cls_df |>
  tabyl(outcome) |>
  adorn_pct_formatting(digits = 1)

> outcome      n percent
> Learner 1906  64.5%
> Native 1051  35.5%

```

So a little less than two-thirds of the texts are from learners. It is important to gauge the distribution of the outcome variable to see if it is balanced or imbalanced. The classes need not be perfectly balanced, but if they are wildly imbalanced it can cause problems for the model.

So in step 1 of our workflow (from Table 9.1), we need to identify the features that we will use to classify the texts. There may be many features that we could use. These could be features derived from raw text (*e.g.* characters, words, n-grams, *etc.*), feature vectors (*e.g.* word embeddings), or meta-linguistic features (*e.g.* part-of-speech tags, syntactic parses, or semantic features) that have been derived from these through manual or automatic annotation.

Let's start simple and use words as the predictor features. This is a simple approach that is often used as a baseline for more complex models. If it doesn't work well, we can try something else.

This provides us the linguistic unit we will use but we still need to decide how to represent these words. Do we use raw token counts? Do we use normalized frequencies? Do we use some type of weighting scheme? These are questions that we need to consider as we embark on this analysis. Since we are exploring we can use trial-and-error or consider the implications of each approach and choose the one that best fits our research question –or both.

As a first pass, let's use raw token counts with our word features.

With our features identified, we can move on to step 2 of our workflow and split the data into training and testing sets. We make the splits to our data at this point to draw a line in the sand between the data we will use to train the model and the data we will use to test the model. A typical approach in supervised machine learning is to allocate around 75-80% of the data to the training set and the remaining 20-25% to the testing set, depending on the number of observations. We have 2957 observations in our data set, so we can allocate 80% of the data to the training set and 20% of the data to the testing set.

In Example 9.4, we will use the `initial_split()` function from the `rsample` package to split the data into training and testing sets. The `initial_split()` function takes a data frame and a proportion and returns a `split` object which contains the training and testing sets. We will use the `strata` argument to stratify the data by the `outcome` variable. This will ensure that the training and testing sets have the same proportion of native and learner texts.

Example 9.4.

```
# Set seed for reproducibility
set.seed(123)

# Split the data into training and testing sets
cls_split <-
  initial_split(
    data = cls_df,
    prop = 0.8,
    strata = outcome
  )

# Create training set
cls_train <- training(cls_split) # 80% of data

# Create testing set
cls_test <- testing(cls_split) # 20% of data
```

A confirmation of the distribution of the data across the training and testing sets as well as a break down of the outcome variable can be seen in Example 9.5.

Example 9.5.

```
# View the distribution of the outcome variables
cls_train |>
  tabyl(outcome) |>
  adorn_totals("row") |>
  adorn_pct_formatting(digits = 1)

> outcome     n percent
> Learner 1524  64.5%
> Native    840  35.5%
> Total    2364 100.0%

cls_test |>
  tabyl(outcome) |>
  adorn_totals("row") |>
  adorn_pct_formatting(digits = 1)

> outcome     n percent
> Learner 382  64.4%
> Native    211  35.6%
> Total    593 100.0%
```

We can see that the split was successful. The training and testing sets have very similar proportion of native and learner texts.

We are now ready to create a ‘recipe’, step 3 in our analysis. A recipe is a set of instructions or blueprint which specify the outcome variable and the predictor variable and determines how to preprocess and engineer the feature variables.

We will use the `recipe()` function from the `recipes` package to create the recipe. The `recipe()` function minimally takes a formula and a data frame and returns a `recipe` object. The formula specifies the outcome variable (y) and the predictor variable(s) ($x_1..x_n$). For example $y \sim x$ can be read as “ y as a function of x ”. In our particular case, we will use the formula `outcome ~ text` to specify that the outcome variable is the `outcome` variable and the predictor variable is the `text` variable. The code is seen in Example 9.6.

Example 9.6.

```

# Create a recipe
base_rec <-
  recipe(
    formula = outcome ~ text,
    data = cls_train
  )

# Preview
base_rec

```

The recipe object at this moment contains just one instruction, what the variables are and what their relationship is.

Tip

R formulas are a powerful way to specify relationships between variables and are used extensively in data modeling including exploratory, predictive, and inferential analysis. The basic formula syntax is $y \sim x$ where y is the outcome variable and x is the feature variable. The formula syntax can be extended to include multiple feature variables, interactions, and transformations. For more information on R formulas, see R for Data Science^a.

^a<https://r4ds.github.io/bookclub-tmwr/r-formula-syntax.html>

The `recipes` package provides a wide range of `step_*`() functions which can be applied to the recipe to specify how to engineer the variables in our recipe call. These include functions to scale (*e.g.* `step_center()`, `step_scale()`, *etc.*) and transform (*e.g.* `step_log()`, `step_pca()`, *etc.*) numeric variables, and functions to encode (*e.g.* `step_dummy()`, `step_labelencode()`, *etc.*) categorical variables.

These step functions are great when we have selected the variables we want to use in our model and we want to engineer them in a particular way. In our case, however, we need to derive features from the text in the `text` column of datasets before we engineer them. To ease this process, the `textrecipes` package provides a number of step functions for preprocessing text data. These include functions to tokenize (*e.g.* `step_tokenize()`), remove stop words (*e.g.* `step_stopwords()`), and to derive meta-features (*e.g.* `step_lemma()`, `step_stem()`, *etc.*) ². Furthermore, there are functions to engineer features in ways that are particularly relevant to text data, such as feature frequencies and weights (*e.g.* `step_tf()`, `step_tfidf()`, *etc.*) and token filtering (*e.g.* `step_tokenfilter()`).

²Note that functions for meta-features require more sophisticated text analysis software to be installed on the computing environment (*e.g.* `spacyr` for `step_lemma()`, `step_pos()`, *etc.*). See the `textrecipes` package documentation for more information.

❖ Dive deeper

For text processing steps for Japanese, see the `washoku` package (Uryu 2024).

So let's build on our basic recipe `cls_rec` by adding steps relevant to our task. To extract our features, we will use the `step_tokenize()` function to tokenize the text into words. The default behavior of the `step_tokenize()` function is to tokenize the text into words, but other token units can be derived and various options can be added to the function call (as the `tokenizers` package is used under the hood). Adding the `step_tokenize()` function to our recipe is seen in Example 9.7.

Example 9.7.

```
# Add step to tokenize the text
cls_rec <-
  base_rec |>
  step_tokenize(text)

# Preview
cls_rec
```

The recipe object now contains two instructions, one for the outcome variable and one for the feature variable. The feature variable instruction specifies that the text should be tokenized into words.

We now need to consider how to engineer the word features. If we add `step_tf()` we will get a matrix of token counts by default. We also have the option to add `step_tfidf()` to get a matrix of term frequencies weighted by inverse document frequency, which effectively down weights words that are common across all documents.

We decided in step 1 that we will start with raw token counts, so we will add `step_tf()` to our recipe. This is seen in Example 9.8.

Example 9.8.

```
# Add step to tokenize the text
cls_rec <-
  cls_rec |>
  step_tf(text)

# Preview
cls_rec
```

To make sure things are in order and that the recipe performs as expected, we can use the functions `prep()` and `bake()` to inspect the recipe. The `prep()` function takes a recipe object and a data frame and returns a `prep` object. The `prep` object contains the recipe and the data frame with the feature variables engineered according to the recipe. The `bake()` function takes a `prep` object and an optional new dataset to apply the recipe to. If we only want to see the application to the training set, we can use the `new_data = NULL` argument.

In Example 9.9, we use the `prep()` and `bake()` functions to create a data frame with the feature variables. We can then inspect the data frame to see if the recipe performed as expected.

Example 9.9.

```
# Prep and bake
cls_bake <-
  cls_rec |>
  prep() |> # create a prep object
  bake(new_data = NULL) # apply to training set

# Preview
cls_bake |> dim()

> [1] 2364 38115

cls_bake[
  c(1000:1001, 2000:2001),      # selected rows
  c(1, 1000:1001, 20000:20001) # selected columns
]

> # A tibble: 4 x 5
>   outcome tf_text_actuales tf_text_actualiadad tf_text_iniciáticas
>   <fct>      <int>           <int>           <int>
> 1 Learner        0             0               0
> 2 Learner        0             0               0
> 3 Native         0             0               0
> 4 Native         0             0               0
> # i 1 more variable: tf_text_iniciativa <int>
```

The resulting engineered features data frame has 2364 observations and 38115 variables. The first variable is the outcome variable and the remaining variables are the engineered features. We can see that the recipe performed as expected and that the feature variables are the token counts for each word in the text.

👉 Tip

When applying tokenization and feature engineering steps to text data the result is often contained in a matrix object. Using the `recipes` package a data frame with a matrix-like structure is returned.

Furthermore, the features are prefixed with the variable name and transformation step labels. In Example 9.9 we applied term frequency to the `text` variable. Therefore we see that our features are prefixed with `tf_text_`.

But we should pause. We have a lot of features! One for every single word in the entire corpus. This is an unwieldy number of features for a model and it is likely that many of these features are not useful for our classification task. Furthermore, the more features we have, the more chance these features capture the nuances of these particular writing samples, thus, we are the more likely we are to overfit the model. All in all, we need to reduce the number of features.

Our domain knowledge about language can be of help us decide on how to approach reducing the feature set. On the one hand, we know that most tokens occur rarely in any sizable corpus. And the lower the frequency, the more likely that the token may reflect nuances of the speaker or the content of particular texts rather than generalizable trends. On the other hand, we know that a relatively small number of the most frequent words quickly account for a large proportion of the tokens in a corpus.

So just with these two considerations, we can see that we can filter out many infrequent words and likely have quite a few viable features. Let's start with an arbitrary threshold of the top 1,000 words by frequency. We can use the `step_tokenfilter()` function to filter out the top 1,000 words by frequency. This particular step needs to be applied before the `step_tf()` step, so we will add it to our recipe before the `step_tf()` step. This is seen in Example 9.10.

Example 9.10.

```
# Rebuild recipe with tokenfilter step
cls_rec <-
  base_rec |>
  step_tokenize(text) |>
  step_tokenfilter(text, max_tokens = 1000) |>
  step_tf(text)

# Prep and bake
cls_bake <-
  cls_rec |>
  prep() |>
  bake(new_data = NULL)
```

```
# Preview  
cls_bake |> dim()
```

```
> [1] 2364 1001
```

```
cls_bake[1:5, 1:10]
```

```
> # A tibble: 5 x 10  
>   outcome tf_text_10 tf_text_2 tf_text_3 tf_text_4 tf_text_a tf_text_abandonado  
>   <fct>     <int>     <int>     <int>     <int>     <int>     <int>  
> 1 Learner      0         0         0         0         0         0  
> 2 Learner      0         0         0         0         2         0  
> 3 Learner      0         1         0         0         5         0  
> 4 Learner      0         0         0         0         0         0  
> 5 Learner      0         0         0         0         2         0  
> # i 3 more variables: tf_text_abuela <int>, tf_text_abuelos <int>,  
> #   tf_text_aburrido <int>
```

We now have a manageable set of features. Only during the interrogation step will we know if they are useful.

👉 Tip

The `prep()` and `bake()` functions are useful for inspecting the recipe and the engineered features, but they are not required to build a recipe. When a recipe is added to a workflow, the `prep()` and `bake()` functions are called automatically as part of the process.

There is one last step we should add to our recipe which concerns the skewed nature of word frequency distributions. The magnitude of the token counts will be highly skewed with a few words having very high counts and most words having relatively low counts, even for the top 1,000 words. This skew can be problematic for some models, so we will add a step to log normalize the token counts. This will not change the rank order, only the magnitude of the differences. Note that we use `all_predictors()` to apply the log transformation to all the word features, as seen in Example 9.11.

Example 9.11.

```
# Add log step to recipe  
cls_rec <-
```

```

cls_rec |>
  step_log(all_predictors(), offset = 1) # add 1 to avoid log(0)

cls_rec

```

We are now ready to turn our attention to step 5 of our workflow, interrogating the data. In this step, we will first select a classification algorithm, then add this algorithm and our recipe to a workflow object. We will then use the workflow object to train and evaluate the model on the training set.

There are many classification algorithms to choose from with their own strengths and shortcomings. In Table 9.4, we list some of the most common classification algorithms and their characteristics.

Table 9.4: Classification algorithms

Algorithm	Strengths	Shortcomings
Logistic regression	Simple, interpretable, fast	Assumes linear relationship between features and outcome
Naive Bayes	Simple, interpretable, fast	Assumes independence between features
Decision trees	Nonlinear relationships, interpretable	Prone to overfitting
Random forest	Nonlinear relationships, interpretable	Prone to overfitting
Support vector machines	Nonlinear relationships, interpretable	Prone to overfitting
Neural networks	Nonlinear relationships, fast	Prone to overfitting, difficult to interpret

In the process of selecting an algorithm, simple, computationally efficient, and interpretable models are preferred over complex, computationally expensive, and uninterpretable models, all things being equal. Only if the performance of the simple model is not good enough should we move on to a more complex model.

With this end mind, we will start with a simple logistic regression model to see how well we can classify the texts in the training set with the features we have engineered. We will use the `logistic_reg()` function from the `parsnip` package to specify the logistic regression model. We then select the implementation engine (`glm` General Linear Model) and the mode of the model (`classification`). The implementation engine is the software that will be used to fit the model. The mode is the type of model, either classification or regression. The code is seen in Example 9.12.

Example 9.12.

```
# Create a model specification
cls_spec <-
  logistic_reg() |>
  set_engine("glm") |>
  set_mode("classification")

# Preview
cls_spec

> Logistic Regression Model Specification (classification)
>
> Computational engine: glm
```

In the `parsnip` package, model specifications are separate from model fitting. This allows us to specify the model once and then fit the model with different datasets. Furthermore, different algorithms will have different hyperparameters that can be tuned. The code in Example 9.12 uses the default hyperparameters for the logistic regression model.

👉 Tip

The `parsnip` package provides a consistent interface to many different models, 105 at the time of writing. You can peruse the list of models by running `parsnip::model_db`. You can also retrieve the list of potential engines for a given model specification with the `show_engines()` function. For example, `show_engines("logistic_reg")` will return a tibble with the engines available for the logistic regression model specification.

Now we will combine our recipe and model specification into a workflow object. The workflow object will allow us to train and evaluate the model on the training set. We will use the `workflow()` function from the `workflows` package to combine the recipe and model specification into a workflow object. The code is seen in Example 9.13.

Example 9.13.

```
# Create a workflow
cls_wf <-
  workflow() |>
  add_recipe(cls_rec) |>
  add_model(cls_spec)
```

```

# Preview
cls_wf

> == Workflow =====
> Preprocessor: Recipe
> Model: logistic_reg()
>
> -- Preprocessor -----
> 4 Recipe Steps
>
> * step_tokenize()
> * step_tokenfilter()
> * step_tf()
> * step_log()
>
> -- Model -----
> Logistic Regression Model Specification (classification)
>
> Computational engine: glm

```

The workflow contains all the preprocessing and the model-specific parameters we've selected. A workflow object at this stage in the analysis is not trained. It is a blueprint for a model. We can use the `fit()` function to apply the workflow to the training data to train the model and update our workflow object with the trained model. The `fit()` function takes a workflow and a data frame and returns an updated workflow object which is trained. The code is seen in Example 9.14.

Example 9.14.

```

# Fit the workflow
cls_wf_fit <-
  fit(
    cls_wf,
    data = cls_train
  )

```

The workflow object now contains the trained model. But things did not go off without a hitch. We receive two warning messages when fitting the workflow to the training data:

Warning messages:

```
1: glm.fit: algorithm did not converge
2: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

Warning messages are a sign that something may be amiss with the features we have chosen, the model we have selected, or both! Warning messages can sometimes be cryptic and steeped in the jargon of the algorithm. When in doubt it is best to consult the documentation of the algorithm and/ or seek help from the R community.

The first warning, the ‘algorithm did not converge’, means that given the data and the model, the algorithm could not estimate a stable solution. The reason or reasons for this can be varied, but it typically due to extreme outliers, collinearity, or a small sample size. Collinearity is when two or more features are highly correlated. Given we are using words as features, it is likely that there is collinearity in the data. We will need to address this.

The second warning is ‘fitted probabilities numerically 0 or 1 occurred’. This means that the model is overfitting the data, (i.e. there are one or more features that perfectly predict the outcome). This very well could be related to the first warning, as a small set of features may be perfectly predicting the outcome in a way that will likely not generalize to new data.

The upshot is that this model specification and/ or the feature engineering needs to be changed. So we step back in the workflow and make changes that will cascade downstream.

It turns out that a regularized logistic regression model often addresses the issues this model is experiencing. We will use the `glmnet` engine to fit a regularized logistic regression model. It is a more complex approach, but it can often mitigate the issues of collinearity and overfitting by penalizing features that are highly correlated and by shrinking the coefficients of features that are not useful for predicting the outcome.

We will build a new model specification using the `logistic_reg()` function and the `glmnet` engine. This time we will use hyperparameters in our `logistic_reg()` call to specify the penalty we want to use and the strength of the penalty. The penalty we will use is the LASSO (L1)³. We now need to decide what value to use for the strength of the penalty, 0 to 1, where 0 indicates no penalty and 1 indicates a maximum penalty. We either experiment with different values one by one or we can implement a range of values in tandem and then select the best value. We will use the latter approach.

The `tune` package provides a number of functions for selecting, or ‘tuning’, hyperparameters. The first is the `tune()` function which we add as the argument of the hyperparameter we want to tune in the model specification, as seen in Example 9.15.

Example 9.15.

³The LASSO (least absolute shrinkage and selection operator) is a type of regularization that penalizes the absolute value of the coefficients. In essence, it smooths the coefficients by shrinking them towards zero to avoid coefficients picking up on particularities of the training data that will not generalize to new data.

```

# Create a model specification for tuning
cls_spec_tune <-
  logistic_reg(penalty = tune(), mixture = 1) |>
  set_engine("glmnet") |>
  set_mode("classification")

# Create a workflow
cls_wf_tune <-
  workflow() |>
  add_recipe(cls_rec) |>
  add_model(cls_spec_tune)

```

We now have a workflow that includes the `tune()` function as a placeholder for a range of values for the `penalty` hyperparameter. We use the `grid_regular()` function from the `dials` package to specify a grid of values for the `penalty` hyperparameter. Let's choose a random set of 10 values, as seen in Example 9.16.

❖ Dive deeper

The hyperparameters `penalty` and `mixture` control which type(s) of regularization to apply and if there is a mixing of the types. In the model specification in Example 9.15, the `penalty` is set to be tuned and the `mixture` is set to 1, which means that only a lasso penalty will be applied.

See the documentation for the `parsnip::logistic_reg()` function for more information.

Example 9.16.

```

# Create a grid of values for the penalty hyperparameter
cls_grid <-
  grid_regular(
    penalty(),
    levels = 10
  )

# Preview
cls_grid

> # A tibble: 10 x 1
>       penalty
>       <dbl>
> 1 0.0000000001

```

```

> 2 0.0000000129
> 3 0.000000167
> 4 0.00000215
> 5 0.0000278
> 6 0.000359
> 7 0.00464
> 8 0.00599
> 9 0.0774
> 10 1

```

The 10 values chosen to be in the grid range from nearly zero to 1, where 0 indicates no penalty and 1 indicates a strong penalty.

Now to perform the tuning and arrive at an optimal value for `penalty` we need to create a tuning workflow. We do this by calling the `tune_grid()` function using our tuning model specification workflow, a resampling object, and our hyperparameter grid and returns a `tune_grid` object.

Now, a resampling object is not something we've seen yet. Resampling is a strategy that allows us to generate multiple training and testing sets from a single data set—in this case the training data we split at the outset. Each variation of the training and testing sets is called a fold. Which is why this type of resampling is called k-fold cross-validation. The `vfold_cv()` function from the `rsample` package takes a data frame and a number of folds and returns a `vfold_cv` object. We will use 10 folds and include the model specification and the hyperparameter grid in the `tune_grid()` function call. The code is seen in Example 9.17.

Example 9.17.

```

# Set seed for reproducibility
set.seed(123)

# Create a resampling object
cls_vfold <-
  vfold_cv(
    cls_train,
    v = 10
  )

# Tune the model
cls_tune <-
  tune_grid(
    cls_wf_tune,
    resamples = cls_vfold,
    grid = cls_grid
  )

```

```

)
# Preview
cls_tune

> # Tuning results
> # 10-fold cross-validation
> # A tibble: 10 × 4
>   splits           id     .metrics     .notes
>   <list>         <chr>  <list>       <list>
> 1 <split [2127/237]> Fold01 <tibble [20 × 5]> <tibble [0 × 3]>
> 2 <split [2127/237]> Fold02 <tibble [20 × 5]> <tibble [0 × 3]>
> 3 <split [2127/237]> Fold03 <tibble [20 × 5]> <tibble [0 × 3]>
> 4 <split [2127/237]> Fold04 <tibble [20 × 5]> <tibble [0 × 3]>
> 5 <split [2128/236]> Fold05 <tibble [20 × 5]> <tibble [0 × 3]>
> 6 <split [2128/236]> Fold06 <tibble [20 × 5]> <tibble [0 × 3]>
> 7 <split [2128/236]> Fold07 <tibble [20 × 5]> <tibble [0 × 3]>
> 8 <split [2128/236]> Fold08 <tibble [20 × 5]> <tibble [0 × 3]>
> 9 <split [2128/236]> Fold09 <tibble [20 × 5]> <tibble [0 × 3]>
> 10 <split [2128/236]> Fold10 <tibble [20 × 5]> <tibble [0 × 3]>

```

The `cls_tune` object contains the results of the tuning for each fold. We can see the results of the tuning for each fold by calling the `collect_metrics()` function on the `cls_tune` object, as seen in Example 9.18.

Example 9.18.

```

# Collect the results of the tuning
cls_tune_metrics <-
  collect_metrics(cls_tune)

# Visualize metrics
cls_tune |> autoplot()

```

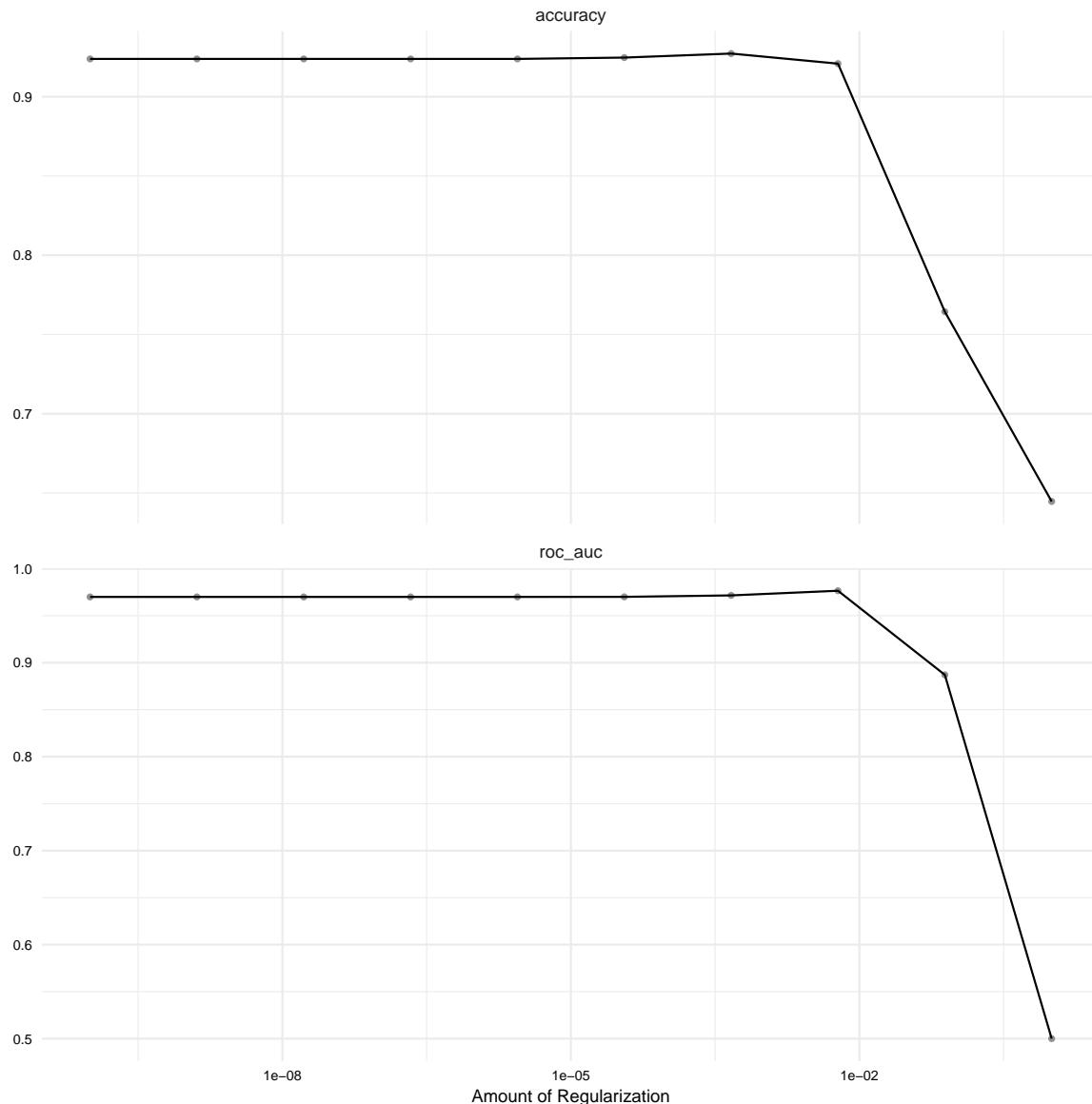


Figure 9.2: Metrics for each fold of the tuning process.

The most common metrics for model performance in classification are accuracy and the area under the receiver operating characteristic curve (ROC-AUC). Accuracy is the proportion of correct predictions. The ROC-AUC is a measure of the trade-off between sensitivity and specificity. Sensitivity is the proportion of true positives that are correctly identified. Specificity is the proportion of true negatives that are correctly identified. The ROC-AUC is a measure of how well the model can distinguish between the two classes.

In the plot of the metrics, we can see that the many of the penalty values performed similarly, with a drop off in performance at the higher values. Conveniently, the `show_best()` function from the `tune` package takes a `tune_grid` object and returns the best performing hyperparameter values. The code is seen in Example 9.19.

Example 9.19.

```
# Show the best performing hyperparameter value
cls_tune |>
  show_best(metric = "roc_auc")
```



```
> # A tibble: 5 x 7
>   penalty .metric .estimator  mean    n std_err .config
>   <dbl> <chr> <chr>     <dbl> <int>  <dbl> <chr>
> 1 0.00599  roc_auc binary    0.977   10  0.00312 Preprocessor1_Model08
> 2 0.000464  roc_auc binary    0.972   10  0.00320 Preprocessor1_Model07
> 3 0.0000359  roc_auc binary    0.970   10  0.00337 Preprocessor1_Model06
> 4 0.0000000001  roc_auc binary    0.970   10  0.00342 Preprocessor1_Model01
> 5 0.00000000129  roc_auc binary    0.970   10  0.00342 Preprocessor1_Model02
```

We can make this selection programmatically by using the `select_best()` function. This function needs a metric to select by. We will use the ROC-AUC and select the best value for the penalty hyperparameter. The code is seen in Example 9.20.

Example 9.20.

```
# Select the best performing hyperparameter value
cls_best <-
  select_best(cls_tune, metric = "roc_auc")
```



```
# Preview
cls_best
```



```
> # A tibble: 1 x 2
>   penalty .config
>   <dbl> <chr>
> 1 0.00599 Preprocessor1_Model08
```

All of that to tune a hyperparameter! Now we can update the model specification and workflow with the best performing hyperparameter value using the previous `cls_wf_tune` workflow and

the `finalize_workflow()` function. The `finalize_workflow()` function takes a workflow and the selected parameters and returns an updated `workflow` object, as seen in Example 9.21.

Example 9.21.

```
# Update model specification
cls_wf_lasso <-
  cls_wf_tune |>
  finalize_workflow(cls_best)

cls_wf_lasso

> == Workflow =====
> Preprocessor: Recipe
> Model: logistic_reg()
>
> -- Preprocessor -----
> 4 Recipe Steps
>
> * step_tokenize()
> * step_tokenfilter()
> * step_tf()
> * step_log()
>
> -- Model -----
> Logistic Regression Model Specification (classification)
>
> Main Arguments:
>   penalty = 0.00599484250318942
>   mixture = 1
>
> Computational engine: glmnet
```

Our model specification and the workflow are updated with the parameters.

Let's now return to fitting the workflow to the training set as we did before for the vanilla logistic regression model. As a reminder we are still working in step 5 of our workflow, interrogating the data. We identified and addressed potential issues in the model specification, leaving the feature selection the same.

We again fit the workflow to the training set, as seen in Example 9.22.

Example 9.22.

```
# Fit the workflow
cls_wf_lasso_fit <-
  fit(
    cls_wf_lasso,
    data = cls_train
  )
```

No warnings, so that is a good sign! –Or at least a better sign than before.

Let's evaluate the performance of the model on the training data. The `predict()` function takes a trained model specification and a data frame and returns a data frame with the predicted outcome. We can join these predicted outcomes with the actual outcomes in the training data. The `metrics()` function takes a data frame with the actual and predicted outcomes and returns a data frame with the metrics for the model. The code is seen in Example 9.23.

Example 9.23.

```
# Evaluate workflow
cls_lasso_fit_preds <-
  bind_cols(
    cls_train,
    predict(cls_wf_lasso_fit, cls_train)
  )

# Calculate accuracy
cls_lasso_fit_preds |>
  metrics(truth = outcome, estimate = .pred_class)
```

```
> # A tibble: 2 x 3
>   .metric   .estimator .estimate
>   <chr>     <chr>        <dbl>
> 1 accuracy  binary      0.969
> 2 kap       binary      0.932
```

Again, no warnings, so we have a functioning model. It also has a high accuracy, but we know that this is not the most reliable metric for the robustness of the model on new data. Similar to what we did to tune the hyperparameters, we can use cross-validation to gauge the variability of the model. The `fit_resamples()` function takes a workflow and a resampling object and returns metrics for each fold. The code is seen in Example 9.24.

Example 9.24.

```
# Cross-validate workflow
cls_lasso_cv <-
  cls_wf_lasso |>
  fit_resamples(
    resamples = cls_vfold,
    control = control_resamples(save_pred = TRUE)
  )
```

We want to aggregate the metrics across the folds to get a sense of the variability of the model. The `collect_metrics()` function takes the results of a cross-validation and returns a data frame with the metrics.

Example 9.25.

```
# Collect metrics
cls_lasso_cv |>
  collect_metrics()
```

```
> # A tibble: 2 × 6
>   .metric  .estimator  mean    n  std_err .config
>   <chr>    <chr>     <dbl> <int>   <dbl> <chr>
> 1 accuracy  binary     0.921     10  0.00627 Preprocessor1_Model1
> 2 roc_auc   binary     0.977     10  0.00312 Preprocessor1_Model1
```

The accuracy has dropped, but is still very high. From these metrics it appears we have a good candidate model. In many cases, however, there may be further room for improvement. A good next step to in these cases is to evaluate the model errors and see if there are any patterns that can be addressed before evaluating the model on the test set.

For classification tasks, a good place to start is to visualize the confusion matrix to assess false negatives and false positives. The `conf_mat_resampled()` function takes a `fit_resamples` object and returns a table (`tidy = FALSE`) with the confusion matrix for the aggregated folds. We can pass this to the `autoplot()` function to plot as in Example 9.26.

Example 9.26.

```
# Plot confusion matrix
cls_lasso_cv |>
```

```
conf_mat_resampled(tidy = FALSE) |>
  autoplot(type = "heatmap")
```

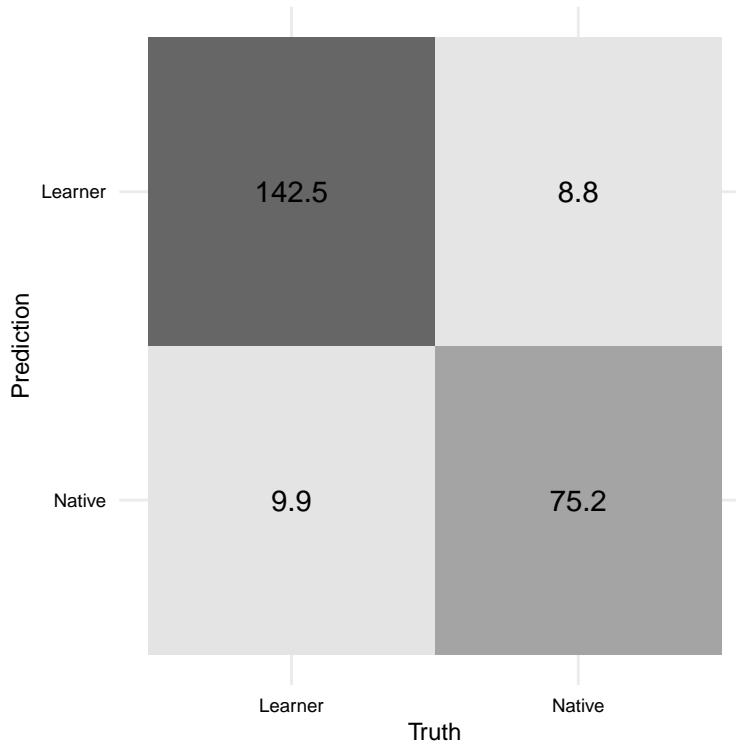


Figure 9.3: Confusion matrix for the aggregated folds of the cross-validation.

The top left to bottom right diagonal contains the true positives and true negatives. The top right to bottom left diagonal contains the false positives and false negatives. The convention is speak of one class being the positive class and the other class being the negative class. In our case, we will consider the positive class to be the ‘learner’ class and the negative class to be the ‘natives’ class.

We can see that there are more learners falsely predicted to be natives than the other way around. This may be due to the fact that there are simply more learners than natives in the data set or this could signal that there are some learners that are more similar to natives than other learners. Clearly this can’t be the entire explanation as the model is not perfect, even some natives are classified falsely as learners! But may be an interesting avenue for further exploration. Maybe these are learners that are more advanced or have a particular style of writing that is more similar to natives.

Another perspective often applied to evaluate a model is the Reciever Operating Characteristic (ROC) curve. The ROC curve is a plot of the true positive rate (TPR) against the false positive rate (FPR) for different classification thresholds. To produce the ROC curve, we pass the resampled fit to the `collect_predictions()` function. We then pass this result to `roc_curve()` function. But we want the results grouped by each fold, so we use `group_by(id)`. Finally, we can pass this to the `autoplot()` function to plot as in Example 9.27.

Example 9.27.

```
# Plot ROC curve
cls_lasso_cv |>
  collect_predictions() |>
  group_by(id) |>
  roc_curve(truth = outcome, .pred_Learner) |>
  autoplot() +
  labs(
    y = "True positive rate",
    x = "False positive rate",
    color = "Fold"
  )
```

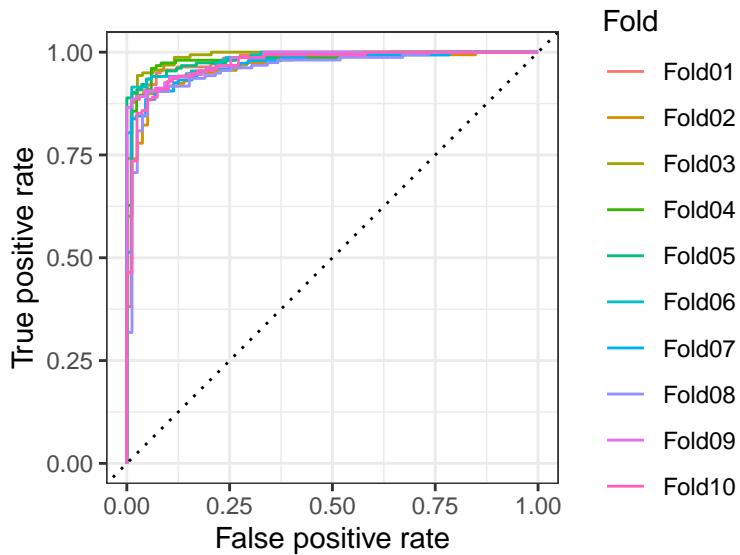


Figure 9.4: ROC curve for the aggregated folds of the cross-validation.

In a ROC curve plot, each line represents a model's performance for varying classification probability thresholds (from near 0 to 1, where 0.5 equal chance). The dotted line represents the null model (*i.e.* random guessing). The further the line is from the dotted line, along the top left to bottom right diagonal, the better the model. Thus, the larger the area under the curve (AUC) implies a more robust model for distinguishing between the two classes.

In Figure 9.4, each fold is plotted. We can see that the AUC is quite large for most of the folds which suggests that our model is robust.

We are now ready to move on to step 7, evaluating the model on the test set. We will use the `predict()` function to predict the outcome on the test set. The `metrics()` function takes a data frame with the actual and predicted outcomes and returns a data frame with the metrics for the model. The code is seen in Example 9.28.

Example 9.28.

```
# [ ] update to use `last_fit()`?
```

```

cls_final_fit <-
  last_fit(
    cls_wf_lasso,
    split = cls_split
  )

cls_final_fit |>
  collect_metrics()

```

```

> # A tibble: 2 x 4
>   .metric  .estimator .estimate .config
>   <chr>    <chr>        <dbl> <chr>
> 1 accuracy  binary      0.927 Preprocessor1_Model1
> 2 roc_auc   binary      0.972 Preprocessor1_Model1

```

```

# Evaluate model on test set
cls_lasso_fit_preds_test <-
  bind_cols(
    cls_test,
    predict(cls_wf_lasso_fit, cls_test)
  )

# Calculate accuracy
cls_lasso_fit_preds_test |>
  metrics(truth = outcome, estimate = .pred_class)

```

```

> # A tibble: 2 x 3
>   .metric  .estimator .estimate
>   <chr>    <chr>        <dbl>
> 1 accuracy  binary      0.927
> 2 kap       binary      0.843

```

The accuracy is as good as the training set, even a tad higher. This is a good sign that the model is robust as it performs well on both training and test sets. We can evaluate the confusion matrix on the test set as well. The code is seen in Example 9.29.

Example 9.29.

```
# Plot confusion matrix
cls_lasso_fit_preds_test |>
  conf_mat(truth = outcome, estimate = .pred_class) |>
  autoplot(type = "heatmap")

cls_final_fit |>
  collect_predictions() |>
  conf_mat(truth = outcome, estimate = .pred_class) |>
  autoplot(type = "heatmap")
```

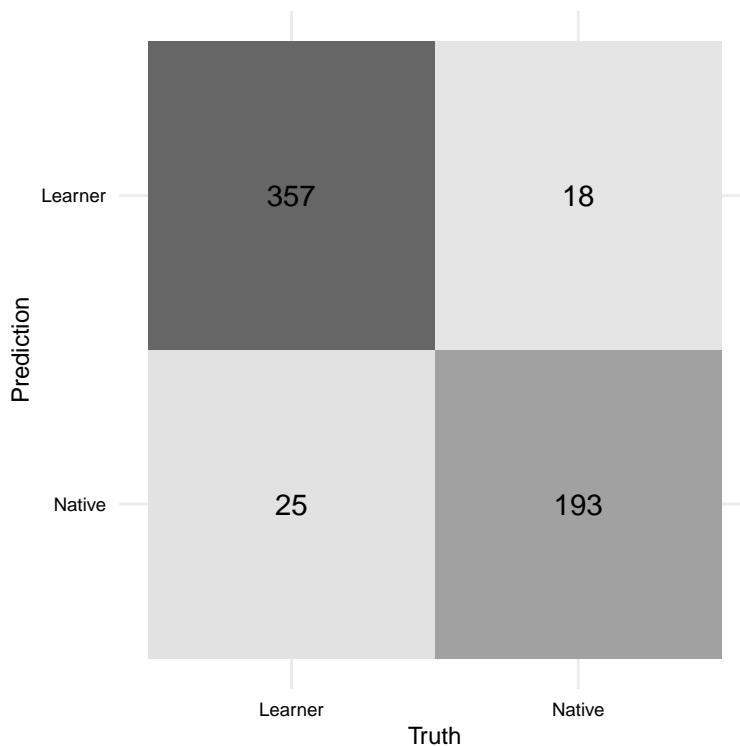


Figure 9.5: Confusion matrix for the test set.

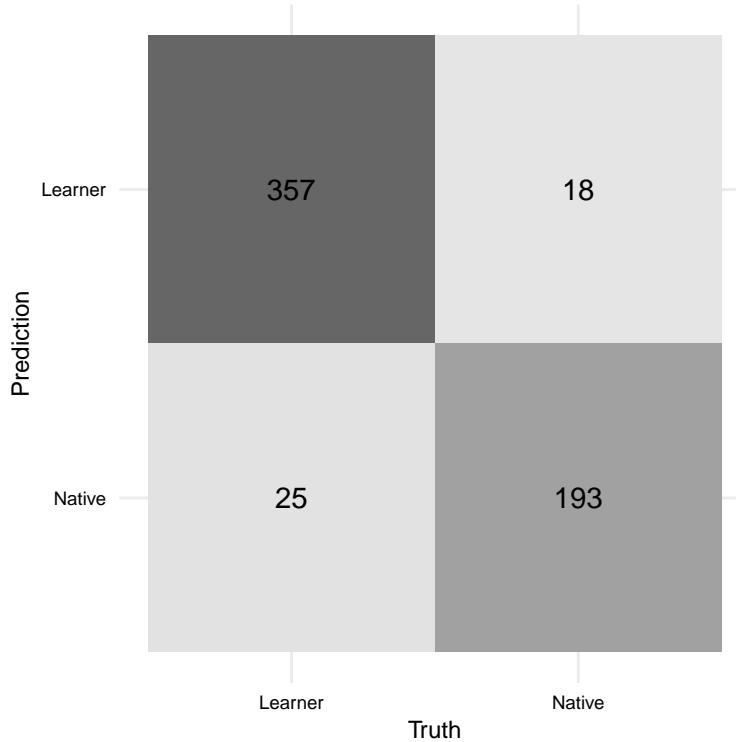


Figure 9.6: Confusion matrix for the test set.

On the test set the false instances look similar to the distribution on the training set, with the exception that learners are more likely to be falsely predicted to be natives than the other way around.

We can inspect the errors on the test set by filtering the data frame to only include the false instances. I will then select the columns with the actual outcome, the predicted outcome, the proficiency level, and the text and separate the predicted outcome to inspect them separately, as seen in Example 9.30.

Example 9.30.

```
# Inspect errors
cls_lasso_fit_preds_test |>
  filter(outcome != .pred_class) |>
  select(outcome, .pred_class, proficiency, text)
```

```
> # A tibble: 43 x 4
```

```

>   outcome .pred_class proficiency      text
>   <fct>   <fct>      <chr>          <chr>
> 1 Learner Native      Upper beginner   "Un dia, El niño estaba durmiendo cua-
> 2 Learner Native      Lower intermediate "Estoy actualmente en mi segundo año ~
> 3 Learner Native      Lower intermediate "La película "Solas" contiene muchos ~
> 4 Learner Native      Upper intermediate "Un día decidí llevarme a casa una ra-
> 5 Learner Native      Lower advanced    "El año pasado nos fuimos al festivál-
> 6 Learner Native      Lower advanced    "Bueno, el año pasado mi novia y yo v-
> 7 Learner Native      Lower advanced    "Me parece que en actualidad, el mund-
> 8 Learner Native      Lower advanced    "Acabo de visitar Barcelona con mi no-
> 9 Learner Native      Lower advanced    "Podría escribir un libro de mis pla-
> 10 Learner Native     Lower advanced    "Un día Miguel y su perro Pepe encont-
> # i 33 more rows

```

```

# Inspect learners falsely predicted to be natives
cls_lasso_fit_preds_test |>
  filter(outcome == "Learner", .pred_class == "Native") |>
  select(outcome, .pred_class, proficiency, text) |>
  count(proficiency, sort = TRUE)

```

```

> # A tibble: 5 x 2
>   proficiency      n
>   <chr>          <int>
> 1 Upper advanced  13
> 2 Lower advanced  8
> 3 Lower intermediate  2
> 4 Upper beginner  1
> 5 Upper intermediate  1

```

- Majority of misclassified learners are advanced, which could be expected as they are more similar to natives. There are some beginners that are misclassified as natives, which is interesting, and not expected. But all models are wrong, but some are useful –George Box.
- Still an open question as to why some natives are classified as learners.

We can inspect the estimates for the features in the model to gain some insight into what features are most important for predicting the outcomes. The `extract_fit_parsnip()` function takes a trained model specification and returns a data frame with the estimated coefficients for each feature. The code is seen in Example 9.31.

Example 9.31.

```

# Extract estimates
cls_wf_lasso_fit |>
  extract_fit_parsnip() |>
  tidy()

> # A tibble: 1,001 x 3
>   term            estimate  penalty
>   <chr>          <dbl>    <dbl>
> 1 (Intercept)    -1.37    0.00599
> 2 tf_text_10      0        0.00599
> 3 tf_text_2       0        0.00599
> 4 tf_text_3       0        0.00599
> 5 tf_text_4       0        0.00599
> 6 tf_text_a       0.350   0.00599
> 7 tf_text_abandonado 0.0222 0.00599
> 8 tf_text_abuela   0        0.00599
> 9 tf_text_abuelos  0        0.00599
> 10 tf_text_aburrido -0.108  0.00599
> # i 991 more rows

```

The estimates are the log odds of the outcome. In a binary classification task, the log odds of the outcome is the log of the probability of the outcome divided by the probability of the other outcome. In our case, the reference outcome is “Learner”, so negative log-odds indicate that the feature is associated with the “Learner” outcome and positive log-odds indicate that the feature is associated with the “Native” outcome.

The estimates are in log-odds, so we need to exponentiate them to get the odds. The odds are the probability of the outcome divided by the probability of the other outcome. The probability of the outcome is the odds divided by the odds plus one. The code is seen in Example 9.32.

Example 9.32.

```

# Calculate probability
cls_wf_lasso_fit |>
  extract_fit_parsnip() |>
  tidy() |>
  mutate(probability = exp(estimate) / (exp(estimate) + 1))

> # A tibble: 1,001 x 4

```

```

>   term          estimate  penalty  probability
>   <chr>        <dbl>    <dbl>    <dbl>
> 1 (Intercept) -1.37    0.00599  0.202
> 2 tf_text_10    0        0.00599  0.5
> 3 tf_text_2     0        0.00599  0.5
> 4 tf_text_3     0        0.00599  0.5
> 5 tf_text_4     0        0.00599  0.5
> 6 tf_text_a     0.350   0.00599  0.587
> 7 tf_text_abandonado 0.0222  0.00599  0.506
> 8 tf_text_abuela  0        0.00599  0.5
> 9 tf_text_abuelos 0        0.00599  0.5
> 10 tf_text_aburrido -0.108   0.00599  0.473
> # i 991 more rows

```

So just looking at the snippet of the features returned from Example 9.32, we can see that the features ‘a’ and ‘abandonado’ are slightly associated with the “Native” outcome and the other features are neutral (**probability** = 0.5).

A quick way to extract the most important features for predicting the each outcome is to use the **vi()** function from the **vip** package. It takes a trained model specification and returns a data frame with the most important features. The code is seen in Example 9.33.

Example 9.33.

```

# Load package
library(vip)

conflicted::conflicts_prefer(vip::vi)

# Extract important features
var_importance_df <-
  cls_wf_lasso_fit |>
  vi()

# Preview
var_importance_df

> # A tibble: 1,000 x 3
>   Variable        Importance Sign
>   <chr>          <dbl> <chr>
> 1 tf_text_todavia  8.67  NEG
> 2 tf_text_eeuu     7.20  NEG

```

```

> 3 tf_text_ésta           6.31 POS
> 4 tf_text_sorpresa      6.31 POS
> 5 tf_text_sienta        6.30 POS
> 6 tf_text_arriba        6.29 NEG
> 7 tf_text_ahí           6.06 POS
> 8 tf_text_encuentran    5.86 NEG
> 9 tf_text_mayoría       5.85 NEG
> 10 tf_text_favorito     5.75 NEG
> # i 990 more rows

```

The `Variable` column contains each feature (with the feature type and corresponding variable `tf_text_`), `Importance` provides the absolute log-odds value, and the `Sign` column indicates whether the feature is associated with the “NEG” (“Learner”) or the “POS” (“Native”) outcome. We can recode the `Variable` and `Sign` columns to make them more interpretable and exponentiate the log-odds to get probabilities and then plot them using `ggplot()`, as in Example 9.34.

Example 9.34.

```

# Recode variable and sign
var_importance_df <-
  var_importance_df |>
  mutate(
    Feature = str_remove(Variable, "tf_text_"),
    Outcome = case_when(Sign == "NEG" ~ "Learner", Sign == "POS" ~ "Native"),
    Importance = exp(Importance) / (exp(Importance) + 1)
  ) |>
  select(Outcome, Feature, Importance)

# Plot
var_importance_df |>
  slice_max(Importance, n = 50) |>
  ggplot(aes(x = reorder(Feature, Importance), y = Importance)) +
  geom_point() +
  coord_flip() +
  facet_wrap(~ Outcome, scales = "free_y") +
  labs(x = NULL, y = "Importance", fill = NULL) +
  theme_minimal()

```

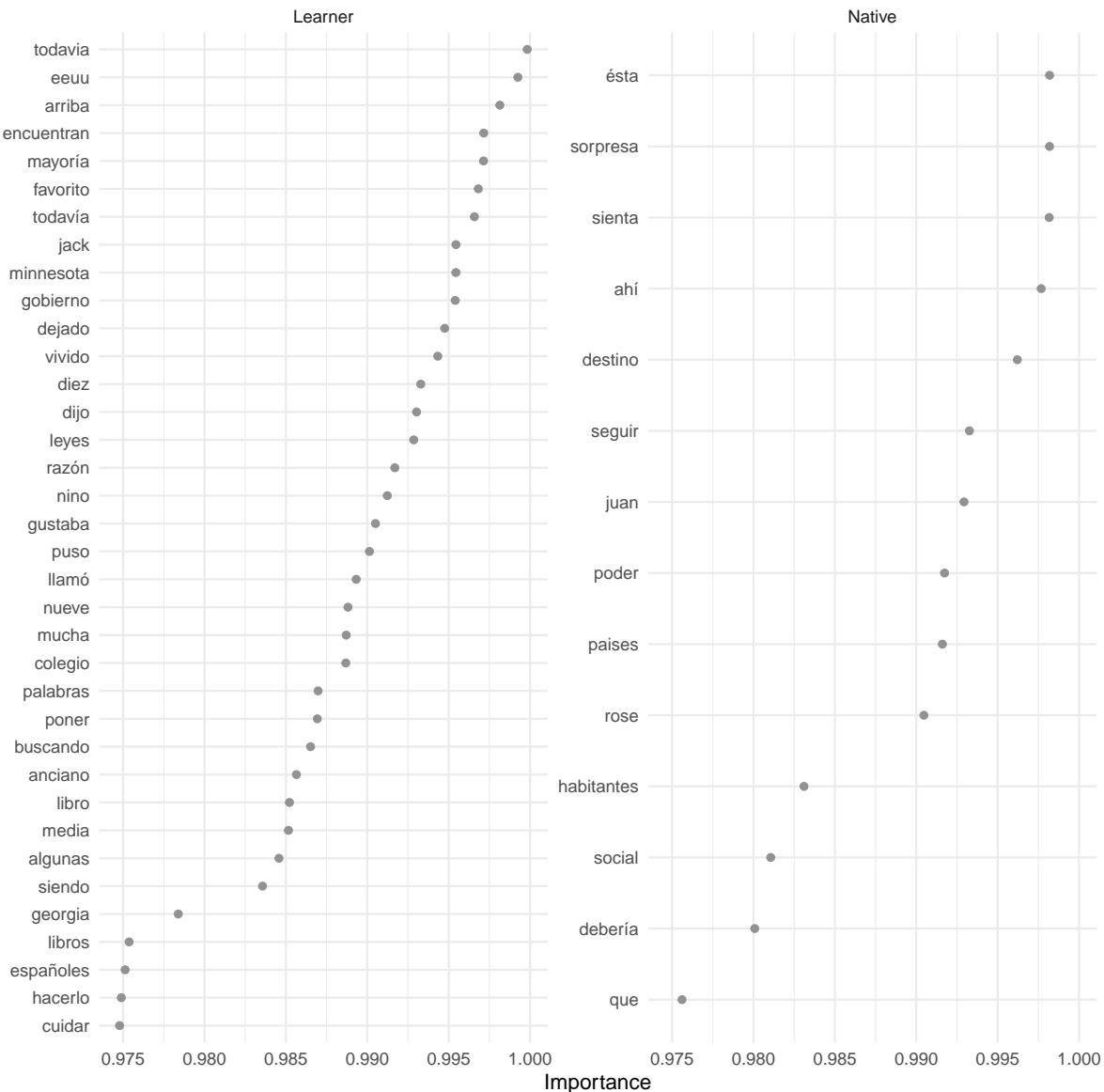


Figure 9.7: Most important features for predicting the outcome.

We can inspect Figure 9.7, and qualitatively assess what these features may be telling us about the differences between the learners and the natives.

In this section we've build a text classifier using a regularized logistic regression model. We've tuned the hyperparameters to arrive at a robust model that performs well on both the training and test sets. We've also evaluated the model errors and inspected the most important features for predicting the outcome.

The `tidymodels` package provides a framework for building and evaluating supervised machine learning models that is modular in nature. This means, that we can quickly and easily change the model specification, the features, feature engineering, and the hyperparameters to arrive at a robust model. If the model is not robust, we can change models in the model specification. If the features are not robust, we can change the recipe. If the model is overfitting, we can tune the hyperparameters.

9.2.2 Text regression

We will now turn our attention to the second task in this section, text regression. In this task, we will use the same original dataset as in the classification task, but we will predict the placement score based on the learner writing samples. Let's start by extracting the observations (only learners) and the relevant variables from the original data set. The code is seen in Example 9.35.

Example 9.35.

```
# Extract observations and relevant variables
reg <-
  df |>
  filter(proficiency != "Native") |>
  select(outcome = placement_score, proficiency, text)

# Preview
reg |> glimpse()

> Rows: 1,906
> Columns: 3
> $ outcome    <dbl> 14.0, 16.3, 16.3, 18.6, 18.6, 18.6, 20.9, 20.9, 20.9,
> $ proficiency <chr> "Lower beginner", "Lower beginner", "Lower beginner", "Low-
> $ text        <chr> "Yo vivo es Alanta, Georgia. Atlanta es muy grande ciudad.~
```

In this task, our outcome variable is numeric so we do not need, or want, to convert it to a factor. Our predictor variable `text` is the same as before. We have already weighed the options for feature engineering and decided to use the term frequency method (raw counts) for the top 1,000. Since we are setting up the same recipe as before, essentially, we can use the same code as before.

Let's first move to step 2, initial split. We will use the `initial_split()` function again, but this time we will not need to stratify the data as we are not predicting a categorical variable. The code is seen in Example 9.36.

Example 9.36.

```
# Set seed for reproducibility
set.seed(123)

# Split data
reg_split <-
  initial_split(reg, prop = 0.8)

# Training set
reg_train <-
  training(reg_split)

# Test set
reg_test <-
  testing(reg_split)
```

The training set has 1524 observations and the test set has 382 observations.

Now we can create the recipe to set up the variable relations, select the features, and engineer the features. The code is seen in Example 9.37.

Example 9.37.

```
# Create a recipe
reg_rec <-
  recipe(outcome ~ text, data = reg_train) |>
  step_tokenize(text) |>
  step_tokenfilter(text, max_tokens = 1000) |>
  step_tf(text) |>
  step_log(all_predictors(), offset = 1)

# Preview
reg_rec
```

At this point we would inspect our recipe to make sure that it looks as expected and gauge the number of features. But since are using the same recipe as before, we can skip this step.

We can now proceed to interrogate the data. As before we will want to start with a simple model and then build up to more complex models. Let's consider some common algorithms for regression tasks in Table 9.5.

Table 9.5: Regression algorithms

Algorithm	Strengths	Shortcomings
Linear regression	Simple, interpretable, fast	Assumes linear relationship between features and outcome
Decision trees	Nonlinear relationships, interpretable	Prone to overfitting
Random forest	Nonlinear relationships, interpretable	Prone to overfitting
Neural networks	Nonlinear relationships, fast	Prone to overfitting, difficult to interpret

Let's start with a with a linear regression model in mind for our model specification. But let's also consider what we learned in our first attempt to build a logistic regression model using word frequencies. We learned that the model was overfitting the training data and we needed to use a regularized model to reduce the variance of the model. So let's start with a regularized linear regression model.

The `linear_reg()` function, just as the `logistic_reg()` function, provides arguments for the regularization hyperparameters when the `glmnet` computational engine is used. Let's tune the `penalty` hyperparameter in the same way as before. The code for the process is seen in Example 9.38.

Example 9.38.

```
# Create model specification
reg_spec_lasso <-
  linear_reg(penalty = tune(), mixture = 1) |>
  set_engine("glmnet") |>
  set_mode("regression")

# Create workflow
reg_wf_lasso <-
  workflow() |>
  add_recipe(reg_rec) |>
  add_model(reg_spec_lasso)

# Create tuning grid
reg_grid <-
  grid_regular(penalty(), levels = 10)
```

```

# Set seed for reproducibility
set.seed(123)

# Create tuning workflow
reg_tune <-
  tune_grid(
    reg_wf_lasso,
    resamples = vfold_cv(reg_train, v = 10),
    grid = reg_grid,
    control = control_resamples(save_pred = TRUE)
  )

# Select best parameter
chosen_penalty <-
  reg_tune |>
  select_best(metric = "rmse")

# Update workflow
reg_final_wf_lasso <-
  reg_wf_lasso |>
  finalize_workflow(chosen_penalty)

reg_final_wf_lasso

```

```

> == Workflow =====
> Preprocessor: Recipe
> Model: linear_reg()
>
> -- Preprocessor -----
> 4 Recipe Steps
>
> * step_tokenize()
> * step_tokenfilter()
> * step_tf()
> * step_log()
>
> -- Model -----
> Linear Regression Model Specification (regression)
>
> Main Arguments:
>   penalty = 1

```

```

>   mixture = 1
>
> Computational engine: glmmnet

```

Now we fit this model to the training data and evaluate the performance using cross-validation. The code is seen in Example 9.39.

Example 9.39.

```

# Cross-validated workflow
reg_cv_lasso <-
  reg_final_wf_lasso |>
  fit_resamples(
    resamples = vfold_cv(reg_train, v = 10),
    control = control_resamples(save_pred = TRUE)
  )

# Collect metrics
reg_cv_lasso |>
  collect_metrics()

```

```

> # A tibble: 2 x 6
>   .metric .estimator  mean     n std_err .config
>   <chr>   <chr>     <dbl> <int>   <dbl> <chr>
> 1 rmse    standard    13.3     10   0.348 Preprocessor1_Model1
> 2 rsq     standard     0.659     10   0.0222 Preprocessor1_Model1

```

Now, the RMSE estimate is 13.3. RMSE is expressed in the same units as the outcome variable. In this case, the outcome variable is the placement test score percent. So the RMSE is 13.3 percentage points. The R^2 (rsq) is 0.659. This means that the model explains 66% of the variance in the outcome variable. Taken together, this isn't the best model.

But how good or bad is it? This is where we can use the null model to compare the model to. The null model is a model that predicts the mean of the outcome variable. We can use the `null_model()` function to create a null model and submit it to cross-validation. The code is seen in Example 9.40.

Example 9.40.

```

# Create null model
null_model <-

```

```

  null_model() |>
  set_engine("parsnip") |>
  set_mode("regression")

# Cross-validate null model
null_cv <-
  workflow() |>
  add_recipe(reg_rec) |>
  add_model(null_model) |>
  fit_resamples(
    resamples = vfold_cv(reg_train, v = 10),
    metrics = metric_set(rmse)
  )

# Collect metrics
null_cv |>
  collect_metrics()

```

```

> # A tibble: 1 x 6
>   .metric .estimator  mean    n std_err .config
>   <chr>   <chr>     <dbl> <int>   <dbl> <chr>
> 1 rmse    standard    22.6     10    0.206 Preprocessor1_Model1

```

Our regression model performs better than the null model (22.608) which means that it is picking up on some signal in the data.

Let's visualize the distribution of the predictions and the errors from our model to see if there are any patterns of interest. We can use the `collect_predictions()` function to extract the predictions of the cross-validation and plot the true outcome against the predicted outcome using `ggplot()`, as in Example 9.58.

Example 9.41.

```

# Visualize predictions
reg_cv_lasso |>
  collect_predictions() |>
  ggplot(aes(outcome, .pred, shape = id)) +
  geom_point(alpha = 0.5, position = position_jitter(width = 0.5)) +
  geom_smooth(method = "lm", se = FALSE, linewidth = 0.5) + # trend for each fold
  labs(
    x = "Truth",

```

```

y = "Predicted score",
shape = "Fold"
)

```

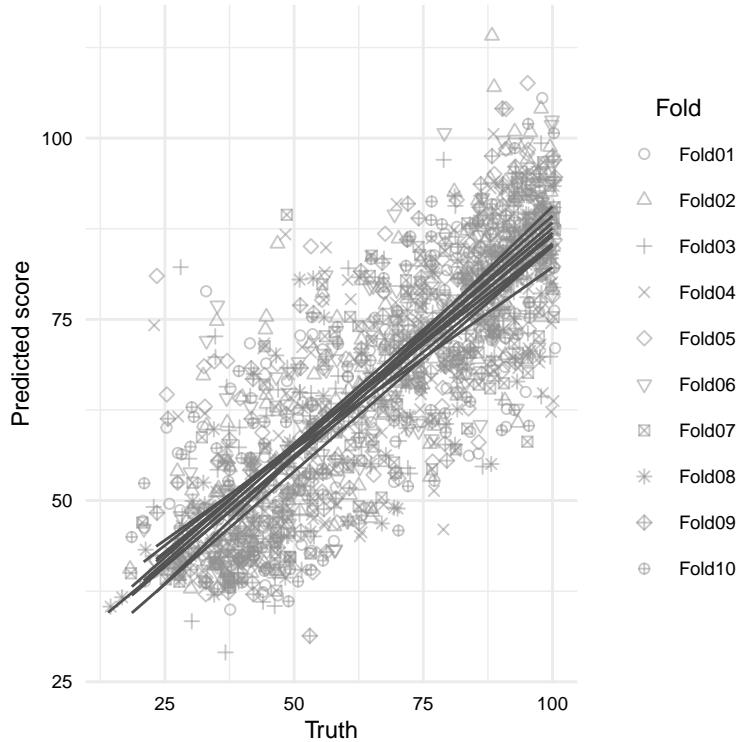


Figure 9.8: Distribution of the RMSE for the cross-validated linear regression model.

From this plot, we see data points for each predicted and truth value pair for each of the ten folds. There is a trend line for each fold which shows the linear relationship between the predicted and truth values for each fold. The trend lines are more similar than different, which is a good sign that the model is not wildly overfitting the training data. Looking closer, however, we can see the errors. Some are noticeably distant from the linear trend lines, *i.e.* outliers, in particular for test scores in the lower ranges.

If the R^2 value is in the ballpark, this means that somewhere around 40% of the variation is not explained by the frequency of the top 1,000 words. This is not surprising, as there are many other factors that contribute to the proficiency level of a text.

We have a model that is performing better than the null model, but it is not performing well enough to be very useful. We will need to update the model specification and/ or the features to try to improve the model fit. Let's start with the model. There are many different model

specifications we could try, but we will likely need to use a more complex model specification to capture the complexity that we observed in the errors from the previous model.

Let's try a decision tree model. **Decision trees** are non-linear models that are able to model non-linear relationships and interactions between the features and the outcome and tend to be less influenced by outliers. These are all desirable characteristics. Decision trees, however, can be prone to overfitting

Along the spectrum of model complexity, decision trees are more complex than linear regression models, but less complex than other models such as neural networks. Furthermore, decision trees are interpretable, which is a nice feature for an exploratory-oriented analysis.

To implement a new model in `tidymodels`, we need to create a new model specification and a new workflow. We will use the `decision_tree()` function from the `parsnip` package to create the model specification. The `decision_tree()` function takes no arguments and returns a `decision_tree` object. We create the new model specification in Example 9.42.

Example 9.42.

```
# Create model specification
reg_spec_tree <-
  decision_tree() |>
  set_engine("rpart") |>
  set_mode("regression")

reg_spec_tree

> Decision Tree Model Specification (regression)
>
> Computational engine: rpart
```

We now have a new model specification. We can now create a new workflow. We will use the same recipe as before, but we will change the model specification to `prof_spec_tree`. We add this to a new workflow and fit the workflow to the training data. The code is seen in Example 9.43.

Example 9.43.

```
# Create workflow
reg_wf_tree <-
  workflow() |>
  add_recipe(reg_rec) |>
```

```

add_model(reg_spec_tree)

# Set seed for reproducibility
set.seed(123)

# Cross-validated workflow
reg_cv_tree <-
  reg_wf_tree |>
  fit_resamples(
    resamples = vfold_cv(reg_train, v = 10),
    control = control_resamples(save_pred = TRUE)
  )

```

We can now evaluate the performance of the model using cross-validation. The code is seen in Example 9.44.

Example 9.44.

```

# Collect metrics
reg_cv_tree |>
  collect_metrics()

> # A tibble: 2 x 6
>   .metric .estimator  mean     n std_err .config
>   <chr>   <chr>     <dbl> <int>   <dbl> <chr>
> 1 rmse    standard    15.1     10   0.404 Preprocessor1_Model1
> 2 rsq     standard     0.554    10   0.0215 Preprocessor1_Model1

```

The metrics for the vanilla decision tree are similar to the regularized linear regression model. The RSME is 15.1 and the R^2 is 0.554. Yet, if we compare the standard error between the two models, we can see that the decision tree model has a larger standard error. This means that the decision tree model is more prone to overfitting the training data.

To minimize overfitting, we can tune hyperparameters of the model. Regularization is one way to reduce overfitting, as we saw with the regularized linear regression model. Another way to reduce overfitting is to reduce the complexity of the model. This can be done by reducing the number of features or by reducing the number of splits in the decision tree, known as **pruning**.

Another approach is to implement a random forest model. A **random forest** is an ensemble model that combines multiple decision trees to make a prediction. A random forest is a type

of ensemble model which means that it combines multiple models to make a prediction. In addition to multiple decision trees, random forests also perform random feature selection. This helps to reduce the correlation between the decision trees and thus reduces the variance of the model.

Let's try a random forest model. We will use the `rand_forest()` function from the `parsnip` package to create the model specification. The `rand_forest()` function takes no arguments and returns a `rand_forest` object. We will select the `ranger` engine and add the `importance` argument to ensure that we can extract feature importance if this model proves to be useful. We create the new model specification in Example 9.45.

Example 9.45.

```
# Create model specification
reg_spec_rf <-
  rand_forest() |>
  set_engine("ranger", importance = "impurity") |>
  set_mode("regression")

reg_spec_rf

> Random Forest Model Specification (regression)
>
> Engine-Specific Arguments:
>   importance = impurity
>
> Computational engine: ranger
```

We can now update the workflow to use the new model specification. The code is seen in Example 9.46.

Example 9.46.

```
# Update workflow
reg_wf_rf <-
  reg_wf_tree |>
  update_model(reg_spec_rf)

# Set seed for reproducibility
set.seed(123)
```

```
# Cross-validated workflow
reg_cv_rf <-
  reg_wf_rf |>
  fit_resamples(
    resamples = vfold_cv(reg_train, v = 10),
    control = control_resamples(save_pred = TRUE)
)
```

We can now evaluate the performance of the model using cross-validation. The code is seen in Example 9.47.

Example 9.47.

```
# Collect metrics
reg_cv_rf |>
  collect_metrics()

> # A tibble: 2 x 6
>   .metric .estimator  mean     n std_err .config
>   <chr>   <chr>     <dbl> <int>   <dbl> <chr>
> 1 rmse    standard    13.1     10   0.305 Preprocessor1_Model1
> 2 rsq     standard     0.680     10   0.0133 Preprocessor1_Model1
```

The random forest model performs better than the decision tree model and the regularized linear regression model. The RSME is 13.1 and the R^2 is 0.68. We also see that the standard error is the lowest of the models we have tried so far. This means that the random forest model is less prone to overfitting the training data.

Before we settle on this model, let's try one more model, a support vector machine (SVM). A **support vector machine** is a supervised machine learning model that can be used for both classification and regression. It is a non-parametric method, which means that it does not make any assumptions about the underlying distribution of the data. It is also a method which can be better suited for high-dimensional data where many values are zero, that is, sparse data, which is often the case with text data.

Let's again specify the model. We will use the `svm_linear()` function from the `parsnip` package to create the model specification and we will use the `LiblineaR` computational engine. We create the new model specification in Example 9.48.

Example 9.48.

```
# Create model specification
reg_spec_svm <-
  svm_linear() |>
  set_engine("LiblineaR") |>
  set_mode("regression")

reg_spec_svm
```

```
> Linear Support Vector Machine Model Specification (regression)
>
> Computational engine: LiblineaR
```

Now let's update the workflow to use the new model specification. The code is seen in Example 9.49.

Example 9.49.

```
# Update workflow
reg_wf_svm <-
  reg_wf_rf |>
  update_model(reg_spec_svm)

# Set seed for reproducibility
set.seed(123)

# Cross-validated workflow
reg_cv_svm <-
  reg_wf_svm |>
  fit_resamples(
    resamples = vfold_cv(reg_train, v = 10),
    control = control_resamples(save_pred = TRUE)
  )
```

Let's evaluate the cross-validation performance of the model. The code is seen in Example 9.50.

Example 9.50.

```

# Collect metrics
reg_cv_svm |>
  collect_metrics()

> # A tibble: 2 x 6
>   .metric .estimator  mean     n std_err .config
>   <chr>   <chr>     <dbl> <int>   <dbl> <chr>
> 1 rmse    standard    14.7     10   0.353 Preprocessor1_Model1
> 2 rsq     standard     0.625     10   0.0152 Preprocessor1_Model1

```

This SVR is not performing better than the linear regression and random forest models and the standard error is not particularly low. So we will not pursue this model further.

So in summary, we've tried four different model specifications. The regularized linear regression model, the decision tree model, the random forest model, and the support vector machine model. The random forest model performed the best. But there stands to be improvement, but it looks as if we may need to update the features.

In the recipe we have used until this point we have limited the word features to 1,000 and used the raw counts of the words. The rationale for this was that we wanted to limit the number of features to reduce the complexity of the model while still capturing the most important features. But we may have limited the features too much, at least now that we are comparing features between the same population (learners). A potentially more informative feature would be the TF-IDF score. This score is a measure of how important a word is to a document in a collection or corpus. Specifically, it is the product of the term frequency and the inverse document frequency. The more dispersed a feature is across the corpus, the lower the TF-IDF score. The more concentrated a feature is across the corpus, the higher the TF-IDF score, and the more informative the feature is for distinguishing between documents.

So we can use the `step_tfidf()` function to update the recipe. The code is seen in Example 9.51.

Example 9.51.

```

# Create a recipe
reg_rec <-
  recipe(outcome ~ text, data = reg_train) |>
  step_tokenize(text) |>
  step_tokenfilter(text, max_tokens = 1000) |>
  step_tfidf(text, smooth_idf = FALSE)

```

```
# Preview  
reg_rec
```

👉 Tip

Two things to note about the code in Example 9.51. First, the `step_tfidf()` function by default add a smoothing term to the inverse document frequency (IDF) calculation. This setting has the effect of reducing the influence of the IDF calculation. Thus, terms that appear in many (or all) documents will not be downweighted as much as they would be if the smoothing term was not added. For our purposes, we want to downweight or eliminate the influence of the most frequent terms, so we will set `smooth_idf = FALSE`. Second, the log-transformation is not necessary when using TF-IDF scores as normalization is built into the TF-IDF calculation.

Another change we can explore is to increase the number of features. But how many features should we use? We can turn to the `tune()` function to help us answer this question. Let's add the `tune()` function to the recipe and tune the `max_tokens` hyperparameter. The code is seen in Example 9.52.

Example 9.52.

```
# Create a recipe  
reg_rec <-  
  recipe(outcome ~ text, data = reg_train) |>  
  step_tokenize(text) |>  
  step_tokenfilter(text, max_tokens = tune()) |>  
  step_tfidf(text, smooth_idf = FALSE)  
  
# Preview  
reg_rec
```

Let's tune the `max_tokens` with the random forest model specification that we created earlier. We will create a tuning workflow, which will tune the `max_tokens` hyperparameter on the training data using cross-validation. The code is seen in Example 9.53.

Example 9.53.

```
# Create tuning workflow  
tune_wf <-  
  workflow() |>
```

```
add_recipe(reg_rec) |>  
add_model(reg_spec_rf)
```

```
tune_wf
```

```
> == Workflow =====  
> Preprocessor: Recipe  
> Model: rand_forest()  
>  
> -- Preprocessor -----  
> 3 Recipe Steps  
>  
> * step_tokenize()  
> * step_tokenfilter()  
> * step_tfidf()  
>  
> -- Model -----  
> Random Forest Model Specification (regression)  
>  
> Engine-Specific Arguments:  
>   importance = impurity  
>  
> Computational engine: ranger
```

The `tune_grid()` function takes a workflow, a resampling method, a tuning grid, and a set of metrics. The tuning grid is a set of hyperparameters and their values. The `tune_grid()` function will tune the hyperparameters on the training data using cross-validation. The code is seen in Example 9.54. This is a computationally intensive process, as it will train a 10 folds, for each hyperparameter value. Each fold in the random forest is 500 trees, so this will train 5,000 trees for each hyperparameter value! So that is 30,000 trees in total. This code will take some time to run.

Example 9.54.

```
# Create tuning grid  
tune_grid <-  
  grid_regular(max_tokens(range = c(500, 3500)), levels = 5)  
  
tune_grid
```

```

> # A tibble: 5 x 1
>   max_tokens
>   <int>
> 1      500
> 2     1250
> 3    2000
> 4    2750
> 5    3500

# Set seed for reproducibility
set.seed(123)

# Create tuning workflow
tune <-
  tune_grid(
    tune_wf,
    resamples = vfold_cv(reg_train, v = 10),
    grid = tune_grid,
    metrics = metric_set(rmse, rsq),
    control = control_resamples(save_pred = TRUE)
  )

tune

> # Tuning results
> # 10-fold cross-validation
> # A tibble: 10 x 5
>   splits           id     .metrics     .notes     .predictions
>   <list>          <chr>  <list>       <list>      <list>
> 1 <split [1371/153]> Fold01 <tibble [10 x 5]> <tibble [0 x 3]> <tibble>
> 2 <split [1371/153]> Fold02 <tibble [10 x 5]> <tibble [0 x 3]> <tibble>
> 3 <split [1371/153]> Fold03 <tibble [10 x 5]> <tibble [0 x 3]> <tibble>
> 4 <split [1371/153]> Fold04 <tibble [10 x 5]> <tibble [0 x 3]> <tibble>
> 5 <split [1372/152]> Fold05 <tibble [10 x 5]> <tibble [0 x 3]> <tibble>
> 6 <split [1372/152]> Fold06 <tibble [10 x 5]> <tibble [0 x 3]> <tibble>
> 7 <split [1372/152]> Fold07 <tibble [10 x 5]> <tibble [0 x 3]> <tibble>
> 8 <split [1372/152]> Fold08 <tibble [10 x 5]> <tibble [0 x 3]> <tibble>
> 9 <split [1372/152]> Fold09 <tibble [10 x 5]> <tibble [0 x 3]> <tibble>
> 10 <split [1372/152]> Fold10 <tibble [10 x 5]> <tibble [0 x 3]> <tibble>

```

Just as we did for the `penalty` hyperparameter, we can visualize the performance of the model as a function of the `max_tokens` hyperparameter. The code is seen in Example 9.55.

Example 9.55.

```
# Visualize tuning results
tune |>
  collect_metrics() |>
  ggplot(aes(max_tokens, mean)) +
  geom_point() +
  geom_line() +
  scale_x_continuous(
    breaks = scales::pretty_breaks(n = 10),
    labels = scales::comma
  ) +
  facet_wrap(~ .metric, scales = "free_y", ncol = 1) +
  labs(
    x = "Max tokens"
  )
```

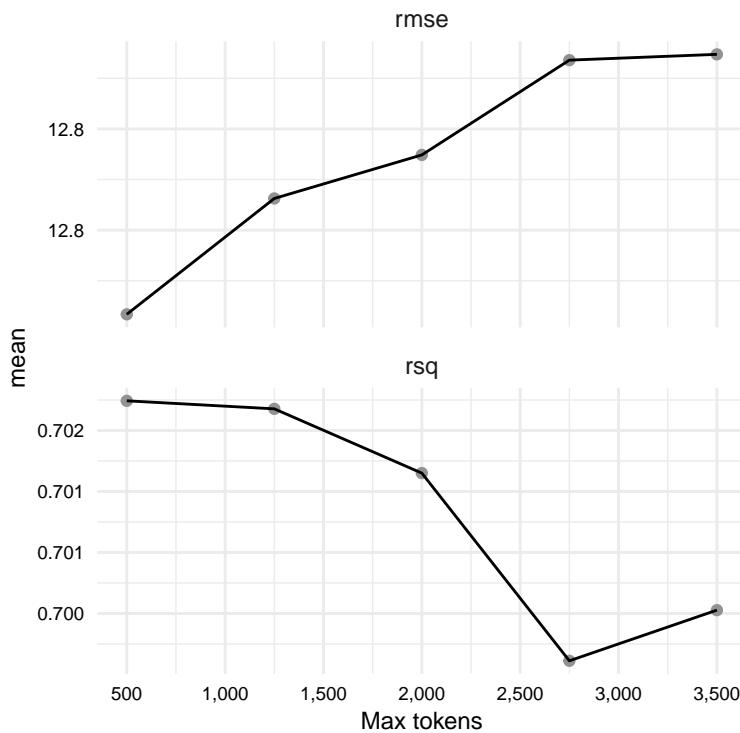


Figure 9.9: Performance of the random forest model as a function of the `max_tokens` hyperparameter.

We added a range of maximum token values to the tuning grid to see if there is a point of diminishing returns. We can see that the performance of the model actually appears to improve, not with more tokens, but instead with less. Our lowest value of 500 tokens appears to perform the best. This is interesting, as it suggests that there are a small number of words that are most informative for predicting the placement test score. It also suggests that individual words, on the whole, are not very informative for predicting the placement test score.

We can now select the best hyperparameter value. The code is seen in Example 9.56.

Example 9.56.

```
# Select best parameter
chosen_max_tokens <-
  tune |>
  select_best(metric = "rmse")

# Update workflow
reg_final_rf <-
  tune_wf |>
  finalize_workflow(chosen_max_tokens)

reg_final_rf

> == Workflow =====
> Preprocessor: Recipe
> Model: rand_forest()
>
> -- Preprocessor -----
> 3 Recipe Steps
>
> * step_tokenize()
> * step_tokenfilter()
> * step_tfidf()
>
> -- Model -----
> Random Forest Model Specification (regression)
>
> Engine-Specific Arguments:
>   importance = impurity
>
> Computational engine: ranger
```

We can now fit the model to the training data and evaluate the performance using cross-validation. The code is seen in Example 9.57.

Example 9.57.

```
# Cross-validated workflow
reg_cv_rf <-
  reg_final_rf |>
  fit_resamples(
    resamples = vfold_cv(reg_train, v = 10),
    control = control_resamples(save_pred = TRUE)
  )

# Collect metrics
reg_cv_rf |>
  collect_metrics()

> # A tibble: 2 x 6
>   .metric .estimator   mean     n std_err .config
>   <chr>   <chr>     <dbl> <int>   <dbl> <chr>
> 1 rmse    standard    12.8     10   0.221 Preprocessor1_Model1
> 2 rsq     standard     0.695    10   0.0137 Preprocessor1_Model1
```

We've improved the model, but not very much. We can see that the RMSE is 13.1 and the R^2 is 0.68. The standard error is NA. This is the lowest standard error we have seen so far, but it is still not as low as we would like.

Let's now visualize the distribution of the predictions and the errors from our word features model to see if there are any patterns of interest. We can use the `collect_predictions()` function to extract the predictions of the cross-validation and plot the true outcome against the predicted outcome using `ggplot()`, as in Example 9.58.

Example 9.58.

```
# Visualize predictions
reg_cv_rf |>
  collect_predictions() |>
  ggplot(aes(outcome, .pred, shape = id)) +
  geom_point(alpha = 0.5, position = position_jitter(width = 0.5)) +
  geom_smooth(method = "lm", se = FALSE) + # trend for each fold
  labs(
```

```

x = "Truth",
y = "Predicted score",
shape = "Fold"
)

```

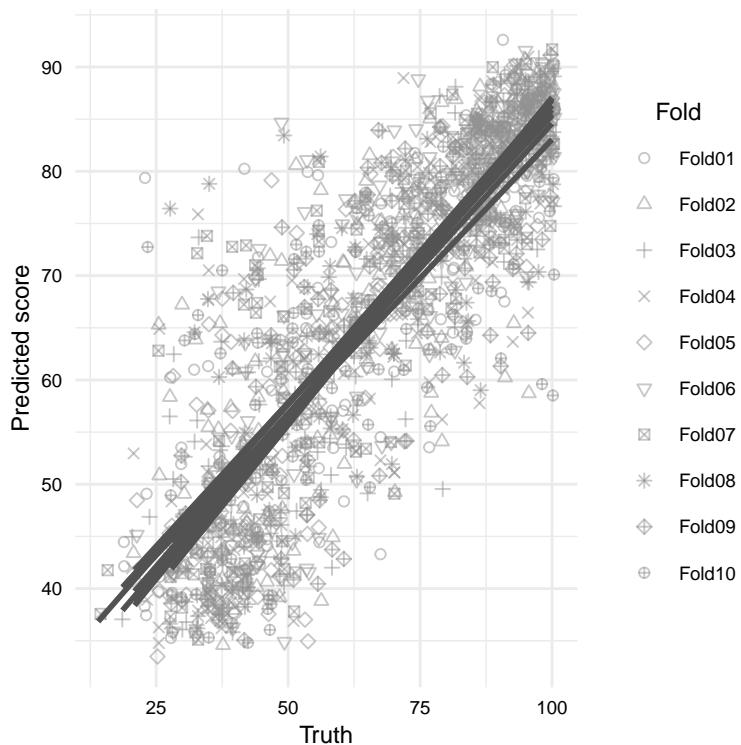


Figure 9.10: Distribution of the RMSE for the cross-validated linear regression model.

There appears to be more cohesion in the predictions, overall. The errors however seem visually to be larger for the lower scores.

At this point we can either consider this model to be good enough or we can try to improve it further. Let's take one more shot at improving the features by including bigrams. To include words (unigrams) and bigrams, we can modify the `step_tokenize()` function in our recipe. We add the `token = "ngrams"` argument and specify the options as `list(n = 2, n_min = 1)`. This will create unigrams and bigrams. The code is seen in Example 9.59.

Example 9.59.

```

# Create a recipe
reg_rec <-
  recipe(outcome ~ text, data = reg_train) |>
  step_tokenize(text, token = "ngrams", options = list(n = 2, n_min = 1)) |>
  step_tokenfilter(text, max_tokens = tune()) |>
  step_tfidf(text, smooth_idf = FALSE)

# Preview
reg_rec

```

Since the features have changed, we won't assume that our tuning of the `max_tokens` is still valid. So we will tune the `max_tokens` hyperparameter again, as in Example 9.52 through Example 9.57. For the sake of brevity, we will not show the code here. We will simply show the results.

```

# Create workflow
reg_wf_rf <-
  workflow() |>
  add_recipe(reg_rec) |>
  add_model(reg_spec_rf)

# Create tuning grid
tune_grid <-
  grid_regular(max_tokens(range = c(500, 3500)), levels = 5)

# Set seed for reproducibility
set.seed(123)

# Create tuning workflow
tune <-
  tune_grid(
    reg_wf_rf,
    resamples = vfold_cv(reg_train, v = 10),
    grid = tune_grid,
    metrics = metric_set(rmse, rsq),
    control = control_resamples(save_pred = TRUE)
  )

# Select best parameter
chosen_max_tokens <-
  tune |>

```

```

select_best(metric = "rmse")

# Update workflow
reg_final_rf <-
  reg_wf_rf |>
  finalize_workflow(chosen_max_tokens)

# Cross-validated workflow
reg_cv_rf <-
  reg_final_rf |>
  fit_resamples(
    resamples = vfold_cv(reg_train, v = 10),
    control = control_resamples(save_pred = TRUE)
  )

# Collect metrics
estimates <-
  reg_cv_rf |>
  collect_metrics() |>
  pull(3)

```

The tuning of `max_tokens` selected 2,000 features as the optimal number. The cross-validation of the training dataset produced an RMSE of 12.8 and an R^2 of 0.698. The standard error is NA. The upshot is that by including bigrams we have not improved, or worsened, the model. Including the unigrams and bigrams together may be more informative for the exploration of the features.

We could continue to try to improve the model, but at this point we have a model that is performing better than the null model and is performing better than the other models we have tried. So we will consider this model to be good enough.

Let's now fit the 1-2 gram model to the testing data and evaluate the performance on the testing set. The code is seen in Example 9.60.

Example 9.60.

```

# Fit model on training data
reg_final_rf_fit <-
  reg_final_rf |>
  fit(reg_train)

# Predict on testing data

```

```

reg_final_rf_pred <-
  bind_cols(
    reg_test,
    predict(reg_final_rf_fit, reg_test)
  )

# Evaluate performance
reg_final_rf_pred |>
  metrics(truth = outcome, estimate = .pred)

> # A tibble: 3 x 3
>   .metric .estimator .estimate
>   <chr>   <chr>       <dbl>
> 1 rmse    standard     12.9
> 2 rsq     standard     0.695
> 3 mae    standard     9.84

```

We can now visualize the feature importance of the model. The code is seen in Example 9.61.

Example 9.61.

```

# Extract predictions
reg_final_rf_fit |>
  vip::vi(scale = TRUE)  |>
  mutate(Variable = str_replace(Variable, "^tfidf_text_", "")) |>
  slice_max(Importance, n = 20) |>
  # reorder variables by importance
  ggplot(aes(reorder(Variable, Importance), Importance)) +
  geom_point() +
  coord_flip() +
  labs(
    x = "Feature",
    y = "Importance"
  )

```

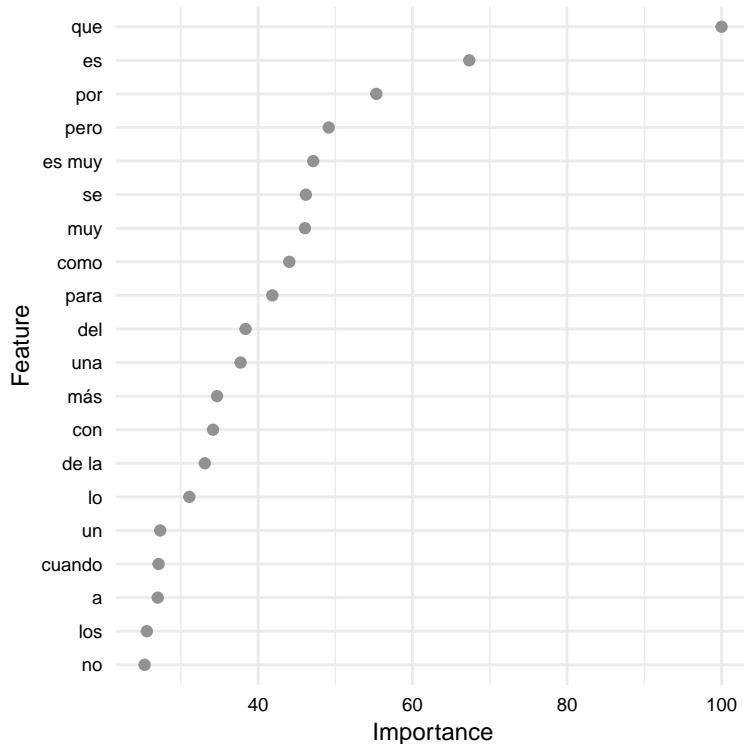


Figure 9.11: Feature importance of the random forest model.

Activities

_recipe

What: Building predictive models^a

How: Read Recipe 9 and participate in the Hypothes.is online social annotation.

Why:  ...

^a<https://qtalr.github.io/qtalrkit/articles/recipe-9.html>

_lab

What: Text classification^a

How: Clone, fork, and complete the steps in Lab 9.

Why:  ...

^a<https://github.com/qtalr/lab-09>

Summary

In this chapter we have learned about supervised machine learning. We have learned about the different types of supervised machine learning methods and how they can be used to predict and classify. We have also learned about the different types of data structures that are used in supervised machine learning. Finally, we have learned about the different types of evaluation metrics that are used to evaluate the performance of supervised machine learning models.

10 Infer

People generally see what they look for, and hear what they listen for.

— Harper Lee, *To Kill a Mockingbird*

▀ Outcomes

- Identify the research goals of inferential data analysis
- Describe the workflow for inferential data analysis
- Indicate the importance of quantifying uncertainty in inferential data analysis

In this chapter, we consider approaches to deriving knowledge from information which can be generalized to the population from which the data is sampled. This process is known as statistical inference. The discussion here implements descriptive assessments, statistical tests, and evaluation procedures for a series of contexts which are common in the analysis of corpus-based data. During our treatment of these contexts, we will establish a foundational understanding of the null hypothesis significance testing (NHST) framework using a simulation-based approach. This approach is more intuitive, easier to implement, and provides a better conceptual understanding of the statistical designs and analyses. The structure of the chapter groups significance testing scenarios by response and explanatory variables, highlighting the commonalities and differences that arise in the statistical designs and analyses.

➤ Lessons

What: Advanced Tables^a

How: In the R Console pane load `swirl`, run `swirl()`, and follow prompts to select the lesson.

Why: ↗ TBD

^a<https://github.com/qtalr/lessons>

10.1 Orientation

The aim of this section is to provide an overview of inferential data analysis (IDA). First we consider the research goal of inferential analysis pointing to key differences with exploratory data analysis (EDA) and predictive data analysis (PDA). Next we outline the Null Hypothesis

Significance Testing (NHST) approach to IDA, highlighting the key steps in the workflow used to conduct analysis.

10.1.1 Research goal

In contrast to exploratory and predictive analyses, inference is not a data-driven endeavor. Rather, the goal of inferential data analysis (IDA) is to make claims about the population and assess the extent to which the data supports those claims. This implicates two key methodological restrictions which are not in play in other analysis methods.

First, the research question and expected findings are formulated *before* the data is analyzed, in fact strictly speaking this should take place even before data collection. This helps ensure that the data is aligned with the research question and that the data is representative of the population and that the analysis has a targeted focus and does not run the risk of becoming a ‘just-so’ story¹ or a ‘significance-finding’ mission² both of which violate the principles of significance testing.

Second, the data used in IDA is only used once. That is to say, that the entire dataset is used a single time to statistically interrogate the relationship(s) of interest. In both EDA and PDA the data can be approached in different ways and the results of the analysis can be used to inform the next steps in the analysis. In IDA, however, the data is used to test a specific hypothesis and the results of the analysis are interpreted in the context of that hypothesis.

10.1.2 Approach

The methodological approach to inferential data analysis (IDA) is the most straightforward of the analysis types covered in this textbook. As the research goal is to test a claim, the steps necessary are fewer than in EDA or PDA, where the exploratory nature of these approaches includes various possible iterations. The workflow for IDA is shown in Table 10.1.

Table 10.1: Workflow for inferential data analysis

Step	Name	Description
1	Identify	Identify and map the hypothesis statement to the appropriate response and explanatory variables
2	Inspect	Assess the distribution of the variable(s) with the appropriate descriptive statistics and visualizations.

¹“Hypothesis After Result is Known” (HARKing) involves selectively analyzing data, trying different variables or combinations until a significant p-value is obtained, or stopping data collection when a significant result is found (Kerr 1998).

²“p-hacking” is the practice of running multiple tests until a statistically significant result is found. This practice violates the principles of significance testing (Head et al. 2015).

Step	Name	Description
3	Interrogate	Apply the appropriate statistical procedure to the dataset.
4	Interpret	Review the statistical results and interpret them in the context of the hypothesis.

Based on the hypothesis statement, we first identify and operationalize the variables. The response variable whose variation we aim to explain. In most statistical designs, one or more explanatory variables are included in the analysis in an attempt to gauge the extent to which these variables account for the variation in the response variable. For both response and explanatory variables, it is key to confirm that your operationalization of the variables is well-defined and that the data is aligned with the operationalization.

 **Consider this**

- Update this callout

Consider the following hypothesis statements:

- *The length of the recipient clause is related to the realization of the recipient clause.*
- *The length of the recipient clause is related to the realization of the recipient clause in spoken language but not in written language.*
- *The length of the recipient clause is related to the realization of the recipient clause in spoken language but not in written language when the length of the theme clause is controlled for.*

What are the explanatory and/ or response variables in each of these statements? What are the operationalizations of these variables? What are the implications for the data that is used to test these hypotheses?

Next, we determine the informational values of the variables. The informational value of each variable will condition how we approach visualization, interrogation, and ultimately interpretation of the results. Note, that some informational types can be converted to other types, specifically higher-order types can be converted to lower-order types. For example, a continuous variable can be converted to a categorical variable, but not vice versa. It is preferable, however, to use the highest informational value of a variable. Simplifying data results in a loss of information –which will result in a loss of information and hence statistical power which may lead to results that obscure meaningful patterns in the data (R. Harald Baayen 2004).

With our design in place, we can now inspect the data. This involves assessing the distribution of the variables using descriptive statistics and visualizations. The goal of this step is to confirm the integrity of the data (missing data, anomalies, etc.), identify general patterns in the data, and identify potential outliers. As much as this is a verification step, it also serves

to provide a sense of the data and the extent to which the data aligns with the hypothesis. This is particularly true when statistical designs are complex and involve multiple explanatory variables. An appropriate visualization provides context for interpreting the results of the statistical analysis.

Interrogating the data involves applying the appropriate statistical procedure to the dataset. In the Null Hypothesis Significance Testing (NHST) paradigm, this process includes calculating a statistic from the data, comparing it to a null hypothesis distribution, and measuring the evidence against the null hypothesis. The null hypothesis distribution is a distribution of statistic values that we would expect if the null hypothesis were true, *i.e.* that there is no difference or relationship between the explanatory and/ or response variables. By comparing the observed statistic to the null hypothesis distribution, we can determine the likelihood of observing the observed statistic if the null hypothesis were true. This likelihood is known as the p-value. When the p-value is below a pre-determined threshold, typically 0.05, the result is considered statistically significant. This means that the observed statistic is sufficiently different from the null hypothesis distribution that we can reject the null hypothesis.

Now let's consider how to approach interpreting the results from a statistical test. The p-value provides a probability that the results of our statistical test could be explained by the null hypothesis. When this probability crosses above the threshold of .05, the result is considered statistically significant, otherwise we have a 'null result' (*i.e.* non-significant).

However, this sets up a binary distinction that can be problematic. On the one hand, what is one to do if a test returns a p-value of .051 or something 'marginally significant'? According to standard practice these results would not be statistically significant. On the other hand, if we get a statistically significant result, do we move on –case closed? To address both of these issues, it is important to calculate a confidence interval for the test statistic. The confidence interval is the range of values for our test statistic that we would expect the true statistic value to fall within some level of uncertainty. Again, 95% is the most common level of uncertainty. The upper and lower bounds of this range are called the confidence limits for the test statistic.

Used in conjunction with p-values, confidence intervals can provide a more nuanced interpretation of the results of a statistical test. For example, if we get a p-value of .051, but the confidence interval is very narrow, we can be more confident that the results are reliable. Conversely, if we get a p-value of .049, but the confidence interval is very wide, we can be less confident that the results are reliable. If our confidence interval contains the null value, then even a significant p-value will require a more nuanced interpretation.

It is important to underscore that the purpose of IDA is to draw conclusions from a dataset which are generalizable to the population. These conclusions require that there are rigorous measures to ensure that the results of the analysis do not overgeneralize (suggest there is a relationship when there is not one) and balance that with the fact that we don't want to undergeneralize (miss the fact that there is a relationship in the population, but our analysis was not capable of detecting it).

10.2 Analysis

In this section, we will discuss the practical application of inferential data analysis. The discussion will be divided into two sections based on the type of response variable: categorical and numeric. We will then explore specific designs for univariate, bivariate, and multivariate tests. Throughout this process, we will focus on null hypothesis testing, covering concepts and methods that are relevant to significance testing and the interpretation of results.

Two datasets are included in this section to provide a context for the inferential data analysis in both categorical and numeric cases. The `dative` dataset is a subset of the `languageR::dative` dataset (R. H. Baayen and Shafeei-Bajestan 2019). It contains over 3k observations describing the realization of the recipient clause in English dative constructions. The `fillers` dataset is drawn from the Switchboard Dialog Act Corpus (University of Colorado Boulder 2008). This dataset contains //FIXME ... observations summarizing the use of fillers by speaker in the corpus.

We will learn and implement null significance testing using a simulation-based method. In contrast to theory-based methods, simulation-based methods tend to be more intuitive, easier to implement, and provide a better conceptual understanding of the statistical designs and analyses (Morris, White, and Crowther 2019; Rossman and Chance 2014). The steps for implementing a simulation-based approach to significance testing are outlined in Table 10.2.

Table 10.2: Simulation-based approach to significance testing

Step	Name	Description
1	Specify	Specify the variables of interest and their relationship
2	Calculate	Calculate the observed statistic
3	Hypothesize	Generate the null hypothesis distribution
4	Visualize	Visualize the null hypothesis distribution
5	Get p-value	Calculate the p-value
6	Get confidence interval	Calculate the confidence interval

The `infer` package (Bray et al. 2024) provides a tidyverse-friendly framework to implement simulation-based methods for statistical inference. Designed to be used in conjunction with the `tidyverse` (Wickham 2023b), `infer` provides a set of functions that can be used to specify the variables of interest, calculate the observed statistic, generate the null hypothesis distribution, visualize the null hypothesis distribution, calculate the p-value, and calculate the confidence interval.

Let's load the necessary packages and import the datasets we will use in this section, as seen in Example 10.1.

Example 10.1.

```
# Load packages
library(infer)      # for statistical inference
library(skimr)       # for descriptive statistics
library(janitor)     # for cross-tabulation

# Load datasets
dative_df <-
  read_csv("../data/derived/dative.csv")

fillers_df <-
  read_csv("../data/derived/fillers.csv")
```

10.2.1 Categorical

Here we demonstrate the application of inferential data analysis (IDA) to categorical response variables. This will include various common statistical designs and analyses. In Table 10.3, we see common design scenarios, the variables involved, and the statistic used in the analysis.

Table 10.3: Statistical test designs for categorical response variables

Scenario	Dependent variable	Independent variable(s)	Statistical test
Univariate Categorical		None	Proportion
Bivariate Categorical		Categorical	Difference in proportions
Bivariate Categorical (>2 levels)		Categorical (>2 levels)	Chi-square
Multivariate Categorical		Categorical or Numeric (>1 variables)	Logistic regression

We will use the `dative_df` dataset to illustrate each of these designs and analyses. To familiarize ourselves with the dataset, let's consider the data dictionary in Table 10.4.

Table 10.4: Data dictionary for the `dative_df` dataset.

variable	name	variable_type	description
realization_of_rcp	Realization of RCP	categorical	The realization of the recipient (NP/ PP)
modality	Modality	categorical	The modality of the utterance (spoken/ written)
length_of_rcp	Length of RCP	numeric	The length of the recipient (number of words)

length_of_thm	Length of THM	numeric	The length of the theme (number of words)
---------------	---------------	---------	---

We see that this dataset has four variables, two categorical and two numeric. In our demonstrations we are going to use the `realization_of_rcp` as the response variable, the variable whose variation we are investigating.

For a bit more context, a dative is the phrase which reflects the entity that takes the recipient role in a ditransitive clause. In English, the recipient (dative) can be realized as either a prepositional phrase (PP) as seen in (1) or as a noun phrase (NP) as seen in (2) below.

Example utterances:

1. John gave the book [to Mary PP].
2. John gave [Mary NP] the book.

Together these two syntactic options are known as the Dative Alternation Bresnan et al. (2007).

From the large set of variables in the original dataset, I've selected three explanatory variables to use in our demonstrations. These variables are:

- `modality`: either written or spoken
- `length_of_rcp`: the length of the recipient clause (in words)
- `length_of_thm`: the length of the theme clause (in words)

In preparation for statistical analysis, we need to convert the character variables to factors. Let's do that and preview the dataset, as seen in Example 10.2.

Example 10.2.

```
# Convert character variables to factors
dative_df <-
  dative_df |>
  mutate(across(where(is.character), factor))

# Preview
glimpse(dative_df)
```

```
> Rows: 3,263
> Columns: 4
> $ realization_of_rcp <fct> NP, ~
> $ modality           <fct> written, written, written, written, written, written, ~
> $ length_of_rcp     <dbl> 1, 2, 1, 1, 2, 2, 1, 1, 1, 2, 2, 1, 2, 1, 1, 4, ~
> $ length_of_thm     <dbl> 14, 3, 13, 5, 3, 4, 4, 1, 11, 2, 3, 3, 5, 2, 8, 2, ~
```

We can see that the dataset includes 3263 observations. We will take a closer look at the descriptive statistics for the variables as we prepare for each analysis.

10.2.1.1 Univariate analysis

The univariate analysis is the simplest statistical design and analysis. It includes only one variable. The goal is to describe the distribution of the levels of the variable. The `realization_of_rcp` variable has two levels: NP and PP. A potential research question is:

- Is there a difference in the proportion of NP and PP realizations of the recipient clause?

This question can be answered using a difference in proportion test. The null hypothesis is that there is no difference in the proportion of NP and PP realizations of the recipient clause. The alternative hypothesis is that there is a difference in the proportion of NP and PP realizations of the recipient clause.

Before we get into statistical analysis, it is always a good idea to cross-tabulate or visualize the question, depending on the complexity of the relationship. In Example 10.3, we see the code that shows the distribution of the levels of the `realization_of_rcp` variable in a cross-table.

Example 10.3.

```
# Cross-tabulation of `realization_of_rcp`  
dative_df |>  
  tabyl(realization_of_rcp) |>  
  adorn_pct_formatting(digits = 2) |>  
  kable() |>  
  kable_styling()
```

Table 10.5: Distribution of the levels of the `realization_of_rcp` variable.

realization_of_rcp	n	percent
NP	2414	73.98%
PP	849	26.02%

From Table 10.5, we see that the proportion of NP realizations of the recipient clause is higher than the proportion of PP realizations of the recipient clause. However, we cannot conclude that there is a difference in the proportion of NP and PP realizations of the recipient clause. We need to conduct a statistical test to determine if the difference is statistically significant.

To determine if the distribution of the levels of the `realization_of_rcp` variable is different from what we would expect if the null hypothesis were true, we need to calculate the difference

observed in the sample and compare it to the differences observed in many samples where the null hypothesis is true.

First, let's calculate the proportion of NP and PP realizations of the recipient clause in the sample. We turn to the `specify()` function from the `infer` package to specify the variable of interest. In this case, we only have the response variable. Furthermore, the argument `success` specifies the level of the response variable that we will use as the 'success'. The term 'success' is used because the `specify()` function was designed for binomial variables where the levels are 'success' and 'failure', as seen in Example 10.4.

Example 10.4.

```
# Specify the variable of interest
dative_spec <-
  dative_df |>
  specify(
    response = realization_of_rcp,
    success = "NP"
  )

dative_spec
```



```
> Response: realization_of_rcp (factor)
> # A tibble: 3,263 x 1
>   realization_of_rcp
>   <fct>
> 1 NP
> 2 NP
> 3 NP
> 4 NP
> 5 NP
> 6 NP
> 7 NP
> 8 NP
> 9 NP
> 10 NP
> # i 3,253 more rows
```

The `dative_spec` is a data frame with attributes which are used by the `infer` package to maintain information about the statistical design for the analysis. In this case, we only have information about what the response variable is.

The next step to calculating the observed proportion is to calculate the proportion statistic. The `calculate()` function from the `infer` package is used to calculate the proportion statistic. The `calculate()` function takes the `dative_spec` data frame as an argument. The `calculate()` function returns a data frame with the proportion statistic in the `stat` column, as seen in Example 10.5.

Example 10.5.

```
# Calculate the proportion statistic
dative_obs <-
  dative_spec |>
  calculate(stat = "prop")

dative_obs

> Response: realization_of_rcp (factor)
> # A tibble: 1 × 1
>   stat
>   <dbl>
> 1 0.740
```

Note, that the observed statistic, proportion, is the same as the proportion we calculated in Table 10.5. In such a simple example, the summary statistic and the observed statistic are the same. But this simple example shows how choosing the ‘success’ level of the response variable is important. If we had chosen the ‘PP’ level as the ‘success’ level, then the observed statistic would be the proportion of PP realizations of the recipient clause. There is nothing wrong with choosing the ‘PP’ level as the ‘success’ level, but it would change the direction of the observed statistic.

Now that we have the observed statistic, our goal will be to determine if the observed statistic is different from what we would expect if the null hypothesis were true. To do this, we simulate many samples where the null hypothesis is true. Simulation means that we will randomly sample from the `dative_df` data frame many times. Note that sampling the dataset in this way is much more feasible with a computer than it would be to do so by hand. This is one of the advantages of using a computer for statistical analysis.

The only addition decision we need to make is how the sampling takes place. Since `realization_of_rcp` is a variable with only two levels, the null hypothesis that both levels are equally likely. In other words, in a null hypothesis world, NP and PP we would expect the proportions to roughly be 50/50.

To formulize this hypothesis with `infer` we use the `hypothesize()` function and set the null hypothesis to “point” and the proportion to 0.5. Then we can `generate()` a number of samples, say 1,000, drawn from our 50/50 world. Finally, the “prop” (proportion) statistic is `calculate()`d for each of the 1,000 samples and returned in a data frame, as seen in Example 10.7.

Example 10.6.

```
# Generate the null hypothesis distribution
dative_null <-
  dative_spec |>
  hypothesize(null = "point", p = 0.5) |>
  generate(reps = 1000, type = "draw") |>
  calculate(stat = "prop")

dative_null

> Response: realization_of_rcp (factor)
> Null Hypothesis: point
> # A tibble: 1,000 x 2
>   replicate   stat
>       <int> <dbl>
> 1       1  0.496
> 2       2  0.499
> 3       3  0.509
> 4       4  0.496
> 5       5  0.492
> 6       6  0.499
> 7       7  0.514
> 8       8  0.499
> 9       9  0.504
> 10     10  0.501
> # i 990 more rows
```

The result of Example 10.7 is a data frame with as many rows as there are samples. Each row contains the proportion statistic for each sample drawn from the hypothesized distribution that the proportion of NP realizations of the recipient clause is 0.5.

To appreciate the null hypothesis distribution, we can visualize it using a histogram. The `infer` package provides a convenient `visualize()` function for visualizing distributions, as seen in Example 10.7.

Example 10.7.

```
# Visualize the null hypothesis distribution
dative_null |>
  visualize()
```

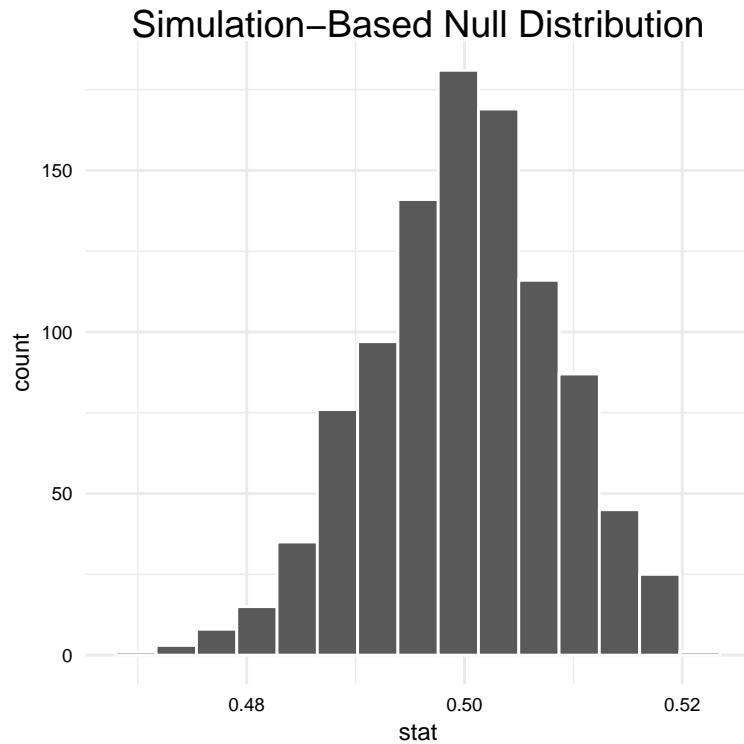


Figure 10.1: Null hypothesis distribution of the proportion of NP realizations of the recipient clause.

On the x-axis is the proportion statistic of NP realizations of the recipient clause that we would expect if the null hypothesis were true. For the 1,000 samples, the proportion statistic ranges from 0.47, 0.52. Importantly we can appreciate that the most of the proportion statistics are around 0.5, which is what we would expect if the null hypothesis were true. But there is variation, as we would also expect.

Why would we expect variation? Consider the following analogy. If we were to flip a fair coin 10 times, we would expect to get 5 heads and 5 tails. But this doesn't always happen. Sometimes we get 6 heads and 4 tails. Sometimes we get 7 heads and 3 tails, and so on. As the number of flips increases, however, we would expect the proportion of heads to be closer to 0.5, but there would still be variation. The same is true for the null hypothesis distribution.

As the number of samples increases, we would expect the proportion of NP realizations of the recipient clause to be closer to 0.5, but there would still be variation. The question is whether the observed statistic we obtained from our data, in Example 10.5, is within some level of variation that we would expect if the null hypothesis were true.

Let's visualize the observed statistic on the null hypothesis distribution, as seen in Figure 10.2, to gauge whether the observed statistic is within some level of variation that we would expect if the null hypothesis were true.

Example 10.8.

```
# Visualize the null hypothesis distribution with the observed statistic
dative_null |>
  visualize() + # note we are adding a visual layer `+`
  geom_vline(
    data = dative_obs,          # the data is the observed statistic
    aes(xintercept = stat),    # the x-axis is the proportion statistic
    color = "red",              # the color of the line is red
    linewidth = 2               # the size of the line is 2
  )
```

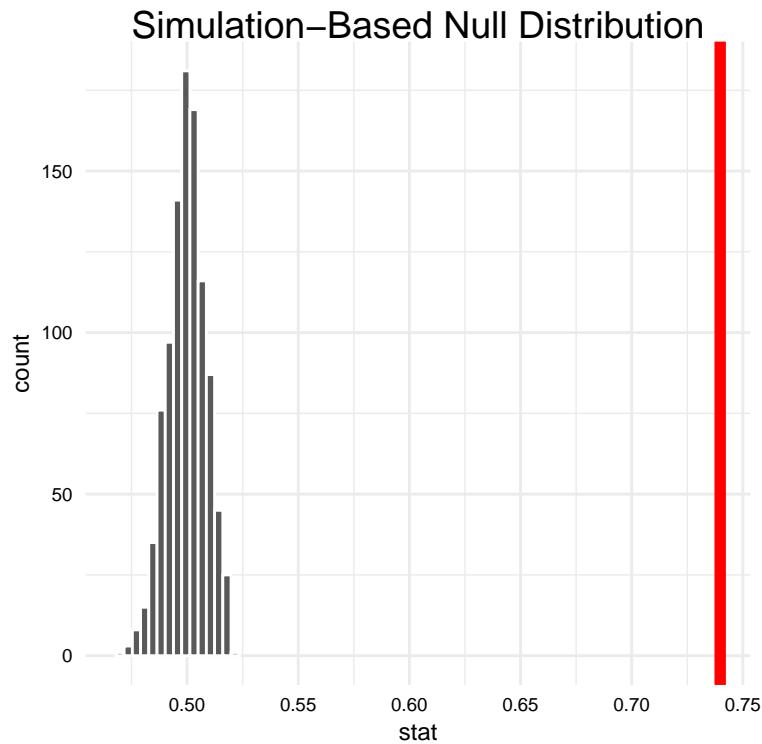


Figure 10.2: Null hypothesis distribution of the proportion of NP realizations of the recipient clause with the observed statistic.

Just from a visual inspection, we can see that the observed statistic lies far away from the null distribution, far right of the right tail. This suggests that the observed statistic is not within some level of variation that we would expect if the null hypothesis were true.

But we need to quantify this. We need to calculate the probability of observing the observed statistic or a more extreme statistic if the null hypothesis were true. This is called the p-value. The p-value is calculated by counting the number of samples in the null hypothesis distribution that are more extreme than expected within some level of uncertainty. 95% is the most common level of uncertainty, which is called the alpha level. The remain 5% of the distribution is the space where the likelihood that the null hypothesis accounts for the statistic is below. This means that if the p-value is less than 0.05, then we reject the null hypothesis. If the p-value is greater than 0.05, then we fail to reject the null hypothesis.

The `shade_p_value()` function from the `infer` package will plot our observed statistic and shade the sample statistics that fall within the alpha level, as seen in Example 10.9.

Example 10.9.

```

# Visualize the null hypothesis distribution with the observed statistic and
# p-value

dative_null |>
  visualize() +
  shade_p_value(
    dative_obs, # the observed statistic
    direction = "two-sided", # the direction of the alternative hypothesis
  )

```

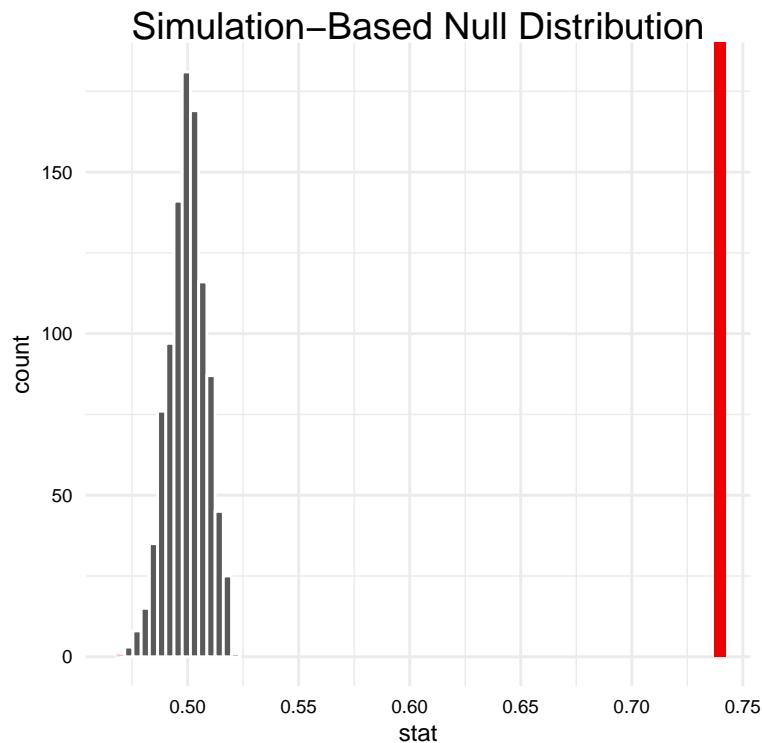


Figure 10.3: Null hypothesis distribution of the proportion of NP realizations of the recipient clause with the observed statistic and p-value.

The two plots we've generated look identical, we cannot appreciate the shading of the p-value range, as our statistic is so far away from the null hypothesis distribution. But if we were to change the observed statistic, to say 0.51, we would see the shading, as seen in Example 10.10.

Example 10.10.

```

# Visualize the null hypothesis distribution with the observed statistic and
# p-value
dative_null |>
  visualize() +
  shade_p_value(
    obs_stat = 0.51, # the observed statistic
    direction = "two-sided", # the direction of the alternative hypothesis
  )

```

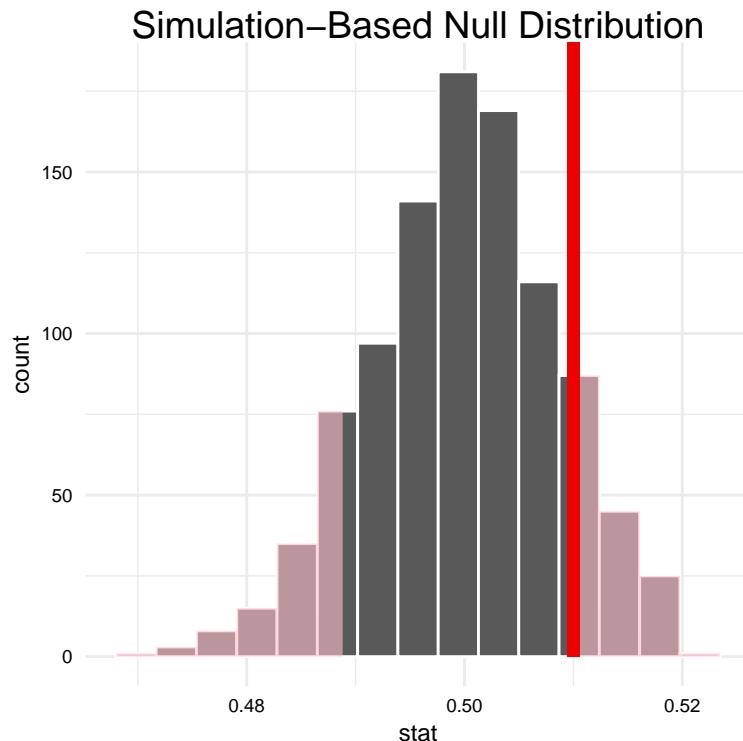


Figure 10.4: Null hypothesis distribution of the proportion of NP realizations of the recipient clause with the observed statistic and p-value with alpha level of 0.1.

Now we can appreciate the shading of the p-value range. We can now talk about the “two-sided” direction we used. The direction of the alternative hypothesis is important because it determines the p-value range. The “two-sided” direction means that we are interested in the proportion of NP realizations of the recipient clause being different from 0.5. If we were only interested in the proportion of NP realizations of the recipient clause being greater than 0.5, then we would use the “greater” direction. If we were only interested in the proportion

of NP realizations of the recipient clause being less than 0.5, then we would use the “less” direction.

Let’s visualize our hypothetical observed statistic of 0.51 on the null hypothesis distribution were the alternative hypothesis is that the proportion of NP realizations of the recipient clause is greater than 0.5, as seen in Example 10.11.

Example 10.11.

```
# Visualize the null hypothesis distribution with the observed statistic and
# p-value
dative_null |>
  visualize() +
  shade_p_value(
    0.51, # the observed statistic
    direction = "greater", # the direction of the alternative hypothesis
  )
```

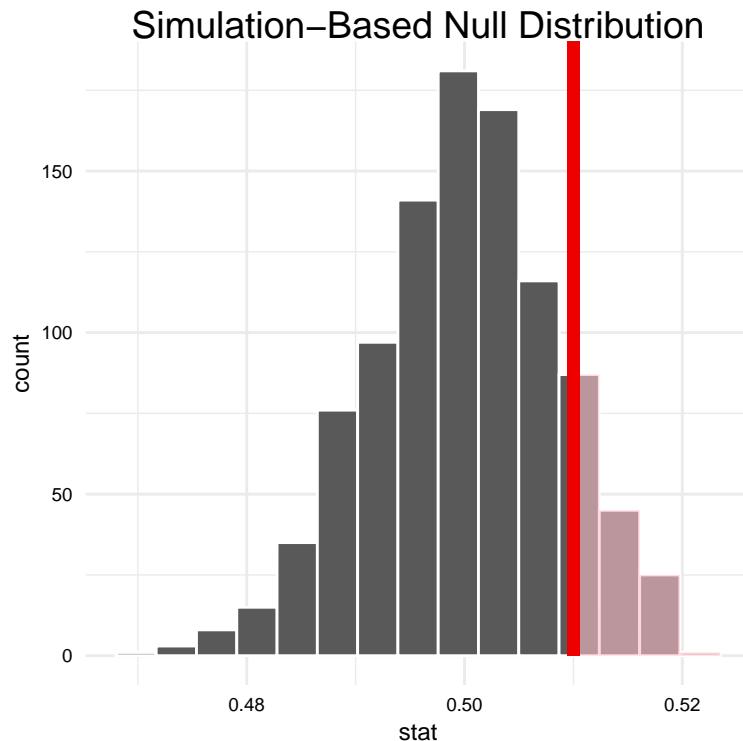


Figure 10.5: Null hypothesis distribution of the proportion of NP realizations of the recipient clause with the observed statistic and p-value with alpha level of 0.1 and alternative hypothesis that the proportion of NP realizations of the recipient clause is greater than 0.5.

As you can now see, the p-value range is dependent on the null hypothesis distribution and the direction of the alternative hypothesis as well as the number of samples. The more samples we have, the more precise the p-value range will likely be.

With `infer` we can calculate the p-value using the `get_p_value()` function. Let's calculate the p-value for our observed statistic and the hypothetical observed statistic of 0.51, as seen in Example 10.12.

Example 10.12.

```
# Calculate the p-value (observed statistic)
dative_null |>
  get_p_value(
    dative_obs, # the observed statistic
```

```

        direction = "two-sided" # the direction of the alternative hypothesis
    )

> # A tibble: 1 × 1
>   p_value
>   <dbl>
> 1      0

# Calculate the p-value (hypothetical observed statistic)
dative_null |>
  get_p_value(
    0.51, # the observed statistic
    direction = "two-sided" # the direction of the alternative hypothesis
  )

> # A tibble: 1 × 1
>   p_value
>   <dbl>
> 1  0.214

```

The p-value for our observed statistic is reported as 0, with a warning that the p-value estimate is contingent on the number of samples we generate in the null distribution. 1,000 is a reasonable number of samples, so we likely have a statistically significant result at the alpha level of 0.05.

The p-value for our hypothetical observed statistic of 0.51 is reported as larger than 0.05, which provides evidence that our hypothetical observed statistic is not sufficiently different from the variation expected in the null distribution to reject the null hypothesis, i.e. we would not have a significant result at the alpha level of 0.05.

The p-value is one, traditionally very common, estimate of uncertainty. Another estimate of uncertainty is the confidence interval. The confidence interval is the range of values for our test statistic that we would expect the true statistic value to fall within some level of uncertainty. Again, 95% is the most common level of uncertainty. The upper and lower bounds of this range are called the confidence limits for the test statistic. The confidence interval is calculated by calculating the confidence limits for the test statistic for many samples from the observed data. But instead of generating a null hypothesis distribution, we generate a distribution based on resampling from the observed data. This is called the bootstrap distribution. The bootstrap distribution is generated by resampling from the observed data, with replacement, many times. This simulates the process of sampling from the population many times. Each

time the test statistic is generated for each sample. The confidence limits are the 2.5th and 97.5th percentiles of the bootstrap distribution. The confidence interval is the range between the confidence limits.

In Example 10.13, we see the code for calculating the confidence interval for our observed statistic.

Example 10.13.

```
# Generate bootstrap distribution
dative_boot <-
  dative_spec |>
  generate(reps = 1000, type = "bootstrap") |>
  calculate(stat = "prop")

dative_ci <-
  dative_boot |>
  get_confidence_interval(level = 0.95) # 95% confidence interval

dative_ci

> # A tibble: 1 x 2
>   lower_ci upper_ci
>     <dbl>    <dbl>
> 1     0.724    0.754
```

Let's visualize the confidence interval for our bootstrapped samples, as seen in Example 10.14.

Example 10.14.

```
# Visualize the bootstrap distribution with the confidence interval
dative_boot |>
  visualize() +
  shade_confidence_interval(
    dative_ci # the confidence interval
  )
```

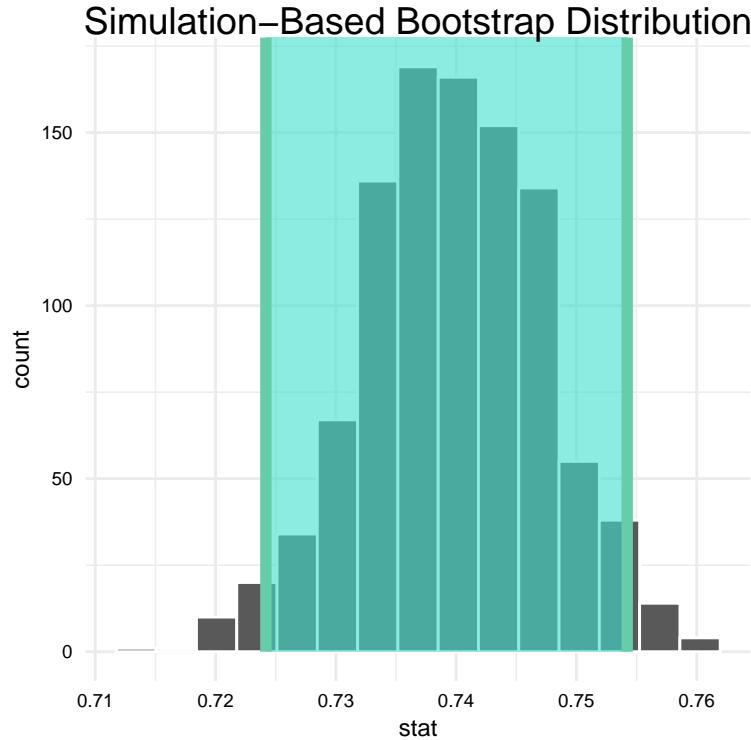


Figure 10.6: Bootstrap distribution of the proportion of NP realizations of the recipient clause with the confidence interval.

The confidence level is the probability that the confidence interval contains the true value. The confidence level is typically set to 0.95 in the social sciences. This means that if the confidence interval contains the null hypothesis value, then we fail to reject the null hypothesis. If the confidence interval does not contain the null hypothesis value, then we reject the null hypothesis.

Our stat is 0.74 and the confidence interval is 0.724 to 0.754. The confidence interval does not contain the null hypothesis value of 0.5, which provides evidence that the proportion of NP realizations of the recipient clause is different from 0.5.

Confidence intervals are often misinterpreted. Confidence intervals are not the probability that the true value is within the range. The true value is either within the range or not. The confidence interval is the probability that the range contains the true value. This is a subtle but important distinction.

Interpreted correctly confidence intervals can enhance our understanding of the uncertainty of our test statistic and reduces the interpretation of p-values (which are based on a relatively arbitrary alpha level) as a binary decision, significant or not significant. Instead, confidence

intervals encourage us to think about the uncertainty of our test statistic as a range of values that we would expect the true value to fall within some level of uncertainty.

10.2.1.2 Bivariate analysis

The univariate case is not very interesting or common in statistical inference, but it is a good place to start to understand the process and the logic of statistical inference. The bivariate case, on the other hand, is much more common and interesting. The bivariate case includes two variables. The goal is to describe the relationship between the two variables.

In the `dative_df` dataset, we can imagine asking the question:

- Is there a difference in the proportion of NP and PP realizations of the recipient clause by modality?

This question can be answered using a difference in proportions test, as both variables are binomial (have two levels). The null hypothesis is that there is no difference in the proportion of NP and PP realizations of the recipient clause by modality. The alternative hypothesis is that there is a difference in the proportion of NP and PP realizations of the recipient clause by modality.

We can cross-tabulate or visualize, but let's visualize this relationship in this case. In Example 10.15, we see the code that shows the distribution of the levels of the `realization_of_rcp` variable by the levels of the `modality` variable.

Example 10.15.

```
# Visualize the relationship between `realization_of_rcp` and `modality`  
dative_df |>  
  ggplot(aes(x = realization_of_rcp, fill = modality)) +  
  geom_bar(position = "fill") +  
  labs(  
    x = "Realization of recipient clause",  
    y = "Proportion",  
    fill = "Modality"  
)
```

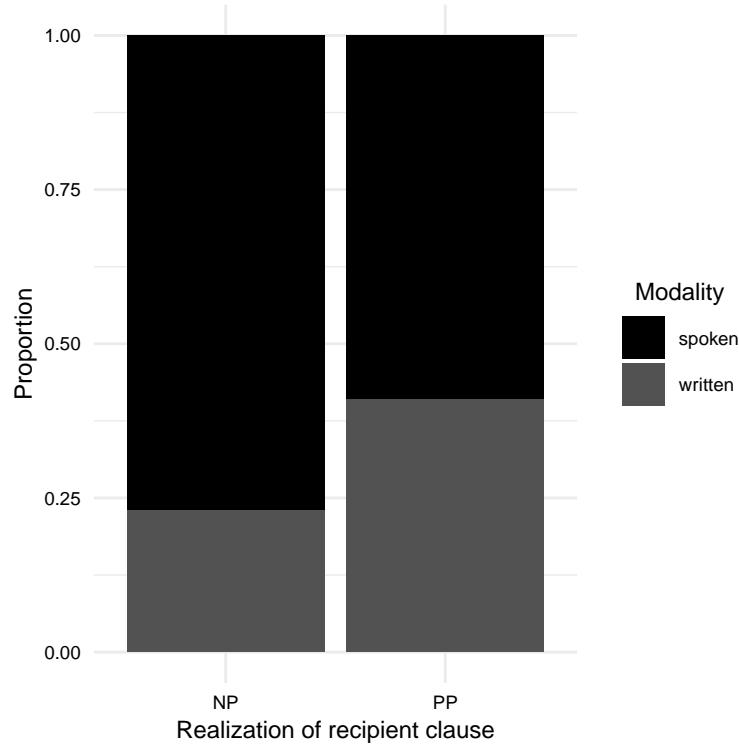


Figure 10.7: Distribution of the levels of the `realization_of_rcp` variable by the levels of the `modality` variable.

From our visualization, we can see that the proportion of NP realizations of the recipient clause is higher in both modalities, as we might expect from our univariate analysis. However, the proportion appears to be different with the spoken modality having a higher proportion of NP realizations of the recipient clause than the written modality. But we cannot conclude that there is a difference in the proportion of NP and PP realizations of the recipient clause by modality. We need to conduct a statistical test to determine if the difference is statistically significant.

Example 10.16.

```
dative_df |>
  tabyl(realization_of_rcp, modality) |> # cross-tabulate
  adorn_totals(c("row", "col")) |> # provide row and column totals
  adorn_percentages("col") |> # add percentages to the columns
  adorn_pct_formatting(rounding = "half up", digits = 0) |> # round the digits
  adorn_ns() |> # add observation number
```

```
adorn_title("combined") |> # add a header title
kable(booktabs = TRUE) |> # pretty table)
kable_styling()
```

Table 10.6: Contingency table for `realization_of_rcp` and `modality`.

realization_of_rcp/modality	spoken	written	Total
NP	79% (1,859)	61% (555)	74% (2,414)
PP	21% (501)	39% (348)	26% (849)
Total	100% (2,360)	100% (903)	100% (3,263)

To determine if the distribution of the levels of the `realization_of_rcp` variable by the levels of the `modality` variable is different from what we would expect if the null hypothesis were true, we need to calculate the difference observed in the sample and compare it to the differences observed in many samples where the null hypothesis is true.

The `infer` package provides a pipeline which maintains a consistent workflow for statistical inference. As such, the procedure is very similar to the univariate analysis we performed, with some adjustments. Let's focus on the adjustments. First, our `specify()` call needs to include the relationship between two variables: `realization_of_rcp` and `modality`. The `response` argument is the response variable, which is `realization_of_rcp`. The `explanatory` argument is the explanatory variable, which is `modality`.

There are two approaches to specifying the relationship between the response and explanatory variables. The first approach is to specify the response variable and the explanatory variable separately as values of the arguments `response` and `explanatory`. The second approach is to specify the response variable and the explanatory variable as a formula using the `~` operator. The formula approach is more flexible and allows for more complex relationships between the response and explanatory variables. In Example 10.17, we see the code for the `specify()` call using the formula approach.

Tip

The formula syntax `y ~ x` can be read as 'y' as a function of 'x'.

Example 10.17.

```
# Specify the relationship between the response and explanatory variables
dative_spec <-
  dative_df |>
  specify(
    realization_of_rcp ~ modality,
```

```

    success = "NP"
)

dative_spec

> Response: realization_of_rcp (factor)
> Explanatory: modality (factor)
> # A tibble: 3,263 x 2
>   realization_of_rcp modality
>   <fct>              <fct>
> 1 NP                 written
> 2 NP                 written
> 3 NP                 written
> 4 NP                 written
> 5 NP                 written
> 6 NP                 written
> 7 NP                 written
> 8 NP                 written
> 9 NP                 written
> 10 NP                written
> # i 3,253 more rows

```

The `dative_spec` now contains attributes about the response and explanatory variables encoded into the data frame.

We now calculate the observed statistic with `calculate()`, as seen in Example 10.18.

Example 10.18.

```

# Calculate the observed statistic
dative_obs <-
  dative_spec |>
  calculate(stat = "diff in props", order = c("spoken", "written"))

dative_obs

> Response: realization_of_rcp (factor)
> Explanatory: modality (factor)
> # A tibble: 1 x 1
>   stat

```

```
> <dbl>
> 1 0.173
```

Two differences are that our statistic is now a difference in proportions and that we are asked to specify the order of the levels of `modality`. The statistic is clear, we are investigating whether the proportion of NP realizations of the recipient clause is different between the spoken and written modalities. The order of the levels of `modality` is important because it determines the direction of the alternative hypothesis, specifically how the statistic is calculated (the order of the subtraction).

So our observed statistic 0.17 is the proportion of NP realizations of the recipient clause in the spoken modality minus the proportion of NP realizations of the recipient clause in the written modality, so the NP realization appears 17% more in the spoken modality compared to the written modality.

The question remains, is this difference statistically significant? To answer this question, we generate the null hypothesis distribution, visualize the p-value range, and calculate the p-value, as seen in Example 10.19.

Example 10.19.

```
# Generate the null hypothesis distribution
dative_null <-
  dative_spec |>
  hypothesize(null = "independence") |>
  generate(reps = 1000, type = "permute") |>
  calculate(stat = "diff in props", order = c("spoken", "written"))

# Visualize the null hypothesis distribution with the observed statistic and
# p-value
dative_null |>
  visualize() +
  shade_p_value(
    dative_obs, # the observed statistic
    direction = "two-sided", # the direction of the alternative hypothesis
  )

# Calculate the p-value
dative_null |>
  get_p_value(
    dative_obs, # the observed statistic
    direction = "two-sided" # the direction of the alternative hypothesis
  )
```

```

> # A tibble: 1 × 1
>   p_value
>   <dbl>
> 1      0

```

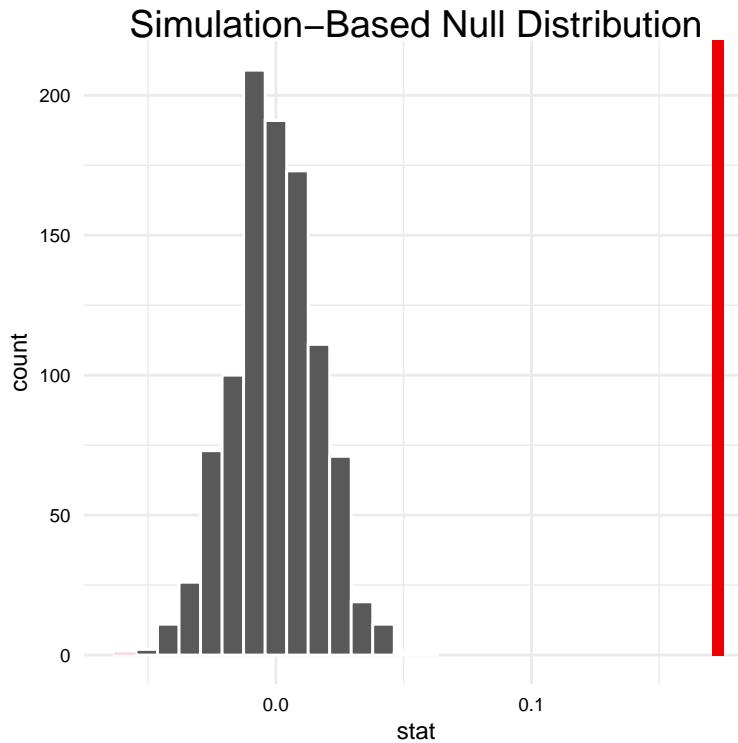


Figure 10.8: Null hypothesis distribution of the difference in proportions of NP realizations of the recipient clause by modality with the observed statistic and p-value.

Note when generating the null hypothesis distribution, we use the `hypothesize()` function with the `null` argument set to “independence”. This is because we are interested in the relationship between the response and explanatory variables. The null hypothesis is that there is no relationship between the response and explanatory variables. When generating the samples, we use the permutation approach, which randomly shuffles the response variable values for each sample. This simulates the null hypothesis that there is no relationship between the response and explanatory variables.

When we plot the null distribution, we see that the statistic values cluster around 0, which is what we expect if there is no difference. We also see that our observed statistic is far away from the null distribution, which suggests that there is a difference in the proportion of NP realizations of the recipient clause by modality.

The p-value underscores this apparent difference. The p-value is reported as 0. To provide some context, we will generate a confidence interval for our observed statistic using the bootstrap method, as seen in Example 10.20.

Example 10.20.

```
# Generate bootstrap distribution
dative_boot <-
  dative_spec |>
  generate(reps = 1000, type = "bootstrap") |>
  calculate(stat = "diff in props", order = c("spoken", "written"))

# Calculate the confidence interval
dative_ci <-
  dative_boot |>
  get_confidence_interval(level = 0.95)

# Visualize the bootstrap distribution with the confidence interval
dative_boot |>
  visualize() +
  shade_confidence_interval(
    dative_ci # the confidence interval
  )
```

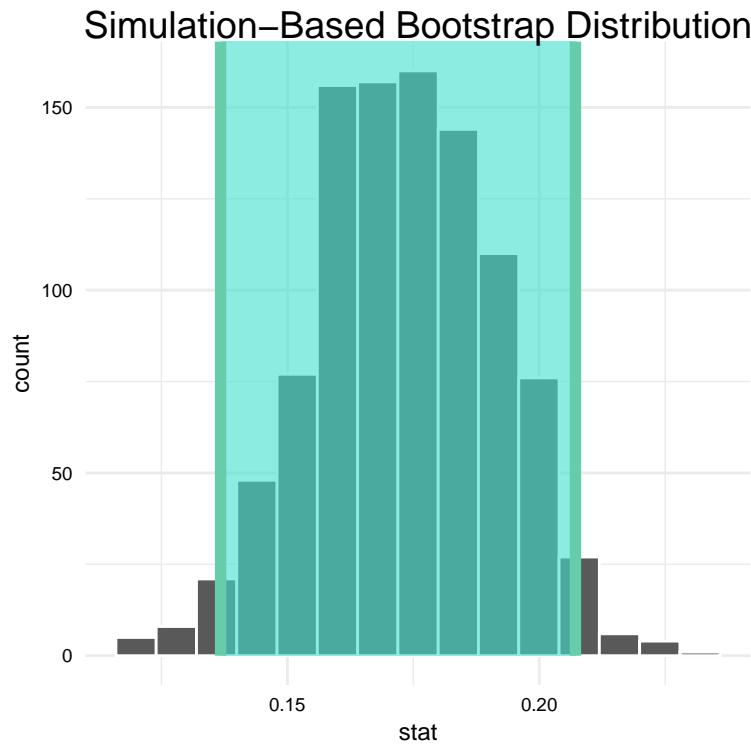


Figure 10.9: Bootstrap distribution of the difference in proportions of NP realizations of the recipient clause by modality with the confidence interval.

The confidence interval does not contain the null hypothesis value of 0, which provides evidence that the proportion of NP realizations of the recipient clause is different between the spoken and written modalities.

10.2.1.3 Multivariate Analysis

In many scenarios, it is common to have multiple explanatory variables that need to be considered. In such cases, logistic regression is a suitable modeling technique. Logistic regression allows for the inclusion of both categorical and continuous explanatory variables. The primary objective of using logistic regression is to assess the association between these variables and the dependent variable. By analyzing this relationship, we can determine how changes in the explanatory variables influence the probability of the outcome occurring.

In our `dative_df` dataset, we can imagine asking the question:

- Is there a difference in the proportion of NP and PP realizations of the recipient clause by modality and length ratio?

The length ratio gets at the length of the recipient clause relative to the length of the theme clause. This ratio is an operationalization of a phenomenon known as ‘Heavy NP’ shift. There are many ways to operationalize this phenomenon, but the length ratio is a simple method to approximate the phenomenon. It attempts to capture the idea that the longer the theme clause is relative to the recipient clause, the more likely the recipient clause will be realized as an NP –in other words, when the theme is relatively longer than the recipient, the theme is ordered last in the sentence, and the recipient is ordered first in the sentence and takes the form of an NP (instead of a PP).

For example,

1. John gave the book [to Mary]. (PP)
2. John gave [Mary] the large book that I showed you in class yesterday. (NP)

The prediction, then, is that the example in (3) would be less likely than (2) because the theme is relatively longer than the recipient.

3. John gave the book that I showed you in class yesterday [to Mary]. (PP)

Let’s consider this variable `length_ratio` and `modality` together as explanatory variables for the realizations of the recipient clause `realization_of_rcp`.

Let’s create the `length_ratio` variable by dividing the `length_of_thm` by the `length_of_rcp`. This will give us values larger than 1 when the theme is longer than the recipient. In Example 10.21, we see the code for creating the `length_ratio` variable.

Example 10.21.

```
# Create the `length_ratio` variable
dative_df <-
  dative_df |>
  mutate(
    length_ratio = length_of_thm / length_of_rcp
  )

# Preview
dative_df |> glimpse()
```

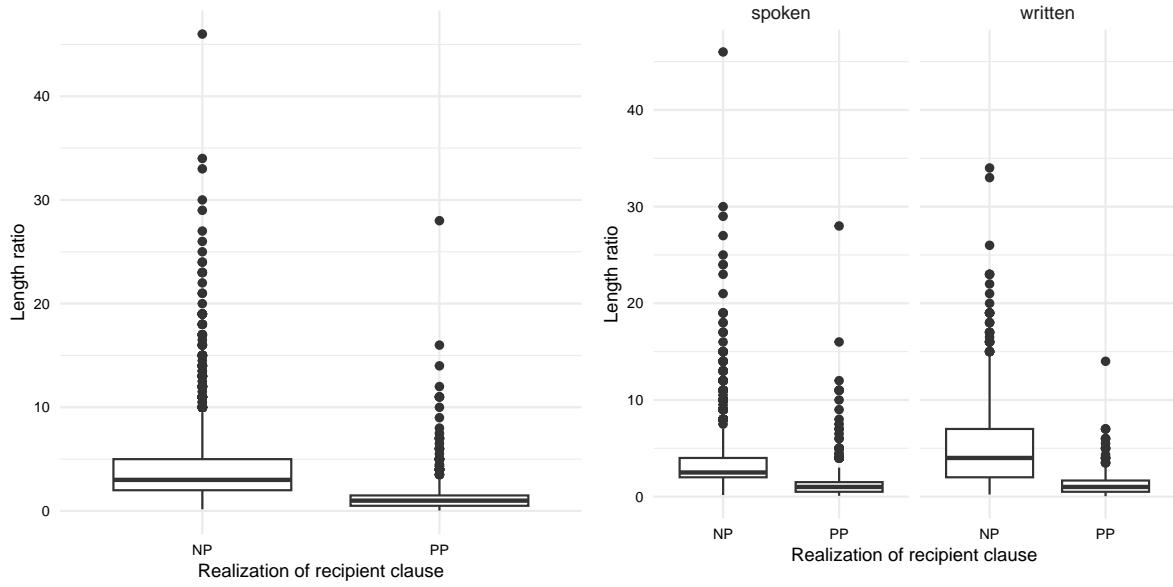
```
> Rows: 3,263
> Columns: 5
> $ realization_of_rcp <fct> NP, ~
> $ modality           <fct> written, written, written, written, written, written, ~
> $ length_of_rcp     <dbl> 1, 2, 1, 1, 2, 2, 1, 1, 1, 2, 2, 1, 2, 1, 1, 4, ~
> $ length_of_thm     <dbl> 14, 3, 13, 5, 3, 4, 4, 1, 11, 2, 3, 3, 5, 2, 8, 2, ~
```

```
> $ length_ratio      <dbl> 14.00, 1.50, 13.00, 5.00, 1.50, 2.00, 2.00, 1.00, 1~
```

Let's visualize the relationship between `realization_of_rcp` and `length_ratio` separately and then together with `modality`, as seen in Example 10.22.

Example 10.22.

```
# Visualize the relationship between `realization_of_rcp` and `length_ratio`  
p1 <-  
  dative_df |>  
  ggplot(aes(x = realization_of_rcp, y = length_ratio)) +  
  geom_boxplot() +  
  labs(  
    x = "Realization of recipient clause",  
    y = "Length ratio"  
)  
  
p1  
  
# Visualize the relationship between `realization_of_rcp` and `length_ratio` by  
# `modality`  
p1 +  
  facet_wrap(~ modality)
```



(a) Length ratio by realization of recipient clause (b) Length ratio by realization of recipient clause by modality

Figure 10.10: Distribution of the levels of the `realization_of_rcp` variable by the levels of the `modality` variable and `length_ratio` variable.

Before jumping in here, the outliers should catch our attention. Each boxplot has a number of outliers. These outliers are likely due to the fact that the `length_ratio` variable is built upon the `length_of_thm` and `length_of_rcp` variables, which are both highly skewed. This is a common problem in statistical inference. The solution is to transform the variables to reduce the skewness. In this case, we can use the log transformation, as seen in Example 10.23.

Example 10.23.

```
# Log transform the 'length_ratio' variable
dative_df <-
  dative_df |>
  mutate(
    length_ratio_log = log10(length_ratio)
  )

dative_df |> glimpse()
```

```
> Rows: 3,263
> Columns: 6
```

```

> $ realization_of_rcp <fct> NP, ~
> $ modality           <fct> written, written, written, written, written, written, ~
> $ length_of_rcp     <dbl> 1, 2, 1, 1, 2, 2, 2, 1, 1, 1, 2, 2, 1, 2, 1, 1, 4, ~
> $ length_of_thm     <dbl> 14, 3, 13, 5, 3, 4, 4, 1, 11, 2, 3, 3, 5, 2, 8, 2, ~
> $ length_ratio      <dbl> 14.00, 1.50, 13.00, 5.00, 1.50, 2.00, 2.00, 1.00, 1~
> $ length_ratio_log  <dbl> 1.146, 0.176, 1.114, 0.699, 0.176, 0.301, 0.301, 0.~
```

Now we can plot the relationships in Figure 10.10 with the log-transformed `length_ratio`, seen in Example 10.24.

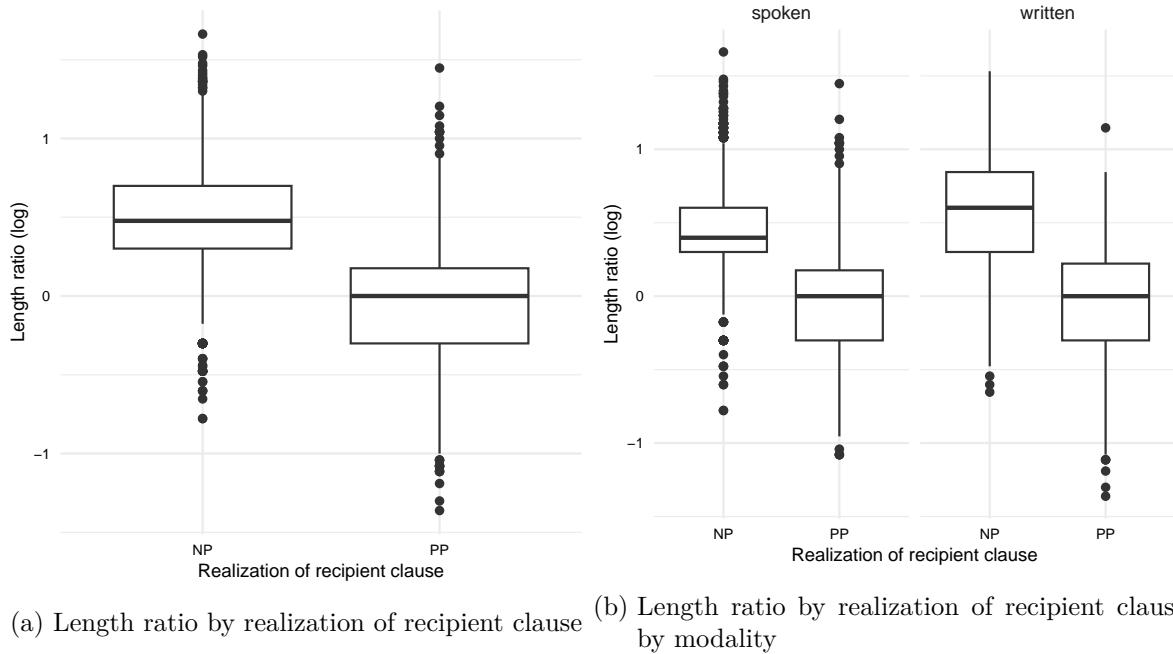
Example 10.24.

```

# Visualize the relationship between `realization_of_rcp` and `length_ratio`
p1 <-
  dative_df |>
  ggplot(aes(x = realization_of_rcp, y = length_ratio_log)) +
  geom_boxplot() +
  labs(
    x = "Realization of recipient clause",
    y = "Length ratio (log)"
  )

p1

# Visualize the relationship between `realization_of_rcp` and `length_ratio` by
#   `modality`
p1 +
  facet_wrap(~ modality)
```



(a) Length ratio by realization of recipient clause (b) Length ratio by realization of recipient clause by modality

Figure 10.11: Distribution of the levels of the `realization_of_rcp` variable by the levels of the `modality` variable and `length_ratio` variable with log transformation.

The log transformation has reduced the skewness of the `length_ratio` variable. Note that the log transformation does not change the rank order of the values, but it does change the scale of the values (the distance between the values) by reducing the magnitude of the values. The boxplots in Figure 10.11 still have outliers, but there are fewer outliers and they are not as extreme.

Now we can return to our question:

- Is there a difference in the proportion of NP and PP realizations of the recipient clause by modality and length ratio?

We can answer this question using a logistic regression. The null hypothesis is that there is no difference in the proportion of NP and PP realizations of the recipient clause by modality and length ratio. The alternative hypothesis is that there is a difference in the proportion of NP and PP realizations of the recipient clause by modality and length ratio.

Let's calculate the statistics (not statistic) for our logistic regression by specifying the relationship between the response and explanatory variables and then using `fit()` to fit the logistic regression model, as seen in Example 10.25.

Example 10.25.

```

# Specify the relationship between the response and explanatory variables
dative_spec <-
  dative_df |>
  specify(
    realization_of_rcp ~ modality + length_ratio_log
  )

# Fit the logistic regression model
dative_fit <-
  dative_spec |>
  fit()

dative_fit

> # A tibble: 3 × 2
>   term      estimate
>   <chr>      <dbl>
> 1 intercept  -0.563
> 2 modalitywritten  1.01
> 3 length_ratio_log -3.76

```

Note I pointed out statistics, not statistic. In logistic regression models, there the number of statistic reported depends on the number of explanatory variables. If there are two variables there will be at least three terms, one for each variable and the intercept term. If one or more variables are categorical, however, there will be additional terms when the categorical variable has three or more levels.

In our case, the `modality` variable has two levels, so there are three terms. The first term is the intercept term, which is the log odds of the proportion of NP realizations of the recipient clause in the written modality when the `length_ratio` is 1. The second term is the log odds of the proportion of NP realizations of the recipient clause in the spoken modality when the `length_ratio` is 1. The third term is the log odds of the proportion of NP realizations of the recipient clause when the `length_ratio` is 1 in the written modality. Notable the spoken modality does not explicitly appear but is implicitly represented the `modalitywritten` term statistic. It is used as the reference level for the `modality` variable.

👉 Tip

The reference level in R is assumed to be the first level alphabetically, unless otherwise specified. We can override this default by using the `fct_relevel()` function from the `forcats` package. The reason we would want to do this is to make the reference level more interpretable. In our case, we would want to make the spoken modality the reference

level it allows us to estimate the difference of the proportion of NP realizations of the recipient as a positive value. Remember that in Figure 10.11b, the proportion of NP realizations of the recipient clause is higher in the written modality than in the spoken modality. If we were to use the written modality as the reference level, the difference would be negative. Not that we couldn't interpret this, but working with positive integers is easier to interpret.

The statistics returned in logistic regression are log odds. Odds are the ratio of the probability of an event occurring to the probability of an event not occurring. Log odds are the natural log of the odds. If we would like to return the statistic as the odds ratio, we can use the `exp()` function, as seen in Example 10.26.

Example 10.26.

```
# Calculate the odds ratio by exponentiating the log odds
dative_fit <-
  dative_fit |>
  mutate(
    odds_ratio = exp(estimate)
  )

dative_fit

> # A tibble: 3 x 3
>   term      estimate odds_ratio
>   <chr>      <dbl>     <dbl>
> 1 intercept   -0.563     0.569
> 2 modalitywritten  1.01      2.75
> 3 length_ratio_log -3.76     0.0233
```

□ TODO: Interpret the odds ratio

The log odds for `writtenmodality` is 1.01. This means that the odds of the proportion of NP realizations of the recipient clause in the written modality when the `length_ratio` is 1 is 2.75 times the odds of the proportion of NP realizations of the recipient clause in the spoken modality when the `length_ratio` is 1.

On the other hand, the log odds for `length_ratio` is -3.76. In this case the `length_ratio` log odds can be interpreted as the log odds of the proportion of NP realizations of the recipient clause as a function of the `length_ratio` when the `modality` is the spoken modality. This is because the `modality` variable is the reference level.

? `length_ratio_log` has been log-transformed with a base of 10. This means that the odds ratio can be exponentiated with a base of 10, to return the odds ratio as a function of the `length_ratio` values, as seen in Example 10.27.

Example 10.27.

```
# Calculate the odds ratio by exponentiating the log odds with a base of 10
dative_fit <-
  dative_fit |>
  mutate(
    odds_ratio = case_when(
      term == "length_ratio_log" ~ 10^odds_ratio,
      TRUE ~ exp(estimate)
    )
  )

dative_fit

> # A tibble: 3 x 3
>   term           estimate odds_ratio
>   <chr>          <dbl>     <dbl>
> 1 intercept     -0.563     0.569
> 2 modalitywritten    1.01     2.75
> 3 length_ratio_log -3.76     1.06
```

So the odds ratio for `length_ratio` is 1.055 when the `modality` is the written modality.

So our logistic regression model as specified considers each explanatory variable independently, controlling for the other explanatory variable. This is an additive model, which is what we stated in our formula $y \sim x_1 + x_2$. We can also specify an interaction between the explanatory variables, as seen in Example 10.28.

Example 10.28.

```
# Specify the relationship between the response and explanatory variables
dative_inter_spec <-
  dative_df |>
  specify(
    realization_of_rcp ~ modality * length_ratio_log
  )
```

```

dative_inter_spec

> Response: realization_of_rcp (factor)
> Explanatory: modality (factor), length_ratio_log (numeric)
> # A tibble: 3,263 x 3
>   realization_of_rcp modality length_ratio_log
>   <fct>           <fct>           <dbl>
> 1 NP              written          1.15 
> 2 NP              written          0.176 
> 3 NP              written          1.11 
> 4 NP              written          0.699 
> 5 NP              written          0.176 
> 6 NP              written          0.301 
> 7 NP              written          0.301 
> 8 NP              written          0      
> 9 NP              written          1.04 
> 10 NP             written          0.301 
> # i 3,253 more rows

```

Replacing the `+` with a `*` tells the model to consider the interaction between the explanatory variables. The interaction is the effect of one explanatory variable on the response variable is dependent on the other explanatory variable. In our case, the interaction is the effect of the `length_ratio` on the proportion of NP realizations of the recipient clause is dependent on the `modality`.

An model with an interaction changes the terms and the estimates. In Example 10.29, we see the terms for the logistic regression model with an interaction.

Example 10.29.

```

# Fit the logistic regression model
dative_inter_fit <-
  dative_inter_spec |>
  fit()

dative_inter_fit

> # A tibble: 4 x 2
>   term                  estimate

```

```

>   <chr>                <dbl>
> 1 intercept              -0.549
> 2 modalitywritten        0.958
> 3 length_ratio_log      -3.88
> 4 modalitywritten:length_ratio_log  0.317

```

The additional term `modalitywritten:length_ratio_log` is the interaction term. We also see the log odds estimates have changed for the previous terms. This is because this interaction draws some of the explanatory power from the other terms. Whether or not we run an interaction model depends on our research question. Whether or not the interaction term, or the other main terms, adds evidence to reject the null hypothesis, is the next step to consider.

Let's return to our additive model and generate the null hypothesis distribution, visualize the p-value range, and calculate the p-value for each of the terms, as seen in Example 10.30.

Example 10.30.

```

# Generate the null hypothesis distribution
dative_null <-
  dative_spec |>
  hypothesize(null = "independence") |>
  generate(reps = 1000, type = "permute") |>
  fit()

# Visualize the null hypothesis distribution with the observed statistics
dative_null |>
  visualize() +
  shade_p_value(
    dative_fit, # the observed statistics
    direction = "two-sided" # the direction of the alternative hypothesis
  )

# Calculate the p-value
dative_null |>
  get_p_value(
    dative_fit, # the observed statistics
    direction = "two-sided" # the direction of the alternative hypothesis
  )

> # A tibble: 3 x 2
>   term          p_value
>   <chr>        <dbl>

```

```

> 1 intercept      0
> 2 length_ratio_log 0
> 3 modalitywritten 0

```

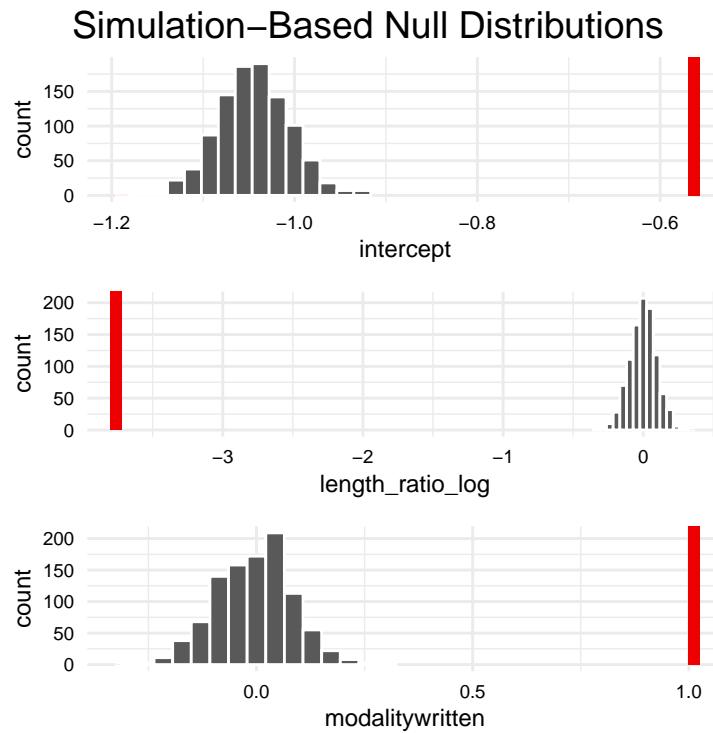


Figure 10.12: Null hypothesis distribution of the proportion of NP realizations of the recipient clause by modality and length ratio with the observed statistic and p-value.

It appears that our main effects, `modality` and `length_ratio`, are statistically significant. Let's generate the confidence intervals for each of the terms, as seen in Example 10.31.

Example 10.31.

```

# Generate bootstrap distribution
dative_boot <-
  dative_spec |>
  generate(reps = 1000, type = "bootstrap") |>
  fit()

# Calculate the confidence interval

```

```

dative_ci <-
  dative_boot |>
  get_confidence_interval(
    point_estimate = dative_fit, # the observed statistics
    level = 0.95
  )

# Visualize the bootstrap distribution with the confidence interval
dative_boot |>
  visualize() +
  shade_confidence_interval(
    dative_ci # the confidence interval
  )

```

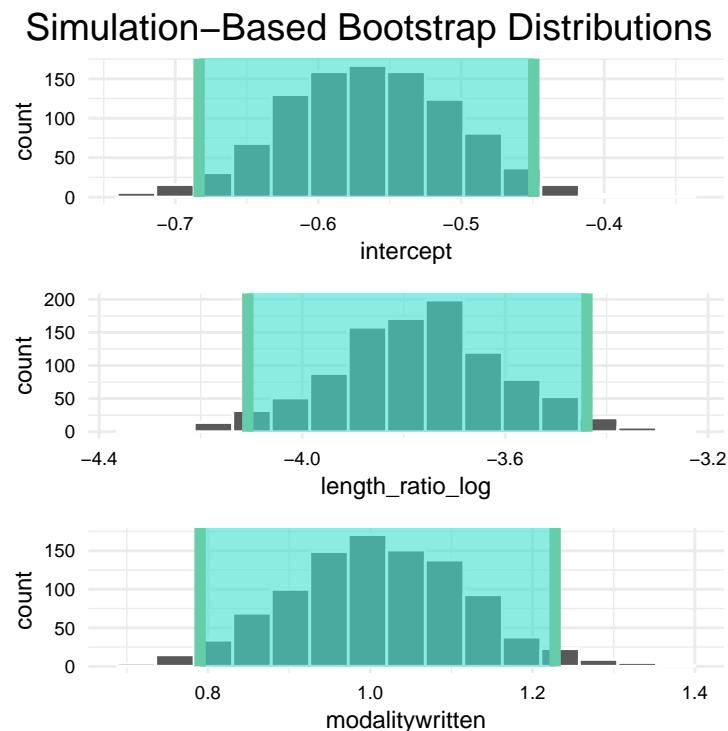


Figure 10.13: Bootstrap distribution of the proportion of NP realizations of the recipient clause by modality and length ratio with the confidence interval.

The confidence intervals for the main effects, `modality` and `length_ratio`, do not contain the null hypothesis value of 0, which provides evidence that each of the explanatory variables is related to the proportion of NP realizations of the recipient clause.

We can quantify the effect size of each of the explanatory variables using the odds ratio to calculate the r and R^2 values. We can use the `logoddsratio_to_r()` function from `effectsize` package to calculate the r value and then square the r value to calculate the R^2 value, as seen in Example 10.32.

Example 10.32.

```
# Calculate the effect size
dative_fit <-
  dative_fit |>
  mutate(
    r = logoddsratio_to_r(estimate),
    r_squared = r^2
  )

dative_fit

> # A tibble: 3 x 5
>   term      estimate odds_ratio      r r_squared
>   <chr>     <dbl>     <dbl> <dbl>     <dbl>
> 1 intercept -0.563     0.569 -0.153    0.0235
> 2 modalitywritten  1.01      2.75  0.269    0.0722
> 3 length_ratio_log -3.76     1.06  -0.720   0.518
```

Beyond the estimates to quantify the likelihood that the null hypothesis is true, the effect size provides a measure of the strength of the relationship between the response and explanatory variables. The r value is the correlation coefficient, which is a measure of the strength of the linear relationship between the response and explanatory variables. The R^2 value is the coefficient of determination, which is a measure of the proportion of the variance in the response variable that is explained by the explanatory variables.

As you can imagine, the larger the R^2 value, the stronger the relationship between the response and explanatory variables. From our effect size evaluation, the `length_ratio` variable has a stronger relationship with the proportion of NP realizations of the recipient clause than the `modality` variable.

Now, knowing “how” strong a given value is can be a little less intuitive. The `effectsize` package provides some guidelines for interpreting effect size measures. Let’s use the `interpret_r2()` function to interpret the R^2 value, as seen in Example 10.33.

Example 10.33.

```
# Interpret the R^2 value
dative_fit |>
  mutate(
    r2_interpretation = interpret_r2(r_squared)
  )

> # A tibble: 3 x 6
>   term      estimate odds_ratio      r r_squared r2_interpretation
>   <chr>      <dbl>      <dbl>      <dbl>      <dbl> <effctsz_>
> 1 intercept  -0.563      0.569  -0.153     0.0235 weak
> 2 modalitywritten  1.01      2.75     0.269     0.0722 weak
> 3 length_ratio_log -3.76      1.06    -0.720     0.518  substantial
```

While the effects for `modality` and `length_ratio` are statistically significant, the effect size for `modality` is small and the effect size for `length_ratio` is much stronger. This can help inform our interpretation of the results.

10.2.2 Numeric

We now turn our attention to the analysis scenarios where the response variable is numeric. Just as for categorical variables, we can have univariate, bivariate, and multivariate analysis scenarios. The statistical tests for numeric variables are summarized in Table 10.7.

Table 10.7: Statistical test design for numeric variables

Scenario	Dependent variable	Independent variable(s)	Statistical test
Univariate	Numeric	None	Mean
Bivariate	Numeric	Numeric	Correlation
Bivariate	Numeric	Categorical	Difference in means
Multivariate	Numeric	Numeric or Categorical (2+)	Linear regression

The dataset we will use here is `fillers_df`. The data dictionary is found in Table 10.8.

Table 10.8: Data dictionary for the `fillers_df` dataset

variable	name	variable_type	description
speaker_id	Speaker ID	numeric	Unique identifier for each speaker

age	Age	numeric	Age of the speaker in years
sex	Sex	categorical	Gender of the speaker
education	Education	ordinal	Level of education attained by the speaker
fillers_per_100	Fillers per 100	numeric	Number of filler words used per 100 utterances
total_fillers	Total Fillers	numeric	Total number of filler words used
total_utterances	Total Utterances	numeric	Total number of utterances made by the speaker

We see the dataset has [FOUR FIXME] variables. The `fillers_per_100` will be used as our response variable and corresponds to the rate of filler usage per speaker, normalized by the number of utterances. The other variables we will consider as explanatory variables are `age`, `sex`, and `education`, providing us a mix of numeric and categorical variables.

The context for these analysis demonstrations comes from the socio-linguistic literature on the use of filled pauses. Filled pauses have often been associated with a type of disfluency; speech errors that occur during speech production. However, some authors have argued that filled pauses can act as sociolinguistic markers of socio-demographic characteristics of speakers, such as gender, age, and educational level (Shriberg 1994; Tottie 2011).

Let's prepare these datasets for analysis by converting the categorical variables to factors and ordering the `education` variable, as seen in Example 10.34.

Example 10.34.

```
# Establish level names and order for the `education` variable
edu_levels <-
  c("More Than College",
    "College",
    "Less Than College",
    "Less Than High School",
    "Unknown")

# Convert categorical variables to factors
fillers_df <-
  fillers_df |>
  mutate(
    sex = factor(sex),
    education = factor(education, levels = edu_levels, ordered = TRUE)
  )

# Preview
glimpse(fillers_df)
```

```

> Rows: 441
> Columns: 7
> $ speaker_id      <dbl> 1000, 1001, 1002, 1004, 1005, 1007, 1008, 1010, 1011, ~
> $ age              <dbl> 38, 52, 29, 34, 36, 27, 53, 60, 28, 35, 45, 25, 47, 3~
> $ sex              <fct> Female, Male, Female, Female, Female, Female, Female, ~
> $ education        <ord> Less Than College, More Than College, College, Colleg~
> $ fillers_per_100   <dbl> 2.14, 25.34, 4.13, 2.41, 3.79, 0.00, 8.33, 1.82, 5.22~
> $ total_fillers    <dbl> 44, 263, 54, 45, 129, 0, 27, 2, 54, 130, 135, 14, 152~
> $ total_utterances <dbl> 2052, 1038, 1308, 1866, 3400, 278, 324, 110, 1034, 20~

```

Our `fillers_df` dataset has 441 observations. Again, we will postpone more descriptive statistics for treatment in the particular scenarios.

10.2.2.1 Univariate analysis

In hypothesis testing, the analysis of a single variable is directed at determining whether or not the distribution or statistic of the variable differs from some expected distribution or statistic. In the case of a single categorical variable with two levels (as in the datives case), we sampled from a binomial distribution by chance. In the case of a single numeric variable, we can sample and compare the observed distribution to a theoretical distribution. When approaching hypothesis testing from a theoretical perspective, it is often necessary to assess how well a numeric variable fits the normal distribution as many statistical tests assume that the data are normally distributed. However, we have adopted the simulation-based approach to hypothesis testing, which does not require that the data fit the normal distribution, or any other distribution for that matter.

The other approach to analyzing a single numeric variable is to compare an observed statistic to an expected statistic. This approach requires a priori knowledge of the expected statistic. For example, imagine we are interested testing the hypothesis that the length of words in a medical corpus tend to be longer than the average length of words in English. We would then calculate the observed mean for the length of words in the medical corpus and then generate a null distribution of means for the length of words in English, as in Example 10.35.

Example 10.35.

```

# Observed mean
obs_mean <-
  medical_df |>
  specify(response = word_length) |>
  calculate(stat = "mean")

# Null distribution of means

```

```
null_mean <-
  medical_df |>
  specify(response = word_length) |>
  hypothesize(null = "point", mu = 5) |>
  generate(reps = 1000, type = "draw") |>
  calculate(stat = "mean")
```

Note that instead of a `p =` argument, as was used in the `hypothesize()` step to generate a null distribution of proportions, we use a `mu =` argument in Example 10.35 to specify the expected mean. The rest of the hypothesis testing workflow is the same as for the null distribution of proportions.

The mean `mu` is not the only statistic we can specify for a numeric variable. We can also specify the median `med`, or the standard deviation `sigma`.

In our case, we do not have a priori knowledge of the expected statistic for the `fillers_per_100` variable, so we will not pursue this approach. However, when looking at the distribution of a numeric variable, it is useful to look at the descriptive statistics the mean, median, and standard deviation in order to get a sense of the central tendency and spread of the data.

We can use the `skim()` function to get the mean, median, and standard deviation of the `fillers_per_100` variable, as seen in Example 10.36.

Example 10.36.

```
fillers_df |>
  skim(fillers_per_100)
```

```
> -- Data Summary -----
>                               Values
> Name                           fillers_df
> Number of rows                  441
> Number of columns                7
> -----
> Column type frequency:
>   numeric                         1
> -----
> Group variables                  None
>
> -- Variable type: numeric -----
>   skim_variable  n_missing complete_rate mean    sd p0   p25   p50   p75   p100 hist
```

```
> 1 fillers_per_100          0          1 9.19 7.03  0 4.11 7.95 13.2 52.8 XXXXX
```

The mean is larger than the median which suggests that the distribution is right-skewed. Furthermore, the standard deviation is large relative to the mean, which suggests that there is a lot of variability in the data.

To get a sense of the distribution of the `fillers_per_100` variable, we can plot a histogram and density plot, as seen in Example 10.37.

Example 10.37.

```
# Histogram
fillers_df |>
  ggplot(aes(x = fillers_per_100)) +
  geom_histogram(bins = 50) +
  labs(x = "Fillers per 100 utterances", y = "Count") +
  theme_bw()

# Density plot
fillers_df |>
  ggplot(aes(x = fillers_per_100)) +
  geom_density() +
  labs(x = "Fillers per 100 utterances", y = "Density") +
  theme_bw()
```

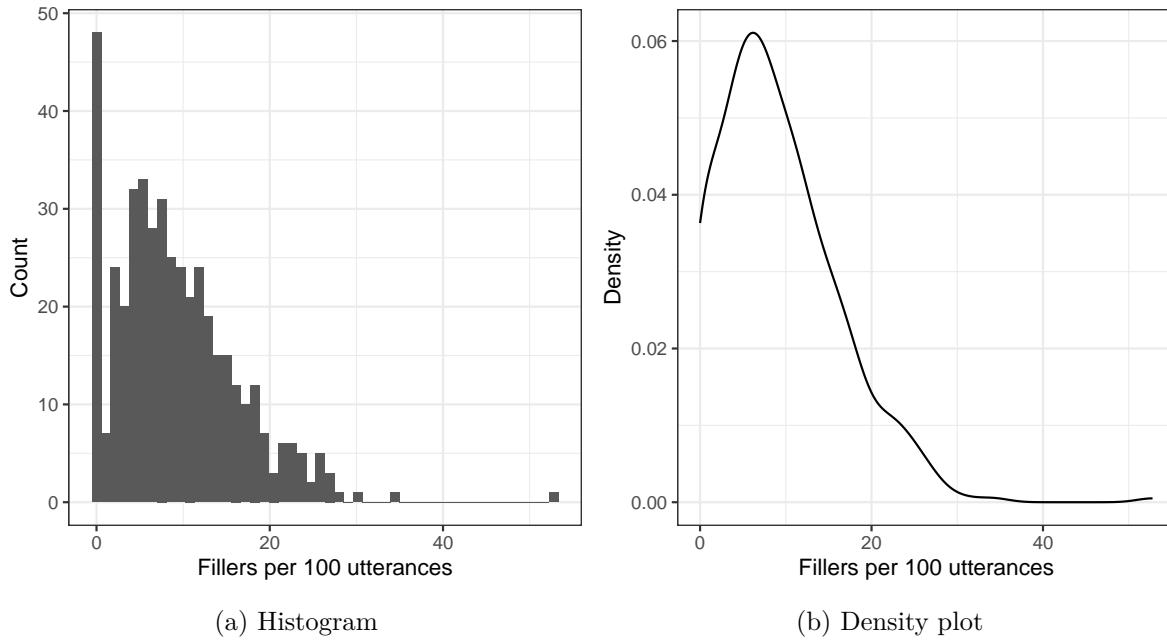


Figure 10.14: Histogram and density plot of the `fillers_per_100` variable

The distribution of `fillers_per_100` is indeed skewed to the right. We might have predicted this given that we are working with ratio based on count data, perhaps not. In any case, the skewing we observe tends to compress the distribution and may make it difficult to see any patterns. To mitigate this, we can log transform the variable. But we will run into a problem if we have any speakers who do not use any fillers at all as these speakers will have a value of zero, as we can see in Figure 10.14b. The log of zero is undefined. So we need to address this.

Eliminating the speakers who do not use any fillers at all is one option. This is quite extreme as we may lose quite a few speakers and it is not clear that removing data in this way will not cause inordinate bias in the results as these speakers may be different in some way from the rest of the speakers. Looking at the speakers with zero fillers in Example 10.38, we can see that there is some potential for bias.

Example 10.38.

```
fillers_df |>
  filter(fillers_per_100 == 0) |>
  tabyl(education, sex)
```

```
>      education Female Male
```

```

> More Than College      3   14
>          College      16   11
> Less Than College     2    0
> Less Than High School 1    0
>          Unknown       1    0

```

Another approach is to add a small value to the `fillers_per_100` variable, for all speakers. This will allow us to log transform the variable and will likely not have any (or very little) impact on the results. It also allows us to keep these speakers.

Adding values can be done in one of two ways. We can add a small constant value to all speakers, or we can add a small random value to all speakers. The former is easier to implement, but means that we will still have a spike in the distribution at the value of the constant. Since we do not expect that speakers that did not use fillers at all would never do so and that when they do we would not expect them to be at exactly the same rate as other speakers, we can add a small random value to all speakers.

In R, we can use the `jitter()` function to add a small amount of random noise to the variable. Note, however, this random noise can be positive or negative. When a negative value is added to a zero value, we are still in trouble. So we need to make sure that none of the jitter produces negative values. We can do this by simply taking the absolute value of the jittered variable with the `abs()` function. Let's see how this works in Example 10.39.

Example 10.39.

```

# Set seed for reproducibility
set.seed(1234)

# Add jitter to fillers
fillers_df <-
  fillers_df |>
  mutate(fillers_per_100_jitter = abs(jitter(fillers_per_100)))

fillers_df

```

```

> # A tibble: 441 x 8
>   speaker_id   age sex   education      fillers_per_100 total_fillers
>   <dbl> <dbl> <fct> <ord>           <dbl>           <dbl>
> 1     1000     38 Female Less Than College     2.14            44
> 2     1001     52 Male   More Than College    25.3            263
> 3     1002     29 Female College            4.13            54
> 4     1004     34 Female College            2.41            45

```

```

> 5      1005    36 Female College      3.79      129
> 6      1007    27 Female College      0          0
> 7      1008    53 Female Less Than College 8.33      27
> 8      1010    60 Male   Less Than College 1.82      2
> 9      1011    28 Female College      5.22      54
> 10     1013    35 Female College      6.23      130
> # i 431 more rows
> # i 2 more variables: total_utterances <dbl>, fillers_per_100_jitter <dbl>

```

The results from Example 10.39 show that the `fillers_per_100_jitter` variable has been added to the `fillers_df` dataset and that zero values for `fillers_per_100` now have a small amount of random noise added to them. Note, that the other values also have a small amount of random noise added to them, but it is so small that rounding to 2 decimal places makes it look like nothing has changed.

Now let's return to log transforming the `fillers_per_100_jitter` variable. We can do this with the `log()` function. Let's see how this works in Example 10.40.

Example 10.40.

```

# Log transform fillers (with jitter)
fillers_df <-
  fillers_df |>
  mutate(fillers_per_100_log = log(fillers_per_100_jitter))

fillers_df

> # A tibble: 441 x 9
>   speaker_id  age sex   education      fillers_per_100 total_fillers
>   <dbl> <dbl> <fct> <ord>          <dbl>          <dbl>
> 1 1000     38 Female Less Than College  2.14          44
> 2 1001     52 Male   More Than College 25.3          263
> 3 1002     29 Female College            4.13          54
> 4 1004     34 Female College            2.41          45
> 5 1005     36 Female College            3.79          129
> 6 1007     27 Female College            0            0
> 7 1008     53 Female Less Than College 8.33          27
> 8 1010     60 Male   Less Than College 1.82          2
> 9 1011     28 Female College            5.22          54
> 10 1013    35 Female College            6.23          130
> # i 431 more rows
> # i 3 more variables: total_utterances <dbl>, fillers_per_100_jitter <dbl>,

```

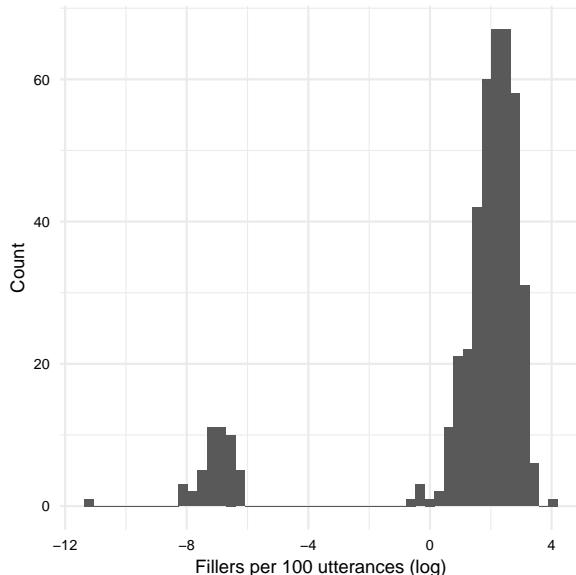
```
> # fillers_per_100_log <dbl>
```

Let's now plot the log-transformed variable, as seen in Example 10.41.

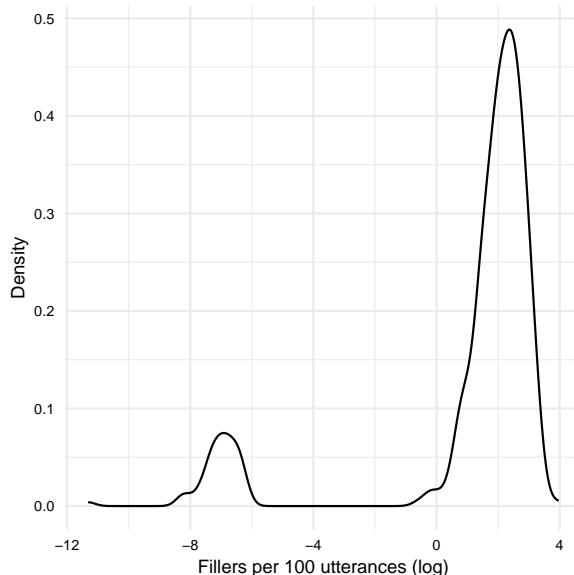
Example 10.41.

```
# Histogram
fillers_df |>
  ggplot(aes(x = fillers_per_100_log)) +
  geom_histogram(bins = 50) +
  labs(x = "Fillers per 100 utterances (log)", y = "Count")

# Density plot
fillers_df |>
  ggplot(aes(x = fillers_per_100_log)) +
  geom_density() +
  labs(x = "Fillers per 100 utterances (log)", y = "Density")
```



(a) Histogram



(b) Density plot

Figure 10.15: Histogram and density plot of the `fillers_per_100_log` variable

The distribution of the log-transformed variable is more spread out now, but the zero-filler speakers do show a low-level spike in the left tail of the distribution. Jitter and log-transformation, however, smooth over their effect to a large degree.

Let's drop some of the variables we no longer need and proceed with the log-transformed variable, as seen in Example 10.42.

Example 10.42.

```
# Drop variables
fillers_df <-
  fillers_df |>
  select(sex, education, age, fillers_per_100_log)
```

10.2.2.2 Bivariate analysis

When considering a numeric responses variable and another variable, it is key to consider the nature of the other variable. If it is a categorical variable with two levels, then we can compare a statistic between the two groups (mean or median). If it is categorical with more than two levels, the F statistic is used to compare the means. Finally, if it is a numeric variable, then we can use a correlation test to see if there is an association between the two variables.

Let's approach each of these bivariate scenarios in turn.

The `datives_df` contains the `sex` variable which is a categorical variable with two levels. According to the literature, filled pauses are associated with differences between men and women Tottie (2014). Sex is one of the variables associated with the rate of filled pauses. The findings suggest that men use fillers at a higher rate than women. Let's test to see if this holds for the SWDA data.

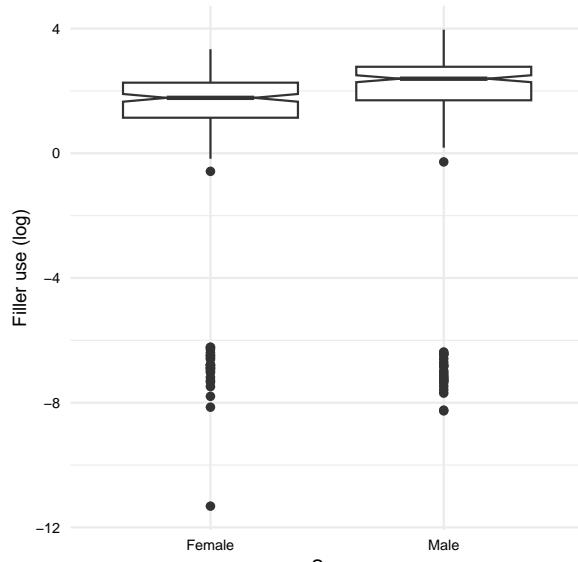
Let's first explore the distribution from a descriptive point of view. With a numeric response variable `fillers_per_100_log` and a categorical explanatory variable `sex`, a boxplot is a natural fit. Let's add a density plot with a `sex` overlay in Example 10.43.

Example 10.43.

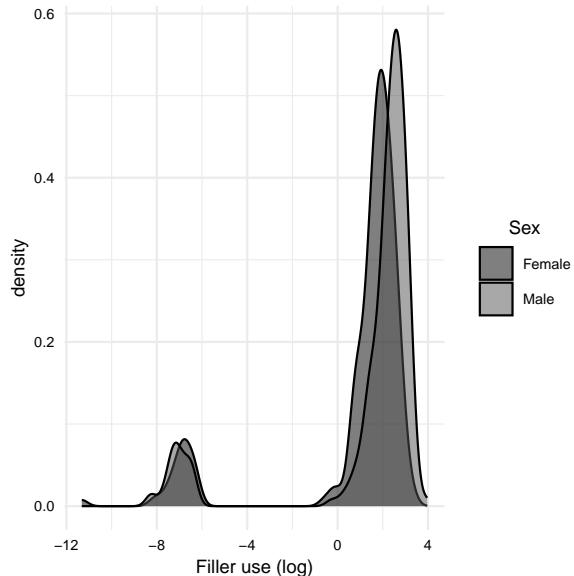
```
fillers_df |>
  ggplot(aes(y = fillers_per_100_log, x = sex)) +
  geom_boxplot(notch = TRUE) +
  labs(
    y = "Filler use (log)",
    x = "Sex"
  )

fillers_df |>
  ggplot(aes(x = fillers_per_100_log, fill = sex)) +
```

```
geom_density(alpha = 0.5) +
  labs(
    x = "Filler use (log)",
    fill = "Sex"
  )
)
```



(a) Boxplot



(b) Density plot

Figure 10.16: Visualizations of the `fillers_per_100_log` variable by `sex`

Looking at the boxplot in Figure 10.16a, we see that there appears to be an overall higher rate of filler use for men, compared to women. We also can see that the random noise added to zero-rate speakers appear as outliers in the left tail. The density plot in Figure 10.16b confirms this and allows us to see the overlap between the two groups. We see that the density distribution is not as concentrated and is slightly lower than that of men.

Consider this

If we focus on the zero-rate outliers, we see there is also a difference in the distribution. Can this difference be attributed to differences between men and women? Why or why not?

Does your answer to this question have an effect on how we interpret the differences between men and women in the main distribution?

Let's follow the simulation-based hypothesis testing workflow and investigate if the apparent difference between men and women is statistically significant, or expected by chance. The first steps are found in Example 10.44.

Example 10.44.

```
# Specify the relationship
fillers_spec <-
  fillers_df |>
  specify(fillers_per_100_log ~ sex) # response ~ explanatory

# Observed statistic
fillers_obs <-
  fillers_spec |>
  # diff in means, Male - Female
  calculate(stat = "diff in means", order = c("Male", "Female"))

# Null distribution
fillers_null <-
  fillers_spec |>
  hypothesize(null = "independence") |> # independence = no relationship
  generate(reps = 1000, type = "permute") |> # permute = shuffle
  calculate(stat = "diff in means", order = c("Male", "Female"))

# Visualize the null distribution w/ observed statistic
fillers_null |>
  visualize() +
  shade_p_value(obs_stat = fillers_obs, direction = "greater") # expect greater

# Calculate the p-value
fillers_null |>
  get_p_value(obs_stat = fillers_obs, direction = "greater")

> # A tibble: 1 x 1
>   p_value
>   <dbl>
> 1 0.033
```

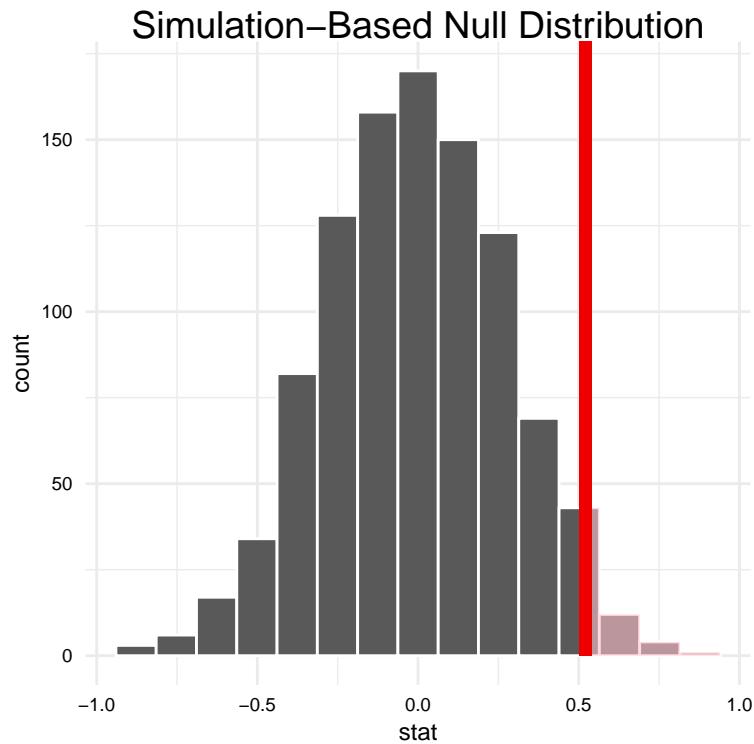


Figure 10.17: Null distribution of the `fillers_per_100_log` variable by `sex`

From the analysis performed in Example 10.44, we can reject the null hypothesis that there is no difference between the rate of filler use between men and women, as the p-value is greater less than 0.05.

To further assess the uncertainty of the observed statistic, and the robustness of the difference, we calculate a confidence interval, as seen in Example 10.45.

Example 10.45.

```
# Resampling distribution
fillers_boot <-
  fillers_spec |>
  generate(reps = 1000, type = "bootstrap") |>
  calculate(stat = "diff in means", order = c("Male", "Female"))

# Calculate the confidence interval
fillers_ci <-
  fillers_boot |>
```

```
get_ci(level = 0.95)

fillers_ci
```

```
> # A tibble: 1 x 2
>   lower_ci upper_ci
>     <dbl>     <dbl>
> 1 -0.00378     1.05
```

```
# Visualize the confidence interval
fillers_boot |>
  visualize() +
  shade_ci(fillers_ci)
```

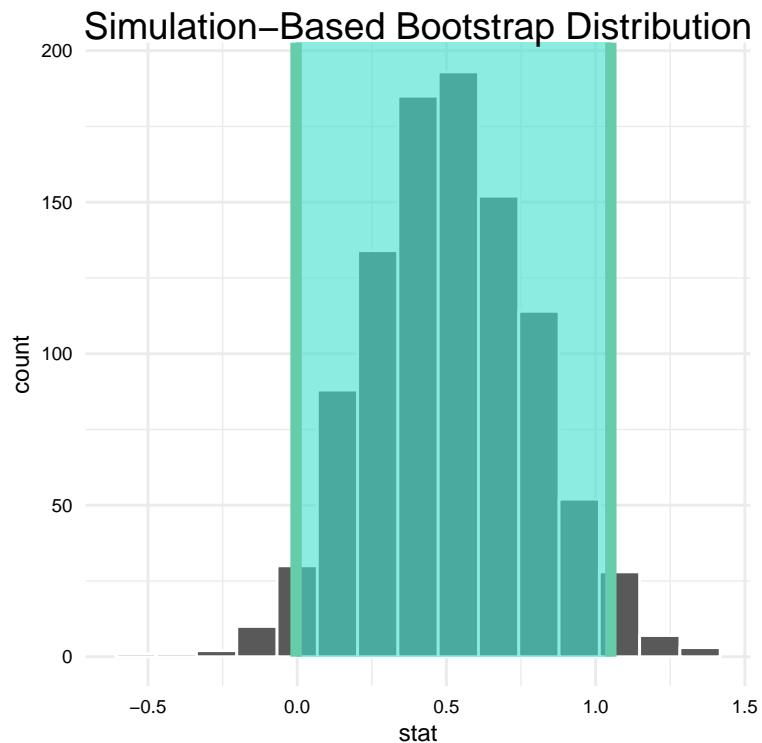


Figure 10.18: Confidence interval generated from bootstrap resampling

The confidence interval includes 0, which suggests that the observed difference is questionable. It is of note, however, that the majority of the interval is above 0, which provides some evidence that the observed difference is not due to chance.

This result highlights how p-values and confidence intervals together can provide a more nuanced picture of the data.

The second bivariate scenario we can consider is when the explanatory variable is categorical with more than two levels. In this case, we can use the F statistic to compare the means of the different levels. The `education` variable in the `fillers_df` dataset is a categorical variable with five levels. Tottie (2011) suggests that more educated speakers use more fillers than less educated speakers. Let's test this hypothesis.

First, we visualize the distribution of the `fillers_per_100_log` variable by `education`, as seen in Example 10.46.

Example 10.46.

```
# Boxplot
fillers_df |>
  ggplot(aes(y = fillers_per_100_log, x = education)) +
  geom_boxplot(notch = TRUE) +
  labs(
    y = "Filler use (log)",
    x = "Education"
  )
```

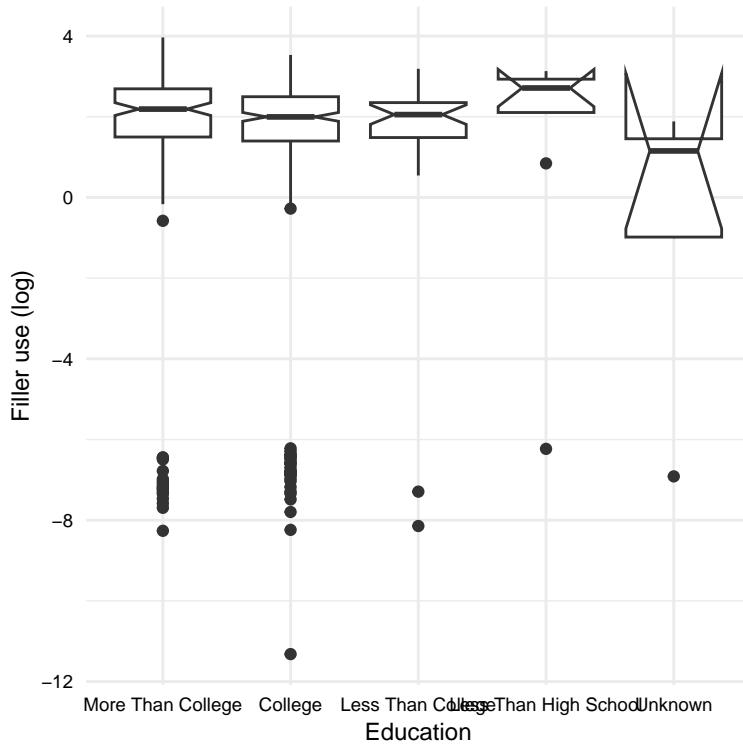


Figure 10.19: Visualizations of the `fillers_per_100_log` variable by `education`

The boxplot in Figure 10.19 does not point to any obvious differences between the levels of the `education` variable. There are a fair number of outliers, however, in the two most educated groups. These outliers are likely due to the random noise added to the 0-rate speakers and it is interesting that they are concentrated in the two most educated groups.

Let's now submit these variables to the simulation-based hypothesis testing workflow to quantify the uncertainty of the observed statistic and determine if the observed difference is statistically significant. The first steps are found in Example 10.47.

Example 10.47.

```
# Specify the relationship
fillers_spec <-
  fillers_df |>
  specify(fillers_per_100_log ~ education) # response ~ explanatory

# Observed statistic
fillers_obs <-
```

```

fillers_spec |>
  calculate(stat = "F") # F = variance between groups / variance within groups

# Null distribution
fillers_null <-
  fillers_spec |>
  hypothesize(null = "independence") |> # independence = no relationship
  generate(reps = 1000, type = "permute") |> # permute = shuffle
  calculate(stat = "F")

# Visualize the null distribution w/ observed statistic
fillers_null |>
  visualize() +
  shade_p_value(obs_stat = fillers_obs, direction = "two-sided") # expect
  ↵ greater

# Calculate the p-value
fillers_null |>
  get_p_value(obs_stat = fillers_obs, direction = "two-sided")

```

```

> # A tibble: 1 × 1
>   p_value
>   <dbl>
> 1 0.426

```

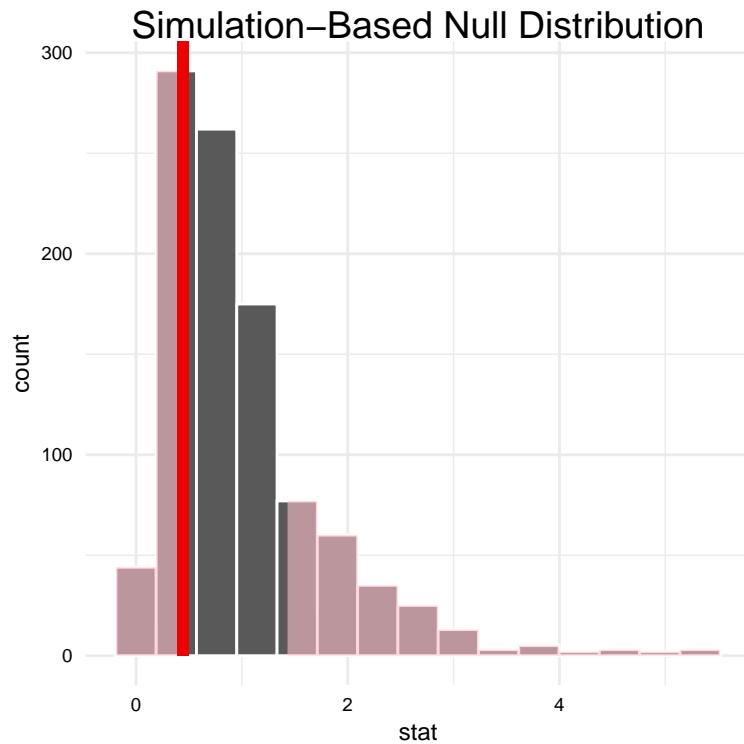


Figure 10.20: Null distribution of the `fillers_per_100_log` variable by `education`

The analysis in Example 10.47 suggests that the observed difference between the means of the different levels of the `education` variable is not significantly different from what we would expect by chance.

The p-value in Example 10.47 was calculated using a two-sided test, which is appropriate when the expected directionality is not known. In this case, while we do have an expected directionality, the visualizations strongly suggest that the observed difference is not in line with our expectations. To account for this uncertainty and to be conservative, we choose to use a two-sided test. This allows us to remain open to the possibility that the observed difference may actually be in the opposite direction, rather than solely focusing on our initial expectation. However, it's important to note that the decision to use a two-sided test should also consider factors such as the specific research question and the context of the analysis.

Let's now calculate a confidence interval to assess the uncertainty of the observed statistic, as seen in Example 10.48.

Example 10.48.

```
# Resampling distribution
fillers_boot <-
  fillers_spec |>
  generate(reps = 1000, type = "bootstrap") |>
  calculate(stat = "F")

# Calculate the confidence interval
fillers_ci <-
  fillers_boot |>
  get_ci(level = 0.95)

fillers_ci
```

```
> # A tibble: 1 × 2
>   lower_ci upper_ci
>     <dbl>    <dbl>
> 1     0.123     4.57
```

```
# Visualize the confidence interval
fillers_boot |>
  visualize() +
  shade_ci(fillers_ci)
```

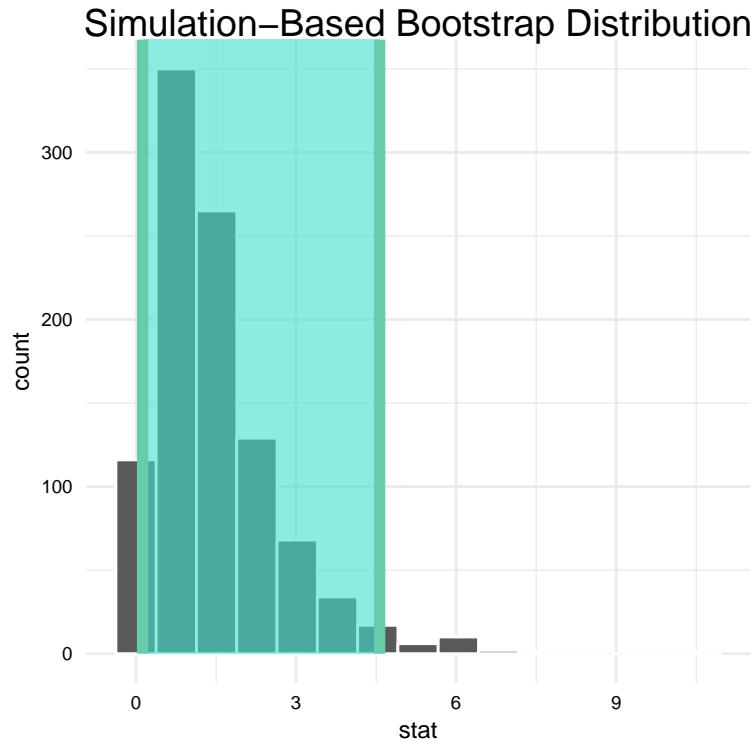


Figure 10.21: Confidence interval generated from bootstrap resampling

In Example 10.48, we see that we are in the opposite situation –the p-value is not significant and but the confidence interval does not include 0. So how do we interpret this? Remember, the p-value is the probability of observing a statistic as extreme or more extreme than the observed statistic, given that the null hypothesis is true. The confidence interval is the range of values that we are 95% confident contains the true population parameter. We should take into consideration two aspects: (1) the confidence interval has a large range (the interval is wide) and (2) that the lower limit is near 0. Take together and in addition to the p-value, we can conclude that the observed difference is not statistically significant, and if there is a difference, it is likely to be small or negligible.

The last bivariate case is when the explanatory variable is numeric. In this case, we can use a correlation test to see if there is an association between the two variables. The `age` variable in the `fillers_df` dataset is a numeric variable. Tottie (2011) suggests that older speakers use more fillers than younger speakers. Let's test this hypothesis.

First, we visualize the distribution of the `fillers_per_100_log` variable by `age`, as seen in Example 10.49.

Example 10.49.

```

# Scatterplot
fillers_df |>
  ggplot(aes(x = age, y = fillers_per_100_log)) +
  geom_point() +
  geom_smooth(method = "lm") +
  labs(
    x = "Age",
    y = "Filler use (log)"
  )

```

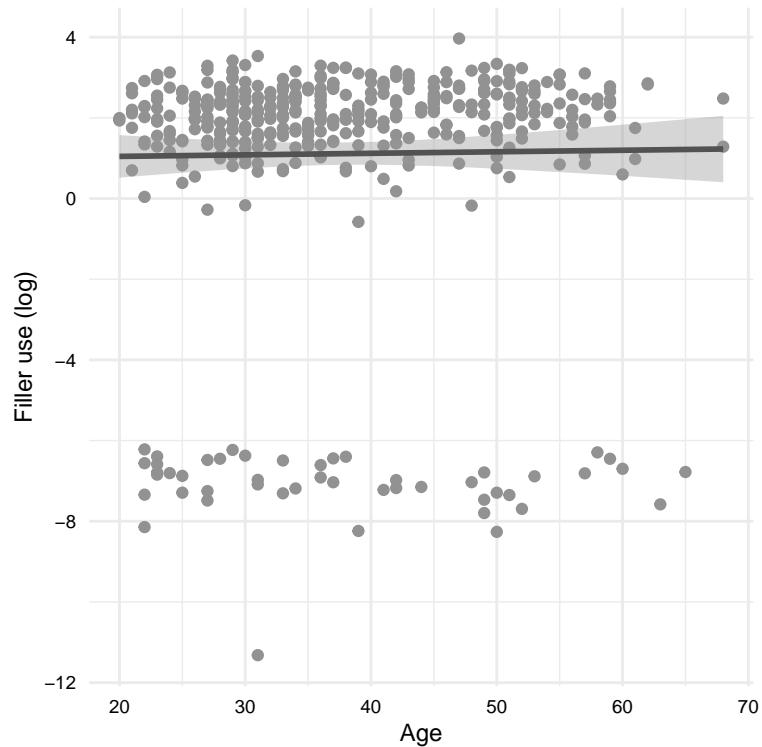


Figure 10.22: Scatterplot of the `fillers_per_100_log` variable by `age`

The trend line in Figure 10.22 does not suggest that there is a strong relationship between the two variables, or even if there is a relationship at all. We can see that the rate of filler use appears constant across the age range.

Let's now submit these variables to the simulation-based hypothesis testing workflow to quantify the uncertainty of the observed statistic and determine if the observed difference is statistically significant. The first steps are found in Example 10.50.

Example 10.50.

```
# Specify the relationship
fillers_spec <-
  fillers_df |>
  specify(fillers_per_100_log ~ age) # response ~ explanatory

# Observed statistic
fillers_obs <-
  fillers_spec |>
  calculate(stat = "correlation") # correlation = r

# Null distribution
fillers_null <-
  fillers_spec |>
  hypothesize(null = "independence") |> # independence = no relationship
  generate(reps = 1000, type = "permute") |> # permute = shuffle
  calculate(stat = "correlation")

# Visualize the null distribution w/ observed statistic
fillers_null |>
  visualize() +
  shade_p_value(obs_stat = fillers_obs, direction = "two-sided") # expect
  ↵ greater

# Calculate the p-value
fillers_null |>
  get_p_value(obs_stat = fillers_obs, direction = "two-sided")
```

```
> # A tibble: 1 × 1
>   p_value
>   <dbl>
> 1 0.762
```

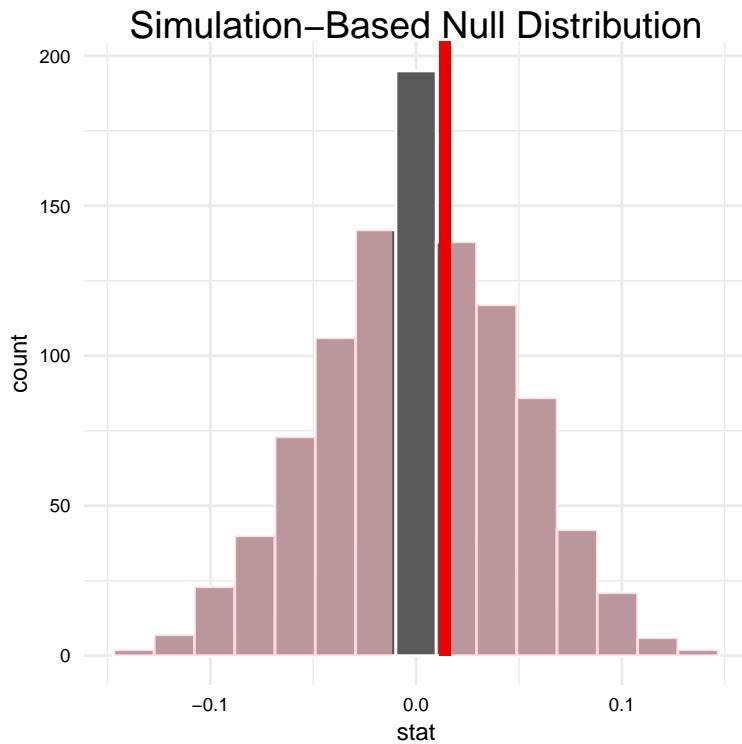


Figure 10.23: Null distribution of the `fillers_per_100_log` variable by `age`

This is a very large p-value and underscores what the scatterplot in Figure 10.22 suggests –there is no relationship between the two variables.

For completeness, we calculate a confidence interval to assess the uncertainty of the observed statistic, as seen in Example 10.51.

Example 10.51.

```
# Resampling distribution
fillers_boot <-
  fillers_spec |>
  generate(reps = 1000, type = "bootstrap") |>
  calculate(stat = "correlation")

# Calculate the confidence interval
fillers_ci <-
  fillers_boot |>
  get_ci(level = 0.95)
```

```
fillers_ci  
  
> # A tibble: 1 × 2  
>   lower_ci upper_ci  
>   <dbl>     <dbl>  
> 1   -0.0867     0.120
```

```
# Visualize the confidence interval  
fillers_boot |>  
  visualize() +  
  shade_ci(fillers_ci)
```

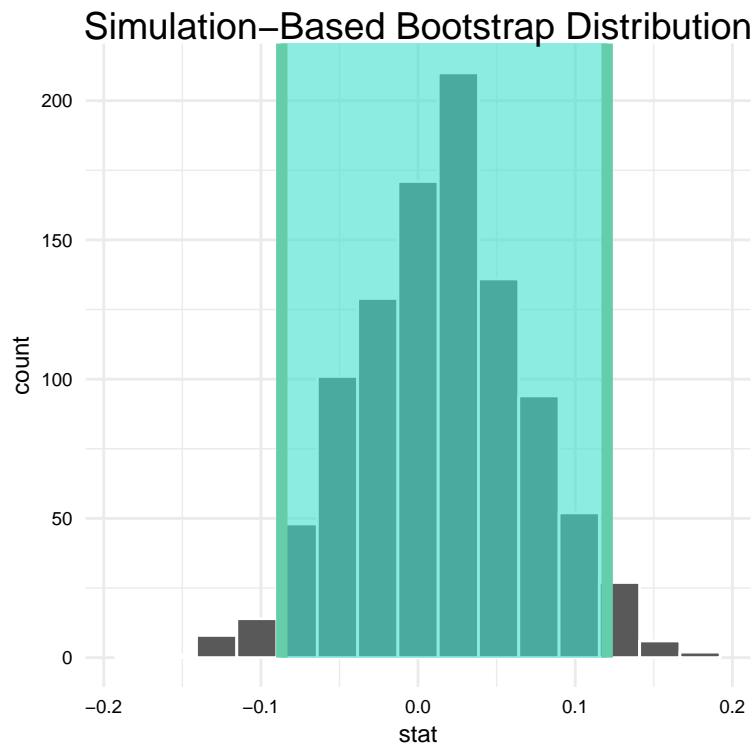


Figure 10.24: Confidence interval generated from bootstrap resampling

The confidence interval includes 0, which suggests that the observed difference is questionable. But in contrast to the confidence interval in Example 10.48, the interval is narrow suggesting more strongly that the observed difference is not due to chance.

10.2.2.3 Multivariate analysis

While bivariate analysis is useful for exploring the relationship between two variables, it is often the case that we want to consider relationships between more than two variables. In this case, we can use multivariate analysis. Linear regression is a common multivariate analysis technique.

In linear regression, we are interested in predicting the value of a numeric response variable based on the values of the explanatory variables. The contribution of the explanatory variables can be considered individually, as an interaction, or as a combination of both.

Let's now pick up the `fillers_type_df` dataset and explore the hypothesis that the rate of filler use varies by the type of filler across the socio-demographic variables `sex`, `education`, and `age`. To do this we will use R formula syntax to specify the variables we want to include in the model.

- Simple effects: `response ~ explanatory_1 + explanatory_2`: the response variable as a function of each explanatory variable.
- Interaction effects: `response ~ explanatory_1:explanatory_2`: the response variable as a function of the interaction between the two explanatory variables.
- Simple and interaction effects: `response ~ explanatory_1 * explanatory_2`: the response variable as a function of each explanatory variable and the interaction between the two explanatory variables.

Let's test the hypothesis that men and women differ in the rates that they use the filler types (`fillers_per_100_log ~ filler_type * sex`). A plot will help us begin to understand the potential relationships. In Example 10.52, we use a boxplot to visualize the relationship between the `fillers_per_100_log` variable and the `filler_type` variable, with a `sex` overlay.

Example 10.52.

```
# Boxplot 'filler_type'  
fillers_type_df |>  
  ggplot(aes(y = fillers_per_100_log, x = filler_type)) +  
  geom_boxplot(notch = TRUE) +  
  labs(  
    x = "Filler type",  
    y = "Fillers per 100 (log)"  
)  
  
# Boxplot 'filler_type' and 'sex'  
fillers_type_df |>
```

```
ggplot(aes(y = fillers_per_100_log, x = filler_type, fill = sex)) +
  geom_boxplot(notch = TRUE) +
  labs(
    x = "Filler type",
    y = "Fillers per 100 (log)",
    fill = "Sex"
  )
)
```

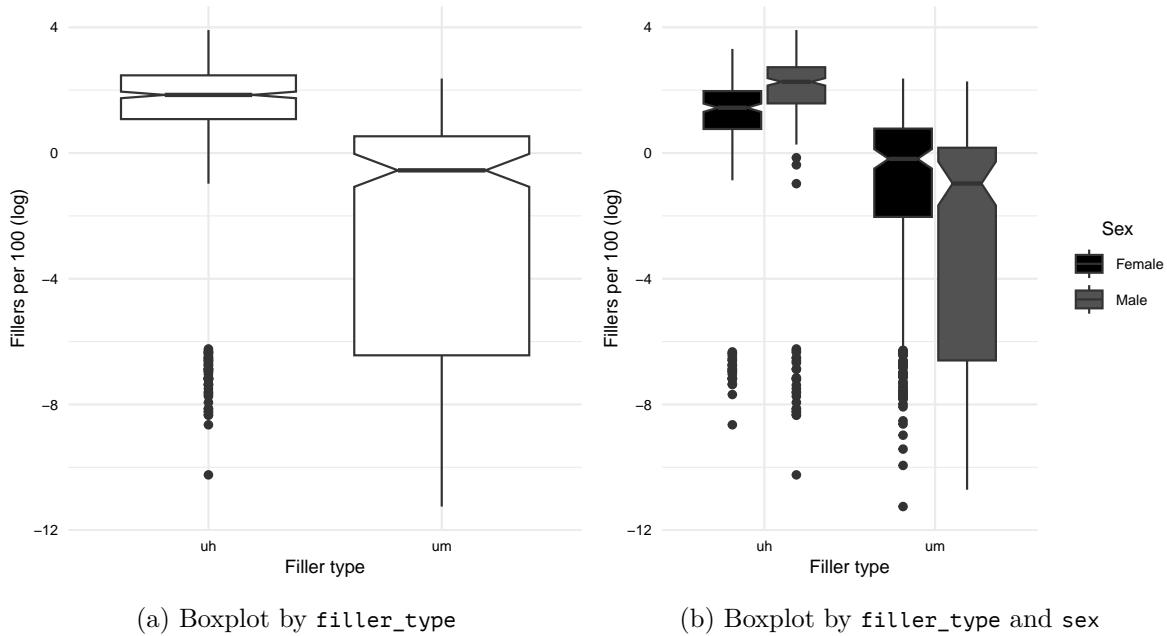


Figure 10.25: Boxplot of the `fillers_per_100_log` variable by `filler_type` and `sex`

Let's interpret the boxplot in Figure 10.25. Focusing on Figure 10.25a first, we see that the filler 'uh' is more frequent than 'um' as the median is distinct and the confidence intervals do not overlap. Now, looking at Figure 10.25b, we see the same distinction between 'uh' and 'um', but we also see that the difference between the use of 'uh' and 'um' is different for males and females. This type of relationship is called an interaction effect. In this case the interaction effect goes in the same direction but the magnitude of the difference is different.

The upshot, men and women both use 'uh' more than 'um' but men are even more likely to use 'uh' over 'um' than women.

Let's test this effect using the `infer` workflow. Calculating the observed statistics for the simple and interaction effects is very similar to other designs, except instead of `calculate()` to derive our statistics we will use the `fit()` function, just as we did for logistic regression. Let's go ahead calculate the observed statistics first, as seen in Example 10.53.

Example 10.53.

```
# Specify the relationship
fillers_type_spec <-
  fillers_type_df |>
  specify(fillers_per_100_log ~ filler_type * sex)

# Observed statistics
fillers_type_obs <-
  fillers_type_spec |>
  fit()

fillers_type_obs

> # A tibble: 4 x 2
>   term            estimate
>   <chr>           <dbl>
> 1 intercept       0.551
> 2 filler_typeum   -2.16
> 3 sexMale         0.657
> 4 filler_typeum:sexMale -1.84
```

The terms in the output from Example 10.53 provide information as to what the reference levels are. For example, `filler_typeum` tells us that the ‘uh’ level is the reference for `filler_type` and by the same logic, ‘Female’ is the reference for `sex`. These terms provide our simple effect statistics. Each can be understood as the difference between the reference level when the other variables are held constant. Our response variable is log transformed, so it is not directly interpretable beyond the fact that smaller units are lower rates of filler use and larger units are higher rates of filler use. So ‘um’ is used less than ‘uh’ and men use more fillers than women.

The statistic returned from a linear regression is the difference in the means of the two levels with the other variables held constant. In this way, the statistic is a measure of the slope of the line between the two levels. This slope quantifies the magnitude of the difference between the two levels.

We can also calculate the effect size by standardizing the statistics (coefficients). This is done by dividing the coefficient by the standard deviation of the response variable. This allows us to compare the effect sizes of different variables.

```

# Standardized effect size
fillers_type_df |>
  group_by(filler_type) |>
  summarize(
    type_sd = sd(fillers_per_100_log)
  )

```

The interaction term `fillertypeum:sexMale` is the difference in the rate of fillers for this combination compared to the reference level combination ('uh' and 'Female'). In this case, the observed rate is lower.

We now need to generate a null distribution to compare the observed statistics to. We will again use the permutation method, but since there is an interaction effect, we need to shuffle the `filler_type` and `sex` variables together. This ensures that any relationship between the two variables is removed. Let's see how this works in Example 10.54.

Example 10.54.

```

# Null distribution
fillers_type_null <-
  fillers_type_spec |>
  hypothesize(null = "independence") |>
  generate(reps = 1000, type = "permute", variables = c("filler_type", "sex")) |>
  fit()

# Visualize the null distribution w/ observed statistics
fillers_type_null |>
  visualize() +
  shade_p_value(obs_stat = fillers_type_obs, direction = "two-sided")

# Calculate the p-values
fillers_type_null |>
  get_p_value(obs_stat = fillers_type_obs, direction = "two-sided")

> # A tibble: 4 x 2
>   term          p_value
>   <chr>        <dbl>
> 1 filler_typeum      0
> 2 filler_typeum:sexMale  0
> 3 intercept        0

```

```
> 4 sexMale          0.066
```

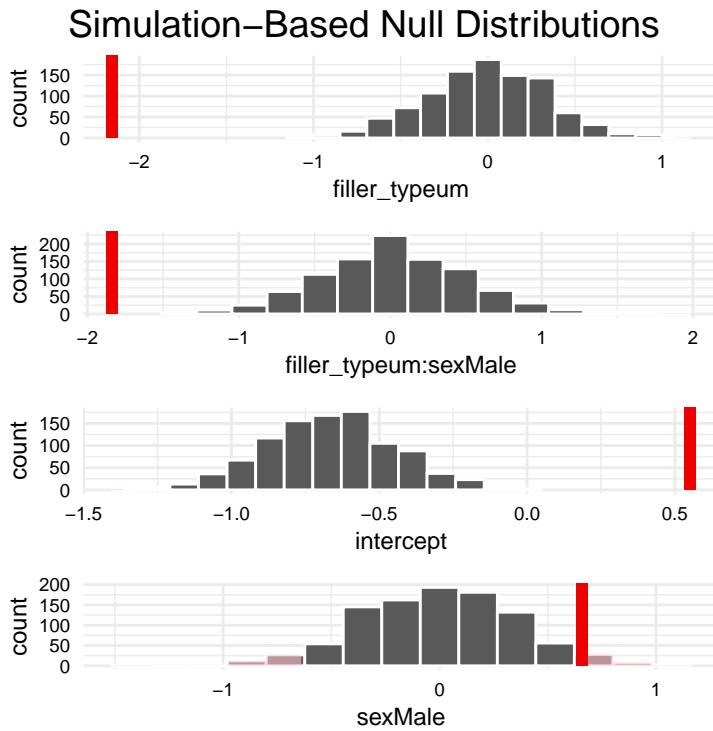


Figure 10.26: Null distribution of the `fillers_per_100_log` variable by `filler_type` and `sex`

For the simple effects, we see that `filler_type` is significant but `sex` is not. Remember, when we only considered `sex` in isolation in the bivariate case, we found it to be significant. So why is it not significant now? It is important to remember that in every statistical design, there are other factors that are not considered. When these are not in the model, our effects may appear to account for more of the variance than they actually do. In this case, the `filler_type` variable is accounting for some of the variance that `sex` was accounting for in the bivariate case, enough, it appears, to make `sex` not significant as a simple effect.

Our interaction effect is also significant meaning the observed difference we visualized in Figure 10.25 is likely not due to chance. The upshot, both men and women use more ‘uh’ compared to ‘um’ but mens’ difference in use is larger than womens’.

As always, let’s calculate a confidence interval to assess the uncertainty of the observed statistic, as seen in Example 10.55.

Example 10.55.

```
# Resampling distribution
fillers_type_boot <-
  fillers_type_spec |>
  generate(reps = 1000, type = "bootstrap") |>
  fit()

# Calculate the confidence intervals
fillers_type_ci <-
  fillers_type_boot |>
  get_ci(level = 0.95, point_estimate = fillers_type_obs)
```

```
fillers_type_ci
```

```
> # A tibble: 4 x 3
>   term            lower_ci  upper_ci
>   <chr>           <dbl>     <dbl>
> 1 filler_typeum   -2.75     -1.54
> 2 filler_typeum:sexMale -2.68     -0.934
> 3 intercept        0.168     0.909
> 4 sexMale          0.0947    1.22
```

```
# Visualize the confidence intervals
fillers_type_boot |>
  visualize() +
  shade_ci(fillers_type_ci)
```

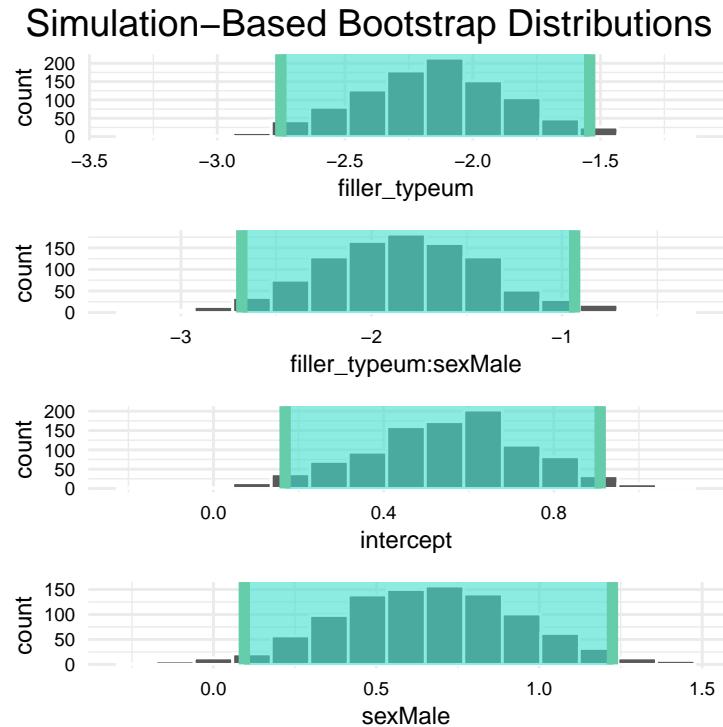


Figure 10.27: Confidence intervals generated from bootstrap resampling

From the confidence intervals, we see that zero is not included in any of the intervals, which suggests that the observed differences are not due to chance. Interpreting the width and the proximity to zero, however, suggests that the observed differences for `filler_type` are stronger than for `sex`, which did not result in a significant simple effect. The interaction effect is also significant, but the confidence interval is quite wide and approximates zero. This should raise some questions about the robustness of the observed effect.

Activities

Recipe

What: Building inference models^a **How:** Read Recipe 10 and participate in the Hypothes.is online social annotation.

Why: TBD

^a<https://qtalr.github.io/qtalrkit/articles/recipe-10.html>

💻 Lab

What: Statistical inference^a **How:** Clone, fork, and complete the steps in Lab 10.

Why: ↗ TBD

^a<https://github.com/qtalr/lab-10>

Summary

...

In sum, in this section we explored the process of statistical inference, specifically the process of hypothesis testing with categorical responses variables. We started with a univariate analysis, which, although not very interesting, allowed us to focus on the process and the logic of statistical inference. We then moved on to bivariate and multivariate analyses. We see that the process is very similar, but the complexity increases with the number of explanatory variables. In each case, we applied a simulation-based approach to statistical inference which may differ from the traditional approach you may have learned in your statistics courses. But as you can appreciate, the simulation-based approach is highly flexible, more intuitive, and more transparent. The `infer` package provides a consistent set of functions and pipeline to maintain a consistent workflow. If you have previous experience with R or find resources on statistical inference using R, you will likely find the traditional, theory-based, approach. I encourage you to explore the both approaches. They have their strengths and weaknesses, but I think you will find the simulation-based approach more intuitive and transparent as a beginner.

...

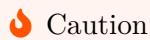
In this chapter we have discussed various approaches to conducting inferential data analysis. Each configuration, however, always includes a descriptive assessment, statistical interrogation, and an evaluation of the results. We considered univariate, bivariate, and multivariate analyses using both categorical and non-categorical dependent variables to explore the similarities and differences between these approaches.

Part V

Communication

In this section, I cover the steps in presenting the findings of the research both as a research document and as a reproducible research project. Both research documents and reproducible projects are fundamental components of modern scientific inquiry. On the one hand a research document provides readers a detailed summary of the main import of the research study. On the other hand making the research project available to interested readers ensures that the scientific community can gain insight into the process implemented in the research and thus enables researchers to vet and extend this research to build a more robust and verifiable research base.

11 Contribute



Caution

Under development.

The reproducibility of studies and the ability to follow up on the work of others is key for innovation in science and engineering.

— Leland Wilkinson

▀ Outcomes

- ...
- ...
- ...

In this chapter, we first examine the role of reporting your research, highlighting the benefits of presenting one's work as a means to develop and refine ideas and conclusions. We then discuss the purpose of a research document, focusing on how its structure effectively conveys the project's rationale, goals, procedures, results, and findings.

Whether for other researchers or for your future self, creating research that is well-documented and reproducible is a fundamental part of conducting modern scientific inquiry. In this chapter we will also emphasize the importance of this endeavor and outline strategies for ensuring your research project is reproducible. This will include directory and file structure, key documentation files as well as how to ensure a reproducible computing environment.

➤_ Lessons

What: ↗ TBA^a

How: In the R Console pane load `swirl`, run `swirl()`, and follow prompts to select the lesson.

Why: ↗ To ...

^a<https://github.com/qtalr/lessons>

11.1 Goals

...

Table 11.1: This is a table too wide for the page.

text_id	sentence_id	sentence
1	1	>Hotel California Fact: Sound is a vibration.
1	2	Sound travels as a mechanical wave through a medium, and in space, there is no medium.
1	3	So when my shuttle malfunctioned and the airlocks didn't keep the air in, I heard nothing.
1	4	After the first whoosh of the air being sucked away, there was lightning, but no thunder.
1	5	Eyes bulging in panic, but no screams.
1	6	Quiet and peaceful, right?
1	7	Such a relief to never again hear my crewmate Jesse natter about his girl back on Earth and ...
1	8	I swore, if I ever had to see a photo of him in a skimpy bathing suit again, giving the came...
1	9	Metaphorically, of course.

11.2 Write ups

11.2.1 Contents

- Introduction
 - Importance of clear and effective communication in research
 - * Enhances understanding of the research
 - * Facilitates collaboration and interdisciplinary work
 - Overview of the chapter content
 - * Research presentations
 - * Research document structure
 - * Citations and references
 - * Figures and tables
 - * Field-specific and publishing house formats
- Research Presentations
 - Importance of research presentations in academia and professional contexts

- * Sharing research findings
 - * Building a professional reputation
- Benefits of presenting research work
 - * Developing and refining ideas and conclusions through feedback and discussion
 - * Receiving feedback and suggestions from peers and experts
 - Conducting peer review can help ensure that the research is conducted appropriately and transparently. Peer review can also identify potential errors or biases in the research design or analysis, and can provide suggestions for improving the study's reproducibility
 - * Enhancing communication and presentation skills
 - * Building professional network and fostering collaboration
- Key elements of an effective research presentation
 - * Structure and organization: logical flow, clear sections, concise points
 - * Visual design and aesthetics: use of color, fonts, visuals, and layout
 - * Delivery and engagement: pacing, tone, body language, and audience interaction
- Using R for creating research presentations
 - * RMarkdown and its integration with presentation formats (e.g., xaringan, slidify)
 - * Incorporating data visualization, tables, and other R-generated content seamlessly
- Tips for delivering engaging and memorable presentations
 - * Practice and preparation
 - * Storytelling and relatability
 - * Addressing diverse audience backgrounds
- Research Documents
 - Purpose of a research document
 - * Communicate research methodology and findings
 - * Contribute to the body of knowledge
 - Benefits of writing a research document
 - * Clarifying and organizing thoughts and ideas
 - * Providing a comprehensive record of research work
 - * Enhancing writing and argumentation skills
 - * Contributing to the body of knowledge in a field
 - * Establishing professional credibility and visibility
 - Components of a research document
 - * Title: concise and informative
 - * Abstract: brief summary of the research
 - * Introduction: background, research question, and objectives

- * Methodology: description of the data, tools, and analysis techniques
 - * Results: presentation of the findings
 - * Discussion: interpretation and implications of the results
 - * Conclusion: summary and future directions
 - * References: list of cited sources
- Tips for organizing and structuring research documents
 - * Outlining the main sections
 - * Maintaining logical flow and consistency
 - * Using clear and concise language
- Citations and References
 - Importance of proper citation and referencing
 - * Acknowledge the work of others
 - * Demonstrate the foundation of your research
 - Different citation styles (APA, MLA, Chicago, etc.)
 - * Overview of common styles
 - * Choosing the appropriate style for your discipline
 - Using R and Quarto for managing citations and references
 - * Integration with reference managers (e.g., Zotero, Mendeley)
 - * Automating citation formatting
 - Integration of citations and references in research documents
 - * In-text citations
 - * Reference list or bibliography
- Figures and Tables
 - Importance of visual representations in research reporting
 - * Aid in understanding complex data
 - * Enhance the readability of the document
 - Creating and customizing figures and tables using R and Quarto
 - * ggplot2 for creating visualizations
 - * kable and gt for generating tables
 - Guidelines for labeling, formatting, and presenting figures and tables
 - * Clear and informative titles and labels
 - * Consistent formatting
 - * Appropriate use of color, fonts, and layout
 - * Proper referencing and integration in the text
 - * Accessibility considerations for diverse readers
- Field-specific and Publishing House Formats
 - Importance of adhering to field-specific and publisher guidelines

- * Consistency and professionalism
 - * Meeting submission requirements for journals, conferences, and other venues
- Overview of common format requirements
 - * Manuscript formatting: margins, line spacing, headings, etc.
 - * Citation and reference style
 - * Figure and table formatting
- Using R and Quarto to apply formatting guidelines
 - * Customizing document templates
 - * Applying and managing style files
- Exporting research documents to various formats
 - * Word: .docx files for collaboration and editing
 - * PDF: .pdf files for sharing and printing
 - * HTML: web-based documents for online publication
 - * ePub: e-book format for digital reading
- Conclusion
 - Recap of the main topics covered in the chapter
 - Importance of clear and effective communication in research reporting
 - Encouragement to practice and refine reporting skills through various research projects

11.2.2 Structure

Example 11.1. Project structure

```
project/
└── process/
    ├── 1_acquire_data.qmd
    ├── 2_curate_data.qmd
    ├── 3_transform_data.qmd
    └── 4_analyze_data.qmd
└── data/
    ├── analysis/
    ├── derived/
    │   ├── datasource_dd.csv
    │   └── datasource/
    │       └── datasource-transformed.csv
    └── original/
        ├── datasource_do.csv
        └── datasource/
```

```
|           └── datasource-set-1.csv
|           └── datasource-set-2.csv
├── reports/
|   ├── figures/
|   ├── tables/
|   ├── manuscript/
|   └── presentation/
├── DESCRIPTION
├── Makefile
└── README
```

Discuss `ggplot2::ggsave()` and `kableExtra::save_kable()` for saving figures and tables, respectively.

11.3 Reproducibility

Whether for other researchers or for your future self, creating research that is well-documented and reproducible is a fundamental part of conducting modern scientific inquiry. In this chapter we will emphasize the importance of this endeavor and outline strategies for ensuring your research project is reproducible. This will include directory and file structure, key documentation files as well as how to effectively use existing software resources and frameworks for publishing your research (either for private use, journal requirements, or general public consumption) on popular repositories such as GitHub and Open Science Framework (OSF).

Reproducibility is the ability to recreate the results of a research project. This is a fundamental part of the scientific process and is a key component of the scientific method. Reproducibility is important for several reasons. First, it allows other researchers to verify the results of a study. Second, it allows other researchers to build on the results of a study. Third, it allows researchers to revisit their own work at a later date. Fourth, it allows researchers to share their work with others. Finally, it allows researchers to use their work as a template for future projects.

- Introduction
- The importance of well-documented and reproducible research in modern scientific inquiry.
 - Ensuring accuracy and reliability of results.
 - Facilitating knowledge sharing and collaboration.
- The role of collaboration in ensuring research reproducibility.
 - Combining expertise from different fields.

- Peer review and feedback.
- Developing a Comprehensive Research Plan
- Organizing your project files for clarity and easy navigation.
 - Creating a logical folder structure.
 - Naming conventions for files and folders.
- Writing essential documentation files (README, LICENSE, CONTRIBUTING, etc.).
 - README: project overview and setup instructions.
 - LICENSE: specifying usage rights and restrictions.
 - CONTRIBUTING: guidelines for collaborators to contribute to the project.
- Creating a detailed research protocol: its importance, components, and best practices.
 - Clear objectives and hypotheses.
 - Detailed methodology, including materials, procedures, and analysis plans.
 - Ethical considerations and approval, if applicable.
- Study pre-registration: concept, benefits, and steps for pre-registering a study.
 - Reducing publication bias and promoting transparency.
 - Process of registering study design, hypotheses, and analysis plans.
 - Platforms for pre-registration.
- Leveraging Open Resources and Tools
- Utilizing open data and open source software: benefits, finding, using, and contributing to resources.
 - Cost-effectiveness and flexibility.
 - Building upon existing work and contributing back to the community.
- An overview of popular software frameworks for managing research projects.
 - Project management tools like Trello, Asana, and Basecamp.
 - Data analysis tools like R.
 - Note-taking and reference management tools like Zotero.
- Version control in collaborative research projects: introduction to Git and other version control systems.
 - Tracking changes and maintaining a history of project files.
 - * Git large file storage (LFS)¹ for managing large files.
 - Collaborating efficiently with multiple researchers.
 - Resolving conflicts in file versions.
- Publishing and Collaborating on Research Projects

¹<https://git-lfs.com/>

- Introduction to popular repositories like GitHub and Open Science Framework (OSF).
 - Hosting and sharing code, data, and documentation.
 - Version control and collaboration features.
- Strategies for uploading and organizing your research project for private use, journal requirements, or public consumption.
 - Preparing files for upload: cleaning data, anonymizing sensitive information, and compressing large files.
 - Creating a clear and informative repository structure.
- Collaboration best practices
 - Copying a repository
 - * Forking a repository and setting up the local environment.
 - * Cloning, configuring Git, and adding upstream remote repository.
 - Editing, syncing, and committing changes
 - * Creating branches, making changes, and committing locally.
 - * Fetching updates from the original repository and merging.
 - * Handling merge conflicts and syncing with the original repository.
 - Suggesting and reviewing changes
 - * Pushing local changes to the forked repository.
 - * Creating, reviewing, discussing, and merging pull requests
 - * Participating in discussions, addressing feedback, and deleting branches after merging.
- Conclusion
- Recap of the key points discussed in the chapter.
 - Importance of well-documented and reproducible research.
 - Developing a comprehensive research plan.
 - Leveraging open resources and tools.
 - Publishing and collaborating on research projects.
- Encouragement to prioritize collaboration, transparency, and reproducibility in future research endeavors.
 - The benefits of embracing these principles for individual researchers and the scientific community as a whole.

Project structure (minimal) (reference to Approaching Analysis)

```
project/
  └── data/
  ...
  
```

Add description of each file/ folder:

- *`_main.R*`
 - Use of `pacman` package to install and load packages
 - Use of `here` package to set working directory
 - Use of `source()` for R scripts or `Rscript -e <filename>` for R scripts
 - Use of `knitr` package to compile Quarto documents
 - Use of `sessioninfo` package to record session information

Project structure (full) (reference to Approaching Analysis)

Functionality:

- Adds `docs/` folder for documentation that may not figure in the main manuscript (e.g., data dictionaries, codebooks, etc.)
- `.renv/` folder for package management

```
project/
```

```
  |--- data/
```

```
  |--- docs/
```

```
  ...
```

Activities

_recipe

What: How: ... Why: ...

_lab

What: How: ... Why: ...

Summary

...

Further reading:

- Rodrigues (2023)
- Gandrud (2020)
- J. D. Blischak, Carbonetto, and Stephens (2019)

- Gentleman and Temple Lang (2007)
- Munafò et al. (2017)

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A Data

A.1 ANC

- ANC

A.2 BNC

- Brown Corpus

A.3 CABNC

- CABNC

A.4 CEDEL2

- CEDEL2

A.5 ENNTT

- ENNTT

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- Europarl
 - Federalist Papers (LOC)
 - SOTU
 - SWDA
 - ...