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My thesis title - edit in index.Rmd

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A dissertation  
submitted in partial fulfillment of the  
requirements for the degree of

Doctor of Philosophy

University of Washington

2021

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**Abstract**

My thesis title - edit in index.Rmd

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“Here is my abstract”

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## ACKNOWLEDGMENTS

“My acknowledgments”



## DEDICATION

“My dedication”

## INTRODUCTION

Welcome to the *R Markdown* thesis template. This template is based on (and in many places copied directly from) the UW LaTeX template, but hopefully it will provide a nicer interface for those that have never used TeX or LaTeX before. Using *R Markdown* will also allow you to easily keep track of your analyses in **R** chunks of code, with the resulting plots and output included as well. The hope is this *R Markdown* template gets you in the habit of doing reproducible research, which benefits you long-term as a researcher, but also will greatly help anyone that is trying to reproduce or build onto your results down the road.

Hopefully, you won't have much of a learning period to go through and you will reap the benefits of a nicely formatted thesis. The use of LaTeX in combination with *Markdown* is more consistent than the output of a word processor, much less prone to corruption or crashing, and the resulting file is smaller than a Word file. While you may have never had problems using Word in the past, your thesis is likely going to be at least twice as large and complex as anything you've written before, taxing Word's capabilities. After working with *Markdown* and **R** together for a few weeks, we are confident this will be your reporting style of choice going forward.

### Why use it?

*R Markdown* creates a simple and straightforward way to interface with the beauty of LaTeX. Packages have been written in **R** to work directly with LaTeX to produce nicely formatting tables and paragraphs. In addition to creating a user friendly interface to LaTeX, *R Markdown* also allows you to read in your data, to analyze it and to visualize it using **R** functions, and also to provide the documentation and commentary on the results of your project. Further, it allows for **R** results to be passed inline to the commentary of your results. You'll see

more on this later.

### **Who should use it?**

Anyone who needs to use data analysis, math, tables, a lot of figures, complex cross-references, or who just cares about the final appearance of their document should use *R Markdown*. Of particular use should be anyone in the sciences, but the user-friendly nature of *Markdown* and its ability to keep track of and easily include figures, automatically generate a table of contents, index, references, table of figures, etc. should make it of great benefit to nearly anyone writing a thesis project.

## Chapter 1

# **RIPARIAN SOIL NITROGEN CYCLING AND ISOTOPIC ENRICHMENT IN RESPONSE TO A LONG-TERM SALMON CARCASS MANIPULATION EXPERIMENT**

### 1.1 ABSTRACT

Pacific salmon acquire most of their biomass in the ocean before returning to spawn and die in coastal streams and lakes, thus providing subsidies of marine-derived nitrogen (MDN) to freshwater and terrestrial ecosystems. Recent declines in salmon abundance have raised questions of whether managers should mitigate for losses of salmon MDN subsidies. To test the long-term importance of salmon subsidies to riparian ecosystems we measured soil N cycling in response to a 20-year manipulation where salmon carcasses were systematically removed from one bank and deposited on the opposite bank along a 2 km stream in southwestern Alaska. Soil samples were taken at different distances from the stream bank along nine paired transects and measured for organic and inorganic nitrogen concentrations, and nitrogen transformation rates. MDN was measured using  $^{15}\text{N}/^{14}\text{N}$  for bulk soils, and  $\text{NH}_4^+$  and  $\text{NO}_3^-$  soil pools. Stable isotope analyses confirmed  $^{15}\text{N}/^{14}\text{N}$  was elevated on the salmon enhanced bank compared to the salmon depleted bank. However,  $^{15}\text{N}/^{14}\text{N}$  values of plant-available inorganic nitrogen exceeded the  $^{15}\text{N}/^{14}\text{N}$  of salmon inputs, highlighting N isotope fractionation in soils that raises significant methodological issues with standard MDN assessments in riparian systems. Surprisingly, despite 20 years of salmon supplementation, the presence of MDN did not cause a long-term increase in soil N availability. This finding indicates the importance of MDN to ecosystem N biogeochemistry and riparian vegetation may be overestimated for some systems. Given that essential nutrients can also be pollutants, we urge more critical analyses of the role of MDN to inform compensatory mitigation programs

targeting salmon nutrient enhancement.

## 1.2 INTRODUCTION

Pacific salmon (*Oncorhynchus spp.*) migration from marine environments to freshwater spawning grounds is a textbook case of cross-ecosystem nutrient subsidies, and dozens of studies have identified the presence of marine-derived nitrogen (MDN) from salmon as crossing ecosystem boundaries from oceans to freshwaters and into the terrestrial environment (sensu, (Polis, Power, & Huxel, 2004; Schindler et al., 2003; Scott M, Richard T, Mary F, & Mark S, 2002). Declines in Pacific salmon populations in many areas, caused by human activities (overharvest, habitat degradation, dams) (Richard et al., 2007), and the concern over loss of MDN to coastal watersheds has made restoration of salmon nutrients a focal point for many management and mitigation strategies. For example, in the Columbia River Basin where Pacific salmon populations have declined, legislation requiring compensatory mitigation has led to nutrient enhancement programs, on the foundation that habitats have lost critical nutrients from salmon and therefore augmentation is necessary to maintain ecosystem function (Collins, Marcarelli, Baxter, & Wipfli, 2015).

Salmon bring nutrients, including phosphorus (P) and other compounds in addition to nitrogen (N), into freshwater and terrestrial food webs through two pathways: 1) direct consumption of tissues by predators and scavengers, and 2) autotrophic or heterotrophic assimilation of nutrients released as salmon spawn, die, and eventually decay (Scott M et al., 2002). Salmon are enriched in the heavy isotope of nitrogen ( $^{15}\text{N}$ ) relative to the light isotope ( $^{14}\text{N}$ ) when compared to terrestrial and watershed-derived N. This isotopic enrichment has been used to quantitatively trace the presence of salmon derived nutrients into watersheds (Schindler et al., 2003). For example, the proportion of N derived from salmon ranges from approximately 30% – 75% in fish and aquatic invertebrates (Naiman, Bilby, Schindler, & Helfield, 2002), 10 – 90% in piscivorous mammals such as bears, and 20 – 40% in piscivorous fishes near salmon spawning grounds (Bilby, Fransen, & Bisson, 1996; Chaloner, Martin, Wipfli, Ostrom, & Lamberti, 2002; Claeson, Li, Compton, & Bisson, 2006; Hilderbrand et

al., 1999).

The annual return of this predictable and abundant, yet temporally limited, high quality resource drives the foraging ecology of both terrestrial and aquatic consumers (Quinn, Helfield, Austin, Hovel, & Bunn, 2018; Schindler et al., 2013). Carcasses and roe are documented food sources for over 22 species of mammals, birds (???), fishes (Scheuerell, Moore, Schindler, & Harvey, 2007), and invertebrates (???; Meehan, Seminet-Reneau, & Quinn, 2005; Winder, Schindler, Moore, Johnson, & Palen, 2005). Bear population density, body size, and reproductive output has been correlated with meat (primarily salmon) consumption, with piscivorous populations having 55 times higher density than their meat-limited counterparts (Hilderbrand et al., 1999). In aquatic ecosystems, salmon carcass abundance has been correlated with elevated growth rates of invertebrates, and with size, density, and condition factor of juvenile salmonids (???; R. E. Bilby, Fransen, Bisson, & Walter, 1998; Wipfli, Hudson, Caouette, & Chaloner, 2003).

The presence of MDN has been documented in aquatic primary producers, though its overall ecological importance remains ambiguous. Via this bottom-up pathway, salmon supply critical limiting nutrients that can increase primary and/or bacterial productivity, which are subsequently transferred to consumers and up through the food web (Chaloner et al., 2002; Holtgrieve & Schindler, 2011; M. S. Wipfli, Hudson, & Caouette, 1998). Higher salmon returns are correlated with MDN signatures in lower trophic levels including zooplankton and periphyton (Finney, 2000; Holtgrieve, Schindler, Gowell, Ruff, & Lisi, 2010; Kline Jr et al., 1993). Both direct ecological and paleolimnological evidence suggest MDN and P positively influence primary production in lakes (Moore et al., 2007). For example, commercial fisheries remove upwards of two-thirds of MDN which would otherwise enter some freshwater lakes in Alaska, resulting in a 3-fold decline in algal production (Schindler, Leavitt, Brock, Johnson, & Quay, 2005). In stream ecosystems, the decomposition of salmon increases dissolved organic and inorganic nutrients, including highly available forms such as orthophosphate ( $\text{PO}_4^{3-}$ ) and ammonia/ammonium ( $\text{NH}_3/\text{NH}_4^+$ ). These nutrients can stim-

ulate epilithon growth (bacteria and algae), though the magnitude of this response is highly variable, and dependent on other growth limiting factors such as sunlight and disturbance (Janetski, Chaloner, Tiegs, & Lamberti, 2009; Johnston, MacIsaac, Tschaplinski, & Hall, 2004; Mitchell & Lamberti, 2005).

In the terrestrial realm, bottom-up effects of MDN from salmon are also thought to be ecologically important, though this has been difficult to demonstrate rigorously. Studies across the range of salmon in North America have inferred that up to 26% of foliar N in riparian plants is marine derived, with foliar N levels often correlating with salmon abundance and distance from the salmon spawning location (e.g., Hocking & Reynolds, 2012; Reimchen & Fox, 2013). While MDN is clearly present in terrestrial producers, direct evidence of the importance of MDN for ecosystem function and productivity is much less evident. Helfield & Naiman (2001) measured tree growth increments in areas with and without salmon and found higher growth in one species (Sitka spruce) in areas where salmon nutrients were present, although these findings were later contested on statistical grounds (Kirchhoff, 2003). Hocking & Reynolds (2012) observed decreased understory plant diversity with increasing salmon abundance, though this pattern was largely attributed to increased dominance of a single N tolerant species (salmonberry). Reimchen & Fox (2013) suggested that salmon abundance increased tree growth, but tree ring  $^{15}\text{N}/^{14}\text{N}$  values were not related to salmon abundance; other growth limiting factors such as temperature and location were important covariates. Most recently, Quinn et al. (2018) examined tree growth increments in the riparian zone of a small Alaskan stream before and after a 20-year, > 200,000 kg, salmon carcass manipulation. In the two decades prior to manipulation, white spruce (*Picea glauca*) on average grew faster on one bank compared to the other. The subsequent decades of carcass manipulation enriched the naturally slower growing side, and were associated with increased growth. However, the growth effect of the carcasses was smaller than the natural side-to-side variation, and other important site and landscape factors such as forest demography, climate, aspect, and water availability were not fully considered, a common trend in MDN studies of

riparian vegetation.

Interpreting the contributions of MDN to terrestrial producers using stable isotopes is often highly simplified, and does not consider how variability of N sources and overall N availability may confound results. MDN analyses apply simple two-source mixing models to infer the proportion of total N derived from salmon. When applied to terrestrial vegetation, the terrestrial end-member for the mixing models is typically determined by sampling the  $^{15}\text{N}/^{14}\text{N}$  of the same species of plant either laterally away from the stream (where MDN contribution is expected to be small), upstream of barriers to salmon migration, or in watersheds without salmon. For the salmon end-member, a single value equal to the average  $^{15}\text{N}/^{14}\text{N}$  of salmon ( $12.62 \pm 0.31$  per mille for sockeye salmon) is typically used (S1). Inherent assumptions with these models therefore include: 1) reference sites are biogeochemically similar to salmon sites and 2) the isotopic signature of salmon is unchanged in the soils prior to plant uptake. N cycling in soils is strongly controlled by position in the landscape and contains a number of chemical reactions which fractionate N isotopically [(???)]; Wheeler, Kavanagh, & Daanen (2014); Figure 1], therefore these assumptions may not be valid.

Experiments examining the contributions of MDN are often limited by short timescales, and relatively few experiments investigate changes in plant-available soil N pools important to plant nutrient uptake and growth (Collins et al., 2015). Studies examining spatial and temporal impacts of salmon on soil inorganic N have identified highly localized responses (effects only observed  $< 30$  cm from carcasses) where soil ammonium ( $\text{NH}_4^+$ ) and nitrate ( $\text{NO}_3^-$ ) increase for weeks to months (???; Gende, Miller, & Hood, 2007; Holtgrieve, Schindler, & Jewett, 2009) and rarely consider long-term N retention in the system. Experiments typically examine the contributions of MDN by nutrient addition not nutrient removal; however, nutrient removal is important for understanding the effects of lower numbers of salmon returning to coastal watersheds due to fishing, habitat reduction, and climate change. In addition, previous research observed a strong effect of watershed slope on  $^{15}\text{N}/^{14}\text{N}$  in riparian plants and attributed this to topography concentrating carcasses near streams (???). However, wa-



tershed topography also influences soil water content and N cycling, which affect N isotopes (???) and therefore complicates MDN assessments.

To resolve the extent to which salmon carcasses contributed MDN to plant-available N pools and the long-term ecological response to this subsidy, we present a second study of the 20-year carcass manipulation experiment described in Quinn et al. (2018). While Quinn et al. (2018) focused on tree growth before and after the manipulation, the objective of this work was to determine whether prolonged enhancement and reduction of salmon subsidies altered long-term soil N cycling, similar to that documented in forests receiving N fertilizer additions (???; Prescott, Corbin, & Parkinson, 1992; Prescott, Kishchuk, & Weetman, 1995). If long-term changes in N availability due to salmon enhancement or reduction were observed, compensatory nutrient subsidies may be valuable for maintaining critical ecosystem functions in riparian areas with reduced salmon returns. If not, then the addition of nutrients as a management response to low salmon returns may have unintended negative consequences (sensu Compton et al., 2006). Specifically, the importance of MDN to riparian ecosystems was assessed by 1) evaluating the presence of MDN in soils enhanced and depleted in salmon carcasses through bulk stable isotope analysis of N, 2) quantifying the response of plant-available N pools ( $[\text{NH}_4^+]$  and  $[\text{NO}_3^-]$ ) and their rate of supply via mineralization and nitrification, 3) considering how fractionation in soils may impact mixing model results by measuring  $^{15}\text{N}/^{14}\text{N}$  of  $\text{NH}_4^+$  and 4) comparing these results to the vegetation responses measured by Quinn et al. (2018) at the same site. This research fills key knowledge gaps by examining the long-term legacy of inorganic N pools, both salmon addition and removal, and considering site variability that may impact the assumption of biogeochemical similarity between test and control sites, following a 20-year manipulation.

## Chapter 2

# MATHEMATICS AND SCIENCE

### 2.1 *Math*

T<sub>E</sub>X is the best way to typeset mathematics. Donald Knuth designed T<sub>E</sub>X when he got frustrated at how long it was taking the typesetters to finish his book, which contained a lot of mathematics. One nice feature of *R Markdown* is its ability to read LaTeX code directly.

If you are doing a thesis that will involve lots of math, you will want to read the following section which has been commented out. If you're not going to use math, skip over or delete this next commented section.

### 2.2 *Chemistry 101: Symbols*

Chemical formulas will look best if they are not italicized. Get around math mode's automatic italicizing in LaTeX by using the argument  `$\mathrm{formula here}$` , with your formula inside the curly brackets. (Notice the use of the backticks here which enclose text that acts as code.)

So, Fe<sub>2</sub><sup>2+</sup>Cr<sub>2</sub>O<sub>4</sub> is written  `$\mathrm{Fe_2^{2+}Cr_2O_4}$` .

Exponent or Superscript: O<sup>-</sup>

Subscript: CH<sub>4</sub>

To stack numbers or letters as in Fe<sub>2</sub><sup>2+</sup>, the subscript is defined first, and then the superscript is defined.

Bullet: CuCl • 7H<sub>2</sub>O

Delta:  $\Delta$

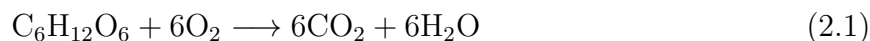
Reaction Arrows:  $\longrightarrow$  or  $\xrightarrow{\text{solution}}$

Resonance Arrows:  $\leftrightarrow$

Reversible Reaction Arrows:  $\rightleftharpoons$

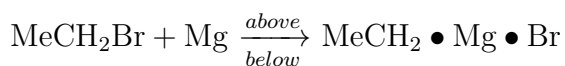
### 2.2.1 *Typesetting reactions*

You may wish to put your reaction in an equation environment, which means that LaTeX will place the reaction where it fits and will number the equations for you.



We can reference this combustion of glucose reaction via Equation (2.1).

### 2.2.2 *Other examples of reactions*



## 2.3 *Physics*

Many of the symbols you will need can be found on the math page <http://web.reed.edu/cis/help/latex/math.html> and the Comprehensive LaTeX Symbol Guide (<http://mirror.utexas.edu/ctan/info/symbols/comprehensive/symbols-letter.pdf>).

## 2.4 *Biology*

You will probably find the resources at <http://www.lecb.ncifcrf.gov/~toms/latex.html> helpful, particularly the links to bst's for various journals. You may also be interested in

TeXShade for nucleotide typesetting (<http://homepages.uni-tuebingen.de/beitz/txe.html>). Be sure to read the proceeding chapter on graphics and tables.

## Chapter 3

# TABLES, GRAPHICS, REFERENCES, AND LABELS

### 3.1 Tables

By far the easiest way to present tables in your thesis is to store the contents of the table in a CSV or Excel file, then read that file in to your R Markdown document as a data frame. Then you can style the table with the `kable` function, or functions in the `kableExtra` package.

In addition to the tables that can be automatically generated from a data frame in **R** that you saw in [R Markdown Basics] using the `kable` function, you can also create tables using *pandoc*. (More information is available at <http://pandoc.org/README.html#tables>.) This might be useful if you don't have values specifically stored in **R**, but you'd like to display them in table form. Below is an example. Pay careful attention to the alignment in the table and hyphens to create the rows and columns. Generally I don't recommend this approach of typing the table directly into your R Markdown document.

Table 3.1: Correlation of Inheritance Factors for Parents  
and Child

Factors	Correlation between Parents & Child	Inherited
Education	-0.49	Yes
Socio-Economic Status	0.28	Slight
Income	0.08	No
Family Size	0.18	Slight

Factors	Correlation between Parents & Child	Inherited
Occupational Prestige	0.21	Slight

We can also create a link to the table by doing the following: Table [3.1](#). If you go back to [Loading and exploring data] and look at the `kable` table, we can create a reference to this max delays table too: Table `??`. The addition of the `(\#tab:inher)` option to the end of the table caption allows us to then make a reference to Table `\@ref(tab:label)`. Note that this reference could appear anywhere throughout the document after the table has appeared.

## 3.2 Figures

If your thesis has a lot of figures, *R Markdown* might behave better for you than that other word processor. One perk is that it will automatically number the figures accordingly in each chapter. You'll also be able to create a label for each figure, add a caption, and then reference the figure in a way similar to what we saw with tables earlier. If you label your figures, you can move the figures around and *R Markdown* will automatically adjust the numbering for you. No need for you to remember! So that you don't have to get too far into LaTeX to do this, a couple **R** functions have been created for you to assist. You'll see their use below.

In the **R** chunk below, we will load in a picture stored as `uw.png` in our main directory. We then give it the caption of "UW logo", the label of "uwlogo", and specify that this is a figure. Make note of the different **R** chunk options that are given in the R Markdown file (not shown in the knitted document).

```
knitr::include_graphics(path = "figure/uw.png")
```

Here is a reference to the UW logo: Figure 3.1. Note the use of the `fig:` code here. By naming the **R** chunk that contains the figure, we can then reference that figure later as done in the first sentence here. We can also specify the caption for the figure via the R chunk option `fig.cap`.



Figure 3.1: UW logo



Below we will investigate how to save the output of an **R** plot and label it in a way similar to that done above. Recall the `flights` dataset from Chapter ?? (Note that we've shown a different way to reference a section or chapter here.) We will next explore a bar graph with the mean flight departure delays by airline from Portland for 2014. Note also the use of the `scale` parameter which is discussed on the next page.

```
flights %>% group_by(carrier) %>%  
  summarize(mean_dep_delay = mean(dep_delay)) %>%  
  ggplot(aes(x = carrier, y = mean_dep_delay)) +  
  geom_bar(position = "identity", stat = "identity", fill = "red")
```

``summarise()`` ungrouping output (override with ``.groups`` argument)

Here is a reference to this image: Figure 3.2.

A table linking these carrier codes to airline names is available at <https://github.com/ismayc/pnwflights14/blob/master/data/airlines.csv>.

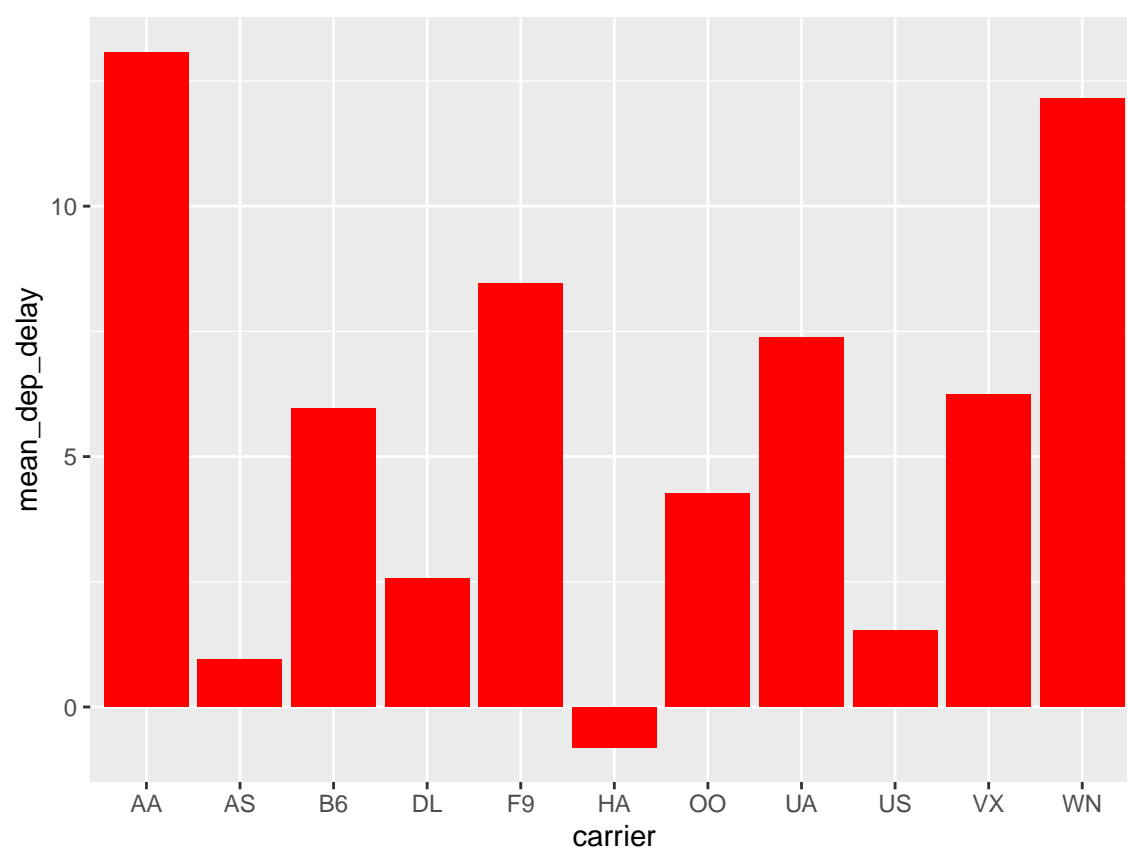


Figure 3.2: Mean Delays by Airline

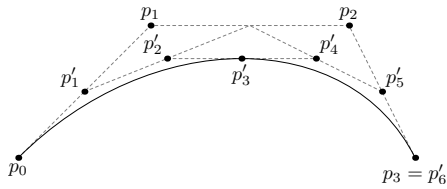


Figure 3.3: Subdiv. graph

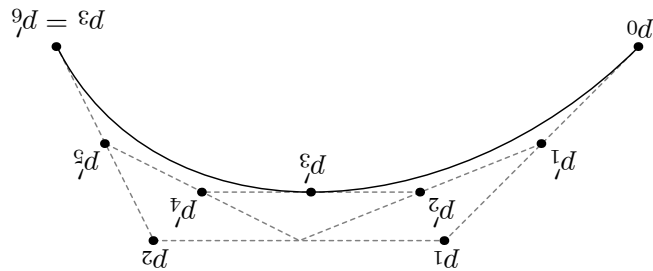


Figure 3.4: A Larger Figure, Flipped Upside Down

Next, we will explore the use of the `out.extra` chunk option, which can be used to shrink or expand an image loaded from a file by specifying "`scale=` ". Here we use the mathematical graph stored in the “subdivision.pdf” file. Here is a reference to this image: Figure 3.3. Note that `echo=FALSE` is specified so that the **R** code is hidden in the document.

### More Figure Stuff

Lastly, we will explore how to rotate and enlarge figures using the `out.extra` chunk option. (Currently this only works in the PDF version of the book.) As another example, here is a reference: Figure 3.4.

### 3.3 Footnotes and Endnotes

You might want to footnote something.<sup>1</sup> The footnote will be in a smaller font and placed appropriately. Endnotes work in much the same way.

---

<sup>1</sup>footnote text

### 3.4 Cross-referencing chapters and sections

The [bookdown documentation](#) is an excellent source for learning how to cross-reference in a bookdown project such as a huskydown document. Here we only cover the most common uses for a typical thesis. If you want something more complex or fancy, please refer to the bookdown documentation and seek help from the developers of that package.

By default, all of your chapter and section headers will get an auto-generated ID label. For example, e.g., `# Chapter 1` will have an auto-generated ID `chapter-1`. Note that the ID label is all lower case, and has no spaces. If you have any kind of punctuation in your header, such as a colon (:), it will not appear in the ID label. Then in your text you can reference chapter one in your Rmd file like this: ‘as discussed in Chapter `\@ref(chapter-1)`’, which will print as ‘as discussed in Chapter 1’

We strongly recommend that you to manually assign ID labels to your chapter header to make it easy to cross-reference. For example, at the top of the Rmd file for this chapter, you can see:

```
# Tables, Graphics, References, and Labels {#ref-labels}
```

The `{#ref-labels}` part of this header is the ID label. It doesn’t show in the output, but is there for us to use for easy cross-referencing, because it can be short, and we don’t need to change it elsewhere our document when we update the chapter header. We can use this custom ID label in our Rmd document like this: ‘as discussed in Chapter `\@ref(ref-labels)`’, which will print as ‘as discussed in Chapter [3](#)’. If you need to show custom text instead of the chapter number, you use this syntax in your Rmd document: `see [my chapter about labels]({#ref-labels}) for more details` which will appear as ‘see [my chapter about labels](#) for more details’

To cross-reference a specific section in the same chapter, we recommend adding a custom ID label to the section header, and using that to cross-reference. For example, earlier in this chapter we have a section on tables and in the Rmd file we see `## Tables`

`{#tables}`. We can cross-reference that in the text like this ‘as discussed in the section on `[tables]({#tables})`’ which will appear as ‘as discussed in the above section on [tables](#)’

To cross-reference a section in a different chapter we can use the ID label from that section directly. For example, we can write in our Rmd document `as discussed in the section on [R code chunks]({#r-chunks}) in Chapter \@ref(rmd-basics)` which will appear as ‘as discussed in the section on [R code chunks](#) in Chapter ??’.

If you prefer to cross-reference by the section number, we can use custom ID labels in our Rmd document. For example, to refer to a section in our first chapter, we can write in the Rmd document: `as discussed in section \@ref(r-chunks) in Chapter \@ref(rmd-basics)`. This will appear with section and chapter numbers like so: as ‘as discussed in section ?? in Chapter ??’.

### 3.5 Bibliographies

Of course you will need to cite things, and you will probably accumulate an armful of sources. There are a variety of tools available for creating a bibliography database (stored with the `.bib` extension). In addition to BibTeX suggested below, you may want to consider using the free and easy-to-use tool called Zotero. Some Zotero documentation is at <http://libguides.reed.edu/citation/zotero>. In addition, a tutorial is available from Middlebury College at <http://sites.middlebury.edu/zoteromiddlebury/>.

*R Markdown* uses *pandoc* (<http://pandoc.org/>) to build its bibliographies. One nice caveat of this is that you won’t have to do a second compile to load in references as standard LaTeX requires. To cite references in your thesis (after creating your bibliography database), place the reference name inside square brackets and precede it by the “at” symbol. For example, here’s a reference to a book about worrying: `(???)`. This `Molina1994` entry appears in a file called `thesis.bib` in the `bib` folder. This bibliography database file was created by a program called BibTeX. You can call this file something else if you like (look at the YAML header in the main `.Rmd` file) and, by default, is to placed in the `bib` folder.

For more information about BibTeX and bibliographies, see (<http://web.reed.edu/cis/help/latex/index.html>)<sup>2</sup>. There are three pages on this topic: *bibtex* (which talks about using BibTeX, at <http://web.reed.edu/cis/help/latex/bibtex.html>), *bibtexstyles* (about how to find and use the bibliography style that best suits your needs, at <http://web.reed.edu/cis/help/latex/bibtexstyles.html>) and *bibman* (which covers how to make and maintain a bibliography by hand, without BibTeX, at <http://web.reed.edu/cis/help/latex/bibman.html>). The last page will not be useful unless you have only a few sources.

If you look at the YAML header at the top of the main .Rmd file you can see that we can specify the style of the bibliography by referencing the appropriate csl file. You can download a variety of different style files at <https://www.zotero.org/styles>. Make sure to download the file into the csl folder.

## Tips for Bibliographies

- Like with thesis formatting, the sooner you start compiling your bibliography for something as large as thesis, the better.
- The cite key (a citation’s label) needs to be unique from the other entries.
- When you have more than one author or editor, you need to separate each author’s name by the word “and” e.g. `Author = {Noble, Sam and Youngberg, Jessica},.`
- Bibliographies made using BibTeX (whether manually or using a manager) accept LaTeX markup, so you can italicize and add symbols as necessary.
- To force capitalization in an article title or where all lowercase is generally used, bracket the capital letter in curly braces.

---

<sup>2</sup>(???)

### 3.6 *Anything else?*

If you'd like to see examples of other things in this template, please [contact us](mailto:bmarwick@uw.edu) (email [bmarwick@uw.edu](mailto:bmarwick@uw.edu)) with your suggestions. We love to see people using *R Markdown* for their theses, and are happy to help.

## CONCLUSION

If we don't want Conclusion to have a chapter number next to it, we can add the `{-}` attribute.

### More info

And here's some other random info: the first paragraph after a chapter title or section head *shouldn't be* indented, because indents are to tell the reader that you're starting a new paragraph. Since that's obvious after a chapter or section title, proper typesetting doesn't add an indent there.



## Appendix A

### THE FIRST APPENDIX

This first appendix includes all of the R chunks of code that were hidden throughout the document (using the `include = FALSE` chunk tag) to help with readability and/or setup.

**In the main Rmd file**

```
# This chunk ensures that the huskydown package is  
# installed and loaded. This huskydown package includes  
# the template files for the thesis.  
if(!require(devtools))  
  install.packages("devtools", repos = "http://cran.rstudio.com")  
if(!require(huskydown))  
  devtools::install_github("benmarwick/huskydown")  
library(huskydown)
```

**In Chapter 3:**

```
# This chunk ensures that the huskydown package is  
# installed and loaded. This huskydown package includes  
# the template files for the thesis and also two functions  
# used for labeling and referencing  
if(!require(devtools))  
  install.packages("devtools", repos = "http://cran.rstudio.com")  
if(!require(dplyr))
```

```
  install.packages("dplyr", repos = "http://cran.rstudio.com")
if(!require(ggplot2))
  install.packages("ggplot2", repos = "http://cran.rstudio.com")
if(!require(ggplot2))
  install.packages("bookdown", repos = "http://cran.rstudio.com")
if(!require(huskydown)){
  library(devtools)
  devtools::install_github("benmarwick/huskydown")
}
library(huskydown)
flights <- read.csv("data/flights.csv")
```

## Appendix B

### **THE SECOND APPENDIX, FOR FUN**

## COLOPHON

This document is set in **EB Garamond**, **Source Code Pro** and **Lato**. The body text is set at 11pt with *lmr*.

It was written in R Markdown and  $\LaTeX$ , and rendered into PDF using **huskydown** and **bookdown**.

This document was typeset using the XeTeX typesetting system, and the **University of Washington Thesis class** class created by Jim Fox. Under the hood, the **University of Washington Thesis LaTeX template** is used to ensure that documents conform precisely to submission standards. Other elements of the document formatting source code have been taken from the **Latex**, **Knitr**, and **RMarkdown templates for UC Berkeley's graduate thesis**, and **Dissertate: a LaTeX dissertation template to support the production and typesetting of a PhD dissertation at Harvard, Princeton, and NYU**

The source files for this thesis, along with all the data files, have been organised into an R package, **xxx**, which is available at <https://github.com/xxx/xxx>. A hard copy of the thesis can be found in the University of Washington library.

This version of the thesis was generated on 2021-05-22 15:09:49. The repository is currently at this commit:

The computational environment that was used to generate this version is as follows:

```
- Session info -----
setting  value
version  R version 4.0.2 (2020-06-22)
os       macOS Catalina 10.15.6
```

```

system    x86_64, darwin17.0
ui         X11
language  (EN)
collate   en_US.UTF-8
ctype     en_US.UTF-8
tz        America/Los_Angeles
date      2021-05-22

```

- Packages -----

package	* version	date	lib	source
assertthat	0.2.1	2019-03-21	[1]	CRAN (R 4.0.0)
backports	1.1.6	2020-04-05	[1]	CRAN (R 4.0.0)
bookdown	0.22.3	2021-05-22	[1]	Github (rstudio/bookdown@aa75b5f)
callr	3.7.0	2021-04-20	[1]	CRAN (R 4.0.2)
cli	2.5.0	2021-04-26	[1]	CRAN (R 4.0.2)
colorspace	1.4-1	2019-03-18	[1]	CRAN (R 4.0.0)
crayon	1.3.4	2017-09-16	[1]	CRAN (R 4.0.0)
desc	1.2.0	2018-05-01	[1]	CRAN (R 4.0.0)
devtools	* 2.3.1	2020-07-21	[1]	CRAN (R 4.0.2)
digest	0.6.27	2020-10-24	[1]	CRAN (R 4.0.2)
dplyr	* 1.0.2	2020-08-18	[1]	CRAN (R 4.0.2)
ellipsis	0.3.0	2019-09-20	[1]	CRAN (R 4.0.0)
evaluate	0.14	2019-05-28	[1]	CRAN (R 4.0.0)
farver	2.0.3	2020-01-16	[1]	CRAN (R 4.0.0)
fs	1.5.0	2020-07-31	[1]	CRAN (R 4.0.2)
generics	0.0.2	2018-11-29	[1]	CRAN (R 4.0.0)
ggplot2	* 3.3.0	2020-03-05	[1]	CRAN (R 4.0.0)
git2r	0.27.1	2020-05-03	[1]	CRAN (R 4.0.2)

glue	1.4.2	2020-08-27	[1]	CRAN	(R 4.0.2)
gtable	0.3.0	2019-03-25	[1]	CRAN	(R 4.0.0)
highr	0.9	2021-04-16	[1]	CRAN	(R 4.0.2)
htmltools	0.5.1.1	2021-01-22	[1]	CRAN	(R 4.0.2)
huskydown	* 0.0.5	2021-05-16	[1]	Github	(benmarwick/huskydown@addb48e)
knitr	1.33	2021-04-24	[1]	CRAN	(R 4.0.2)
labeling	0.3	2014-08-23	[1]	CRAN	(R 4.0.0)
lifecycle	0.2.0	2020-03-06	[1]	CRAN	(R 4.0.0)
magrittr	2.0.1	2020-11-17	[1]	CRAN	(R 4.0.2)
memoise	1.1.0	2017-04-21	[1]	CRAN	(R 4.0.2)
munsell	0.5.0	2018-06-12	[1]	CRAN	(R 4.0.0)
pillar	1.4.3	2019-12-20	[1]	CRAN	(R 4.0.0)
pkgbuild	1.0.6	2019-10-09	[1]	CRAN	(R 4.0.0)
pkgconfig	2.0.3	2019-09-22	[1]	CRAN	(R 4.0.0)
pkgload	1.0.2	2018-10-29	[1]	CRAN	(R 4.0.0)
png	0.1-7	2013-12-03	[1]	CRAN	(R 4.0.2)
prettyunits	1.1.1	2020-01-24	[1]	CRAN	(R 4.0.0)
processx	3.5.2	2021-04-30	[1]	CRAN	(R 4.0.2)
ps	1.6.0	2021-02-28	[1]	CRAN	(R 4.0.2)
purrr	0.3.4	2020-04-17	[1]	CRAN	(R 4.0.0)
R6	2.4.1	2019-11-12	[1]	CRAN	(R 4.0.0)
remotes	2.2.0	2020-07-21	[1]	CRAN	(R 4.0.2)
rlang	0.4.11	2021-04-30	[1]	CRAN	(R 4.0.2)
rmarkdown	2.8	2021-05-07	[1]	CRAN	(R 4.0.2)
rprojroot	1.3-2	2018-01-03	[1]	CRAN	(R 4.0.0)
rstudioapi	0.11	2020-02-07	[1]	CRAN	(R 4.0.0)
scales	1.1.0	2019-11-18	[1]	CRAN	(R 4.0.0)
sessioninfo	1.1.1	2018-11-05	[1]	CRAN	(R 4.0.2)

stringi	1.6.2	2021-05-17	[1]	CRAN	(R 4.0.2)
stringr	1.4.0	2019-02-10	[1]	CRAN	(R 4.0.0)
testthat	3.0.2	2021-02-14	[1]	CRAN	(R 4.0.2)
tibble	3.0.1	2020-04-20	[1]	CRAN	(R 4.0.0)
tidyselect	1.1.0	2020-05-11	[1]	CRAN	(R 4.0.0)
usethis	* 1.6.1	2020-04-29	[1]	CRAN	(R 4.0.2)
vctrs	0.3.4	2020-08-29	[1]	CRAN	(R 4.0.2)
withr	2.4.2	2021-04-18	[1]	CRAN	(R 4.0.2)
xfun	0.23	2021-05-15	[1]	CRAN	(R 4.0.2)
yaml	2.2.1	2020-02-01	[1]	CRAN	(R 4.0.0)

[1] /Library/Frameworks/R.framework/Versions/4.0/Resources/library

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