### Enzymatic Promiscuity

 $\label{eq:approx} \mbox{ A Thesis}$   $\mbox{ Presented to}$   $\mbox{ The Division of Mathematics and Natural Sciences}$   $\mbox{ Reed College}$ 

In Partial Fulfillment of the Requirements for the Degree Bachelor of Arts

Nelly Selem

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Approved for the Division (Mathematics)

Francisco Barona Gomez

# Acknowledgements

I want to thank a few people.

# Preface

This is an example of a thesis setup to use the reed thesis document class.

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# Abstract

The preface pretty much says it all. Second paragraph of abstract starts here.

# Dedication

You can have a dedication here if you wish.

## Introduction

Welcome to the *R Markdown* thesis template. This template is based on (and in many places copied directly from) the 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 about twice as large and complex as anything you've written before, taxing Word's capabilities. After working with Markdown and  $\mathbf R$  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 PTEX. Packages have been written in R to work directly with PTEX to produce nicely formatting tables and paragraphs. In addition to creating a user friendly interface to PTEX, PTEX,

#### 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

# **EvoMining**

**EvoMining** needs. Functional genomics uses genomes in the study of gene and protein function[].

- 1. Genomes DB
- 2. Natural Products DB
- 3. Central Pathways DB

Archaea, Actinobacteria, Cyanobacteria were used as genome DB, MIBiG was used as Natural Product DB and different Central Pathways were used. http://rmarkdown.rstudio.com.

### 1.1 Genome DB

RAST annotation of genomes was done.

### Phylogeny To capture differences on genomes we sort them phylogenetically. Phylogenies can be constructed using different paradigms as Parsimony, Maximum Likelihood, and Bayesian inference. Short descriptions of the main phylogeny methods are included below.

- Parsimony
- Maximum Likelihood
- Mr bayes

#### General Trees

Actinobacteria Tree, Archaea Tree, Cyanobacteria Tree.

It's easy to create a list. It can be unordered like

To create a sublist, just indent the values a bit (at least four spaces or a tab). (Here's one case where indentation is key!)

- 1. Item 1
- 2. Item 2
- 3. Item 3

- Item 3a
- Item 3b ## Central DB
- BBH Best Bidirectional Hits with studied enzymes from Central Actinobacterial pathways were selected.
- By abundance
- By expansions on genomes

#### 1.2 Natural Products DB

Natural products was improved from previous version

### 1.3 Reproducibility on EvoMining code

EvoMining Code was packaged on Docker ## Archaeas Results Archaea is a kingdom of recent discovery were not many natural products has been known. On Actinobacteria, evoMining has proved its value to find new kinds of natural products. The clue to this discovery was that Actinobacteria has genomic expansions. Now Archaea has genomic expansions, even more has central pathways genomic expansions. Are this expansions derived from a genomic duplication?

Has Archaea natural products detected by antismash, and if not, where are this NP's or may Archaea doesn't have NP's.

applying EvoMining to Archaea

# 1.4 Otras estrategias para los clusters Argon context Idea

Argon When you click the **Knit** button above a document will be generated that includes both content as well as the output of any embedded  $\mathbf{R}$  code chunks within the document. You can embed an  $\mathbf{R}$  code chunk like this (cars is a built-in  $\mathbf{R}$  dataset):

#### summary(cars)

spe	eed	dis	t
Min.	: 4.0	Min. :	2.00
1st Qu.	:12.0	1st Qu.:	26.00
Median	:15.0	Median :	36.00
Mean	:15.4	Mean :	42.98
3rd Qu.	:19.0	3rd Qu.:	56.00
Max.	:25.0	Max. :	120.00

1.5. Inline code

#### 1.5 Inline code

If you'd like to put the results of your analysis directly into your discussion, add inline code like this:

The cos of  $2\pi$  is 1.

Another example would be the direct calculation of the standard deviation:

The standard deviation of speed in cars is 5.2876444.

One last neat feature is the use of the ifelse conditional statement which can be used to output text depending on the result of an R calculation:

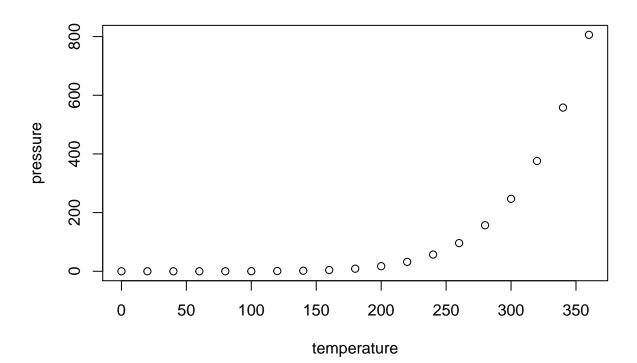
The standard deviation is less than 6.

Note the use of > here, which signifies a quotation environment that will be indented.

As you see with \$2 \pi\$ above, mathematics can be added by surrounding the mathematical text with dollar signs. More examples of this are in [Mathematics and Science] if you uncomment the code in Math.

### 1.6 CORASoN

You can also embed plots. For example, here is a way to use the base **R** graphics package to produce a plot using the built-in **pressure** dataset:



Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated the plot. There are plenty of other ways to add chunk options. More information is available at http://yihui.name/knitr/options/.

Another useful chunk option is the setting of cache = TRUE as you see here. If document rendering becomes time consuming due to long computations or plots that are expensive to generate you can use knitr caching to improve performance. Later in this file, you'll see a way to reference plots created in  $\mathbf{R}$  or external figures.

### 1.7 Loading and exploring data

Included in this template is a file called flights.csv. This file includes a subset of the larger dataset of information about all flights that departed from Seattle and Portland in 2014. More information about this dataset and its R package is available at http://github.com/ismayc/pnwflights14. This subset includes only Portland flights and only rows that were complete with no missing values. Merges were also done with the airports and airlines data sets in the pnwflights14 package to get more descriptive airport and airline names.

We can load in this data set using the following command:

```
flights <- read.csv("data/flights.csv")</pre>
```

The data is now stored in the data frame called **flights** in **R**. To get a better feel for the variables included in this dataset we can use a variety of functions. Here we can see the dimensions (rows by columns) and also the names of the columns.

```
dim(flights)
[1] 52808    16
```

```
names(flights)
```

```
[1] "month"
                     "day"
                                      "dep_time"
                                                      "dep_delay"
                                      "carrier"
 [5] "arr_time"
                     "arr_delay"
                                                      "tailnum"
 [9] "flight"
                     "dest"
                                      "air time"
                                                      "distance"
                                      "carrier name"
[13] "hour"
                     "minute"
                                                      "dest name"
```

Another good idea is to take a look at the dataset in table form. With this dataset having more than 50,000 rows, we won't explicitly show the results of the command here. I recommend you enter the command into the Console **after** you have run the **R** chunks above to load the data into **R**.

#### View(flights)

While not required, it is highly recommended you use the dplyr package to manipulate and summarize your data set as needed. It uses a syntax that is easy to understand using chaining operations. Below I've created a few examples of using dplyr to get information about the Portland flights in 2014. You will also see the use of the ggplot2 package, which produces beautiful, high-quality academic visuals.

We begin by checking to ensure that needed packages are installed and then we load them into our current working environment:

```
# List of packages required for this analysis
pkg <- c("dplyr", "ggplot2", "knitr", "devtools")
# Check if packages are not installed and assign the
# names of the packages not installed to the variable new.pkg
new.pkg <- pkg[!(pkg %in% installed.packages())]
# If there are any packages in the list that aren't installed,
# install them
if (length(new.pkg))
   install.packages(new.pkg, repos = "http://cran.rstudio.com")
# Load packages
library(dplyr)
library(ggplot2)
library(knitr)</pre>
```

The example we show here does the following:

- Selects only the carrier\_name and arr\_delay from the flights dataset and then assigns this subset to a new variable called flights2.
- Using flights2, we determine the largest arrival delay for each of the carriers.

```
flights2 <- flights %>% dplyr::select(carrier_name, arr_delay)
max_delays <- flights2 %>% group_by(carrier_name) %>%
   summarize(max_arr_delay = max(arr_delay, na.rm = TRUE))
```

We next introduce a useful function in the knitr package for making nice tables in *R Markdown* called kable. It produces the LaTeX code required to make the table and is much easier to use than manually entering values into a table by copying and pasting values into Excel or LaTeX. This again goes to show how nice reproducible documents can be! There is no need to copy-and-paste values to create a table. (Note the use of results = "asis" here which will produce the table instead of the code to create the table. You'll learn more about the \\labellater.) The caption.short argument is used to include a shorter version of the title to appear in the List of Tables at the beginning of the document.

Table 1.1. Maximum Delays by An	le 1.1: Maximum Delays by	/ Airline
---------------------------------	---------------------------	-----------

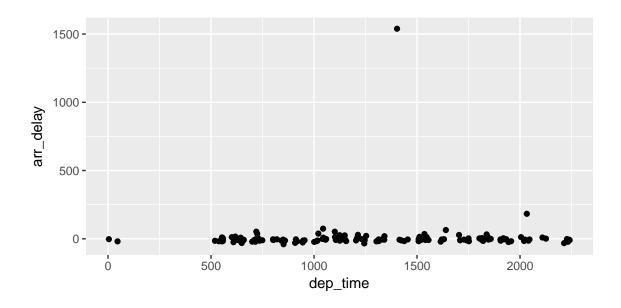
Airline	Max Arrival Delay
Alaska Airlines Inc.	338
American Airlines Inc.	1539
Delta Air Lines Inc.	651
Frontier Airlines Inc.	575
Hawaiian Airlines Inc.	407
JetBlue Airways	273
SkyWest Airlines Inc.	421
Southwest Airlines Co.	694
United Air Lines Inc.	472
US Airways Inc.	347
Virgin America	366
_	

We can further look into the properties of the largest value here for American Airlines Inc. To do so, we can isolate the row corresponding to the arrival delay of 1539 minutes for American in our original flights dataset.

```
dep_time dep_delay arr_time tailnum flight dest air_time distance
1  1403  1553  1934  N595AA  1568  DFW  182  1616
```

We see that the flight occurred on March 3rd and departed a little after 2 PM on its way to Dallas/Fort Worth. Lastly, we show how we can visualize the arrival delay of all departing flights from Portland on March 3rd against time of departure.

```
flights %>% dplyr::filter(month == 3, day == 3) %>%
  ggplot(aes(x = dep_time, y = arr_delay)) +
  geom_point()
```



### 1.8 Additional resources

- Markdown Cheatsheet https://github.com/adam-p/markdown-here/wiki/Markdown-Cheatsheet
- R Markdown Reference Guide https://www.rstudio.com/wp-content/uploads/2015/03/rmarkdown-reference.pdf
- Introduction to dplyr https://cran.rstudio.com/web/packages/dplyr/vignettes/introduction.html
- ggplot2 Documentation http://docs.ggplot2.org/current/

# Chapter 2

# **PriA Family**

- Julian simulation
- Who has TrpF

#### 2.1 Math

TEX is the best way to typeset mathematics. Donald Knuth designed TEX 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 Lagrange 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_2^{2+}Cr_2O_4 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  $Fe_2^{2+}$ , the subscript is defined first, and then the superscript is defined.

Angstrom: Å

Bullet: CuCl • 7H<sub>2</sub>O Double Dagger: ‡

Delta:  $\Delta$ 

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

Resonance Arrows:  $\leftrightarrow$ 

Reversible Reaction Arrows:  $\rightleftharpoons$  or  $\stackrel{solution}{\longleftarrow}$  (the latter requires the chemarr LaTeX package which is automatically loaded in this template)

### 2.2.1 Typesetting reactions

You may wish to put your reaction in a figure environment, which means that LATEX will place the reaction where it fits and you can have a figure caption. You'll see further description of this R label function in . (Note the use of the double backslash here as well as the echo = FALSE which hides the code from the output.)

$$C_6H_{12}O_6 + 6O_2 \longrightarrow 6CO_2 + 6H_2O$$

Figure 2.1: Combustion of glucose

#### 2.2.2 Other examples of reactions

$$NH_4Cl_{(s)} \rightleftharpoons NH_{3(g)} + HCl_{(g)}$$
 $MeCH_2Br + Mg \xrightarrow{above} MeCH_2 \bullet Mg \bullet Br$ 

### 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 bsts for various journals. You may also be interested in TeXShade for nucleotide typesetting (http://homepages.unituebingen.de/beitz/txe.html). Be sure to read the proceeding chapter on graphics and tables.

# Chapter 3

# Archaeas result Tables, Graphics, References, and Labels

#### 3.1 Tables

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.

1able 5.1:	Correlation	oI	Inneritance	ractors	IOT	Parents	ana	Chiia

Factors	Correlation between Parents & Child	Inherited
Education	-0.49	Yes
Socio-Economic Status	0.28	Slight
Income	0.08	No
Family Size	0.18	$\operatorname{Slight}$
Occupational Prestige	0.21	Slight

We can also create a link to the table by doing the following: Table 5.1. If you go back to Loading and exploring data and look at the kable function code, you'll see that I added in a similar \\lambdabel to be able to reference that table later. (The extra backslash there is a way that *Markdown* interfaces with LaTeX.) We can create a reference to the max delays table: Table 1.1.

The addition of the \label{} option to the end of the table caption allows us to then use the LaTeX autoref function to produce the link. The ref function in R allows for tables and figures to be referenced in the document easily without having to directly use the autoref function. It will automatically add "Table" before your number if you add the "tab:" prefix to your label. Note that this reference could appear anywhere throughout the document.

### 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 reed.jpg in our main directory. We then give it the caption of "Reed logo", the label of "reed", and specify that this is a figure. Note again the use of the results = "asis" specification to automatically include and compile the LATEX code.



Figure 3.1: Reed logo

Here is a reference to the Reed logo: Figure 5.1. Note the use of the inline **R** code here. By default "figure" is specified as the type. For clarity, we could have also added the label and type to the parameter specifications and this would give us the same result: Figure 5.1.

3.2. Figures 15

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 . (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.

```
delay_airline <- 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")
ggsave("figure/delays.pdf", plot = delay_airline,
   height = 3, width = 6)
```



Figure 3.2: Mean Delays by Airline

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

Next, we will explore the use of the scale parameter which can be used to shrink or expand an image. Here we use the mathematical graph stored in the "subdivision.pdf" file. Note that we didn't specify the caption = or label = here, but we could have.

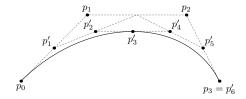


Figure 3.3: Subdiv. graph

Here is a reference to this image: Figure 5.3. (Move this around throughout the document as you wish.)

#### More Figure Stuff

Lastly, we will explore how to rotate figures using the angle parameter.

```
label("figure/subdivision.pdf",
    "A Larger Figure, Flipped Upside Down",
    scale = 1.5,
    angle = 180,
    label = "subd2")
```

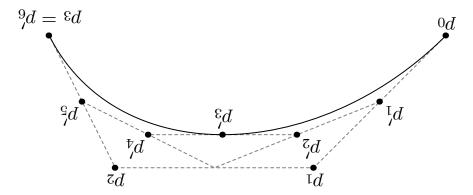


Figure 3.4: A Larger Figure, Flipped Upside Down

As another example, here is a reference to this figure: Figure 5.4.

#### **Common Modifications**

The following figure features the more popular changes thesis students want to make to their figures. We can add math to the caption that displays below the picture, specify the size of our caption to display below the figure (list of sizes available at this link), and also specify that a different caption alt.cap be what appears in the Table of Figures for this figure.

If you'd like to make further tweaks to figures, you might need to invoke some LATEX code. Please email us at data@reed.edu if you need assistance.

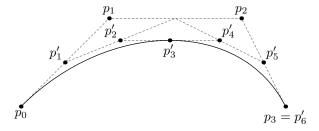


Figure 3.5: You can see that  $p_3 = p_6'$ 

### 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. More information can be found about both on the CUS site or feel free to reach out to data@reed.edu.

### 3.4 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. The Reed librarians have created Zotero documentation at http://libguides.reed.edu/citation/zotero. In addition, a tutorial is available from Middlebury College at http://sites.middlebury.edu/zoteromiddlebury/.

<sup>&</sup>lt;sup>1</sup>footnote text

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: (Molina & Borkovec, 1994). 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 our CUS site (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. Typing in source after source is mind-numbing enough; do you really want to do it for hours on end in late April? Think of it as procrastination.
- 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.
- You can add a Reed Thesis citation<sup>3</sup> option. The best way to do this is to use the phdthesis type of citation, and use the optional "type" field to enter "Reed thesis" or "Undergraduate thesis."

<sup>&</sup>lt;sup>2</sup>Reed College (2007)

 $<sup>^{3}</sup>$ Noble (2002)

## 3.5 Anything else?

If you'd like to see examples of other things in this template, please contact the Data @ Reed team (email data@reed.edu) with your suggestions. We love to see people using R Markdown for their theses, and are happy to help.

# Chapter 4

# Actinobacteria EvoMining Results

Actinobacteria is an ancient phylum {Referencia de luis}

### 4.1 Tables

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.

Table 4.1: Correlation of Inheritance Factors for Parents and Child

Factors	Correlation between Parents & Child
GenomeDB	1245
Families	65

We can also create a link to the table by doing the following: Table 5.1. If you go back to Loading and exploring data and look at the kable function code, you'll see that I added in a similar \\lambdabel to be able to reference that table later. (The extra backslash there is a way that Markdown interfaces with LaTeX.) We can create a reference to the max delays table: Table 1.1.

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### 4.2 Figures

Lets analize Phosphoribosyl\_isomerase\_3 family

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Figure 4.1: Reed logo

Here is a reference to the Reed logo: Figure 5.1. Note the use of the inline **R** code here. By default "figure" is specified as the type. For clarity, we could have also added the label and type to the parameter specifications and this would give us the same result: Figure 5.1.

4.2. Figures 23

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 . (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.

```
delay_airline <- 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")
ggsave("figure/delays.pdf", plot = delay_airline,
   height = 3, width = 6)
```



Figure 4.2: Mean Delays by Airline

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

Next, we will explore the use of the scale parameter which can be used to shrink or expand an image. Here we use the mathematical graph stored in the "subdivision.pdf" file. Note that we didn't specify the caption = or label = here, but we could have.

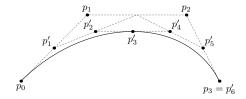


Figure 4.3: Subdiv. graph

Here is a reference to this image: Figure 5.3. (Move this around throughout the document as you wish.)

#### More Figure Stuff

Lastly, we will explore how to rotate figures using the angle parameter.

```
label("figure/subdivision.pdf",
    "A Larger Figure, Flipped Upside Down",
    scale = 1.5,
    angle = 180,
    label = "subd2")
```

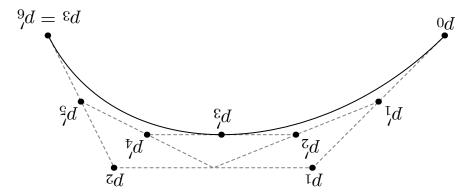


Figure 4.4: A Larger Figure, Flipped Upside Down

As another example, here is a reference to this figure: Figure 5.4.

#### **Common Modifications**

The following figure features the more popular changes thesis students want to make to their figures. We can add math to the caption that displays below the picture, specify the size of our caption to display below the figure (list of sizes available at this link), and also specify that a different caption alt.cap be what appears in the Table of Figures for this figure.

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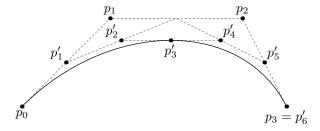


Figure 4.5: You can see that  $p_3 = p_6'$ 

### 4.3 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. More information can be found about both on the CUS site or feel free to reach out to data@reed.edu.

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For more information about BibTeX and bibliographies, see our CUS site (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.

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### Tips for Bibliographies

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- Bibliographies made using BibTeX (whether manually or using a manager) accept LaTeX markup, so you can italicize and add symbols as necessary.
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## 4.5 Anything else?

If you'd like to see examples of other things in this template, please contact the Data @ Reed team (email data@reed.edu) with your suggestions. We love to see people using R Markdown for their theses, and are happy to help.

# Chapter 5

# Cyanobacteria EvoMining Results

Cyanobacteria is phylum {Referencia de luis}

## 5.1 Tables

Table 5.1: Families on Cyanobacteria

Factors	Correlation between Parents & Child
GenomeDB	1245
Families	65

```
library(ggplot2)
#setwd("/home/nelly/GIT/phd/Thesis/tesis/chap5_files")
CyanosCentral <- read.table("chapter5/CyanosCentral", header=TRUE, sep="\t")
CyanosHeatPlot <- read.table("chapter5/CyanosHeatPlot", header=TRUE, sep="\t")
CyanosNp <- read.table("chapter5/CyanosNp", header=TRUE, sep="\t")
Warning in scan(file = file, what = what, sep = sep, quote = quote, dec = dec, : EOF within quoted string

CyanosSMASH <- read.table("chapter5/CyanosSMASH", header=TRUE, sep="\t")
CyanosTaxa <- read.table("chapter5/CyanosTaxa", header=TRUE, sep="\t")</pre>
```

### 5.2 Cyanobacterias AntiSMASH

## 5.3 Figures

Lets analize Phosphoribosyl\_isomerase\_3 family

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 reed.jpg in our main directory. We then give it the caption of "Reed logo", the label of "reed", and specify that this is a figure. Note again the use of the results = "asis" specification to automatically include and compile the LATEX code.

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5.3. Figures 31



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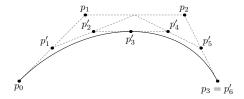


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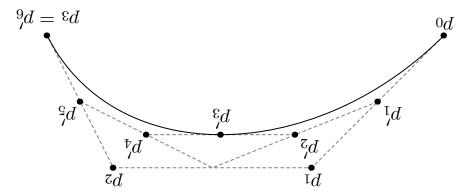


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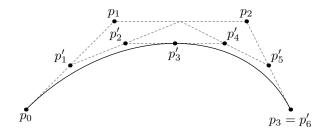


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# Conclusion

If we don't want Conclusion to have a chapter number next to it, we can add the {.unnumbered} attribute. This has an unintended consequence of the sections being labeled as 3.6 for example though instead of 4.1. The LATEX commands immediately following the Conclusion declaration get things back on track.

#### 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 readibility and/or setup.

#### In the main Rmd file:

```
# This chunk ensures that the reedtemplates package is
# installed and loaded. This reedtemplates 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(reedtemplates)){
   library(devtools)
   devtools::install_github("ismayc/reedtemplates")
}
library(reedtemplates)
```

#### In:

```
# This chunk ensures that the reedtemplates package is
# installed and loaded. This reedtemplates package includes
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# 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(reedtemplates)){
   library(devtools)
   devtools::install_github("ismayc/reedtemplates")
   }
library(reedtemplates)
flights <- read.csv("data/flights.csv")</pre>
```

Appendix B

The Second Appendix, for Fun

## References

- Angel, E. (2000). *Interactive computer graphics : A top-down approach with opengl.* Boston, MA: Addison Wesley Longman.
- Angel, E. (2001a). Batch-file computer graphics: A bottom-up approach with quicktime. Boston, MA: Wesley Addison Longman.
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