

# Enzymatic Promiscuity

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A Thesis  
Presented to  
The Division of Mathematics and Natural Sciences  
Reed College

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In Partial Fulfillment  
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Bachelor of Arts

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Approved for the Division  
(Mathematics)

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# 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 L<sup>A</sup>T<sub>E</sub>X template, but hopefully it will provide a nicer interface for those that have never used T<sub>E</sub>X or L<sup>A</sup>T<sub>E</sub>X 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 L<sup>A</sup>T<sub>E</sub>X 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 **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 L<sup>A</sup>T<sub>E</sub>X. Packages have been written in **R** to work directly with L<sup>A</sup>T<sub>E</sub>X to produce nicely formatting tables and paragraphs. In addition to creating a user friendly interface to L<sup>A</sup>T<sub>E</sub>X, *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

## 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, ArchaeaTree, CyanobacteriaTree.

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 **R** code chunks within the document. You can embed an **R** code chunk like this (`cars` is a built-in **R** dataset):

```
summary(cars)
```

speed	dist
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

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:

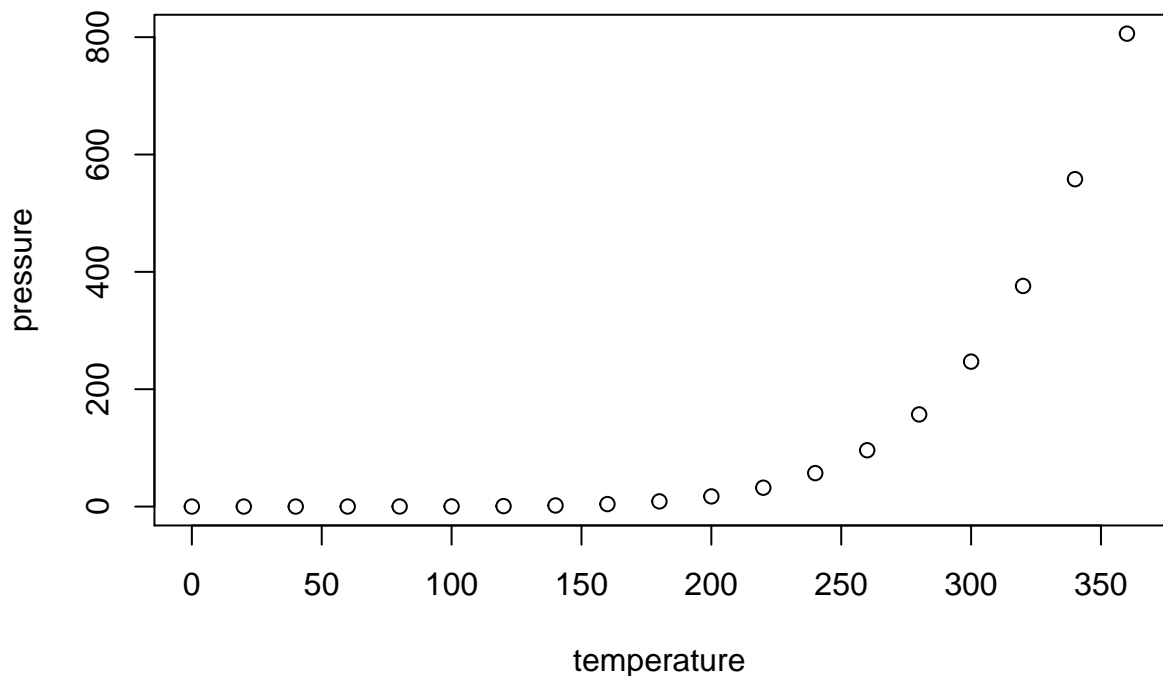
The standard deviation is less than 6.

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 **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")
```

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"
[5] "arr_time"   "arr_delay"  "carrier"    "tailnum"
[9] "flight"     "dest"       "air_time"   "distance"
[13] "hour"       "minute"     "carrier_name" "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)
```

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  $\text{\LaTeX}$  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  $\text{\LaTeX}$ . 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 `\label` later.) 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.

```
kable(max_delays, col.names = c("Airline", "Max Arrival Delay"),
      caption = "Maximum Delays by Airline \\label{tab:max_delay}",
      caption.short = "Max Delays by Airline")
```

Table 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

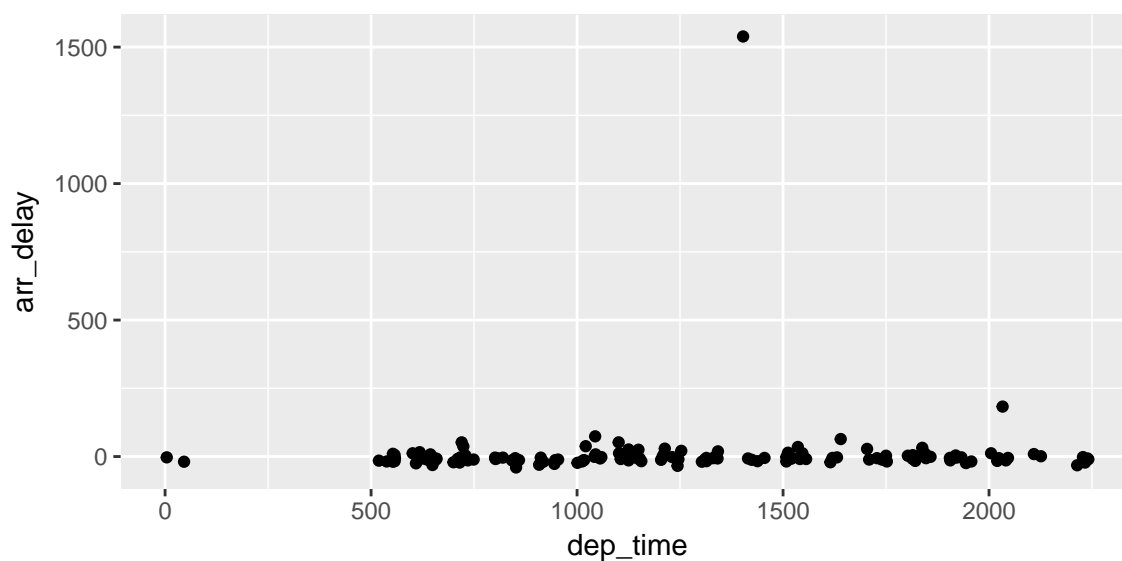
We can further look into the properties of the largest value here for American Airlines Inc. To do so, we can isolate the row corresponding to the arrival delay of 1539 minutes for American in our original `flights` dataset.

```
flights %>% dplyr::filter(arr_delay == 1539,
                          carrier_name == "American Airlines Inc.") %>%
  dplyr::select(-c(month, day, carrier, dest_name, hour,
                   minute, carrier_name, arr_delay))
```

```
  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

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 L<sup>A</sup>T<sub>E</sub>X 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 L<sup>A</sup>T<sub>E</sub>X 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.

Angstrom: Å

Bullet: CuCl • 7H<sub>2</sub>O

Double Dagger: ‡

Delta: Δ

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

Resonance Arrows:  $\leftrightarrow$

Reversible Reaction Arrows:  $\rightleftharpoons$  or  $\xrightleftharpoons{\text{solution}}$  (the latter requires the `chemarr` L<sup>A</sup>T<sub>E</sub>X 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 L<sup>A</sup>T<sub>E</sub>X will place the reaction where it fits and you can have a figure caption. You'll see further description of this `\Rlabel` function in . (Note the use of the double backslash here as well as the `echo = FALSE` which hides the code from the output.)

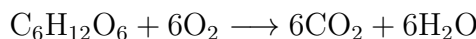
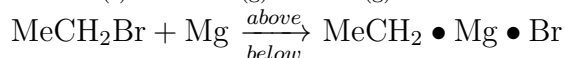


Figure 2.1: Combustion of glucose

### 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 L<sup>A</sup>T<sub>E</sub>X 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.

```
ArchaeasCentral <- read.table("chapter3/ArchaeasCentral", header=TRUE, sep="\t")
ArchaeasHeatPlot <- read.table("chapter3/ArchaeasHeatPlot", header=TRUE, sep="\t")
ArchaeasNp <- read.table("chapter3/ArchaeasNp", header=TRUE, sep="\t")
ArchaeasSMASH <- read.table("chapter3/ArchaeasSMASH", header=TRUE, sep="\t")
ArchaeasTaxa <- read.table("chapter3/ArchaeasTaxa", header=TRUE, sep="\t")
```

## 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.

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
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 `\\label` to be able to reference that table later. (The extra backslash there is a way that *Markdown* interfaces with *L<sup>A</sup>T<sub>E</sub>X*.) 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 *L<sup>A</sup>T<sub>E</sub>X* `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 L<sup>A</sup>T<sub>E</sub>X 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 L<sup>A</sup>T<sub>E</sub>X code.

```
label(path = "figure/reed.jpg", caption = "Reed logo",  
      label = "reed", type = "figure")
```



Figure 3.1: Reed logo

Here is a reference to the Reed logo: Figure 4.1. 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 4.1.



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)
```

```
label(path = "figure/delays.pdf",  
  caption = "Mean Delays by Airline",  
  label = "delays", type = "figure")
```

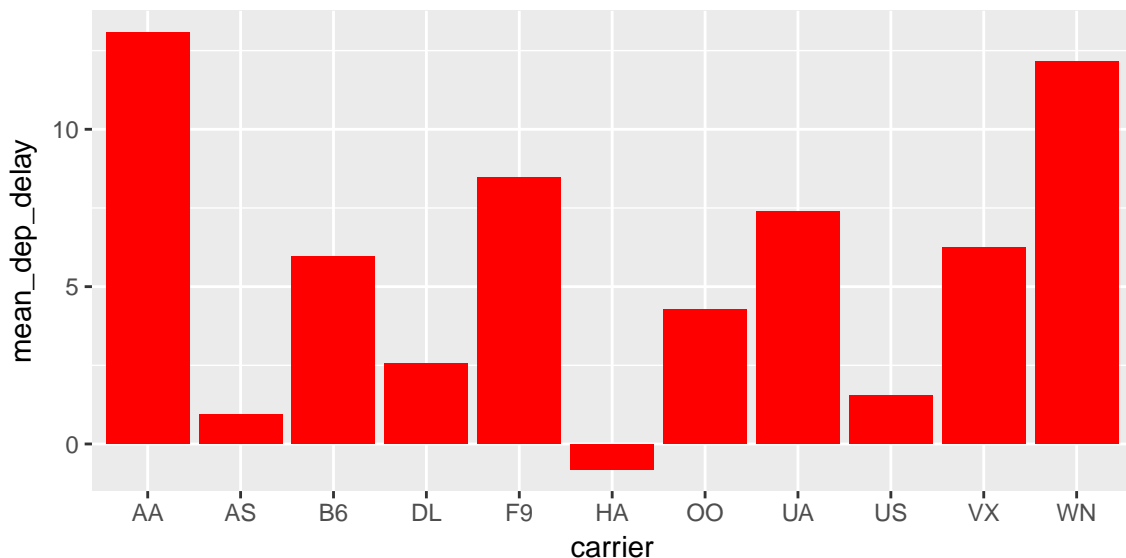


Figure 3.2: Mean Delays by Airline

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.

```
label("figure/subdivision.pdf", "Subdiv. graph", "subd",
      scale = 0.75)
```

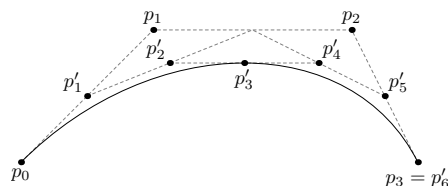


Figure 3.3: Subdiv. graph

Here is a reference to this image: Figure 4.3. (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")
```

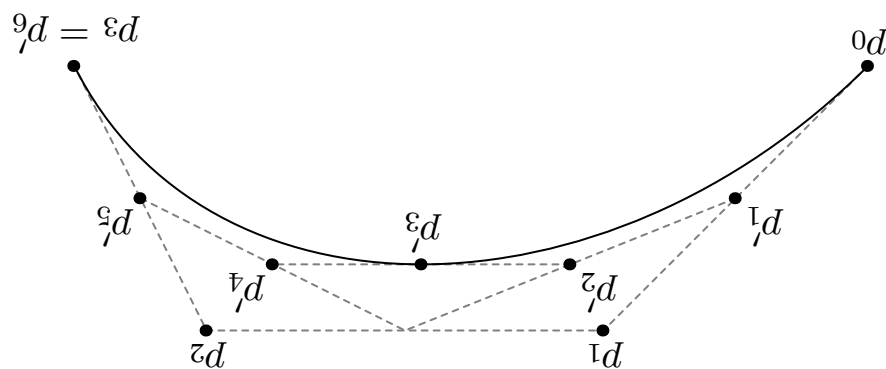


Figure 3.4: A Larger Figure, Flipped Upside Down

As another example, here is a reference to this figure: Figure 4.4.

### 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  $\text{\LaTeX}$  code. Please email us at `data@reed.edu` if you need assistance.

```
label("figure/subdivision.pdf",
      caption = "Subdivision of arc segments",
      alt.cap = "You can see that  $p_3 = p_6^{\prime}$ ",
      cap.size = "footnotesize",
      label = "subd3")
```

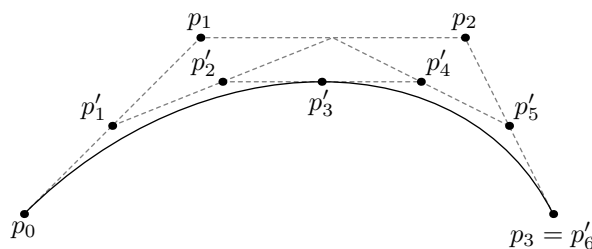


Figure 3.5: You can see that  $p_3 = p_6'$

## 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

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---

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- 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 L<sup>A</sup>T<sub>E</sub>X 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>2</sup>Reed College (2007)

<sup>3</sup>Noble (2002)

## 3.5 Anything else?

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```
ActinoCentral <- read.table("chapter4/ActinoCentral", header=TRUE, sep="\t")
ActinoHeatPlot <- read.table("chapter4/ActinoHeatPlot", header=TRUE, sep="\t")
ActinoNp <- read.table("chapter4/ActinoNp", header=TRUE, sep="\t")
ActinosSmashResults <- read.table("chapter4/ActinosSmashResults", header=TRUE, sep="\t")
ActinoTaxa <- read.table("chapter4/ActinoTaxa", header=TRUE, sep="\t")
```



# 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 `\\label` to be able to reference that table later. (The extra backslash there is a way that *Markdown* interfaces with *L<sup>A</sup>T<sub>E</sub>X*.) 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 *L<sup>A</sup>T<sub>E</sub>X* **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.

## 4.2 Figures

Lets analyze 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 L<sup>A</sup>T<sub>E</sub>X 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 L<sup>A</sup>T<sub>E</sub>X code.

```
label(path = "figure/reed.jpg", caption = "Reed logo",  
      label = "reed", type = "figure")
```



Figure 4.1: Reed logo

Here is a reference to the Reed logo: Figure 4.1. 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 4.1.



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)
```

```
label(path = "figure/delays.pdf",  
  caption = "Mean Delays by Airline",  
  label = "delays", type = "figure")
```

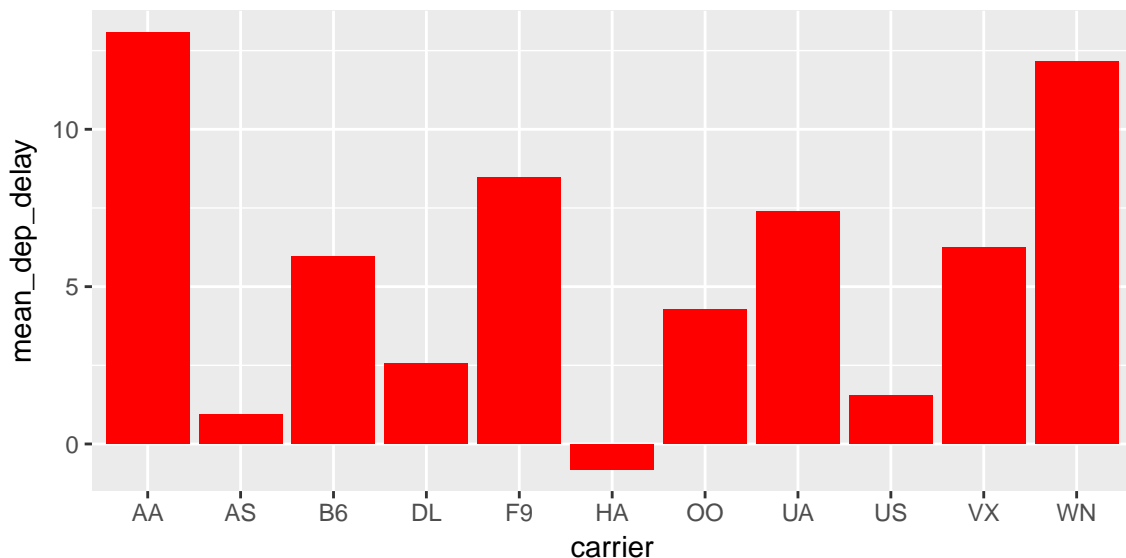


Figure 4.2: Mean Delays by Airline

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.

```
label("figure/subdivision.pdf", "Subdiv. graph", "subd",
      scale = 0.75)
```

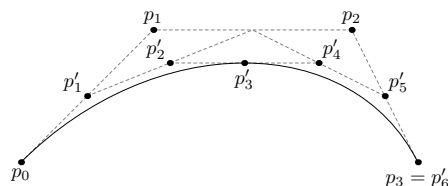


Figure 4.3: Subdiv. graph

Here is a reference to this image: Figure 4.3. (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")
```

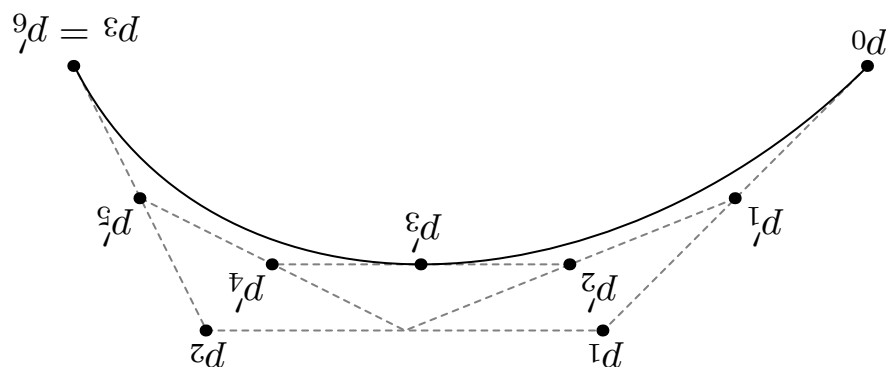


Figure 4.4: A Larger Figure, Flipped Upside Down

As another example, here is a reference to this figure: Figure 4.4.

## 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  $\text{\LaTeX}$  code. Please email us at `data@reed.edu` if you need assistance.

```
label("figure/subdivision.pdf",
      caption = "Subdivision of arc segments",
      alt.cap = "You can see that  $p_3 = p_6^{\prime}$ ",
      cap.size = "footnotesize",
      label = "subd3")
```

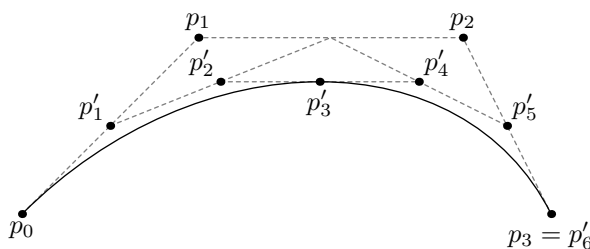


Figure 4.5: You can see that  $p_3 = p_6'$

## 4.3 Footnotes and Endnotes

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- Bibliographies made using BibTeX (whether manually or using a manager) accept L<sup>A</sup>T<sub>E</sub>X 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.
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---

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## 4.5 Anything else?

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# Chapter 5

## Cyanobacteria EvoMining Results

Cyanobacteria phylum {Referencia de luis}

### 5.1 Tables

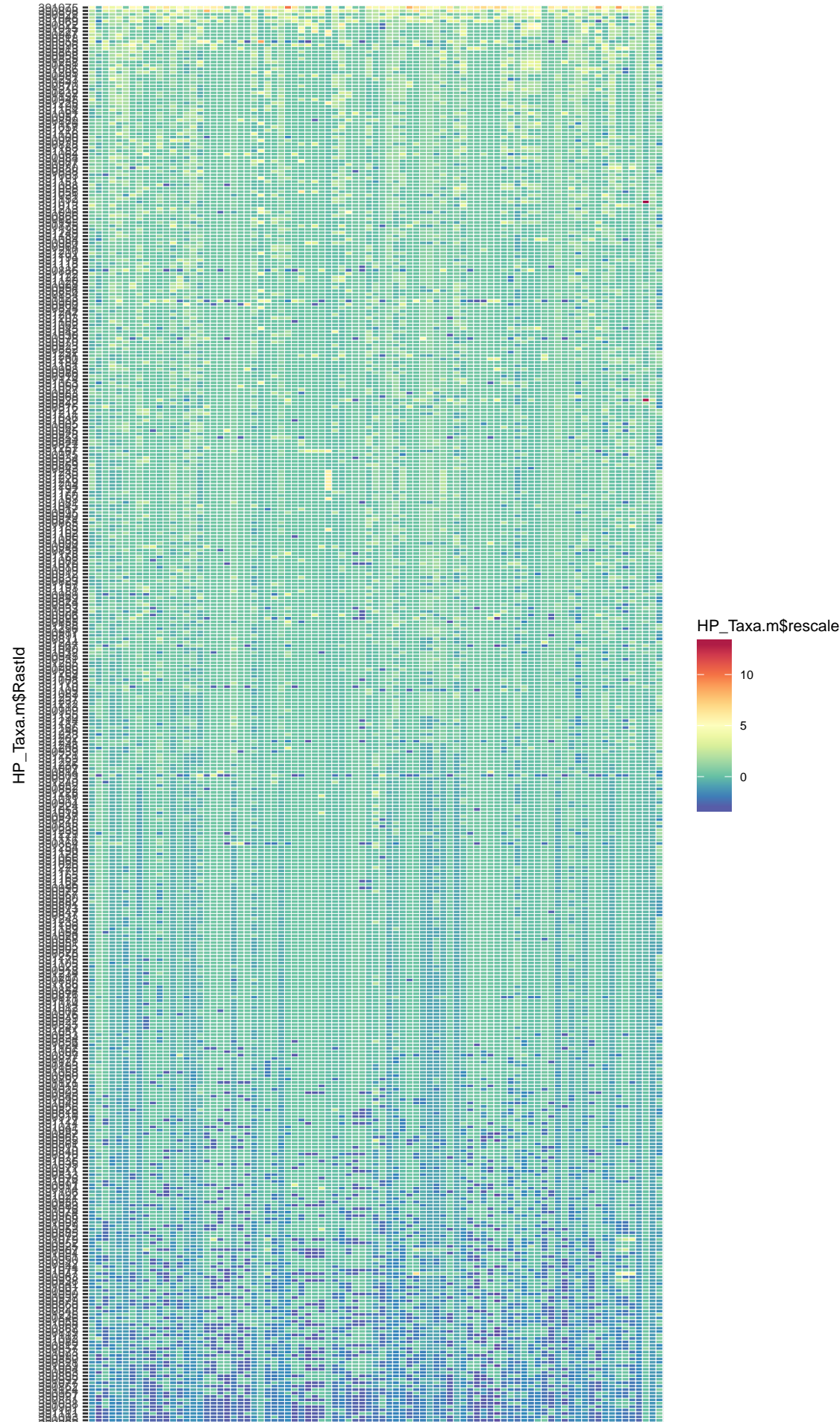
Table 5.1: Families on Cyanobacteria

Factors	Correlation between Parents & Child
GenomeDB	1245
Families	65

## 5.2 Central pathway expansions

Here is a reference to the HeatPlot: Figure 5.1.





Natural product recruitments

```
EXP_SMASH<-merge(CyanosHeatPlot,CyanosSMASH,by.x="RastId",by.y="RastIds")

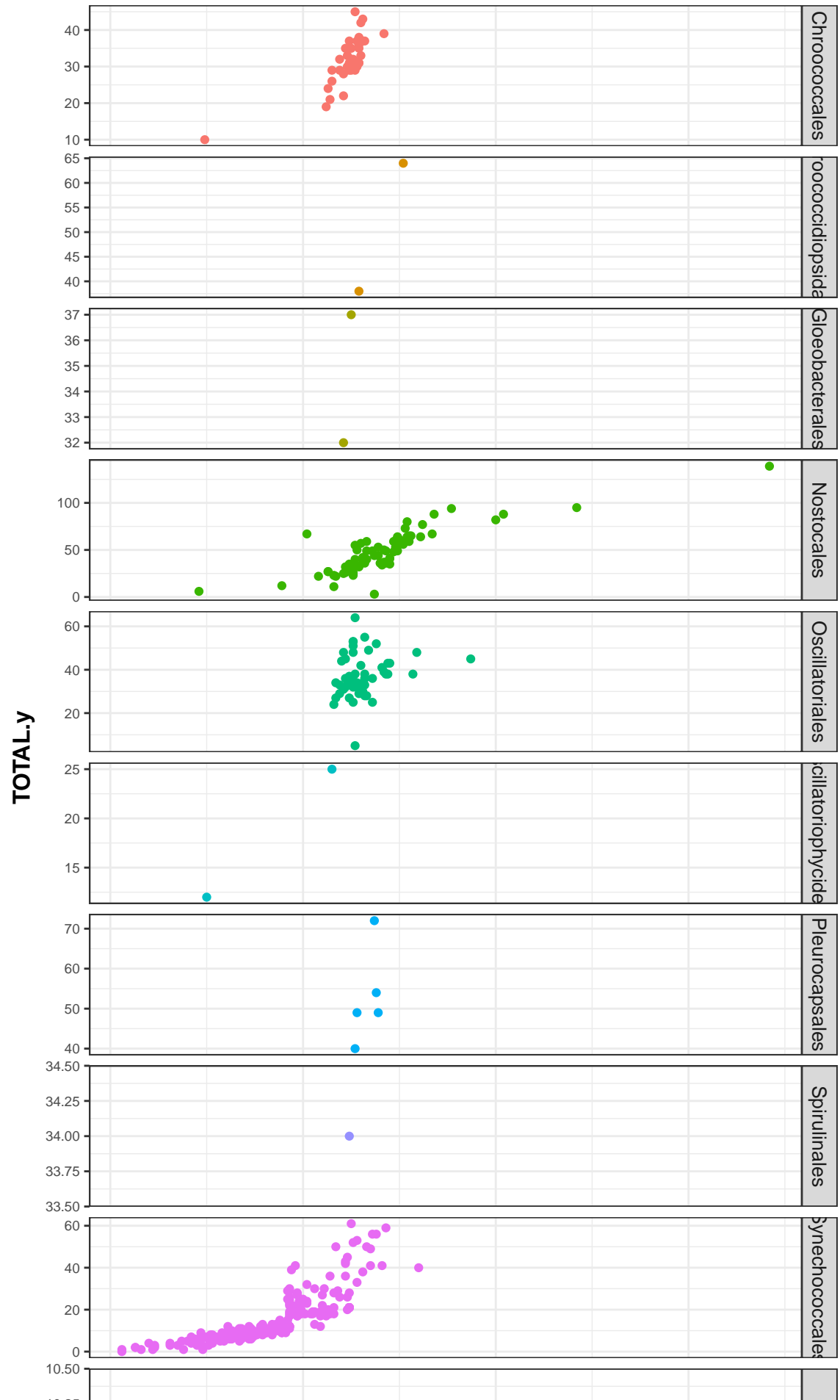
EXP_SMASH2<-merge(CyanosTaxa, EXP_SMASH, by.x="RastId",by.y="RastId")

#qplot(Total.x, Total.y, data = EXP_SMASH, colour=Order)+theme_bw()+
#
sn<-qplot(TOTAL.x, TOTAL.y, data = EXP_SMASH2,colour=Order)+theme_bw()+facet_grid(EXP_S
  theme(legend.position    ="bottom",plot.title = element_text(size = 14, face = "b
    text = element_text(size = 12),
    axis.title = element_text(face="bold"),
    axis.text.x=element_text(size = 12),
    axis.text.y=element_text(size = 7))
ggsave("chapter5/SMASHvsExpansionsbyOrder.pdf", plot = sn,height = 12, width = 6)

## Looking for color modifications
#sn + scale_color_brewer(palette="Dark2(100)")
#n + scale_color_brewer(palette=hm.palette(10))
## sn+ scale_color_hue(l=40, c=35)
```

uuuf

Here is a reference to the HeatPlot: Figure 5.1.

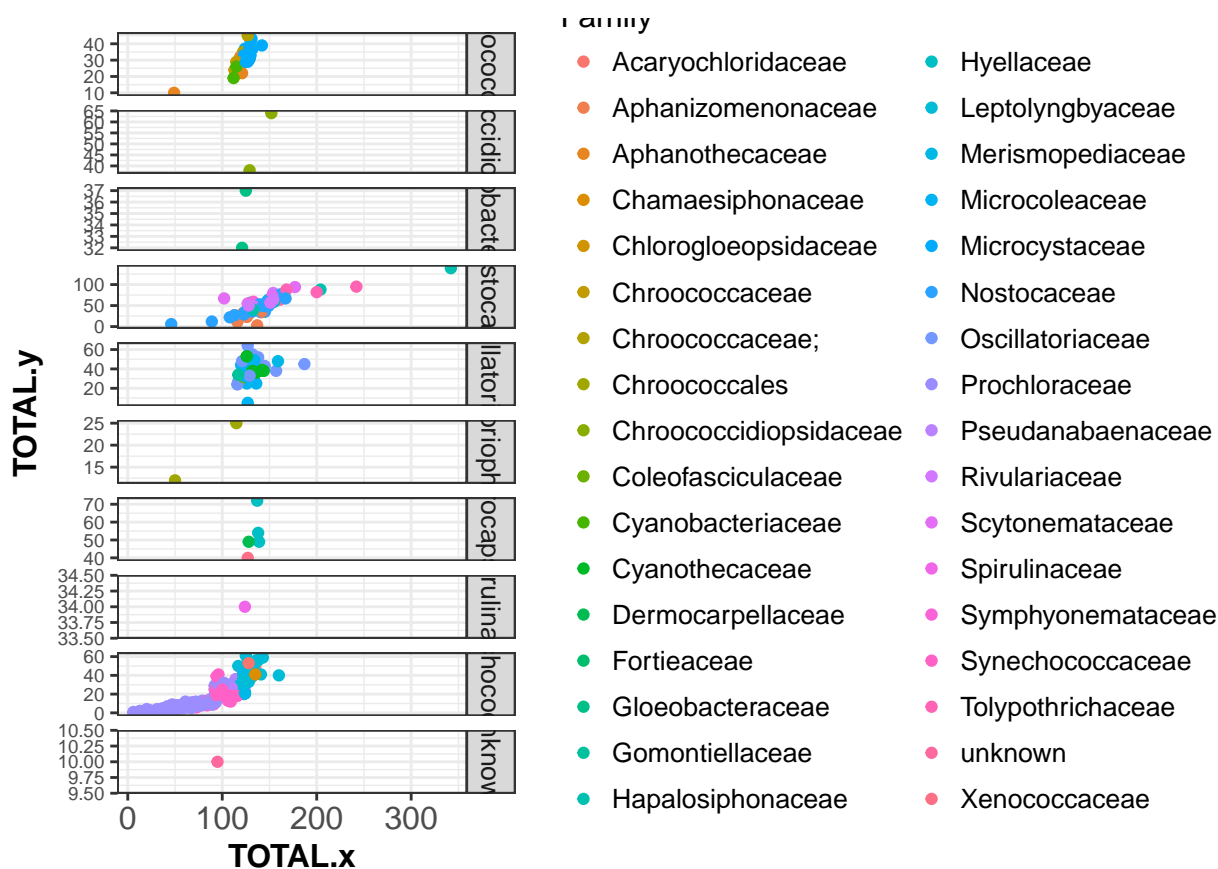


Aqui una correlacion entre en talla de genoma y los productos de antismash Aqui una correlacion entre talla de genoma y expansiones

```
EXP_SMASH<-merge(CyanosHeatPlot,CyanosSMASH,by.x="RastId",by.y="RastIds")
```

```
EXP_SMASH2<-merge(CyanosTaxa, EXP_SMASH, by.x="RastId",by.y="RastId")
```

```
qplot(TOTAL.x, TOTAL.y, data = EXP_SMASH2,colour=Family)+theme_bw()+facet_grid(EXP_SMASH2~Family,
  theme( plot.title = element_text(size = 14, face = "bold"),
    text = element_text(size = 12),
    axis.title = element_text(face="bold"),
    axis.text.x=element_text(size = 12),
    axis.text.y=element_text(size = 7))
```



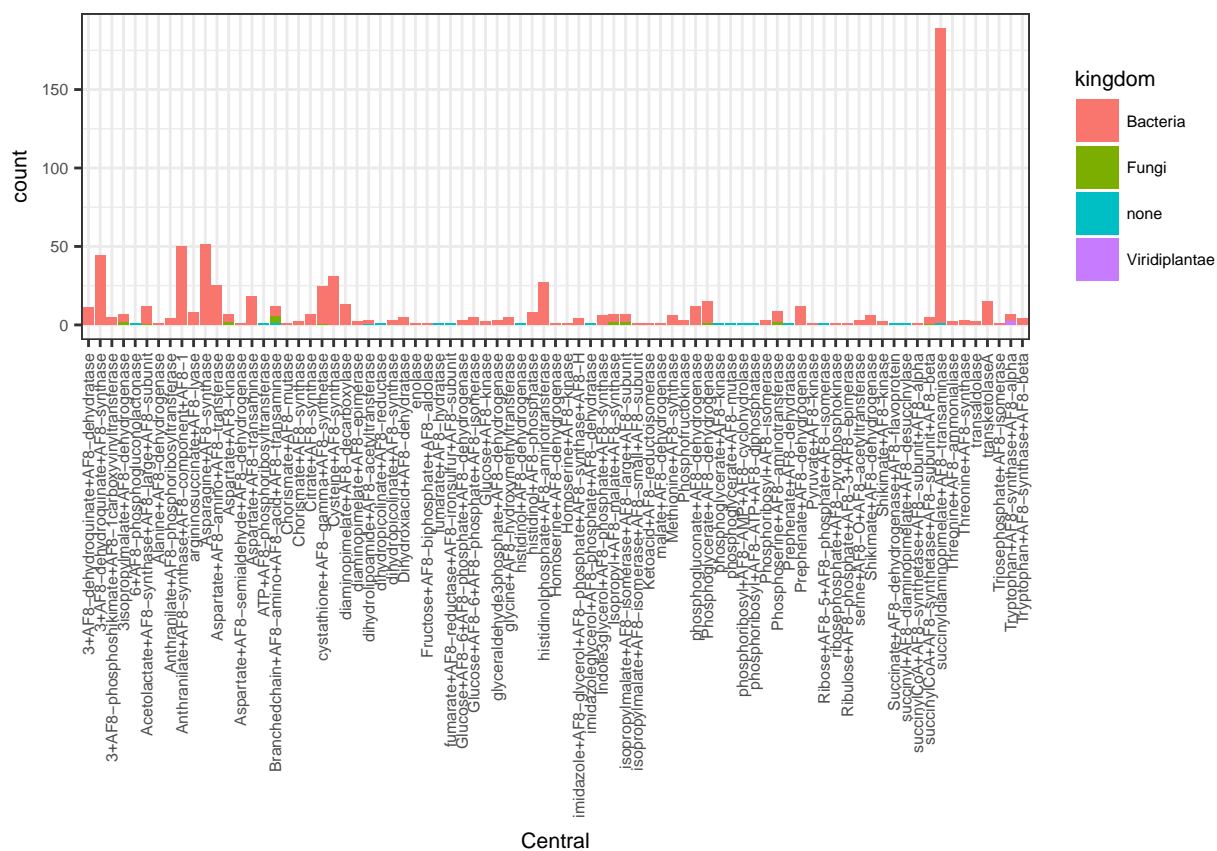
```
#facet_grid(EXP_SMASH$Order~., scales="free")+
```

### 5.3 Natural products recruitments

We can see natural products origin by kingdom Natural products recruited by metabolic family, colored by phylogenetic origin.

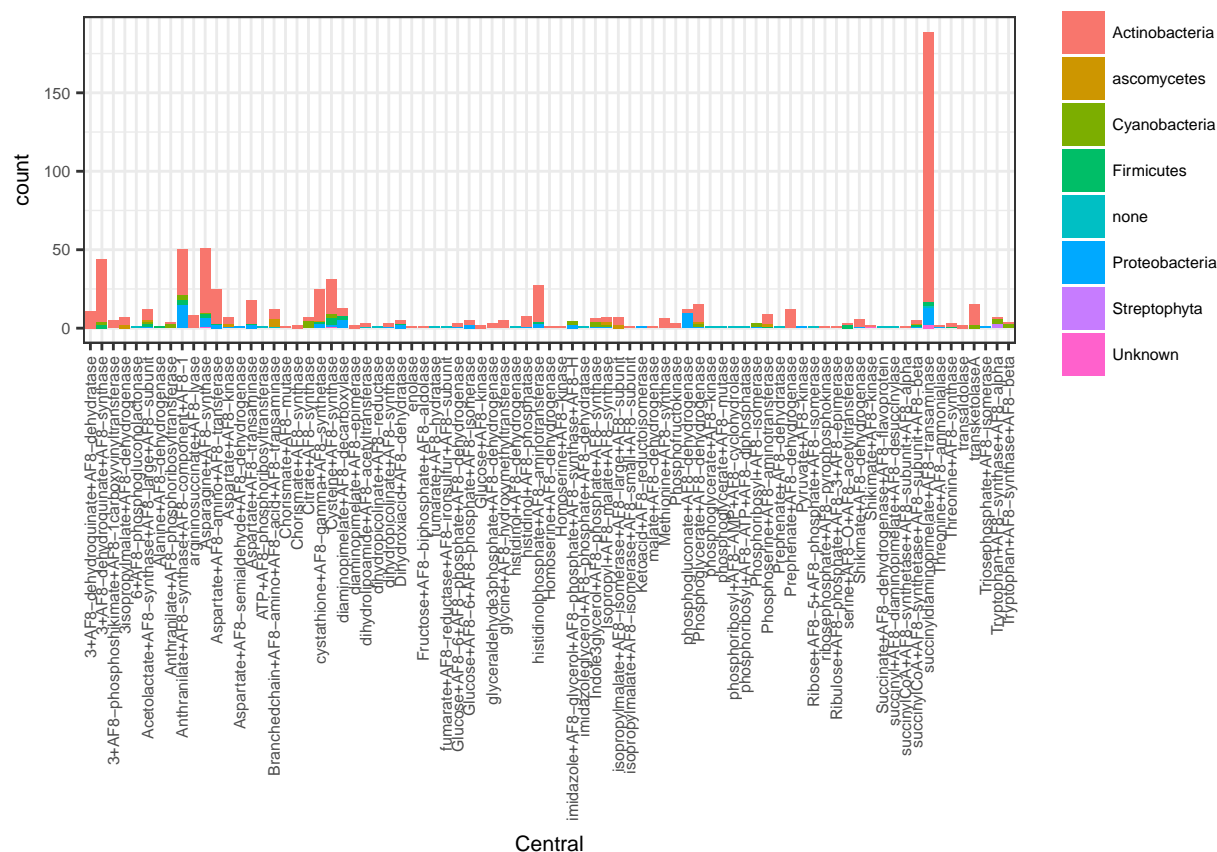
```
qplot(x=Central, data=CyanosNp, geom="bar", fill=kingdom, position="stack")+theme_
```

Warning: `position` is deprecated



```
qplot(x=Central, data=CyanosNp, geom="bar", fill=taxa, position="stack")+theme_bw()
```

Warning: `position` is deprecated



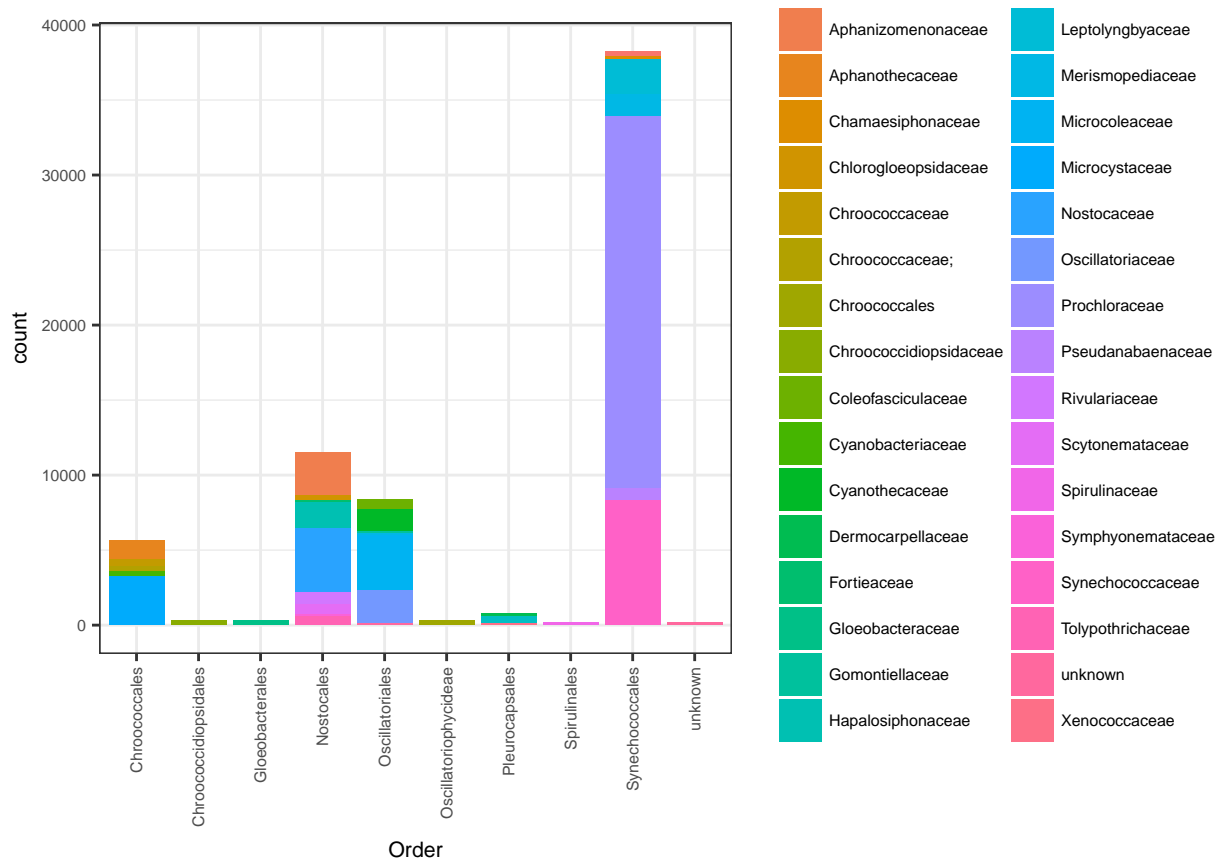
## 5.4 Cyanobacterias AntiSMASH

Phylogenetical diversity on Cyanobacterial dataset

```
## merge tables
m1 <- merge(CyanosTaxa, CyanosSMASH, by.x = "RastId", by.y = "RastIds")
m1.m <- melt(m1, id = c("RastId", "Name", "Phylum", "Class", "Order", "Family", "Contigs", "Si
m2.m <- subset(m1.m, value > 0)

qplot(x=Order, data=m1.m, geom="bar", fill=Family, position="stack")+theme_bw()+ theme(
```

Warning: `position` is deprecated



```
table(m1.m$Order>0,m1.m$Family>0)
```

Warning in Ops.factor(m1.m\$Order, 0): '>' not meaningful for factors

Warning in Ops.factor(m1.m\$Family, 0): '>' not meaningful for factors

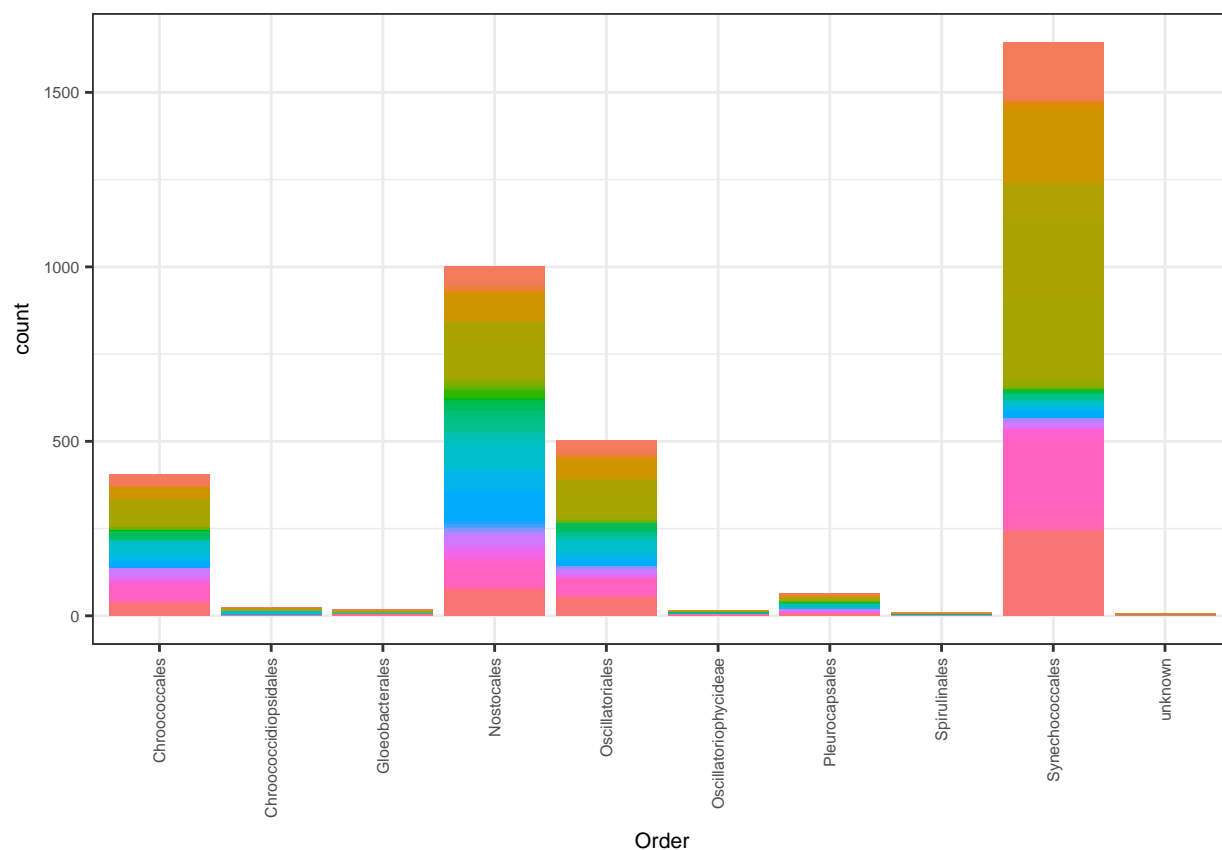
< table of extent 0 x 0 >

```
#qplot(x=clarity, data=diamonds, geom="bar", fill=cut, position="stack")
```

```
qplot(x=Order, data=m2.m, geom="bar", fill=variable, position="stack",colours = hm
```

Warning: `position` is deprecated

Warning: Ignoring unknown parameters: colours



```
table(m1.m$Order>0,m1.m$Family>0)
```

```
Warning in Ops.factor(m1.m$Order, 0): '>' not meaningful for factors
```

```
Warning in Ops.factor(m1.m$Family, 0): '>' not meaningful for factors
```

```
< table of extent 0 x 0 >
```

```
head(table(m2.mOrder,m2.mvariable))
```



```
#summary(CyanosHeatPlot.m)
#table(CyanosHeatPlot.m$scale >=0,Deltas$DeltaPRO>=0)
```

mm

```
expansion_plot<-ggplot(CyanosHeatPlot.m, aes(x=CyanosHeatPlot.m$variable, y=CyanosHeatPlot.m$rescale))
#ggplot(CyanosHeatPlot.m, aes(x=CyanosHeatPlot.m$variable, y=CyanosHeatPlot.m$rescale))
#+facet_grid(CyanosTaxa$class~.,scales="free")
#ggplot(CyanosHeatPlot.m, aes(x=CyanosHeatPlot.m$variable,y=CyanosHeatPlot.m$rescale))
# +facet_grid(CyanosHeatPlot.m$rescale~.,scales="free")

ggsave("chapter5/expansion_plot.pdf", plot = expansion_plot,height = 6, width = 7)
```

why figure is not here?

```
label(path = "chapter5/expansion_plot.pdf", caption = "Expansions Boxplot", label = "Cyan")
```

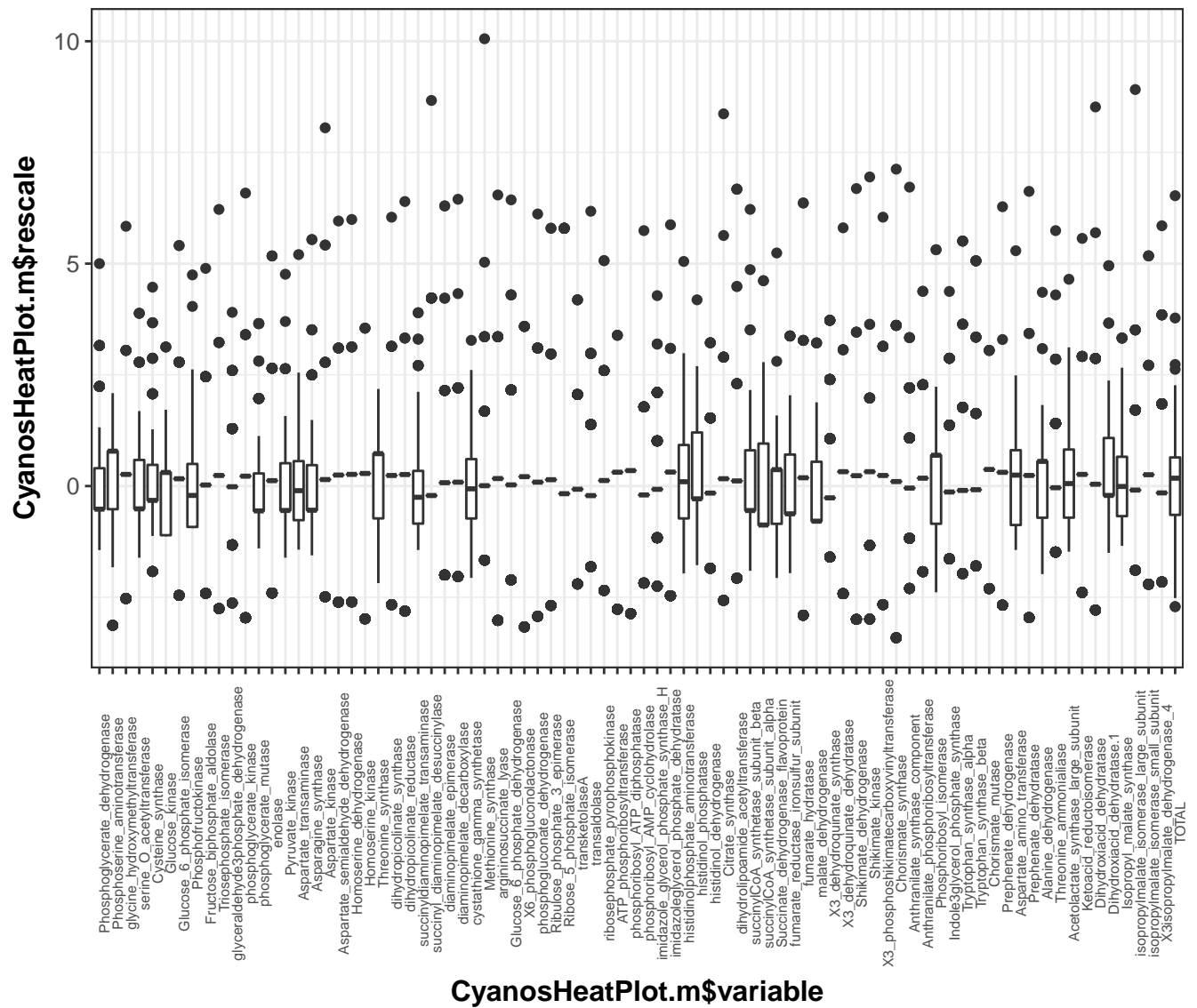


Figure 5.3: Expansions Boxplot

Here is a reference to the expansion boxplot: Figure 5.3.

## **5.5 Selected trees from EvoMining**

### **5.6 Lets analyze Phosphoribosyl\_isomerase\_3 family**

Figure from EvoMining

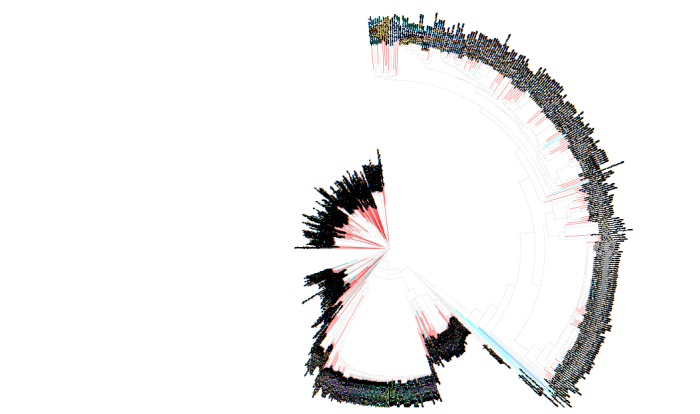


Figure 5.4: Phosphoribosyl isomerase EvoMiningtree

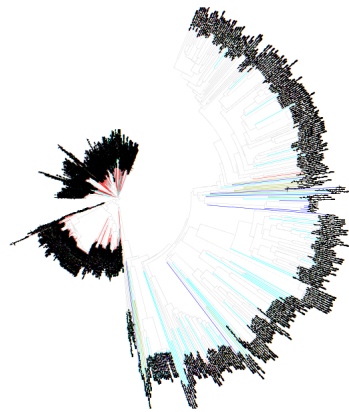


Figure 5.5: Phosphoribosyl isomerase EvoMiningtree

## 5.7 Footnotes and Endnotes

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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  $\text{\LaTeX}$  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 readability 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  
# 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(reedtemplates)){  
  library(devtools)  
  devtools::install_github("ismayc/reedtemplates")  
}  
library(reedtemplates)  
flights <- read.csv("data/flights.csv")
```

## Appendix B

The Second Appendix, for Fun



# References

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