

Evolution of Canidae

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Abstract

We can use markdown syntax to *italicize* or **bold** or ~~strikethrough~~ text. Since Markdown doesn't include small-caps functionality, we can still use L^AT_EXfunctionality to WRITE IN SMALL CAPS.

Introduction

However, there are some limits to markdown- for example, we can't resize the figure to make it larger. We can always turn to L^AT_EXcode to specify options for the image:



Figure 1: Here are different Canis Species

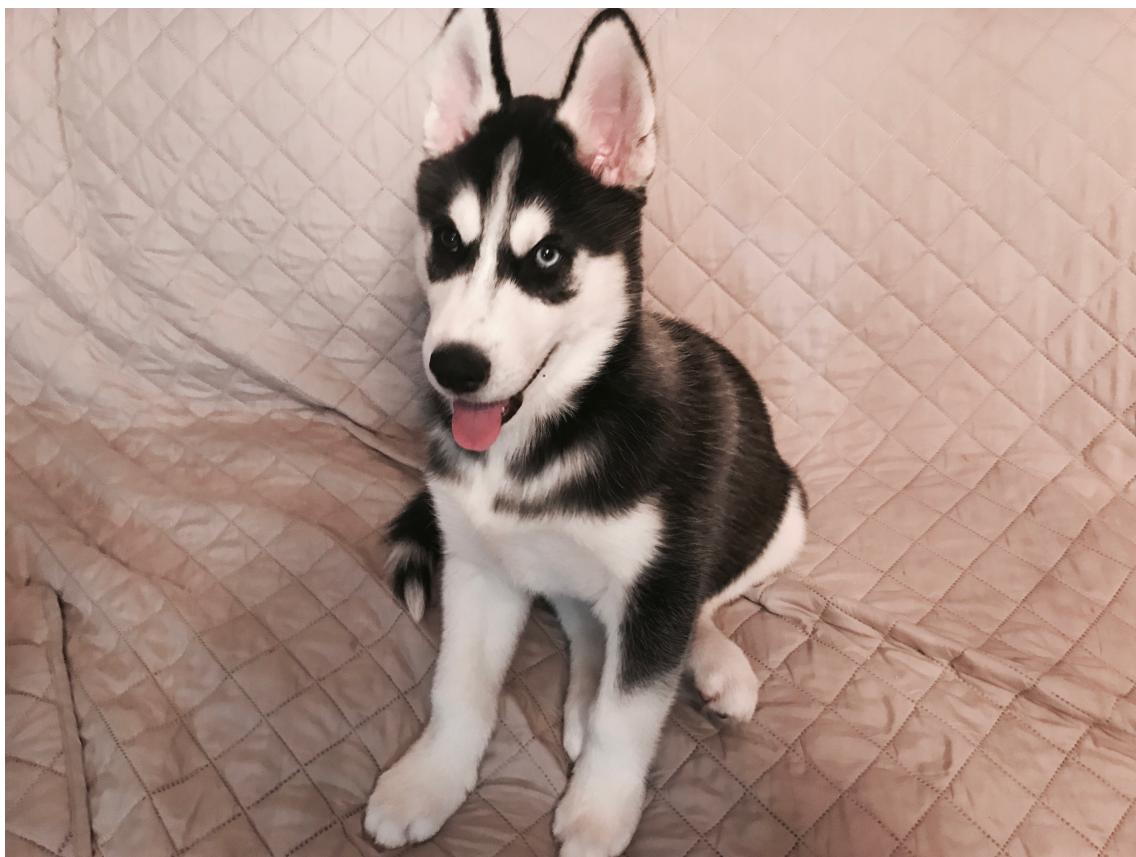


Figure 2: Here are different Canis Species

Methods

Figure 1 - Map: Fossil Records Canidae

```
library(ggplot2)
canis_lnglat <- read.csv("~/Desktop/eeb-177/eeb-174-final-project/formatted-Canis_Occurrence.csv",
  header = F, as.is = T) #grab the .csv data
colnames(canis_lnglat) <- c("species", "accepted_rank",
  "max_ma", "min_ma", "lng", "lat")
# what the data columns are define what
# is in the data
head(canis_lnglat)

# first of all we needed to import a
# world map
library(ggplot2)
library(maps)

world_map <- map_data("world")

# make a base plot with ggplot2
p <- ggplot() + coord_fixed(ratio = 1) +
  xlab("") + ylab("")

# Add map to base plot
base_world_version1 <- p + geom_polygon(data = world_map,
  aes(x = long, y = lat, group = group),
  colour = "green ", fill = "green")

# overlay lng and lat on base_map
map_data1 <- base_world_version1 + geom_point(data = canis_lnglat,
  aes(x = lng, y = lat), colour = "Red",
  pch = 2, size = 0.1, alpha = I(1)) +
  labs(title = "Map: Fossil Records Canidae",
    x = "Longitude", y = "Latitude") +
  theme(plot.title = element_text(hjust = 0.5,
    size = 20, face = "bold"), axis.title = element_text(size = 12))

# INSERT MAP

map_data1
```

Figure 2: Number of Species

```
library(dplyr)
library(ggplot2)

## Assuming the data is in the file 'Types.csv'
canis_dat <- read.csv("~/Desktop/eeb-177/eeb-174-final-project/Canis_Occurrences_725_head"

canis_dat_summary <-
  canis_dat %>% # Pipe df into group_by
  group_by(accepted_name) %>% # grouping by 'type' column
  summarise(name_count = n()) # calculate the name count for each group
## 'canis_dat_summary' now contains the summary data for each 'type'
canis_dat_summary

#### Two ways to plot using ggplot

## (1) Plot pre summarized data: 'canis_dat_summary'.
ggplot(canis_dat_summary, aes(accepted_name, name_count)) +
  geom_bar(stat = 'identity') + # stat='identity' is used for summarized data.
  #coord_flip(xlim = NULL)
  coord_flip(expand = TRUE)
  #coord_flip(ylim = NULL)
```

Figure 3: Early Interval of Canidae Species

```
library(dplyr)
library(ggplot2)

## Assuming the data is in the file 'Types.csv'
early_interval_dat <- read.csv("~/Desktop/eeb-177/eeb-174-final-project/Canis_Occurrences_725_head

early_interval_dat_summary <-
  canis_dat %>% # Pipe df into group_by
  group_by(early_interval) %>% # grouping by 'type' column
  summarise(name_count = n()) # calculate the name count for each group
## 'canis_dat_summary' now contains the summary data for each 'type'
# early_interval_dat_summary
```

```

### Two ways to plot using ggplot

## (1) Plot pre summarized data: 'canis_dat_summary'.
ggplot(early_interval_dat_summary, aes(early_interval, name_count )) +
  geom_bar(stat = 'identity') + # stat='identity' is used for summarized data.
  coord_flip(expand = TRUE)

```

Figure 4: Canidae Fossil Occurrences

```

library(forcats)
library(ggplot2)
canis <- read.csv("~/Desktop/eeb-177/eeb-174-final-project/formatted-Canis_Occurrences_ge
  header = F, as.is = T)  #grab the .csv data
names(canis) <- c("genus", "species", "minage",
  "maxage")  # what the data columns are

# plot the graph of y = species, x = ma
# ago , genus colored )
canis_occ <- ggplot(canis, aes(species, ymin = maxage,
  ymax = minage, colour = genus))
canis_occ <- canis_occ + geom_linerange(aes(ymin = minage,
  ymax = maxage)) + theme(legend.position = "none") +
  coord_flip() + theme(axis.text.y = element_text(size = 10)) +
  theme(axis.ticks.y = element_blank()) +
  scale_y_continuous(limits = c(0, 25),
    expand = c(0, 0), breaks = c(0, 5,
      10, 15, 20, 25)) + labs(title = "Canidae Fossil Occurrences",
  x = "Species", y = "Ma ago") + theme(plot.title = element_text(hjust = 0.5,
  size = 18, face = "bold"), axis.title = element_text(size = 20))

canis_occ

```

Figure 5: Canidae Diversity through Time

```

library(tidyr)
library(dplyr)
# creating a diversity charge
diversity <- canis %>% gather(key = type,
  value = age, minage, maxage) %>% mutate(count = ifelse(type ==

```

```

"maxage", 1, -1)) %>% group_by(age) %>%
summarise(count = sum(count)) %>% arrange(age,
count) %>% mutate(diversity = cumsum(count))

# plot diversity v age adding labels
canis_div <- ggplot(diversity, aes(x = age,
y = diversity)) + geom_step() + labs(title = "Canidae Diversity through Time") +
theme(plot.title = element_text(hjust = 0.5,
size = 18, face = "bold"), axis.title = element_text(size = 16))
canis_div

```

Figure 6: PyRate R script (in shell)

```

#!/bin/bash

# Script to run full pyrate pipeline on Canidae

# download the data
wget -O canis_occ.csv "https://paleobiodb.org/data1.2/occs/list.csv?base_name=Canidae&sh

# use the R script we had created to format the data into a pyrate-friendly file
# NOTE!
# if the output files from the R script already exist in the working directory,
# THIS STEP WILL NOT WORK!
# The existent files are NOT overwritten!
Rscript process_canis_data.R

# Verify that the data formatting worked, and redirect the output into a file called
# data_summary.txt so that it may be inspected later.
python ~/PyRate/PyRate.py canis_occ_PyRate.py -data_info > data_summary.txt

# And then, run PyRate!
python ~/PyRate/PyRate.py canis_occ_PyRate.py -n 1000000

```

Results

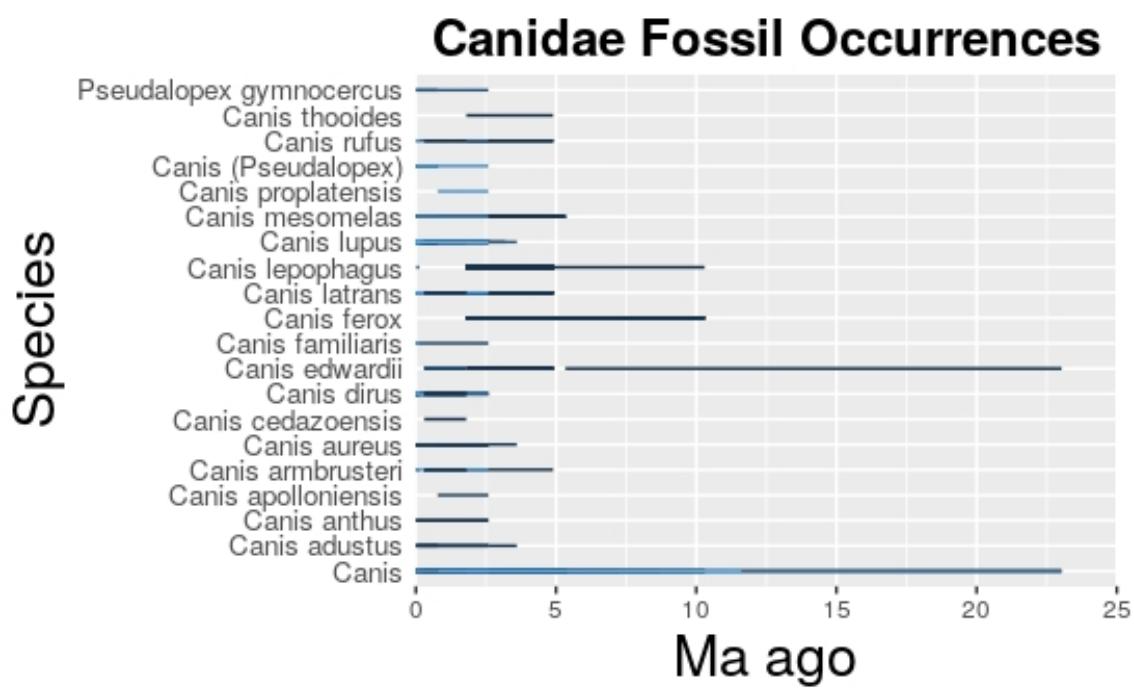


Figure 3: Map: Fossil Records Canidae

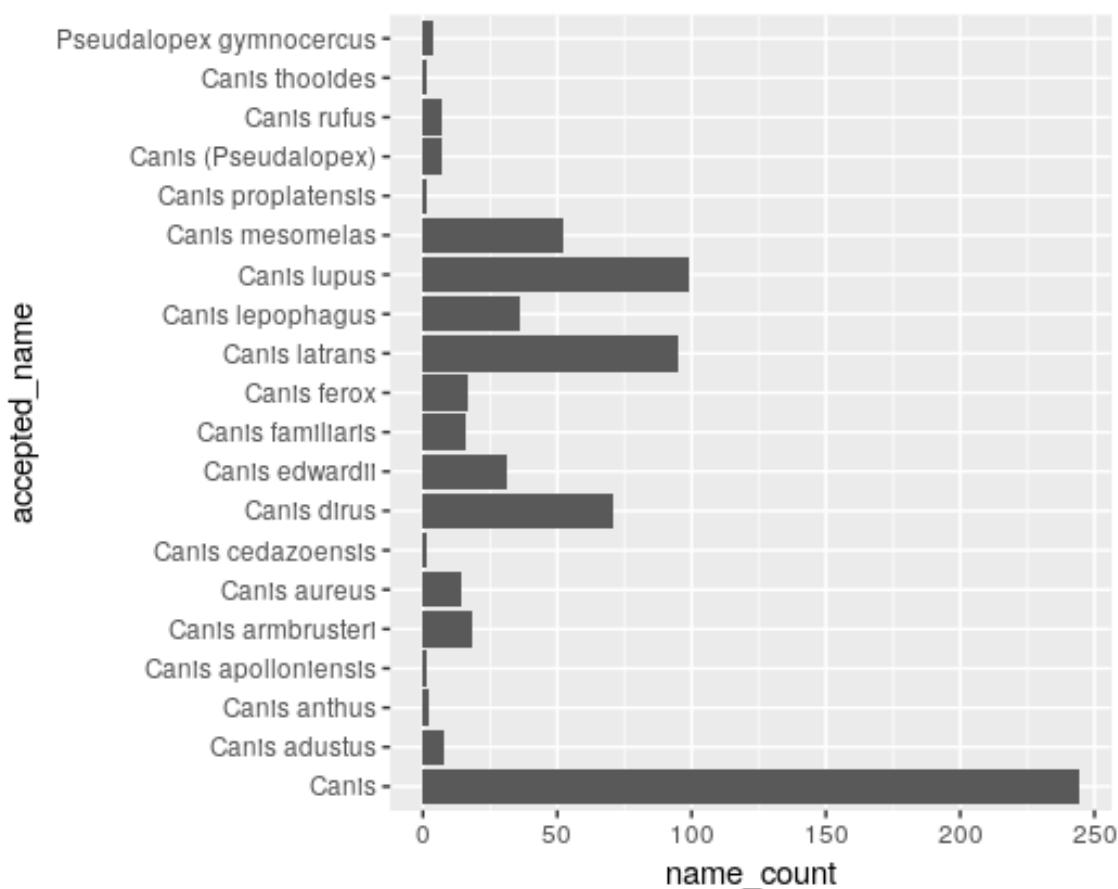


Figure 4: Number of Species

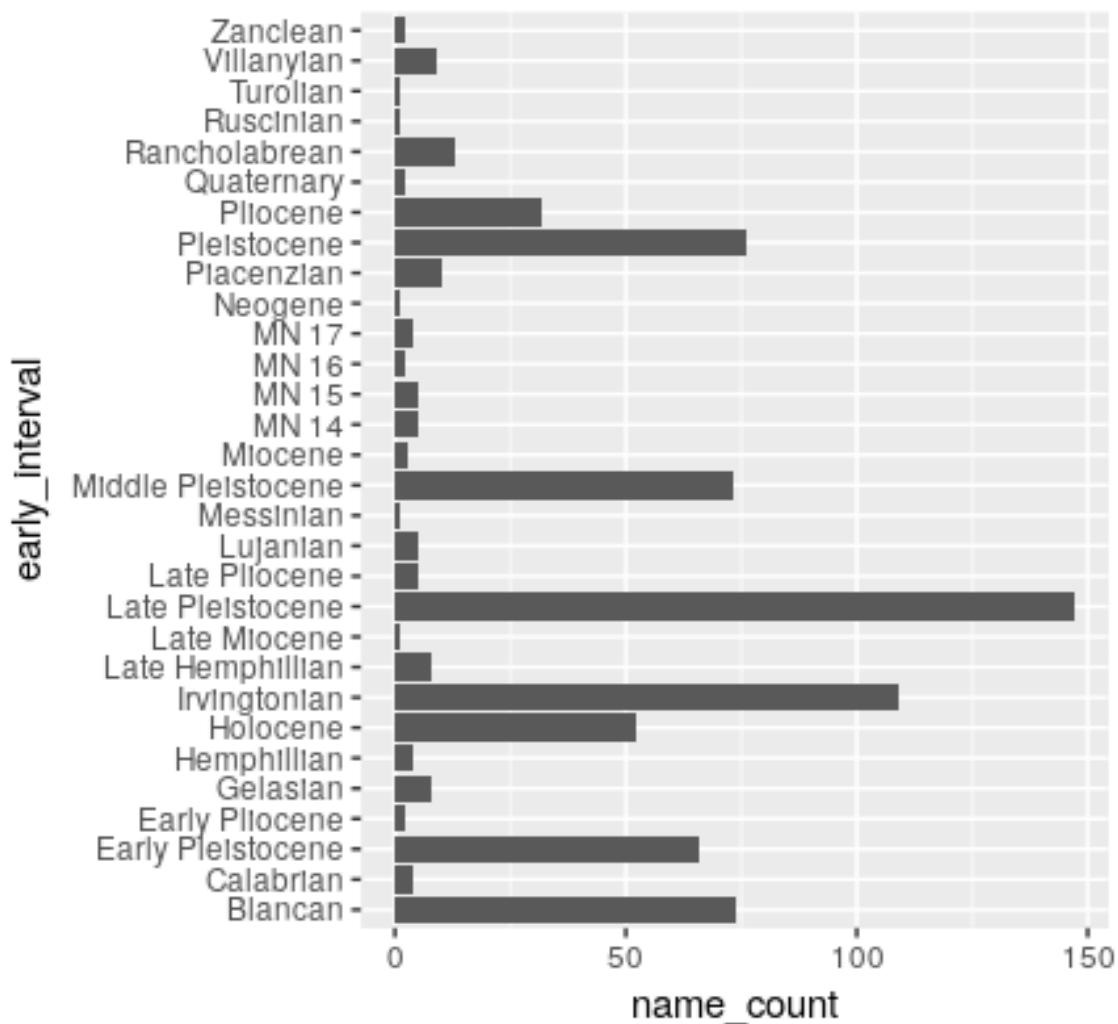


Figure 5: Early Interval of Canidae Species

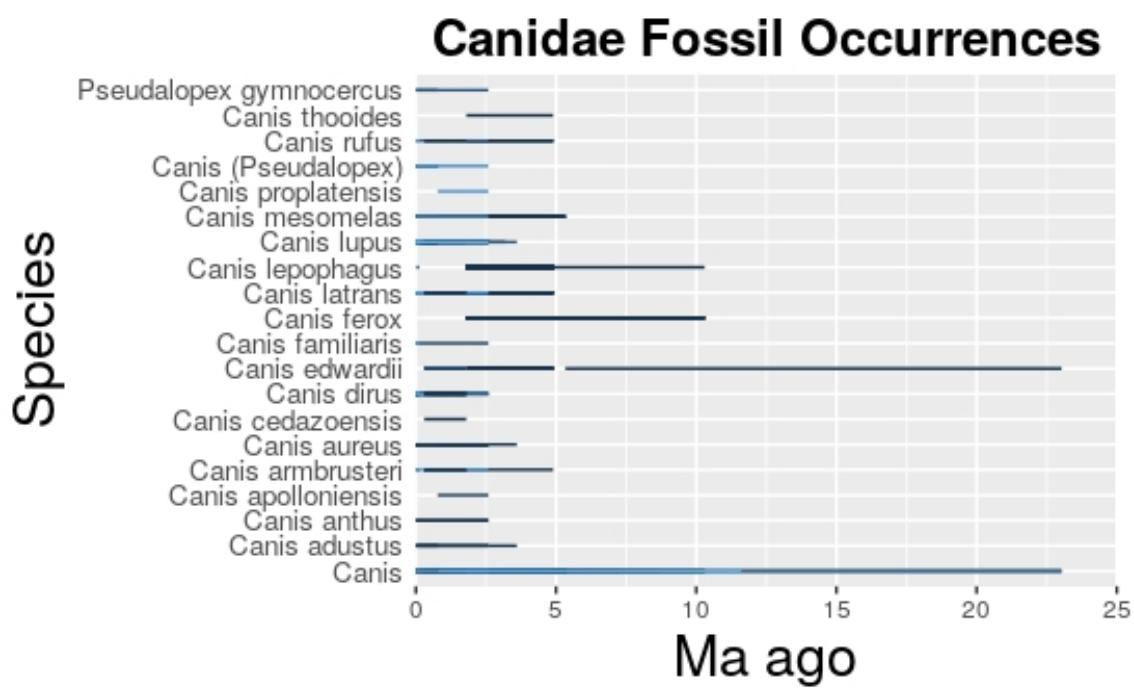


Figure 6: Canidae Fossil Occurrences

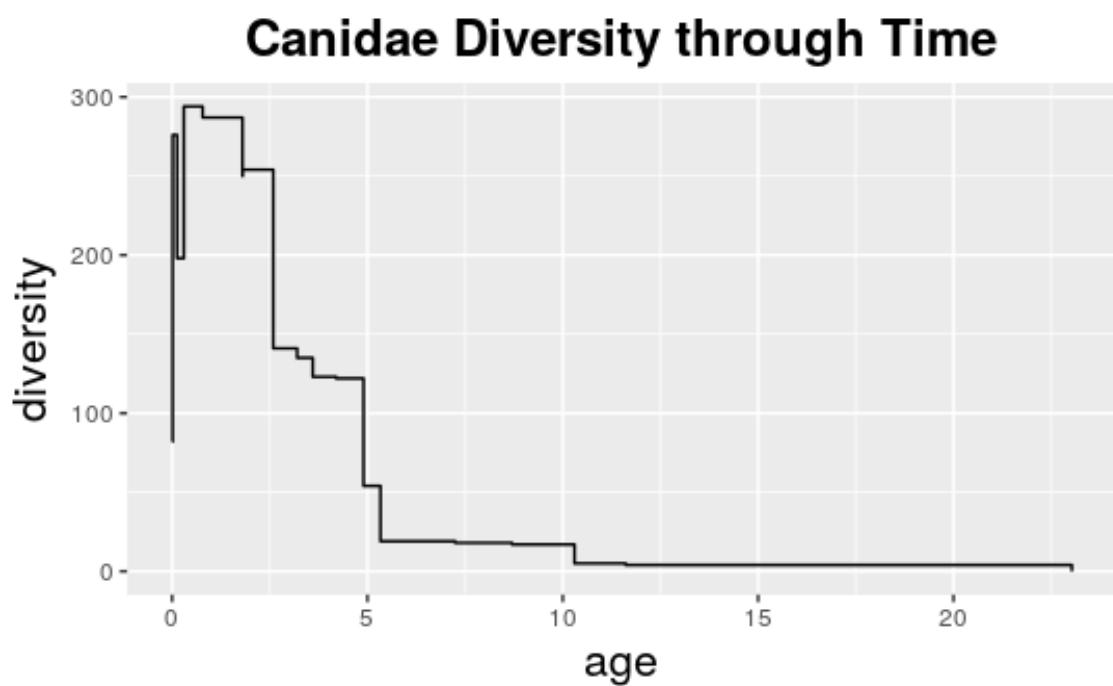


Figure 7: Canidae Diversity through Time

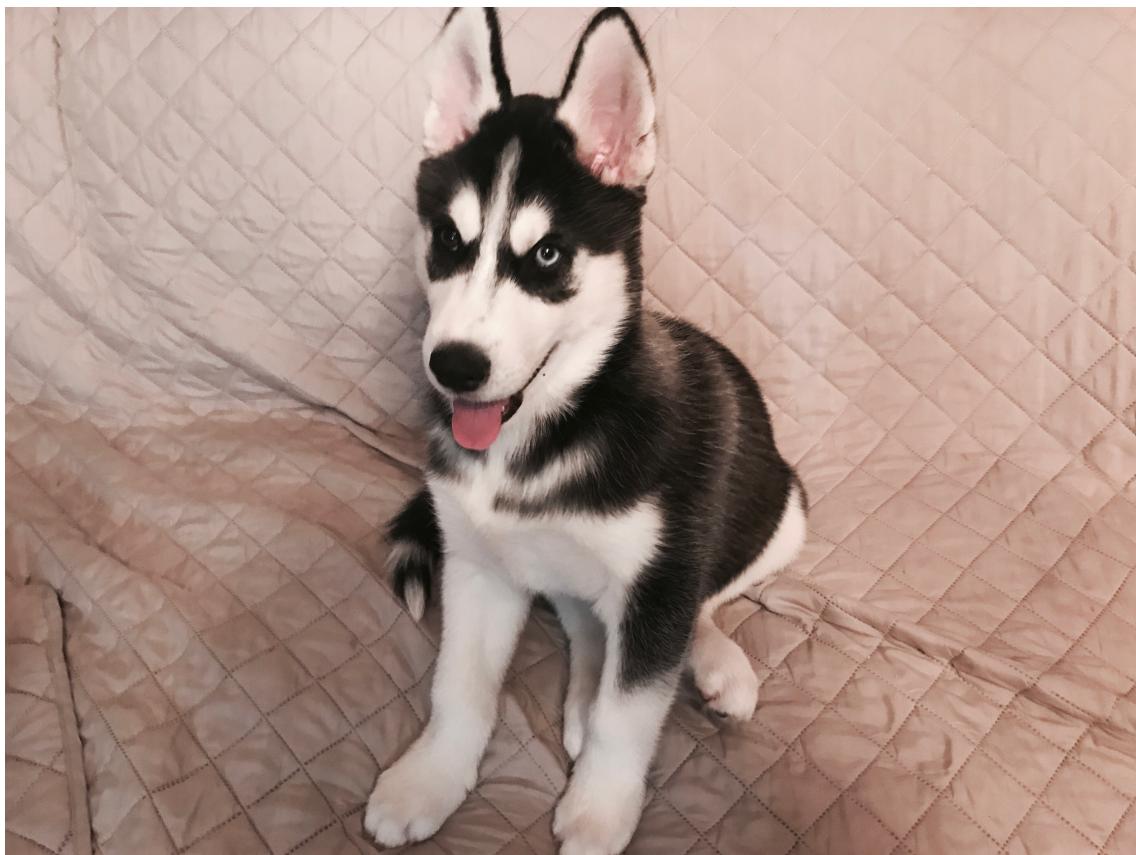


Figure 8: PyRate R script (in shell)

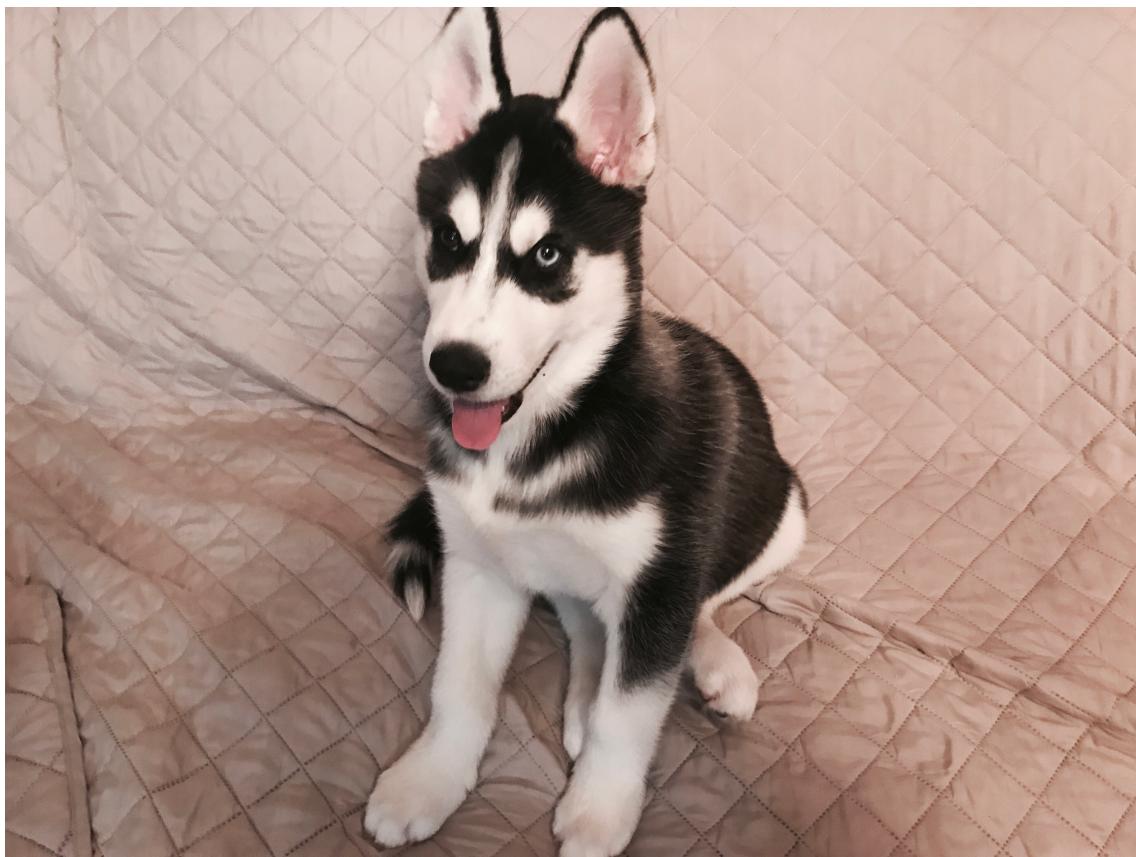


Figure 9: PyRate R script (in shell)

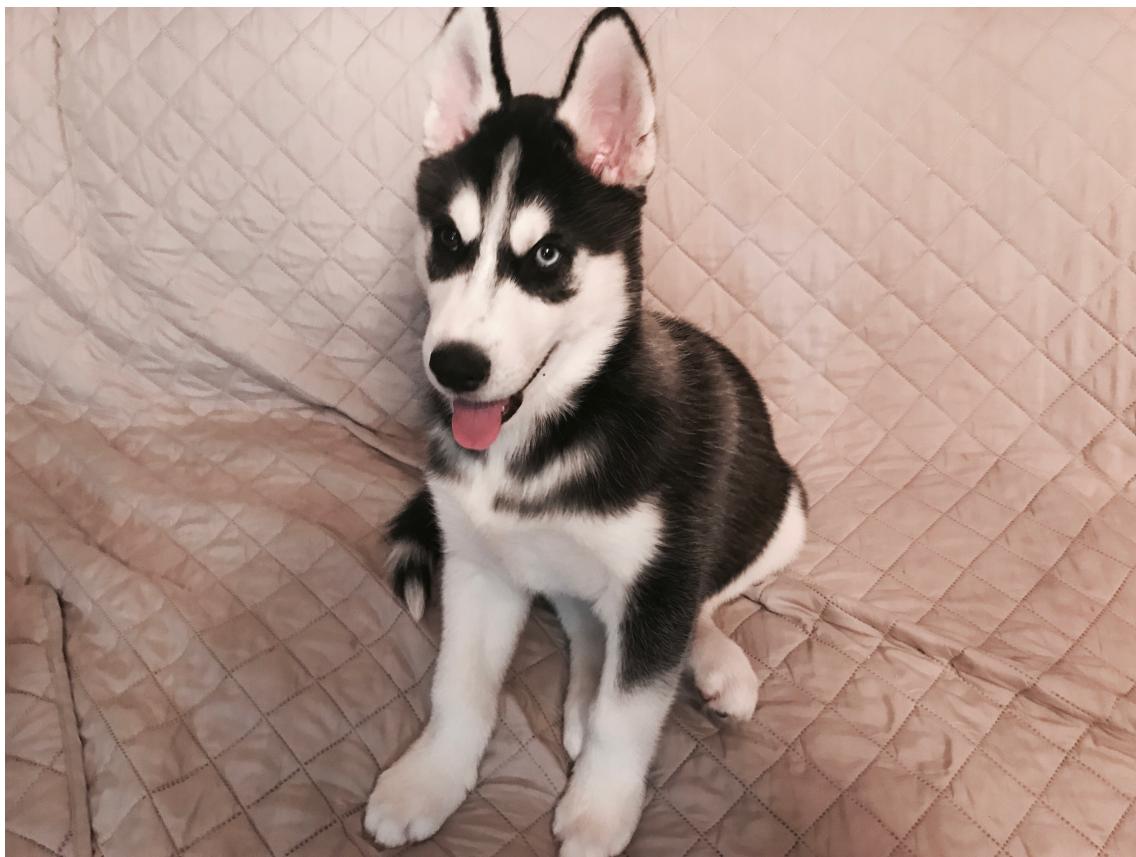


Figure 10: PyRate R script (in shell)

Discussion

Insert Discussion

Conclusion

Insert Conclusion

Citing documents

In this RMarkdown+ \LaTeX world, citing documents becomes super easy. We have included the following lines in the YAML header:

```
bibliography: biblio-1.bib  
csl: ecology-letters.csl
```

The first line here tells the software that knits our document that the bibliography for the document is stored in `biblio-1.bib`; the second line tells the software that a style-guide that describes exactly how we want our references formatted is saved at `ecology-letters-1.csl`. **Note:** You can download the style sheet for your journal of choice from this repository of style sheets¹.

Let's quickly inspect the contents of the files `biblio-1.bib`, which contains the BibTeX formatted citations for the Cooney et al. paper that we have used as a source for beak morphology data and for PyRate. **NOTE** also that we are using the `system()` function in R to execute shell commands from R- you may find this handy later on!

```
system("cat biblio-1.bib", intern = T)
```

```
## [1] "@article{Cooney_2017,"  
## [2] "\tdoi = {10.1038/nature21074}, "  
## [3] "\turl = {https://doi.org/10.1038%2Fnature21074}, "  
## [4] "\tyear = 2017, "  
## [5] "\tmonth = {feb}, "  
## [6] "\tpublisher = {Springer Nature}, "  
## [7] "\tvolume = {542}, "  
## [8] "\tnumber = {7641}, "  
## [9] "\tpages = {344--347}, "  
## [10] "\tauthor = {Christopher R. Cooney and Jen A. Bright and Elliot J. R. Capp and A  
## [11] "\ttitle = {Mega-evolutionary dynamics of the adaptive radiation of birds}, "  
## [12] "\tjournal = {Nature}"  
## [13] "}"  
## [14] "@article{Silvestro_2014,"
```

¹<https://www.zotero.org/styles>

```
## [15] "\tdoi = {10.1111/2041-210x.12263},"
## [16] "\turl = {https://doi.org/10.1111%2F2041-210x.12263},"
## [17] "\tyear = 2014,"
## [18] "\tmonth = {sep},"
## [19] "\tpublisher = {Wiley-Blackwell},"
## [20] "\tvolume = {5},"
## [21] "\tnumber = {10},"
## [22] "\tpages = {1126--1131},"
## [23] "\tauthor = {Daniele Silvestro and Nicolas Salamin and Jan Schnitzler},"
## [24] "\teditor = {Liam Revell},"
## [25] "\ttitle = {{PyRate}: a new program to estimate speciation and extinction rates"
## [26] "\tjournal = {Methods in Ecology and Evolution}"
## [27] "}"
## [28] ""
```

References