Evolutionary History of Family Felidae

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Introduction

Felidae is a taxonomic family of cats. Members of Felidae range from the domestic cat to extant big cats, such as lions and tigers, but also extinct members such as the saber-toothed tiger. This project aims to analyze the diversity of Felidae through time and space. Throughout the history of Felidae, some interesting events include the divergenece between modern cats and now extinct saber-toothed cats, such as the smilodon, and the Late Miocene Radiation, which spiked another wave of speciation. Various graphs of diversity will illustrate these events. Most clades, according to models created by Raia, Carotenuto, et.al, are predicted to fall in species richness after large diversification events like the late Miocene and divergence of sabertooths. Felidae is indeed in decline, and many species, such as the tiger, are endangered today.

Figure 1: Members of Felidae (clockwise from top left): Panthera leo, Felis catus, Smilidon populator, Panthera tigris

Methods

The data utilized in this project is found on the PaleoBiology Database online at paleodb.org. Occurrence data of fossils is downloadable as a CSV file with species name, and an estimate for the age of each fossil in the collection. In order to find species diversity through time, the files are cleaned up with UNIX, then run through python functions to get the data into a plottable format, and finally visualized using R. R is used to plot species diversity through time. Since the fossil ages are estimates, we can use PyRate to statistically analyze more accurate estimates for speciation and extinction. In addition to occurrence data, the paleobiology database also houses collection data with information on the locations of the fossils as well as their ages. This information can be used to plot the fossil through time, showing the geographic distribution of Felidae through history, creating a GIF with python.

Mapping by Fossil Age(python)

```python
min_ma = column_extractor("formatted_felidae_col.csv", 0, 11) #extract lower bound of f
max_ma = column_extractor("formatted_felidae_col.csv", 0, 12) #extract upper bound of f
#iterate through data, find average fossil age, add it to a new dictionary with averag
avg_ma = {}
for key in min_ma.keys():
    avg = ( float(max_ma[key]) + float(min_ma[key]) ) / 2
    avg_ma[key] = avg


longitude = column_extractor("formatted_felidae_col.csv", 0, 3) #extract longitude colu
latitude = column_extractor("formatted_felidae_col.csv", 0, 4) #extract latitude column

strat_lng = stratify(avg_ma, longitude) #stratify longitude by avg_ma
strat_lat = stratify(avg_ma, latitude) #stratify latitude by avg_ma

unique_avg_ma ={} #empty dictionary to hold values of avg_ma as keys
#for use as titles in map
#populate dictionary with for loop
for value in avg_ma.values():
    unique_avg_ma[value] = 1



strat_lng2 = [] #new dictionaries to add longitude for each avg_ma and lower avg_ma
strat_lat2 = [] #same as above but for latitude

#this for loop will add all previous points to each current list of points
for i in range(0, len(strat_lng)):
    new_dict = {} #new dictionary for use in for loop
```

```python
        index = i #variable to decrement for use in while loop
        while(index > 0): #loop will decrement index until 0
            for key in strat_lng[index].keys():
                new_dict[key] = strat_lng[index][key]
            index = index - 1 #decrement to previous index
        strat_lng2.append(new_dict)


#now we do the same for latitude
for i in range(0, len(strat_lat)):
    new_dict = {}
    index = i
    while(index > 0):
        for key in strat_lat[index].keys():
            new_dict[key] = strat_lat[index][key]
        index = index - 1
    strat_lat2.append(new_dict)

unique_avg_ma ={} #empty dictionary to hold values of avg_ma as keys
#populate dictionary with for loop
for value in avg_ma.values():
    unique_avg_ma[value] = 1
#create list of uniqe ages
unique_ages = list(sorted(unique_avg_ma.keys()))
#reverse the order of list
unique_ages.reverse()

#this for loop will go through the fossils by avg_ma and
#create a fossil map for each fossil age stratified over
#saved as png in folder maps
for i in range(0, len(strat_lng3)):
    x = strat_lng3[i]
    y = strat_lat3[i]
    title = str(round(unique_ages[i], 2)) + " Ma ago"
    filename = "maps/map{}.png".format(i) #reverse order
    map_plotter(x, y, filename, title)
```

Converting to GIF(python)

```python
import imageio

filenames =[]
```

```python
for i in range(0, 48):
    filenames.append("maps/map{}.png".format(i))
images = []

for filename in filenames:
    images.append(imageio.imread(filename))
imageio.mimsave('maps/movie.gif', images)
#file called movie.gif is created within the maps folder
```

Output to R: Fossil Occurrences(python)

```python
felid_ranges = extract_fossil_ages("formatted_felidae_occ.csv")

dict_to_file(felid_ranges, "felidae_ranges.csv")
```

Reading in data(R)

```r
library(ggplot2)
#file created using pyton code (shown above)
felids <- read.csv("felidae_ranges.csv", header = F, as.is = T)
names(felids) <- c("genus", "species", "minage", "maxage")
head(felids)
```

Plotting Occurrences(R)

```r
library("forcats")
felids <- felids %>% arrange(maxage)
felids$maxage <- felids$maxage+0.5
felid_occ <- ggplot(felids, aes( x = fct_reorder(species, minage, .desc = T), maxage, co
felid_occ <- felid_occ + geom_linerange(aes(ymin = minage, ymax = maxage + 0.5))
felid_occ <- felid_occ + theme(legend.position="none")
felid_occ <- felid_occ + coord_flip()
felid_occ <- felid_occ +  theme(axis.text.y = element_text(size=3))
felid_occ <- felid_occ + theme(axis.ticks.y=element_blank())
felid_occ <- felid_occ + scale_y_continuous(limits=c(0, 20), expand = c(0, 0), breaks=c
felid_occ <- felid_occ + labs(title = "Felid Fossil Occurrences", x = "Species", y = "Ma

felid_occ
```

Plotting Diversity(R)

```r
library(tidyr)
library(dplyr)
#create new variable diversity which is the number of species
diversity <- felids %>% gather(key = type, value = age, minage, maxage) %>% mutate(count

#plot diversity v age
felid_div <- ggplot(diversity, aes(x = age, y = diversity)) + geom_step()

#add labels and theme
felid_div <- felid_div + labs(title = "Felidae Diversity Through Time", x = "Ma ago", y
felid_div
```

PyRate R script(shell)

```bash
#! /bin/bash

# Script to run full pyrate pipeline on Felidae

# navigate to the working directory
cd ~/Desktop/eeb-177/eeb177-final-project/PyRate

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

# 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_felid_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 felidae_occ_PyRate.py -data_info > data_summary.txt

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

#change directory to the newly created
cd pyrate_mcmc_logs/
```

```
#create graphs
python ~/PyRate/PyRate.py -plot felidae_occ_1_marginal_rates.log
```
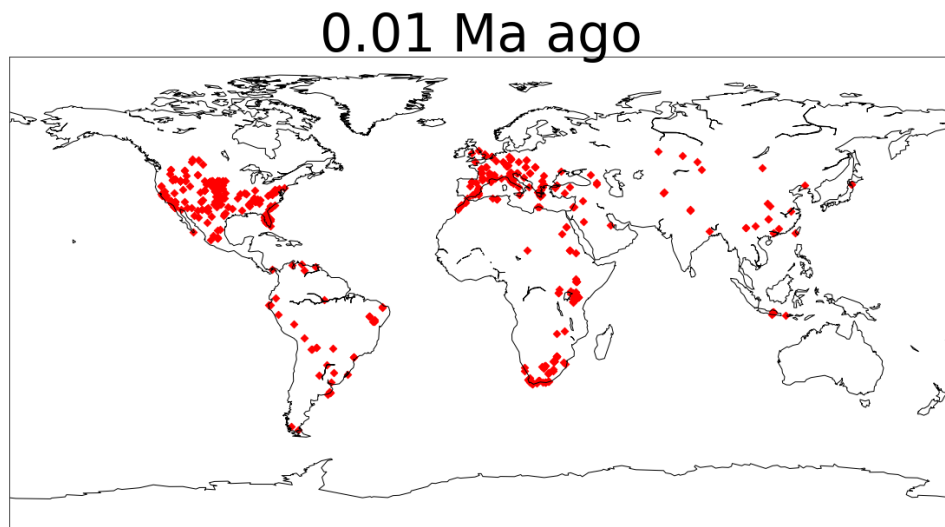
Results

0.01 Ma ago

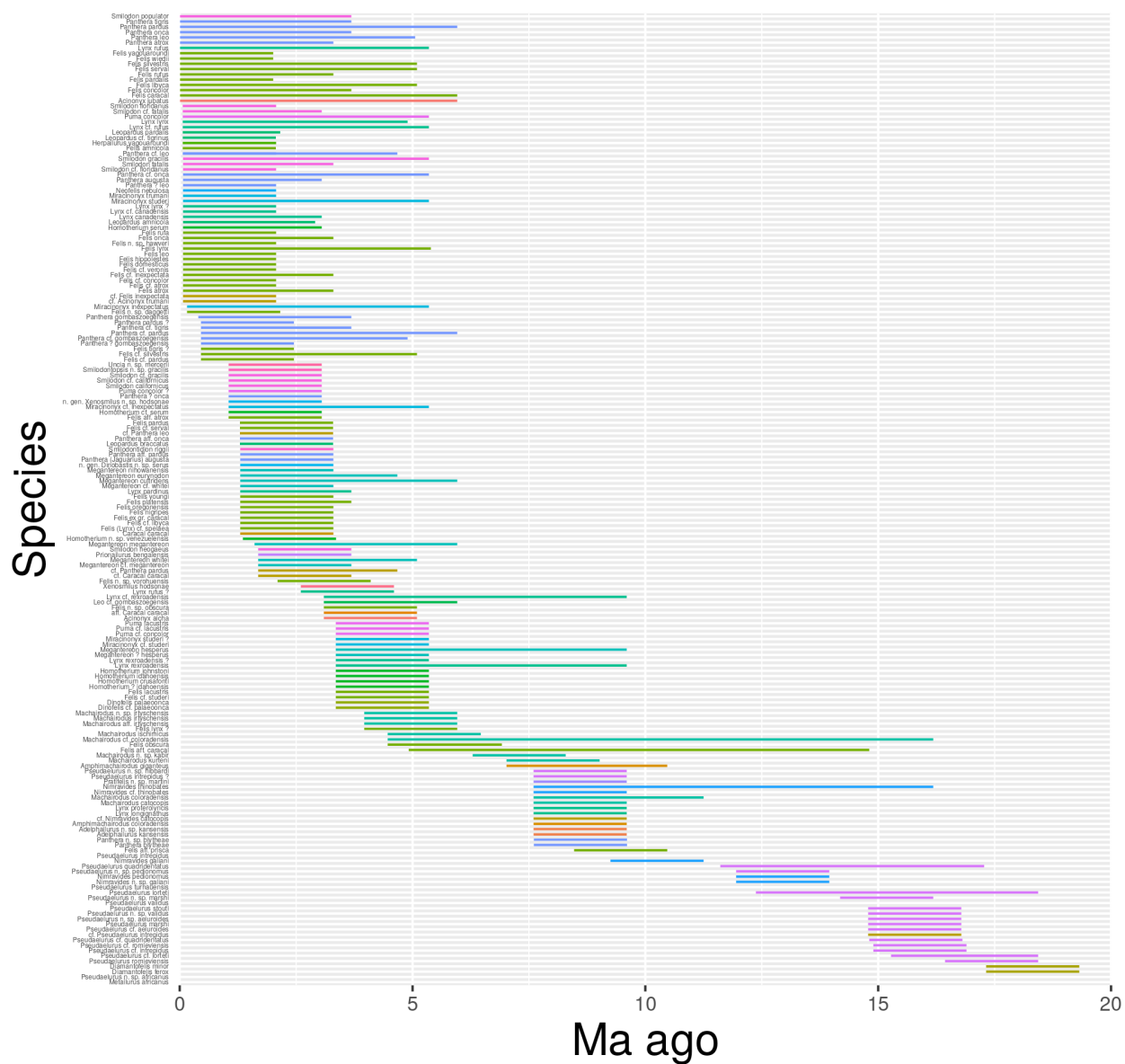Figure 2: Occurrences of Felidae through space, made in python

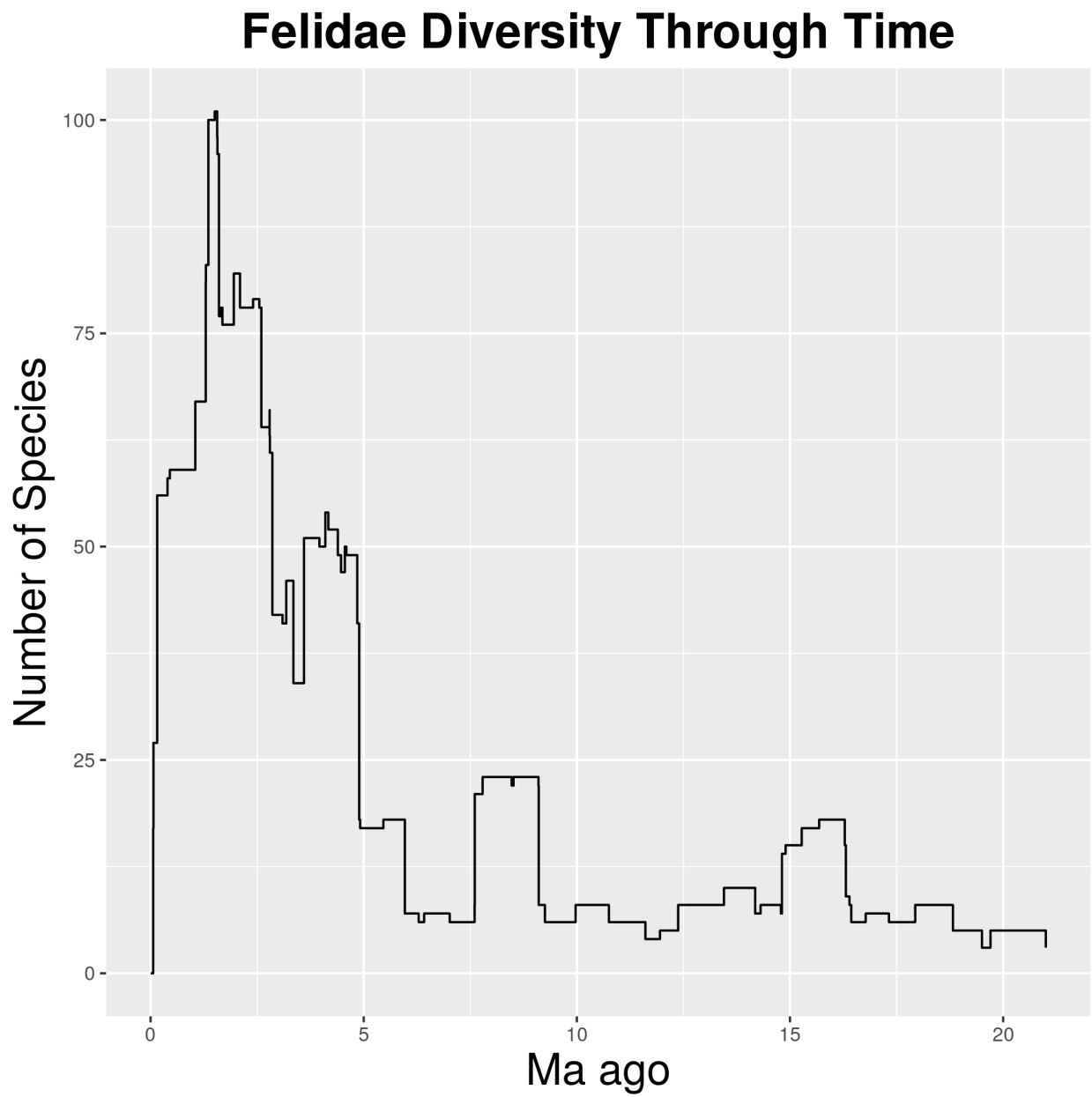Figure 3: Occurrences of Felidae through time, made in R

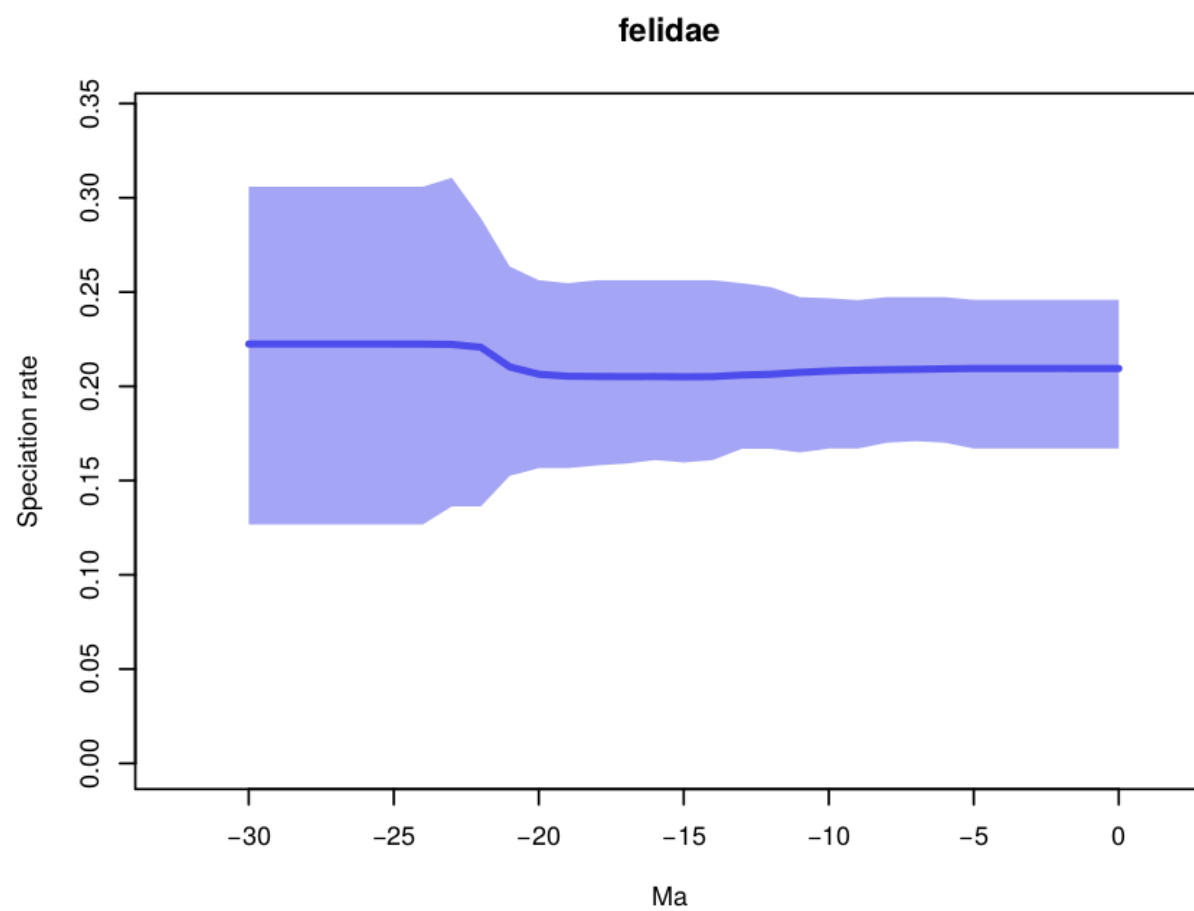Figure 4: Felid Diversity through time, made in R

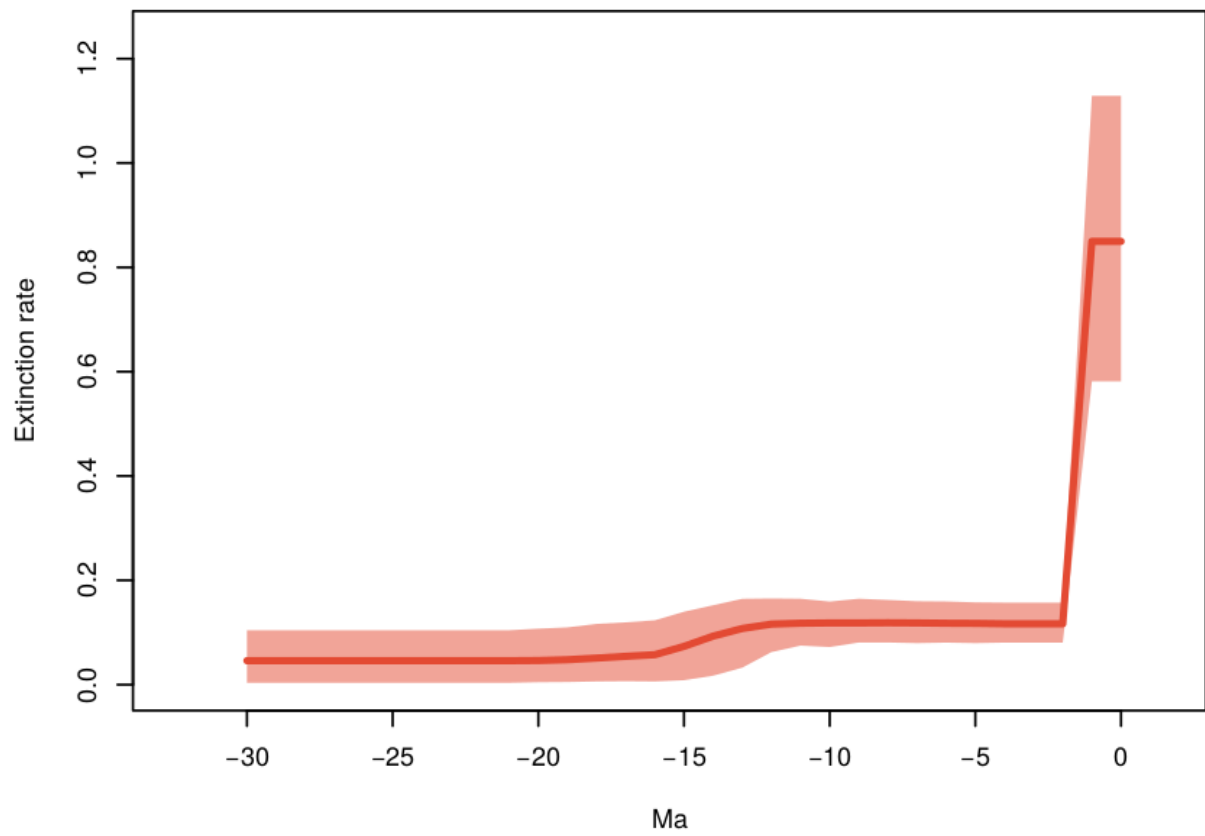Figure 5: Speciation through time, made using PyRate

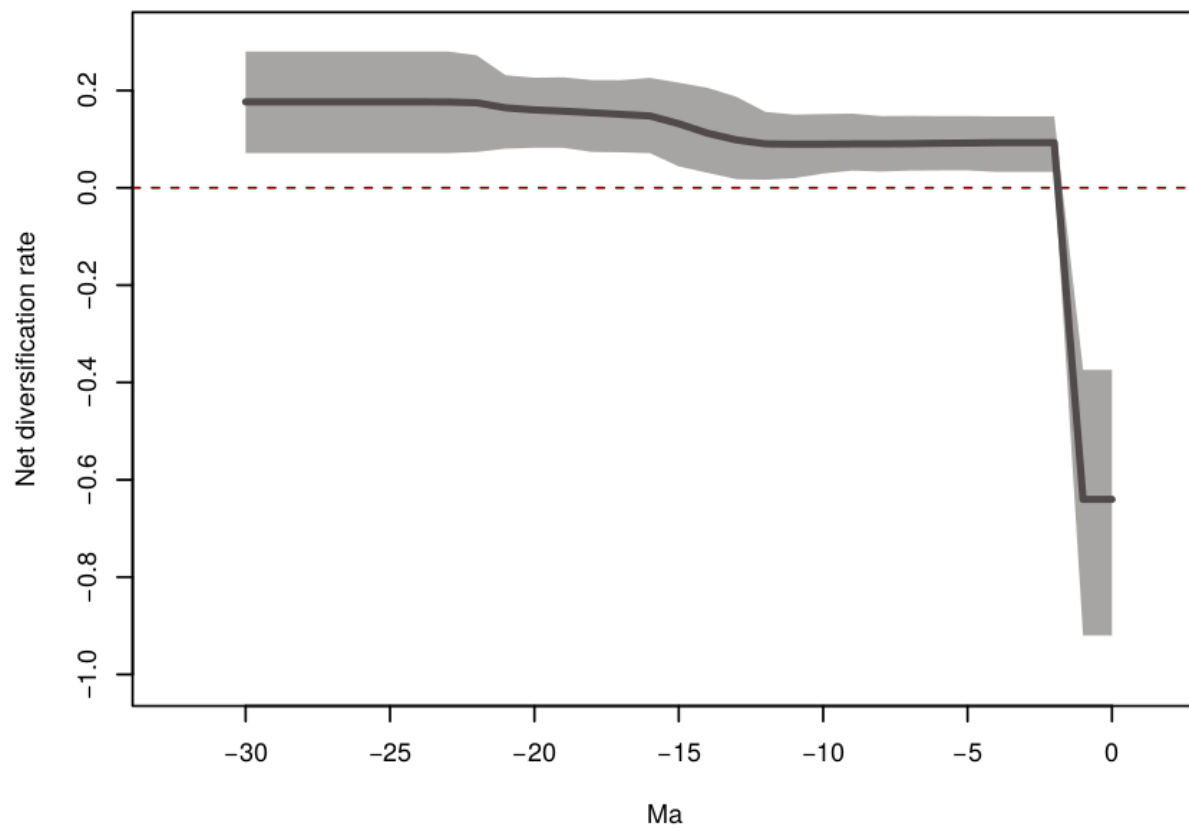Figure 6: Extinction through time, made using PyRate

Figure 7: Net Diversification through time, made using PyRate
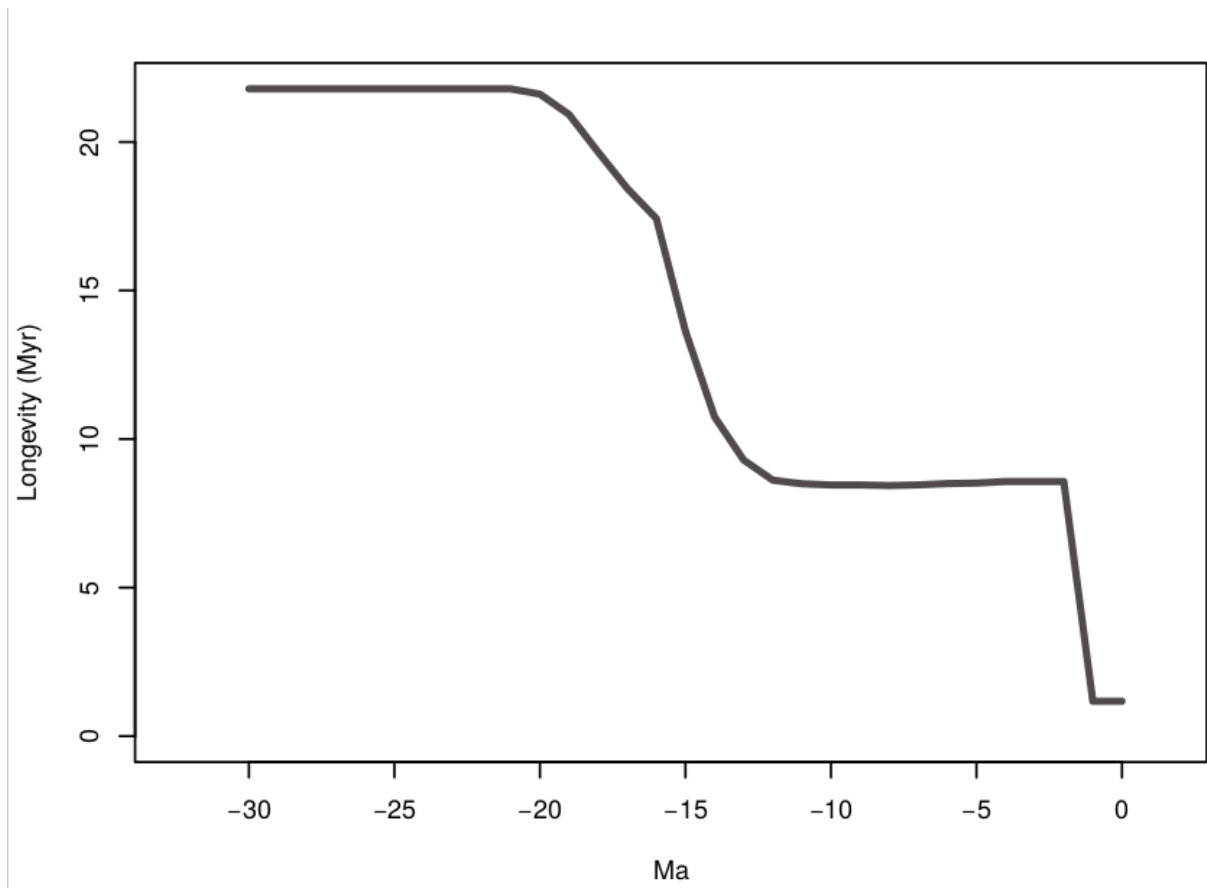
Discussion

Github links:

https://github.com/seanmathew95/eeb-177-final-project

Week 10 Lightning Presentation:

contains python code for functions used above in jupyter notebook format
https://github.com/seanmathew95/eeb-177-final-project/blob/master/Week10_lightning_
presentation.ipynb

PyRate materials:

https://github.com/seanmathew95/eeb-177-final-project/blob/master/PyRate/full-pyrate-run.
sh

https://github.com/seanmathew95/eeb-177-final-project/blob/master/PyRate/process_
felid_data.R

Rmarkdown file:

https://github.com/seanmathew95/eeb-177-final-project/blob/master/Analysis_of_
Felidae.md

References