Speciation, Extinction, and Diversification rates of Neotropic Birds in the Neoave Clade

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Introduction

The Resplendent Quetzals are regarded as one of the most beautiful birds in the world, with their colorful feathers and long tail. They are found in the Southern Mexico and Central America. The resplendent quetzal is the national bird and the name of the currency in Guatemala. Quetzals are part of the order Trogonifromes. This project arose as a personal interest due to my Guatemalan heritage. It is also came about due to the resplendent quetzal having a status of Near Threatened. Although considered at a low risk, understanding what occurs to its habitat is crucial in order to protect these beautiful species.

Fossil records trace back to 49 million years ago, the early Eocene. The greatest diversity of these birds is in the neotropics with some species found in southeast Asia.Although these birds are found in the neotropic regions, their exact origin is not known. The as earliest fossil was found in Denmark in the Eocene Epoch, 54 mya. Others have been found in Germany, Switzerland, and France. Thus Trogons are thought to have an Old World Origin.(Skutch & others 1999; Mayr 2003; Moyle 2005)

Using occurrence data from Paleobiology Database we can see that there is not many occurrences available for the trogon family. I expanded my search to include all neotropic birds, in order to better understand the evolution of the Trogon family in the Neotropical New World. I chose to focus on the evolution of the clade Neoaves, particularly in in the Neotropic regions; North and South America, not including United States nor Canada.

The overall goal of this project was to explore the speciation, extinction, and diversification rates of this clade Eventually an attempt in recreating the phylogeny of Neoaves was made by plotting a time-scaled phylogeny against the international geological time scale.
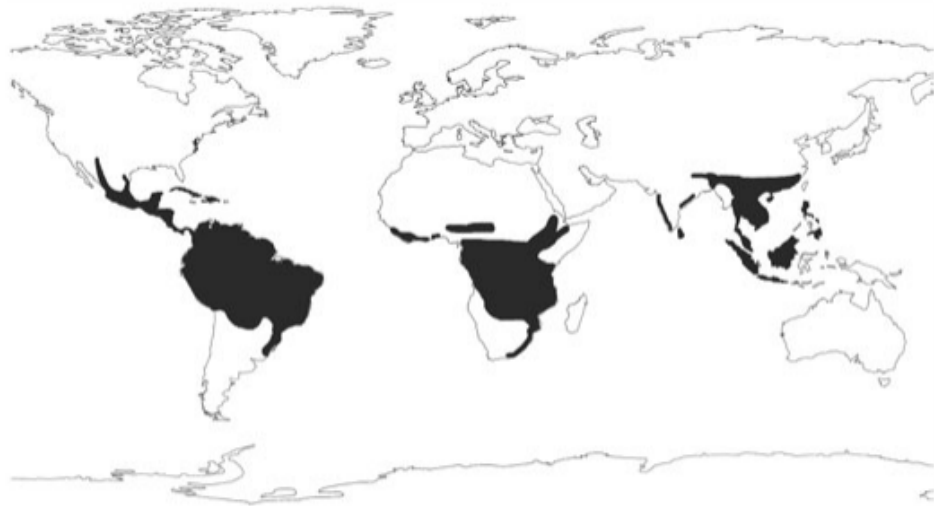
Figure 1: Resplendant Quetzal

Figure 2: Map of the world showing distribution of Trogons in black

Methods

Map of Trogon Occurences

```
from pylab import rcParams
%matplotlib inline
rcParams['figure.figsize'] = (8,6)
from mpl_toolkits.basemap import Basemap
# Create empty lists for the data we are interested in.
latitude = []
longitude = []
timestrings = []

#read in the file
in_file = open ( "/home/eeb177-student/Desktop/eeb-177/eeb-174-final-project/trogones.cs

#get rid of the header
in_file.readline()


    # Store the latitudes and longitudes in the appropriate lists.
for line in in_file:
    lats = line.split('","')[19]
    lons = line.split('","')[18]
    latitude.append(float(lats))
    longitude.append(float(lons))
    import matplotlib.pyplot as plt
import numpy as np
import PIL
# Make the plot larger.
plt.figure(figsize=(16,12))

eq_map = Basemap(projection='robin', resolution = 'l', area_thresh = 1000.0,lat_0=0, lon
eq_map.drawcoastlines()
eq_map.drawcountries()
eq_map.fillcontinents(color = 'gray')
eq_map.bluemarble()
eq_map.drawmapboundary()
eq_map.drawmeridians(np.arange(0, 360, 30))
eq_map.drawparallels(np.arange(-90, 90, 30))

x,y = eq_map(longitude, latitude)
eq_map.plot(x, y, 'ro', markersize=6)
```

```
plt.figtext(.5,.9,'Stratigraphic Location: Trogones', fontsize=40, ha='center')
```
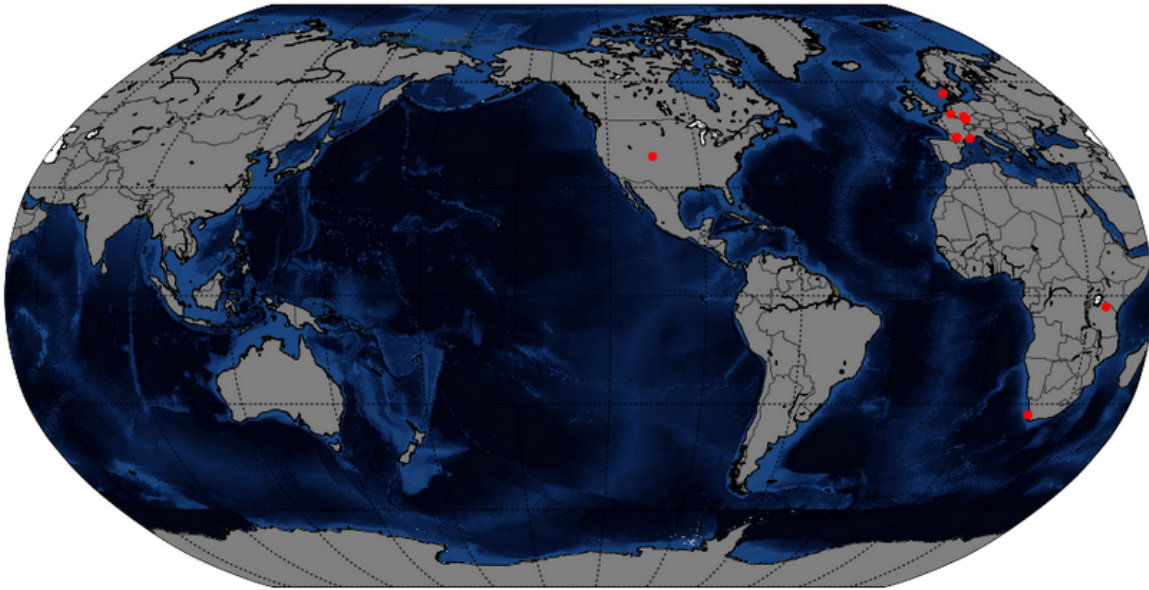
Stratigraphic Location: Trogones

Figure 3: Map of PBDB occurences

Creating a list of species and determing extant species for Pyrate Analysis

```
import csv

output = open("neoaves_extant.csv", "w")
#create and define function that takes an integer from the min_ma as the argument and

def still_exists(string):
    for ma in (item [11]):
        if ma == '0':
            exists.append (0)
            output.write(item[5] + '\n')
            return ('0')
        else:
            exists.append(1)
```

```python
        return('1')


#read in the file
in_file = open ( "/home/eeb177-student/Desktop/eeb-177/eeb-174-final-project/neoaves/neo
#make a dictionary of taxon of either extinct or extanct
#mames a list of 0 or 1
taxon = {}
exists = []

#get rid of the header
in_file.readline()


for line in in_file:

    #split so we can access the different columns in the lines
    item = line.split('","')

    taxons = item [5]
    ma = item [11]

    #populate our dictionaries
    taxon[taxons] = still_exists (ma)

list_species = [] #empty list to store species in

for line in in_file:
    species = line.split('","')[6]
    name_of_species = line.split('","')[5]
    if "species" in species:
        list_species.append(name_of_species)
number_species = len ( list_species)
```

Output to R for fossil occurrences and time scaled phylogeny

```python
import csv

in_file = open ( "/home/eeb177-student/Desktop/eeb-177/eeb-174-final-project/neoaves/neo


#get rid of the header
in_file.readline()
```

```python
# use default dict
from collections import defaultdict
species_ranges = defaultdict(list)


for line in in_file:
    name_of_species = line.split('","')[5]
    minage = line.split('","')[11]
    maxage = line.split('","')[10]
    mean_age = (float(minage) + float(maxage))/2
    species_ranges[name_of_species].append(mean_age) # add species as keys
output = open("aves-ranges.csv", "w")
output1 = open("neoaves_trees.csv", "w")
header = "{}, {}, {},\n".format("Species","FA", "LA")
output1.write(header)

#get oldest and youngest
#species_ranges.values()
for key in species_ranges.keys():
    ages = species_ranges[key]
    minage = min(ages)
    maxage = max(ages)
    genus = key.split(" ")[0]
    species = key
    outline= "{},{},{},{}\n".format(genus, species, minage, maxage)
    output.write(outline)
    outline1 = "{},{},{},\n".format(species, minage, maxage)

    output1.write(outline1)
```

Plotting Occurences in R

```r
library ( ggplot2)
install.packages("forcats", repos="http://cran.rstudio.com/")
library (forcats)
setwd("/home/eeb177-student/Desktop/eeb-177/eeb-174-final-project/Weekly_HW")

aves <- read.csv("/home/eeb177-student/Desktop/eeb-177/eeb-174-final-project/Weekly_HW/a

names(aves) <- c( "genus", "species", "minage", "maxage")
head(aves)
```

```r
aves_occ <- ggplot(aves, aes( x = fct_reorder (species, minage, .desc = T), maxage, col
# everything
aves_occ + geom_linerange(aes(ymin = minage, ymax = maxage + 0.5)) + theme(legend.positi
```

Plotting a time-scaled phylogeny against the international geological time scale

```r
install.packages("strap")
library(strap)
neoaves <- read.csv("/home/eeb177-student/Desktop/eeb-177/eeb-174-final-project/Weekly_H

data("neoaves")

tree_l <- DatePhylo(neoaves$tree, neoaves$ages, method="equal", rlen=1)
geoscalePhylo(tree=tree_l, boxes="Age", cex.tip=0.4)
# Plotting the tree with the stratigraphical ranges included
geoscalePhylo(tree=tree_l, ages=neoaves$ages, boxes="Age", cex.tip=0.4)
# Including all temporal units into the stratigraphic column
geoscalePhylo(tree_l, neoaves$ages, units = c("Eon","Era","Period","Epoch","Age"),
boxes="Age", cex.tip=0.4)
# Plotting the numerical values on the time scale at Age resolution
geoscalePhylo(tree_l, neoaves$ages, units = c("Eon","Era","Period","Epoch","Age"),
boxes="Age", cex.tip=0.4,tick.scale="Age")
```

Pyrate R Script

```bash
#! /bin/bash


# Script to run full pyrate pipeline on Neoaves


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

# 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_ave_data.R

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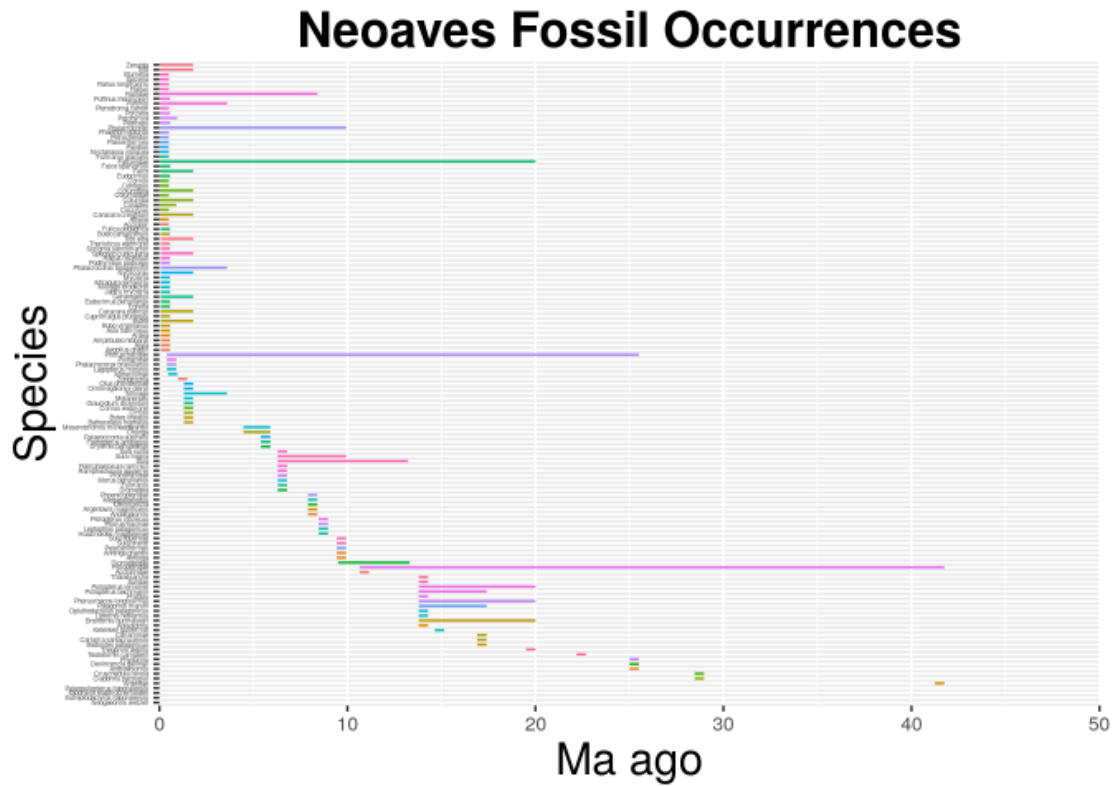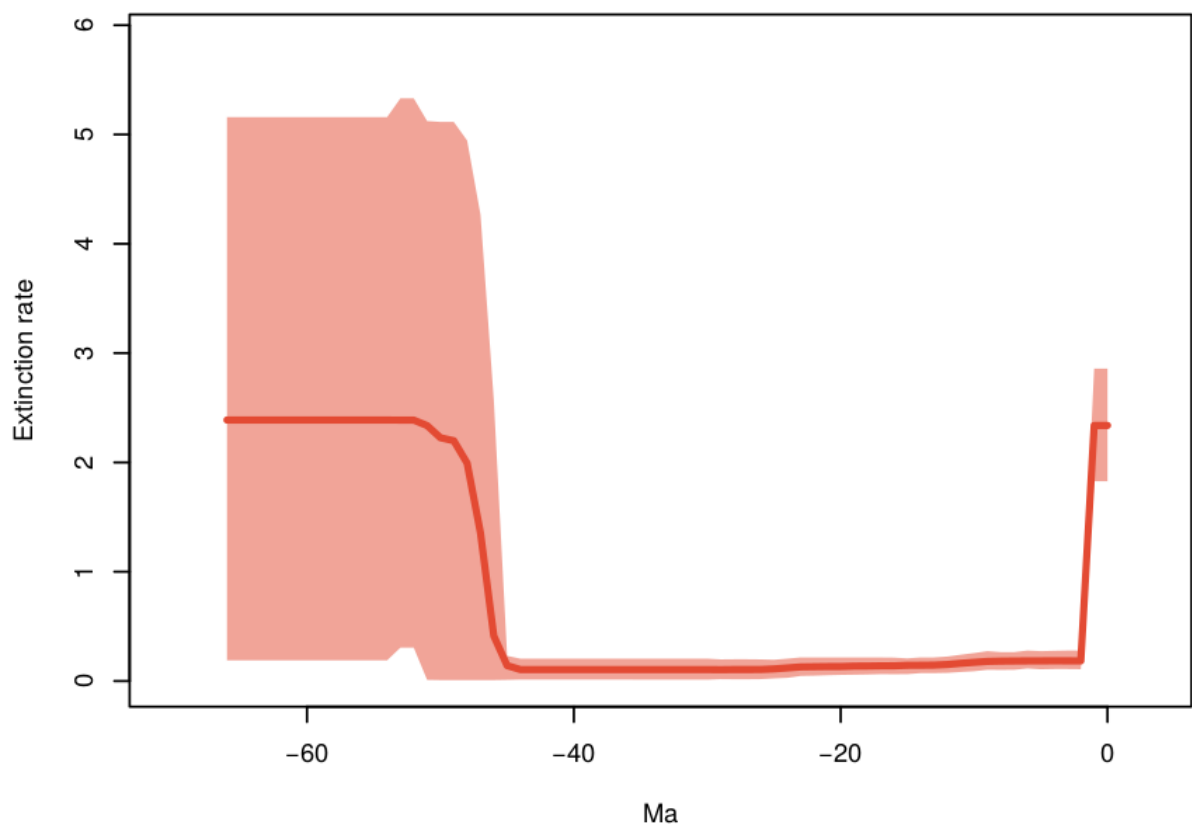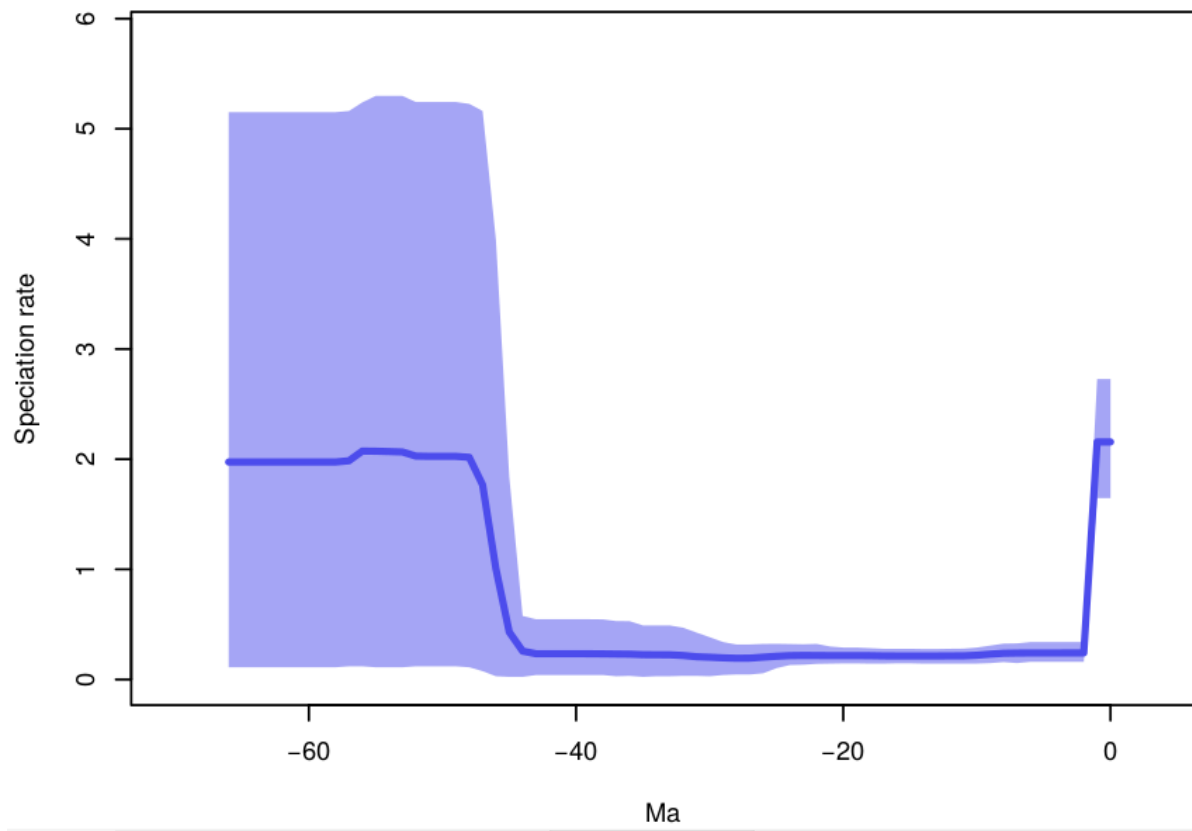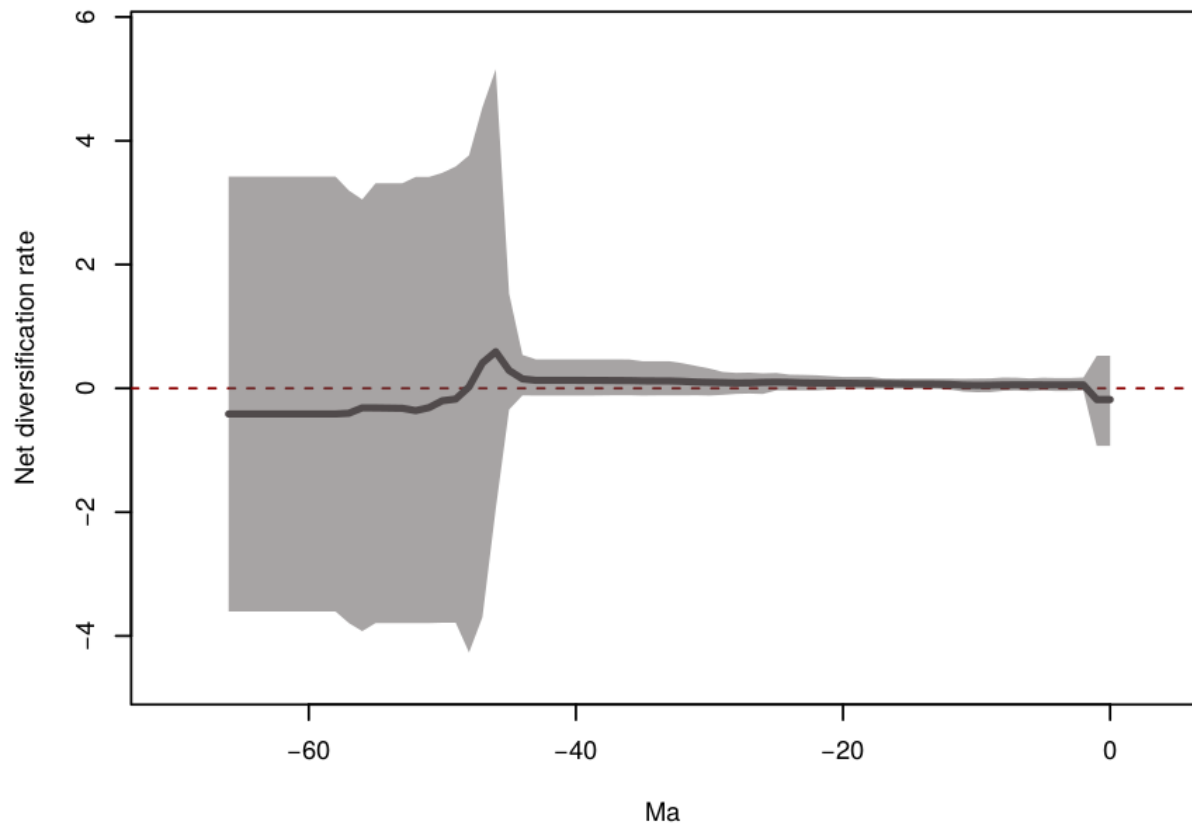
```
# data_summary.txt so that it may be inspected later.
python ~/PyRate/PyRate.py newaves_PyRate.py -data_info > data_summary.txt

# And then, run PyRate!
python ~/PyRate/PyRate.py newaves_PyRate.py -n 1000000
```
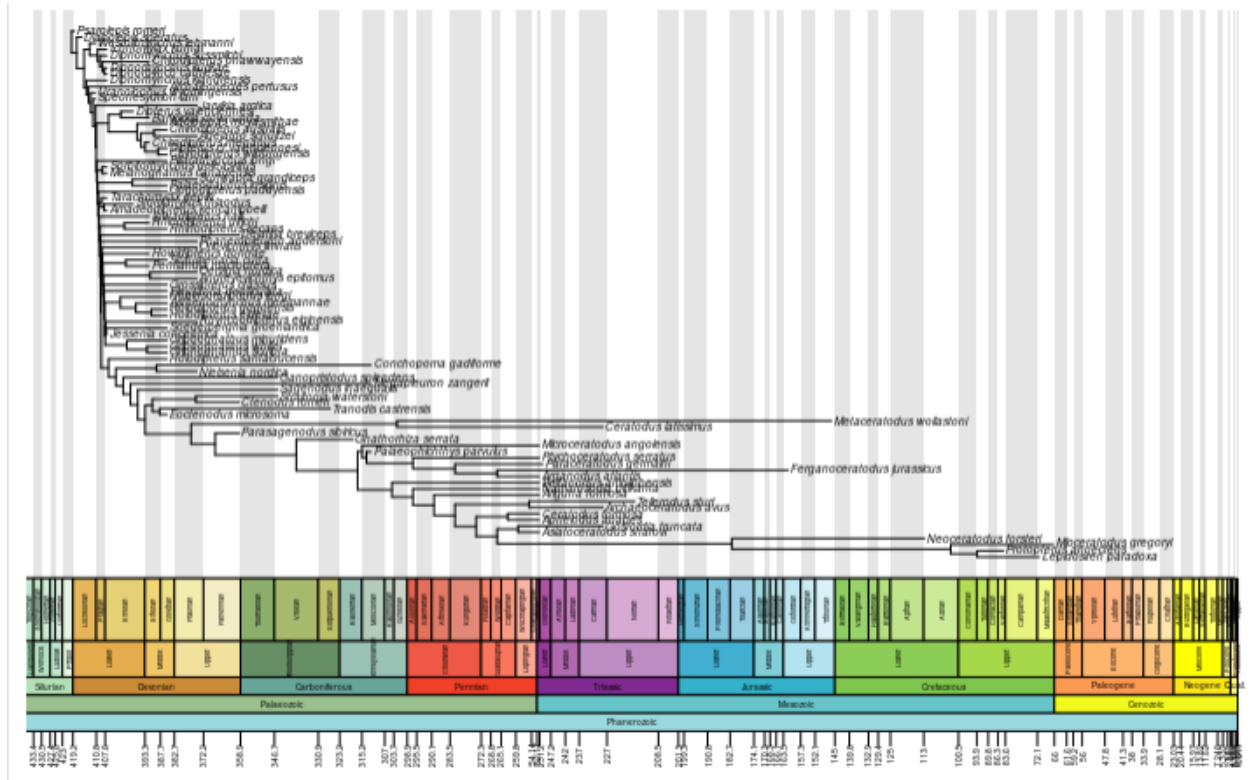
Results

Neoaves Fossil Occurrences

Figure 4: Plot of a time-scaled phylogeny against the international geological time scale

Discussion

Through the analysis using PyRaTe we are able to see the speciation, extinction, and diversification rates. All three graphs had a significantly large confidence interval as shown by the shaded area around the mean rate estimates, the solid lines. Speciation is the formation of the new and distinct species while diversification rate is the species becoming more diverse. Here we see that the extinction and speciation rates were very similar. Both had a decrease in rates around 38 MYA. Along the same time the diversification rates has a short peak. The diversification rate is shown constant throughout time and sees a decrease more recently in the last million years. The occurrence data shows us that there has been much more occurrences of Neotropic birds in the past two million years.In the phylogeny graph we see much more species originating in the Devonian period. Mapping the Neoave occurrence data through time could let us visualize how these Neotropics came about.

GitHub Link

https://github.com/lauratrejo44/eeb-174-final-project/tree/master/eeb-174-final-project

References

Mayr, G. (2003). On the phylogenetic relationships of trogons (aves, trogonidae). *Journal of Avian Biology*, **34**, 81–88.

Moyle, R.G. (2005). Phylogeny and biogeographical history of trogoniformes, a pantropical bird order. *Biological Journal of the Linnean Society*, **84**, 725–738.

Skutch, A.F. & others. (1999). *Trogons, laughing falcons, and other neotropical birds.* Texas A & M University Press.