

The Evolution of Proboscidea

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Abstract

The number of extinctions of megafaunal species in the last few thousand years was incredibly high. In this project, order *Proboscidea* would be studied to understand the reason of extinction. A series of graphs would be generated using the datas from PaleoBiology Database to see the pattern of these species. Overall, appearance of humans and climate change were the main reasons for such fast extinction in last 1 ma. Only species that lived far away from humans were able to survive till recent days.

Introduction

Proboscidea is a taxonomic order of Afrotherian mammals. The fossil occurrence records, from **PaleoBiology Database**(PBDB)¹, showed that the earliest fossil records were from 57.6 million years ago, which was from the earliest species of Proboscidea – *Eritherium azzouzorum*. Moreover, the database gave a total of 115 unique species, from them only 3 extant species, which are all from family *Elephantidea*; the information from **PBDB** gives us an important information: that during almost 58 million years, 97.39% of *Proboscidean* species went extinct, leaving only 2.61% of all species living today.



Figure 1: Evolution of Proboscidea

¹<https://paleobiodb.org>

Proboscidea were first originated in Africa and managed to spread to all continents across the World, except Australia and Antarctica (Shoshani 2001). They reached the peak diversity with around 100 species during Miocene Epoch, 24-5 million years ago. According to Shoshani, the reason for an expansion of *Proboscidea* was due to the appearance of grasses on the Earth during those times.

In this project, we will be producing evolutionary graphs using the data from **PaleoBiology Database**. The generated graphs will be used to understand the dispersal of *Proboscidea* and the reason of extinction of this taxa.

Methods and Figures

In this project, many data will be used in producing figures: such as occurrence, early appearance, late appearance, genus, species name, and location.

1. Species would be used to construct a graph showing how many species lived at each particular time. The graph would be in form of geom graph.
2. Another graph will be showing how long each species lived (aka stratigraphic record). In this graph, both early appearance and late appearance will be used.
3. Occurrence data would be used in PyRate to plot graphs such as extinction, speciation, and diversification rates.

Overall, more than three graphs would be made to understand the data.

Problem

One of the biggest problems was getting the database. The name *Proboscidea* is not only order of afrotherian mammals, it is also an order of class *Insecta*; therefore, when getting the data from **PBDB**, the data that showed up were from wrong class. In order to fix this issue, instead of searching for *Proboscidea*, I used *Tethytheria*, which is the higher classification level (clade) in which *Proboscidea* are found. And using these data, I was able to use “grep -w Proboscidea” to extract all the *Proboscidea* data and removed data from its sister order.

1. Generating Occurrence graph and Diversity graph of the Species

In order to create beautiful graphs in Rmarkdown, we first need to manipulate the data and get the data that we need. Python was used to do this task, below are the codes that were used (the below code was borrowed from the lecture of Professor Alfaro):

```
# first we needed to open the file and read the file in python
infile = "/home/eeb177-student/Desktop/eeb-177/eeb-177-final-project/data_file/occurrence
with open(infile, 'r') as ff:
    proboscidea_recs = ff.readlines()
```

```

# second step is we needed to create a dictionary
# use defaultdict
from collections import defaultdict

species_ranges = defaultdict(list)

# make a dictionary
for line in proboscidea_recs:
    species = line.split(',')[5]
    minage = line.split(',')[10]
    maxage = line.split(',')[11]
    mean_age = (float(minage)+float(maxage))/2
    species_ranges[species].append(mean_age) #add species as keys and mean ages as

# create an output file
output = open("/home/eeb177-student/Desktop/eeb-177/eeb-177-final-project/data_file/occu

# use sorted so the output will be sorted in alphabetical order
for key in sorted(species_ranges.keys()):
    ages = species_ranges[key]
    min_age = min(ages) #getting min_age and max_age from the mean data values
    max_age = max(ages)
    genus = key.split(" ")[0]
    species = key
    print(genus,species, max_age,min_age)
    outline = "{},{},{},{}\n".format(genus, species, max_age, min_age)
    output.write(outline)
    output.close

```

Below shows the data table that was produced:

##	genus	species	minage	maxage
## 1	Afrochoerodon	Afrochoerodon kisumuensis	16.4350	13.795
## 2	Amahuacatherium	Amahuacatherium peruvium	9.5000	9.433
## 3	Amebelodon	Amebelodon britti	14.1815	7.600
## 4	Amebelodon	Amebelodon floridanus	14.1815	7.600
## 5	Amebelodon	Amebelodon fricki	9.2500	7.600
## 6	Amebelodon	Amebelodon grandincisivus	9.2000	9.200

Using these data and the codes given in lecture, I was able to recreate the figures with my own taxa (the codes will not be shown)

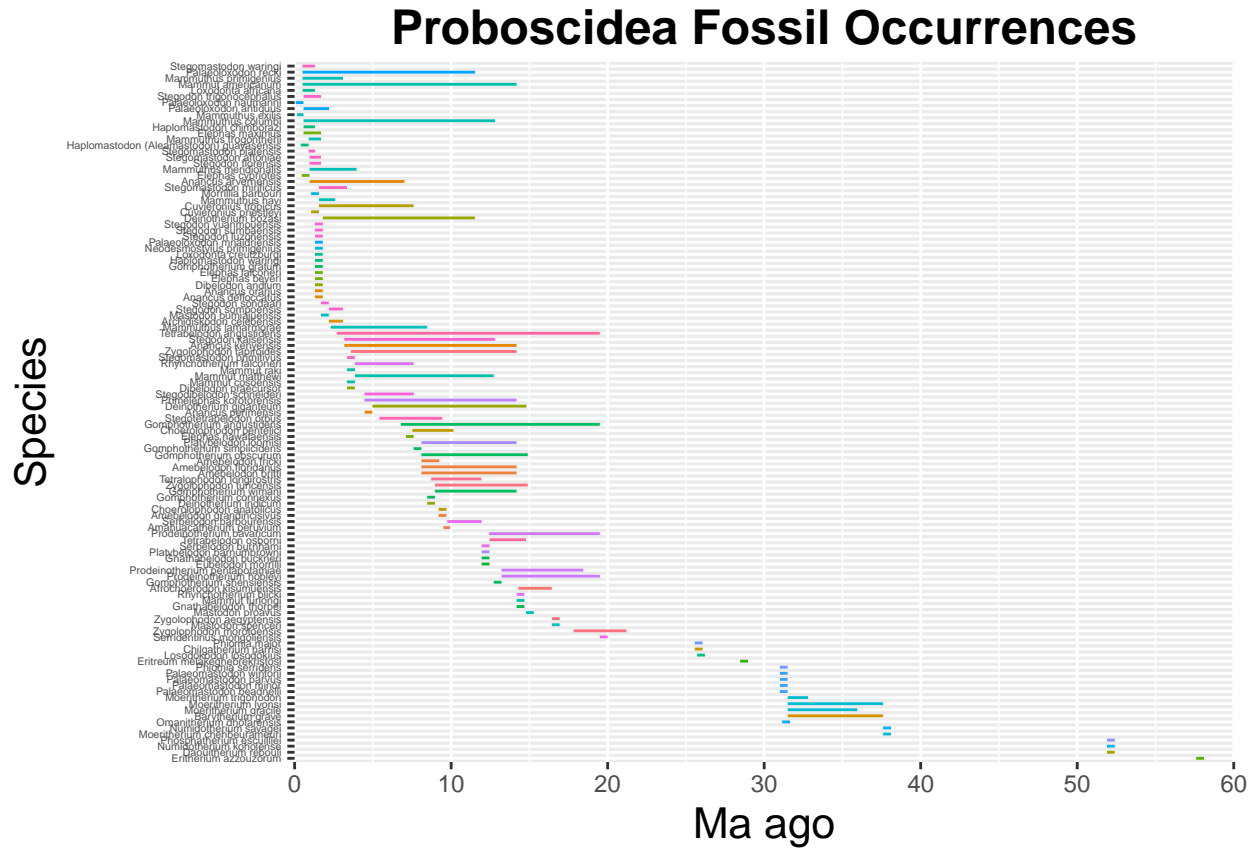


Figure 2: Fossil Occurance of *Proboscidea* Species on Time Scale

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
```

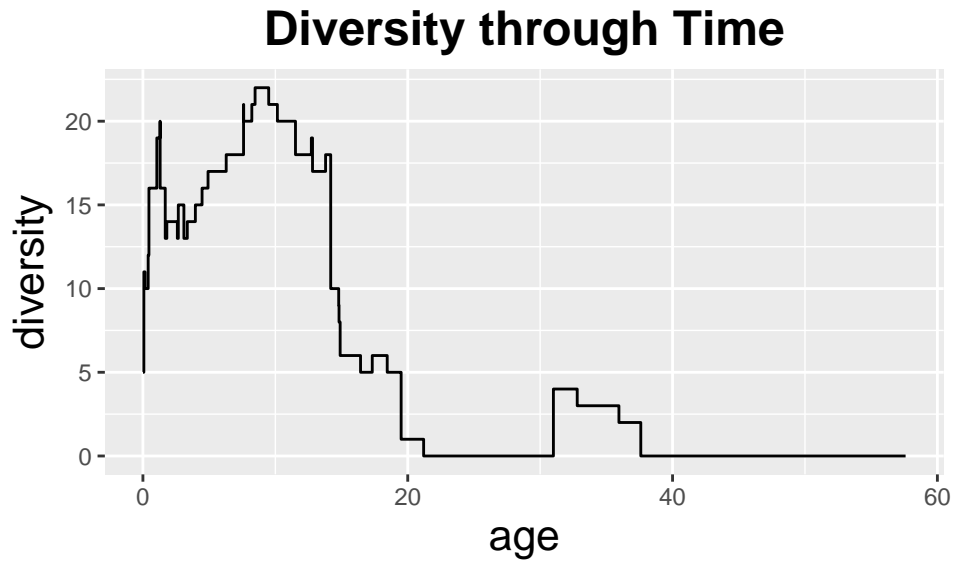


Figure 3: Diversity of *Proboscidea* Species through Time

2. Creating Fossil Records Graph on World Map

In order to create a graph showing where the *Proboscidea* were found, we needed the **PaleoBiology Database** to output location (latitude and longitude). The data was modified through the shell(not python) using [cut -d “,” -f 6,7,11,12,17,18,20,21 location.csv > formatted-location.csv]. The data were not modified through python because in order to show all the fossil records, creation of dictionary was needed. In total 8 colums were outputted: accepted name, accepted rank, max_ma, min_ma, family, genus, longitude, and latitude. Accepted_rank, max_ma, and family were outputted in order to manipulate the graphs according to different classifications.

```
##      accepted_name accepted_rank max_ma min_ma      family      genus
## 1 Gomphotherium      genus    8.700 5.3330 Gomphotheriidae Gomphotherium
## 2 Tetralophodon      genus    8.700 5.3330 Gomphotheriidae Tetralophodon
## 3 Zygolophodon      genus    8.700 5.3330      Mammutidae Zygolophodon
## 4      Stegodon      genus   11.608 5.3330      Elephantidae Stegodon
## 5      Elephas      genus    0.781 0.0117      Elephantidae Elephas
## 6      Stegodon      genus    0.781 0.0117      Elephantidae Stegodon
##          lng          lat
## 1 102.06667 25.01667
## 2 102.06667 25.01667
## 3 102.06667 25.01667
## 4  76.66666 31.53333
## 5 111.56667 22.76667
## 6 111.56667 22.76667
```

Below shows the function in creating the Graph:

```
# first of all we needed to import a world map
library(maps)
library(ggplot2)
world_map <- map_data("world")

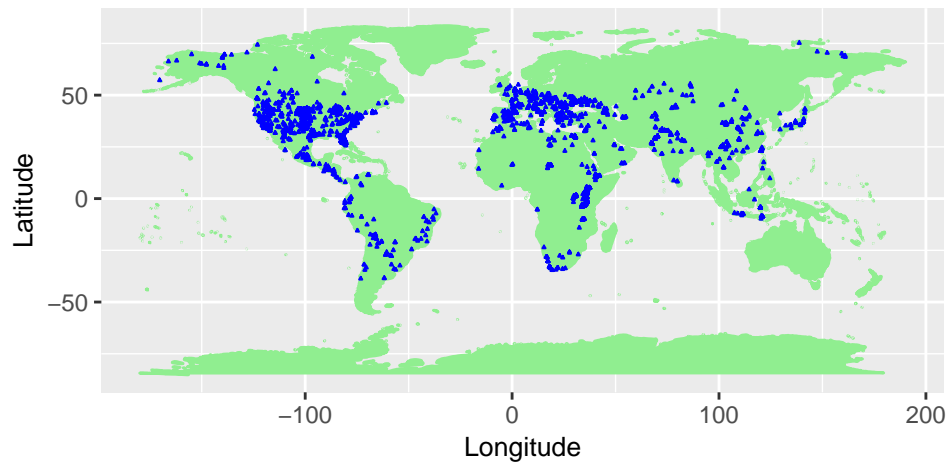
#Then, we needed to create a base plot with ggplot2
p <- ggplot() + coord_fixed() + xlab("") + ylab("")

#Add map to base plot
base_world_messy <- p + geom_polygon(data=world_map, aes(x=long, y=lat, group=group), co

# next we need to put the data(lng and lat) to the map
map_data <-
  base_world_messy + geom_point(data=proboscidea,aes(x=lng, y=lat), colour="Blue",pch=2,

# show the map
map_data
```

Fossil Records on World Map



In order to see *Proboscidea* appearance over time, a graph with coloring according to time was created. This shows us not only the appearance of fossil fuels, we can also use this graph to see the pattern of spreading of *Proboscidea*.

```
#Create a base plot with ggplot2
p <- ggplot() + coord_fixed() + xlab("") + ylab("")

#Add map to base plot
base_world_messy1 <- p + geom_polygon(data=world_map, aes(x=long, y=lat, group=group), co

# I added this step to make the graph more colorful and more easy to identify the clas
library(RColorBrewer)
```

```
myPalette <- colorRampPalette(rev(brewer.pal(11, "Spectral")))
sc <- scale_colour_gradientn(colours = myPalette(100), limits=c(0, 50))

# plot the data on the graph
map_data <- base_world_messy1 + geom_point(data=proboscidea, aes(x=lng, y=lat, colour=max_ma))

map_data
```

Fossil Records according to Time

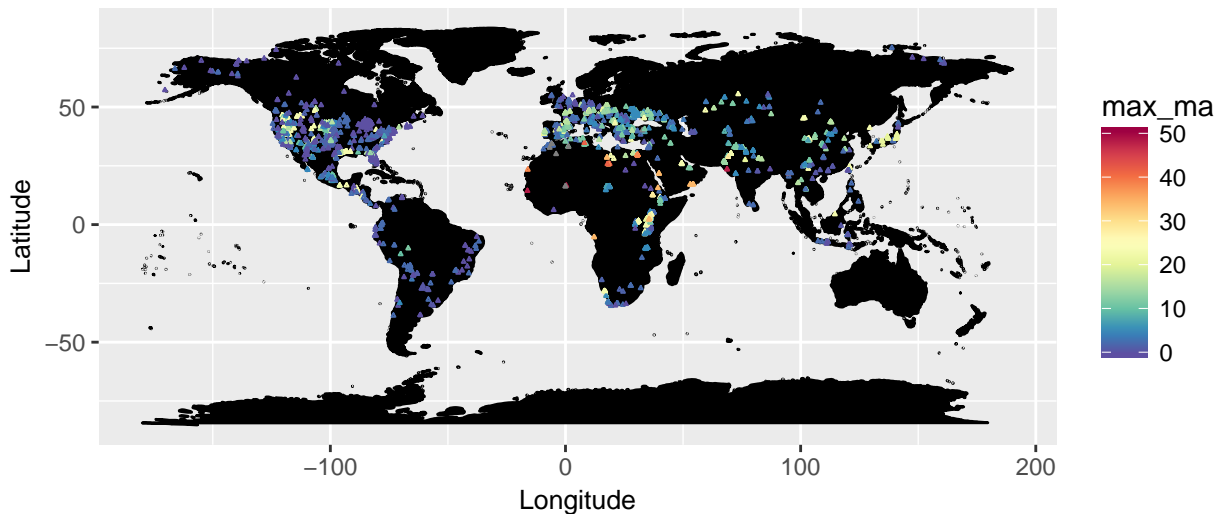
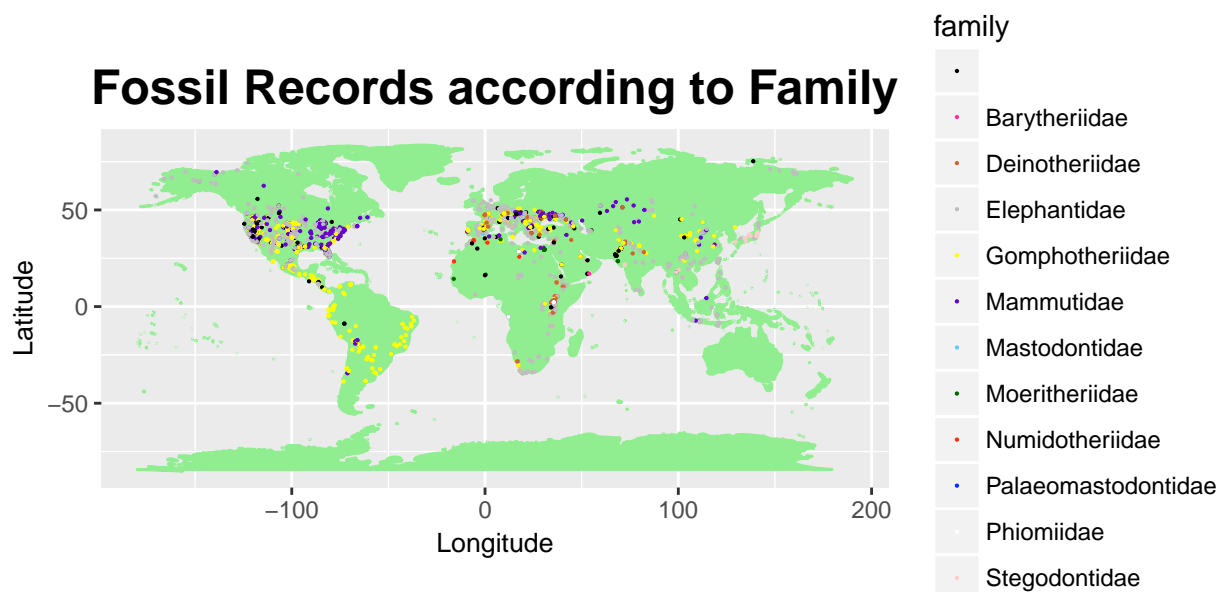


Figure 4: Fossil Records Found and Classifying Them According to Time

By changing the color according to the Family, we get a map that shows where each family was found, which can be later used to understand dispersal pattern:



3. Generating extinction, speciation, and diversification graphs through shell

In order to find out the rates of extinction, speciation, and diversification, the steps we learned in the lab were used to create the figures. The script needed to know the extant species of *Proboscidea*, in this case, the extant species were *Loxodonta cyclotis*, *Loxodonta africana*, *Elephas maximus*.

The PyRate uses the equation below to estimate the rates of speciation and extinction² :

$$P(X|s, e, q) = \prod_{i=1}^n P_{NHPP}(t_1^i, \dots, t_{k_i}^i | s_i, e_i, q)$$

In order to get a flawless data, 10000000 steps in the MCMC chain were used to run PyRate analysis. By using the code (python ~/PyRate/PyRate.py -plot proboscidea_1_marginal_rates.log) in the shell, a PDF with the speciation, extinction, and diversification rates was created.

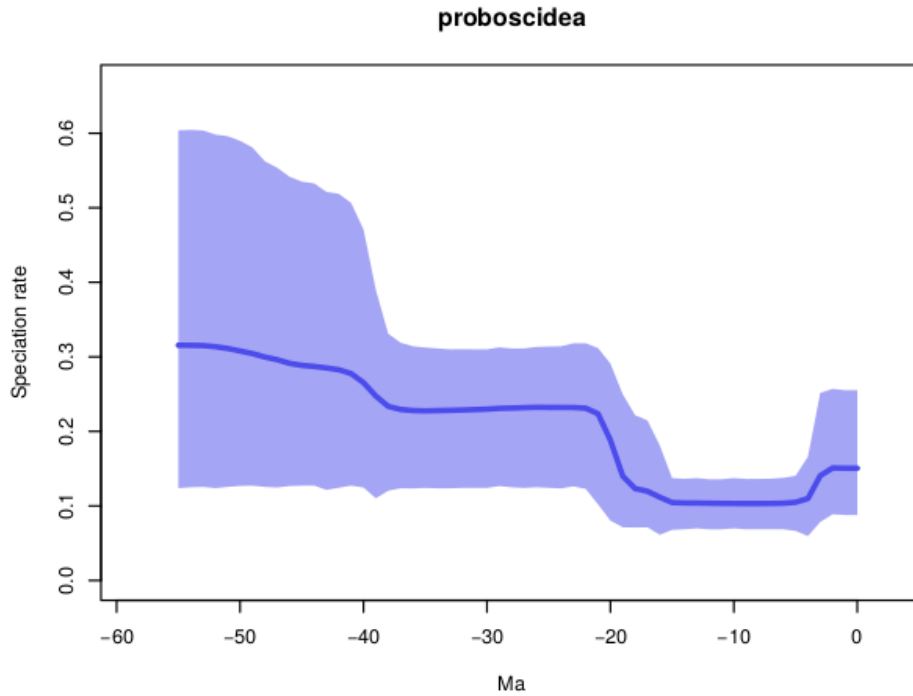


Figure 5: Speciation Rate of Proboscidea

²<https://academic.oup.com/sysbio/article/63/3/349/1650079/Bayesian-Estimation-of-Speciation-and-Extinction>

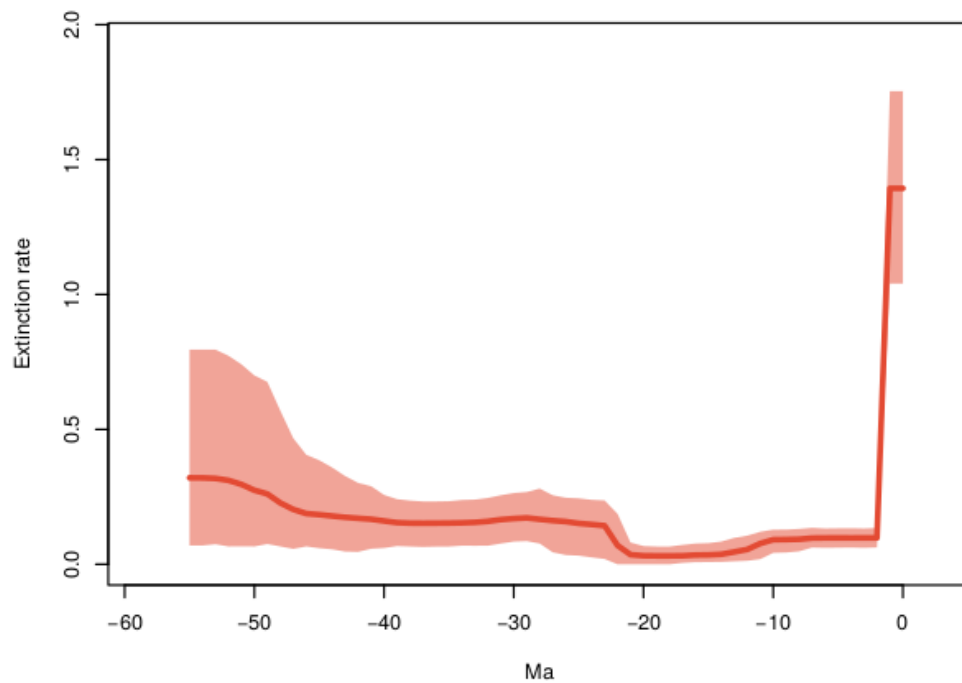


Figure 6: Extinction Rate of Proboscidea

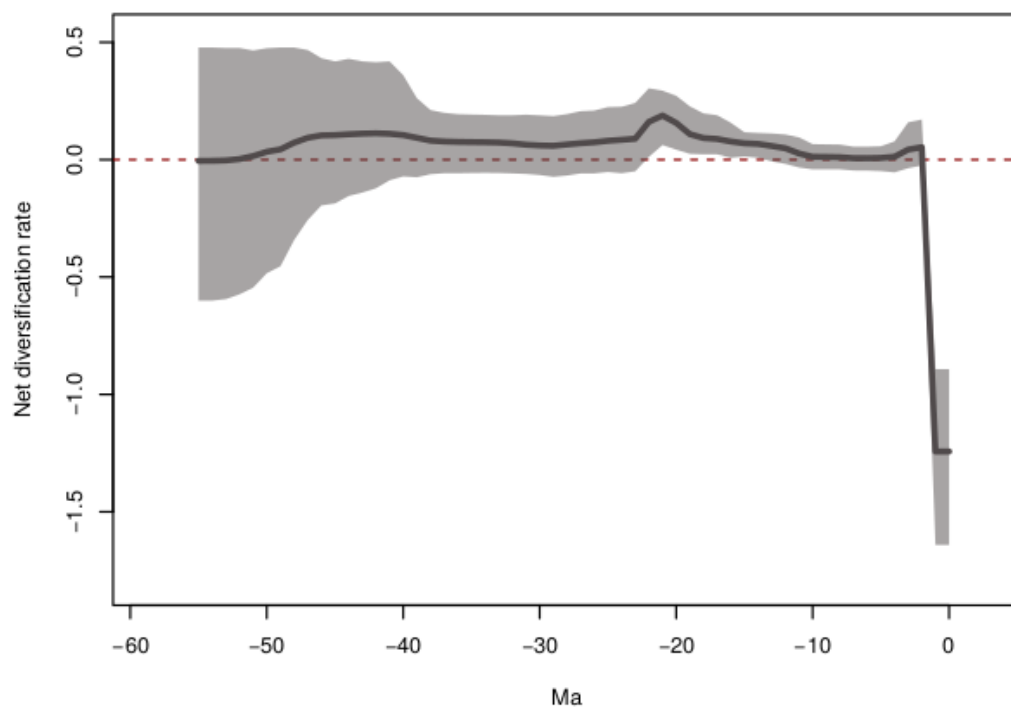


Figure 7: Net Diversification Rate of Proboscidea

Results

Proboscidea is one of the orders that used to be widely spread. According to Proboscidea Fossil Occurrence figure (Figure 2): there were only 4 species of *Proboscidea* recorded during 58-52 ma; no species were recorded during 52-38 ma; since 38 ma to present the number of species recorded raised dramatically, while there was a steep fall in recent years. Moreover, Figure 2 and Figure 3 shows that the number of unique species reached the peak around 10 ma, with a total of 23 species, and another peak around 2 ma, with a total of 20 species. Furthermore, since the colors in Figure 2 are classified by genus, you can see that each genus contains one species that has widest occurrence range, from here we can assume that other species from same genus were evolved from those species.

Figures 3, 4, and 5 show the Fossil Records found on a World Map. As Figure 4 shown, most of the early fossil records are found in Africa, the location of where *Proboscidea* was first originated. They were spreading around the African continent until 35 ma, and reached other continents, such as Europe, Asia and North America, around 25 ma; around 15 ma the first fossil records appeared on South America. Moreover, as seen on the map, most of the fossil records of *Proboscidea* in Europe were from 15-10 ma, while most of the fossil records that were found in North and South America are 2-0 ma. South East Asia also contained records of *Proboscidea* that are from 2-0 ma. Figure 5 shows the fossil records according to the family, which tells us that most widespread families around the world were Gomphotheriidae, Mammutidae, and Elephantidae. While the rest of the species mainly inhabited only one area.

As shown on Figure 3, the diversity of *Proboscidean* were fluctuating in the past 10 ma, with a sharp decrease in last 1 ma. The extinction rate has always been decreasing at a slow rate, however, during the past 1 million year the rate increased from 0.2 to as high as 1.4, as shown on Figure 6. The speciation rate, see Figure 5, was also been slowly decreasing, from 0.3 to 0.1, since the appearance of *Proboscideans* and leveled off to 0.15 in the last 1 ma. The net diversification rate since 60 ma was constant, positively close to 0, as seen on Figure 7. However, the last 1 ma really impacted diversity of *Proboscideans*, the net diversification rate sharply dropped from close to 0 to almost -1.3.

Discussion

Proboscidea once occupied wide variety of habitats, from mountain tops to deserts (Shoshani 1998). As the figure 3 shown, they occupied whole world, except Australia and Antarctica. These large mammals managed to adapt to different environments and spread around the world. But how did they manage to swim across the ocean? No, they did not swim across Atlantic Ocean or Pacific Ocean to get to North America. The continents used to be close to each other million years ago (the next page contains two figures of the Earth: one is 50 million years ago and another one is 35 million years ago). During the time when *Proboscidea* first appeared on the Earth, continents were connected. The first fossil records of *Proboscidea* species that managed to get to North America were around 25 ma, and to South America were around 15 ma; which means that the *Proboscidea* first came to North America, then

gradually moved to South America. Since there were no fossil records on Greenland, the *Proboscideans* never lived or passed Greenland, which means they managed to reach North America directly.



Figure 8: Continent Map - 100 MYA³



Figure 9: Continent Map - 50 MYA⁴

Proboscidea managed to spread around the world in past 60 ma, however, the incoming of humans to their habitats swept them away in just few thousand years (Koch & Barnosky 2006; Lima-Ribeiro *et al.* 2013). Since human geographic ranges were located closely to the ranges of *Proboscidea* habitats, the expansion of human ranges created local extinctions of those species (Surovell *et al.* 2005). In fact, the last-appearance records of *Proboscidea* in South America and the first-appearance records of humans in South America closely correspond (Prado *et al.* 2015). One of the reasons, why human hunting have created such a huge impact on density of these mammals, is *Proboscideans* are considered as slow-breeding mammals, k-selected species (Koch & Barnosky 2006). Since they reproduce slowly and on average they have few amounts of offsprings, in order for them to recover to previous capacity, it would take them a long time (Surovell *et al.* 2005), and with human interference it would take them even longer; therefore, over time the net growth decreased sharply. Another prove that one of the main causes of extinction of *Proboscidean* species is human hunting is that locations, such as sub-Saharan Africa and East Asia, still have wild elephants (Surovell *et al.* 2005). These locations have relatively small amount of people living due insuitable habitats for

³the picture taken from <http://www.nationalgeographic.org/encyclopedia/continental-drift/>

⁴the picture taken from <http://www.nationalgeographic.org/encyclopedia/continental-drift/>

humans to survive. And without human hunting and interference in those locations, species of *Proboscidea* managed to survive till recent days.

Human hunting was not only a reason why *Proboscideans* went extinct, in fact, it was a reason that accelerated the whole rate of extinction (Lima-Ribeiro *et al.* 2013). As seen on figure 6, the extinction rate sharply increased during last thousands to 1 ma, while it was pretty constant before. During the last 1 ma, humans have been populating many places, and in order for them to survive, they had to hunt mammals to gain sufficient energy. Without human hunting, *Proboscideans* would have went extinct 3 times slower due to climatic changes, which was also a reason of extinction (Shoshani 1998). The climate change can alter the habitat range in which the species can live and diversity of fauna, which were the diets of *Proboscideans*. The evidences from Eurasia showed that climate change paced the decline of late Pleistocene megafaunal populations (Koch & Barnosky 2006). Moreover, the change in climate reduced the habitat range, bringing more megafaunal populations together, creating competition for food and space (Shoshani 1998).

Conclusion

Overall, the two main reason of extinction of *Proboscideans* were human hunting and climate change. Although habitat change, competition, and fauna diversity also impacted the extinction, they all considered as the effects of climate change. Right now, there are only 3 extant species (Shoshani & Tassy 2005), out of 115 unique species that lived in this Planet. We need to protect these species and help them to reproduce, so future generations can still have chance to see these beautiful mammals. Humans are creating the sixth mass extinction (Ceballos *et al.* 2015) and every mass extinction kills, on average, over 70% of species. We need to find ways to protect these species, so they won't get completely wiped away from the Earth.

Please click on the text below to see the whole Github of the final project:

Linna's Github link

References

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