

## BEAST Tutorial

BEAST is used for Bayesian evolutionary analysis of molecular sequences using MCMC and the inference is derived using rooted, time measured phylogenetic tree. Various utilities programs are used for the analysis such as BEAUti (Bayesian Evolutionary Analysis Utility), LogCombiner, TreeAnnotator, Tracer and FigTree.

The following tutorial was used for the analysis of the divergence times of the bears:

<https://taming-the-beast.github.io/tutorials/FBD-tutorial>

All the steps were followed in accordance with the tutorial and the files obtained are included. And finally, R package was used to visualize the summary tree with a geological timescale.

# Installing the strap package

```
install.packages("strap", dependencies=TRUE)
```

# Installing the phytools package

```
install.packages("phytools", dependencies=TRUE )
```

# Installing the remotes package

```
install.packages("remotes")
```

# Using the remotes package to install phyloch package

```
remotes::install_github("fmichonneau/phyloch")
```

# Loading the strap package and reading the tree using the ape function read.nexus()

```
library("strap")  
tree<-read.nexus("C:/Users/ssapkot1/Desktop/CourseMaterials/EEB
```

# Setting the variable tree\$root.time (age of the root)

```
tree$root.time <- max(dist.nodes(tree))
```

# Plotting the tree using dist.nodes() function from ape

```
geoscalePhylo(tree=ladderize(tree,right=FALSE ),label.offset=0)
```

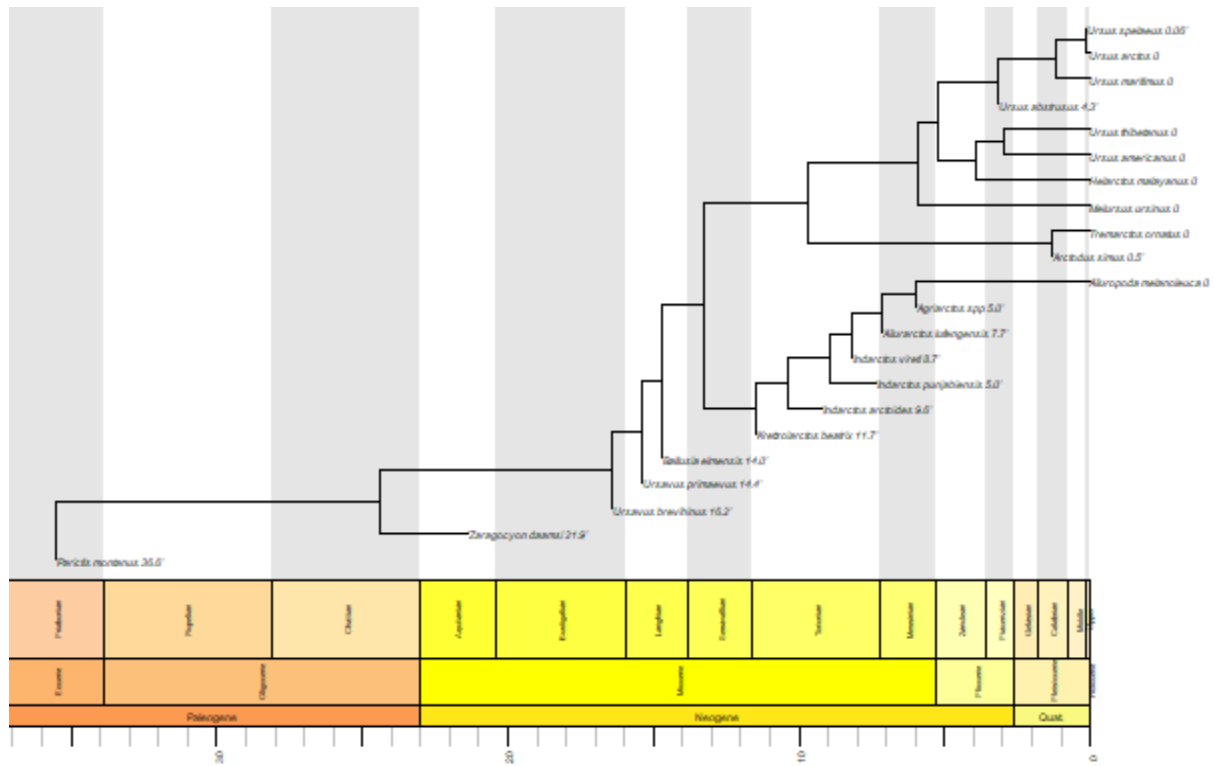


Figure: The maximum clade credibility tree plotted using the strap package in R