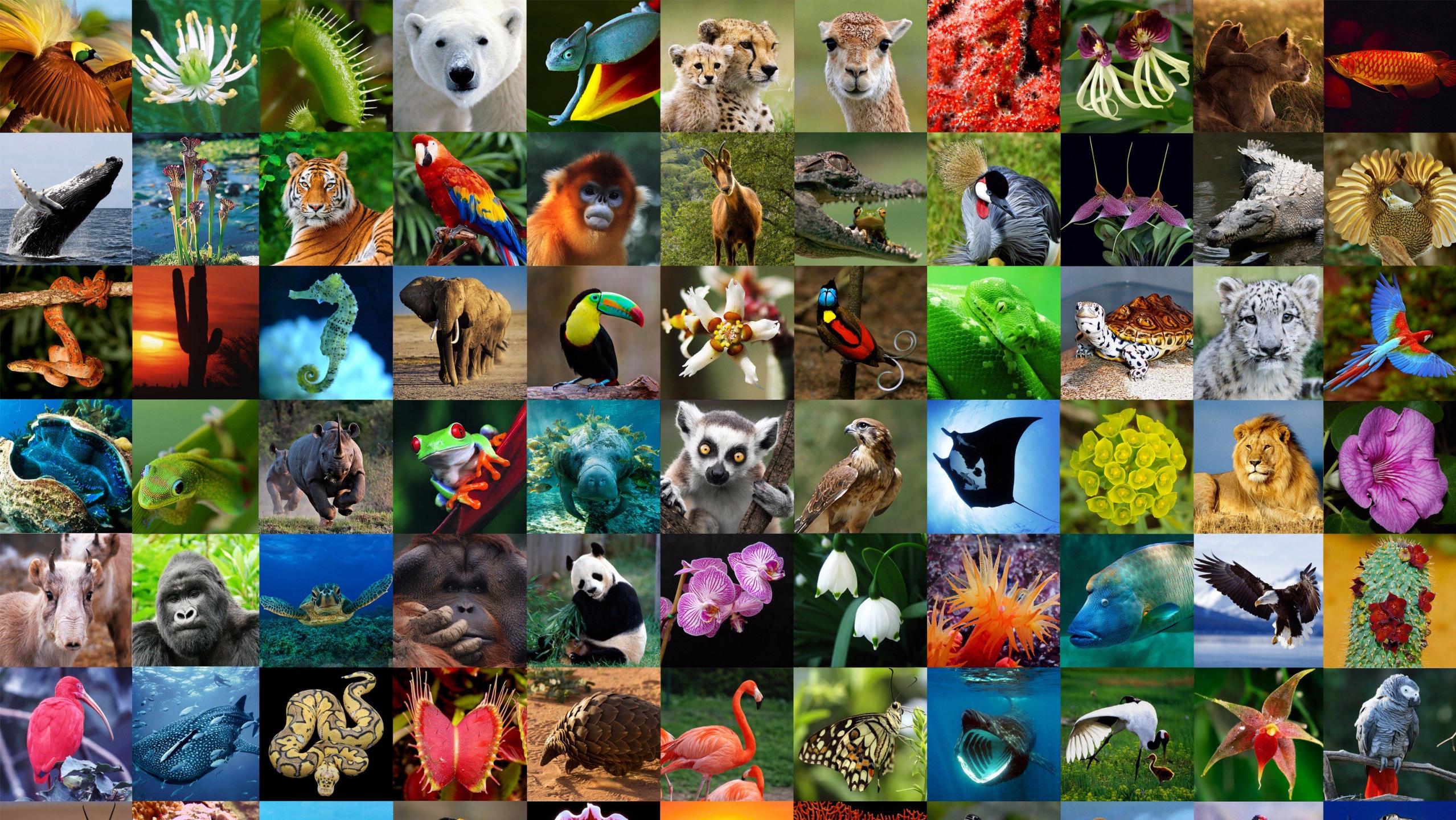




A picture is worth 3.7 billion  
years  
showing evolution in R

Carrie M. Tribble, PhD  
University of Hawai`i at Mānoa





David Patte/ U.S. Fish and Wildlife Service



David Patte/ U.S. Fish and Wildlife Service



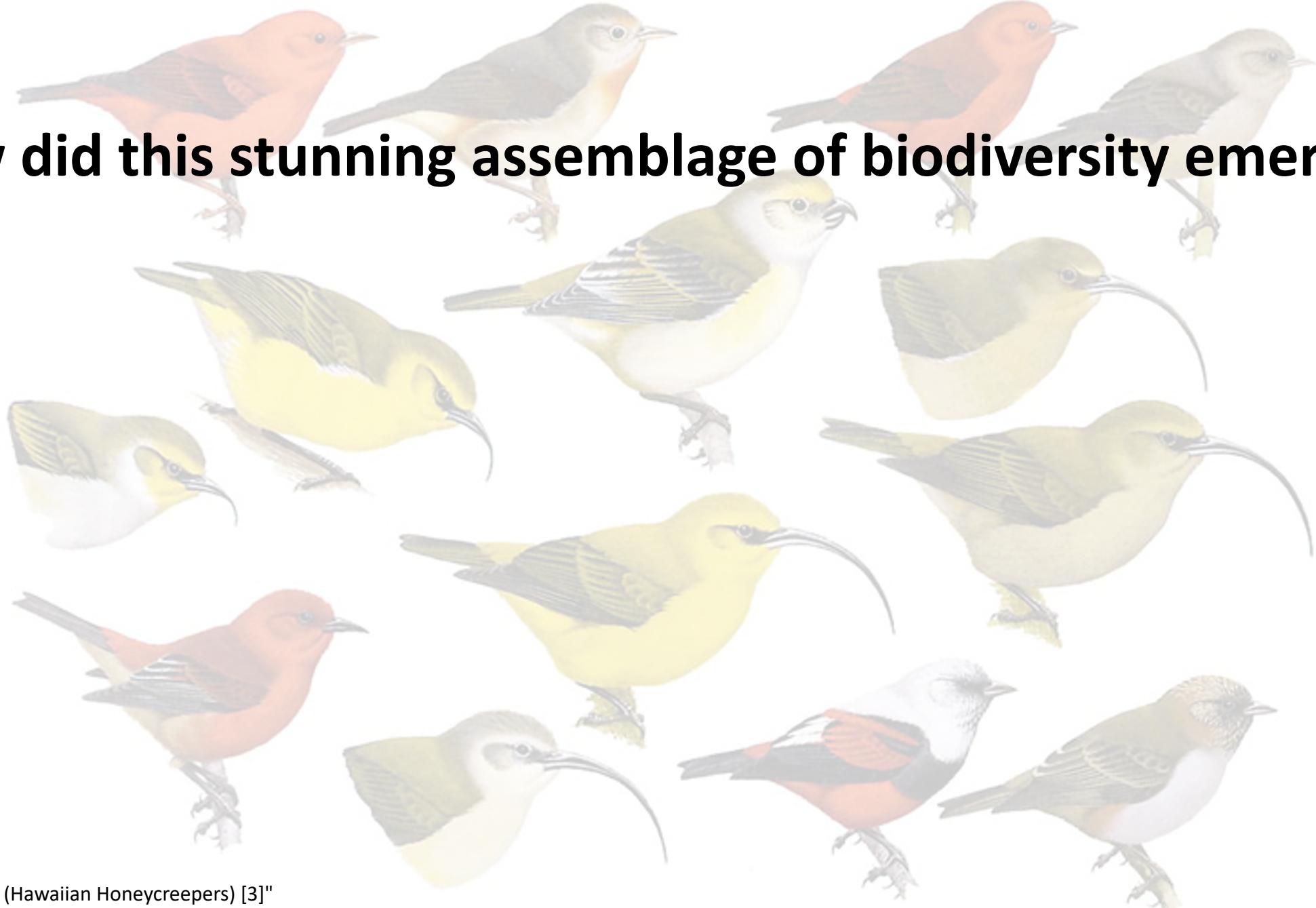
Mikaela Nordborg/ Australian Institute of Marine Science



"Family Drepanididae (Hawaiian Honeycreepers) [3]"

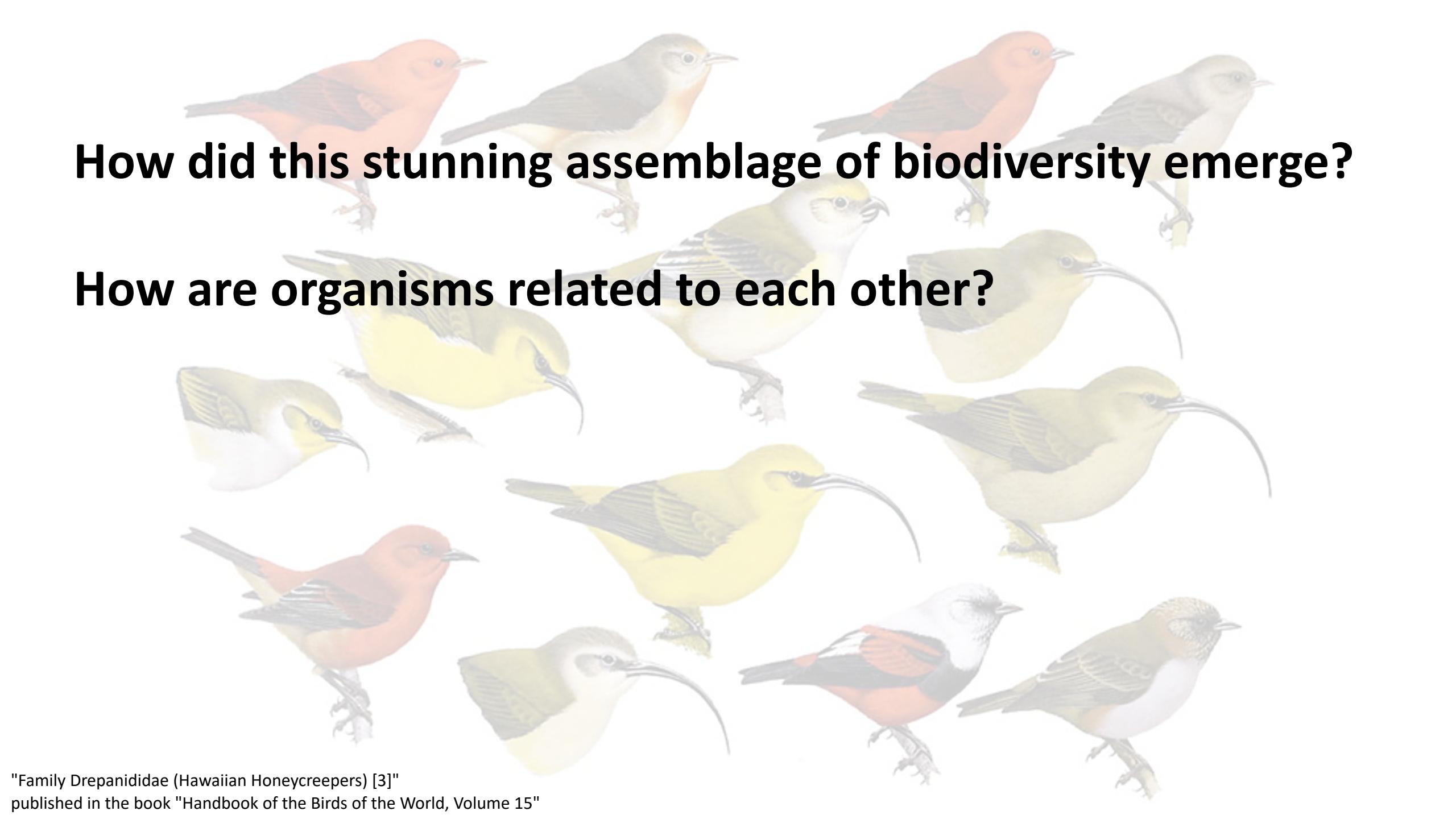
published in the book "Handbook of the Birds of the World, Volume 15"

# How did this stunning assemblage of biodiversity emerge?



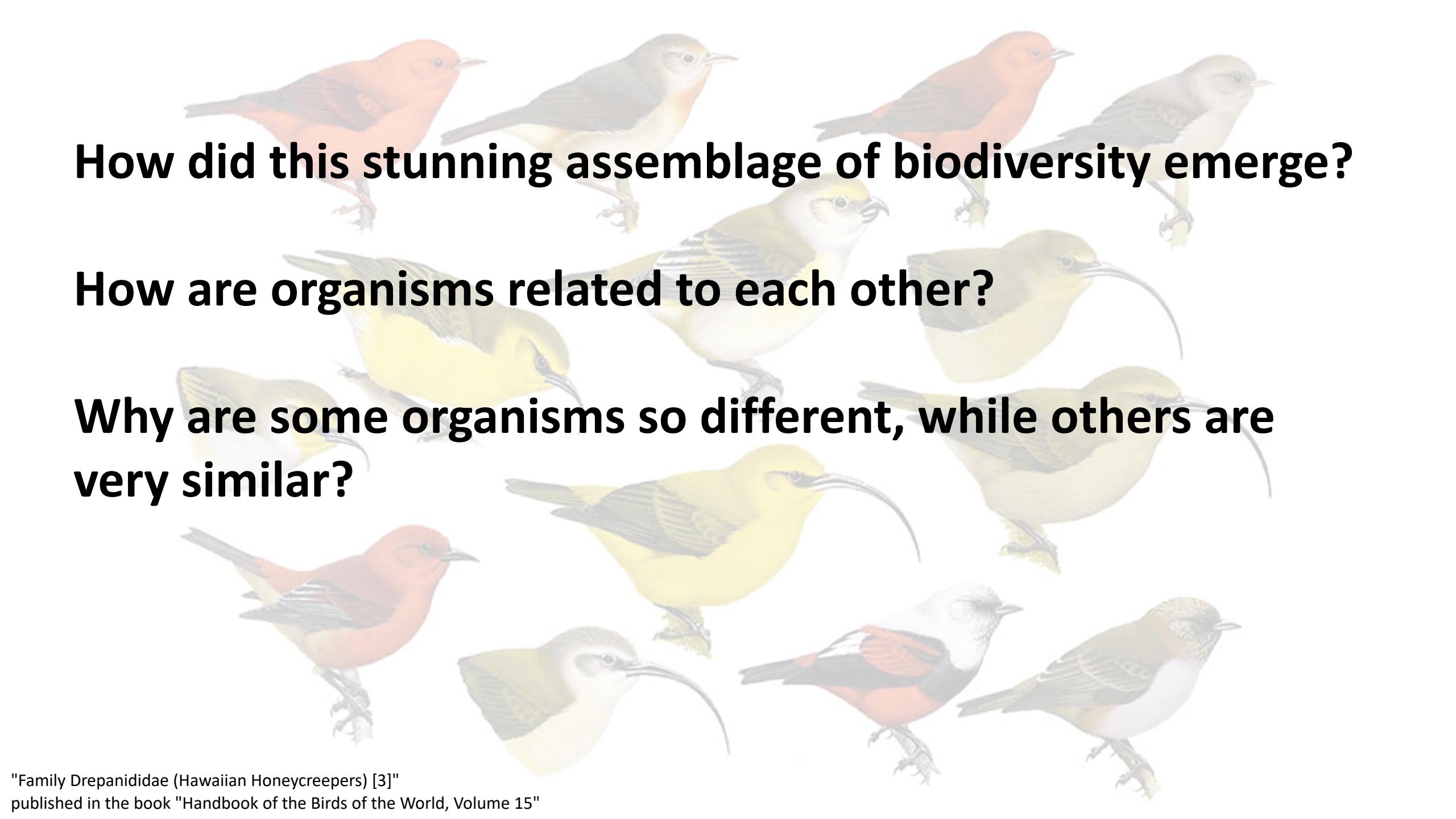
"Family Drepanididae (Hawaiian Honeycreepers) [3]"

published in the book "Handbook of the Birds of the World, Volume 15"



**How did this stunning assemblage of biodiversity emerge?**

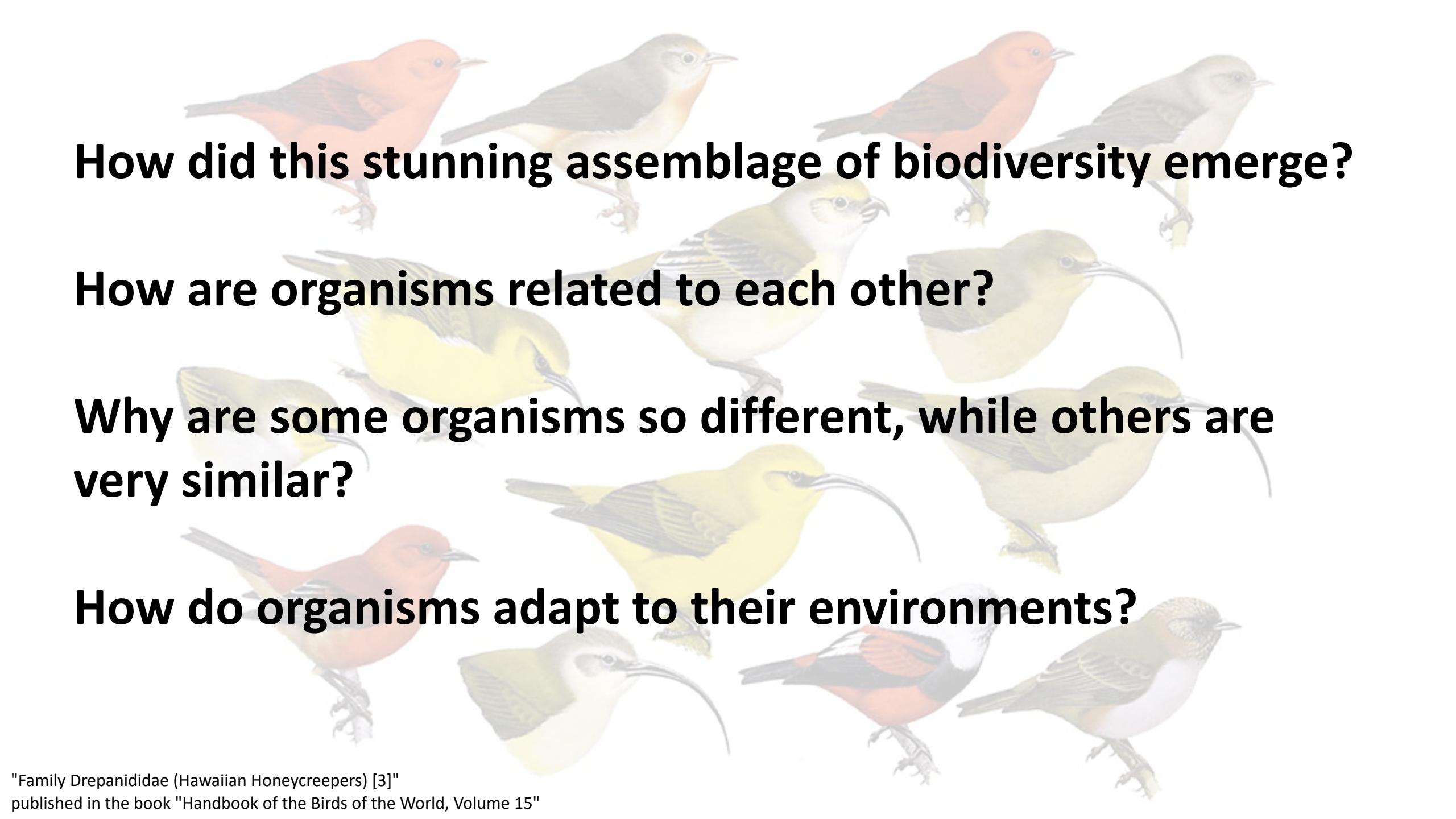
**How are organisms related to each other?**



**How did this stunning assemblage of biodiversity emerge?**

**How are organisms related to each other?**

**Why are some organisms so different, while others are very similar?**



**How did this stunning assemblage of biodiversity emerge?**

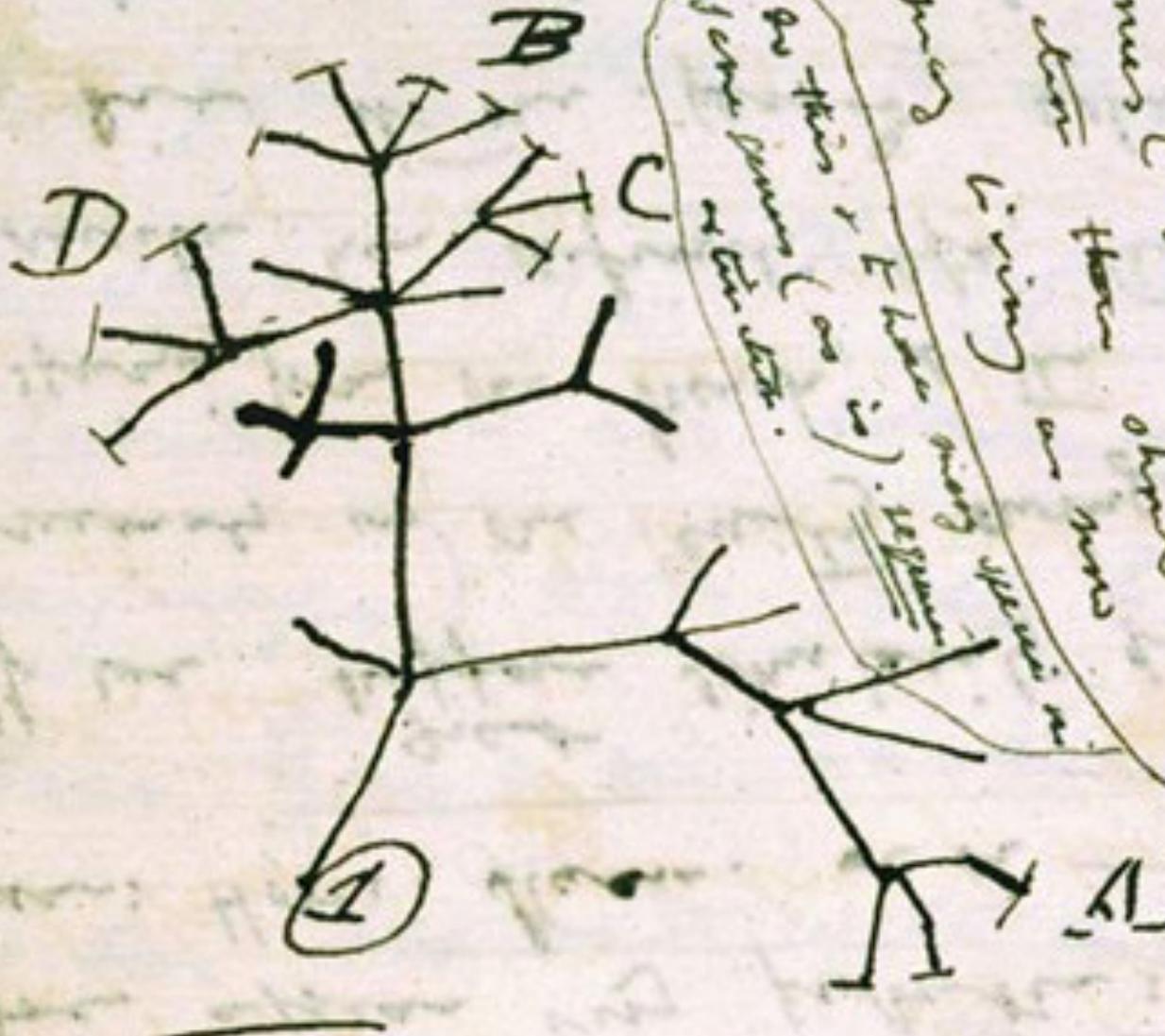
**How are organisms related to each other?**

**Why are some organisms so different, while others are very similar?**

**How do organisms adapt to their environments?**

b

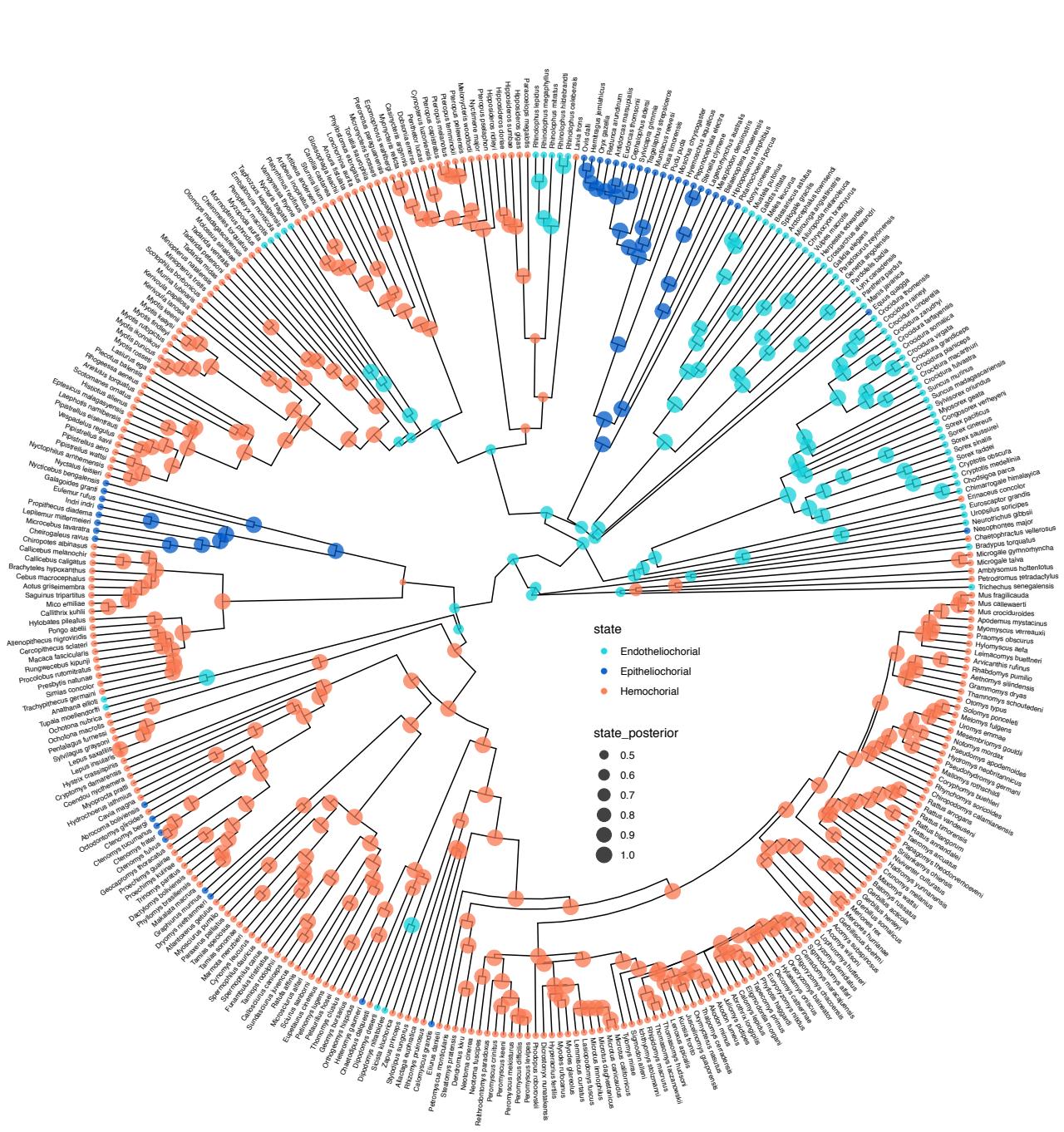
I think there are  
more to be shown in  
one mass than there  
seem to be living or now  
existing many species.  
— now —  
— as this is to have many species  
Do as this is to have many species  
done now (as it is).



I think

# Phylogenetics

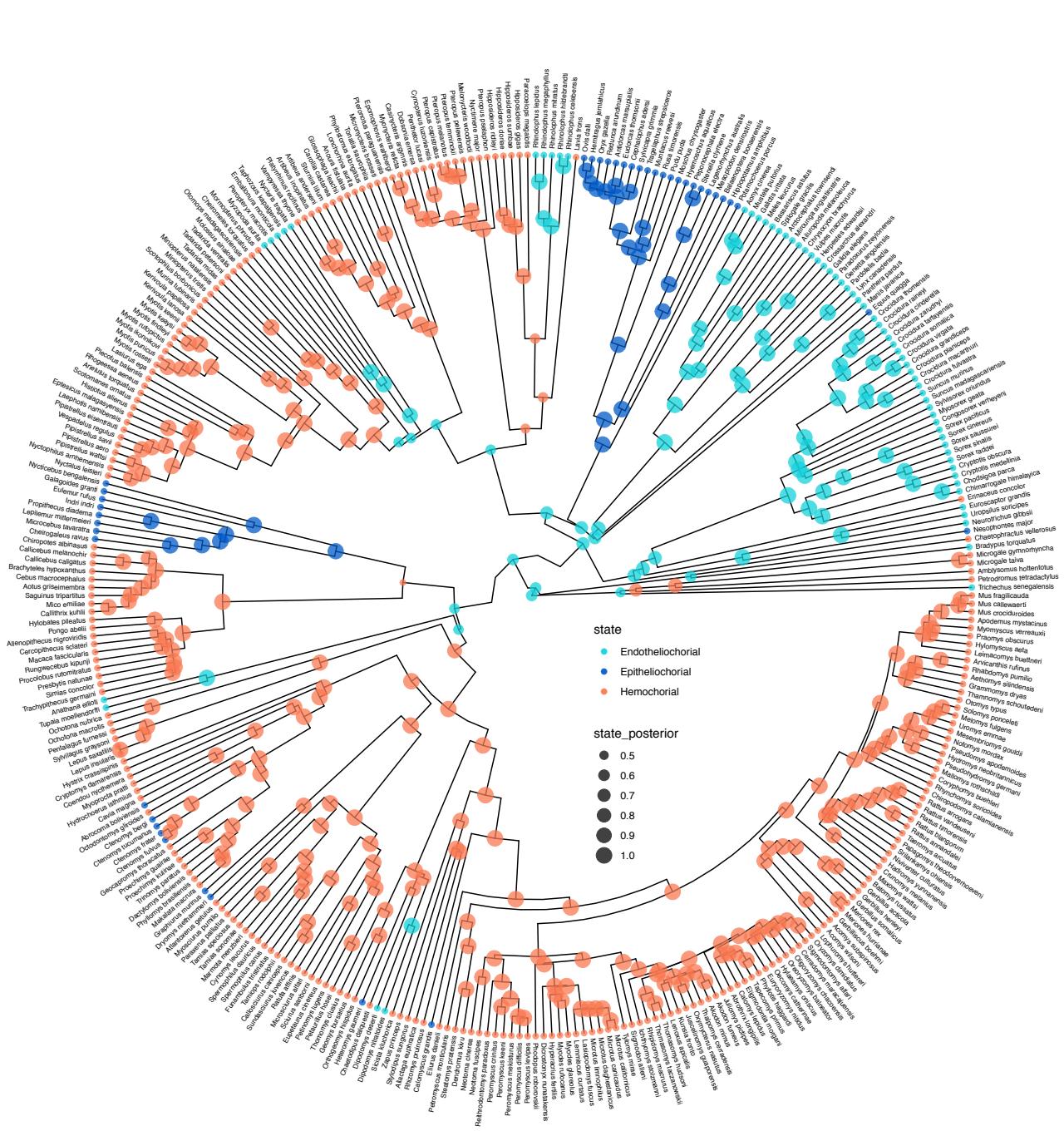
Model relationships between living things



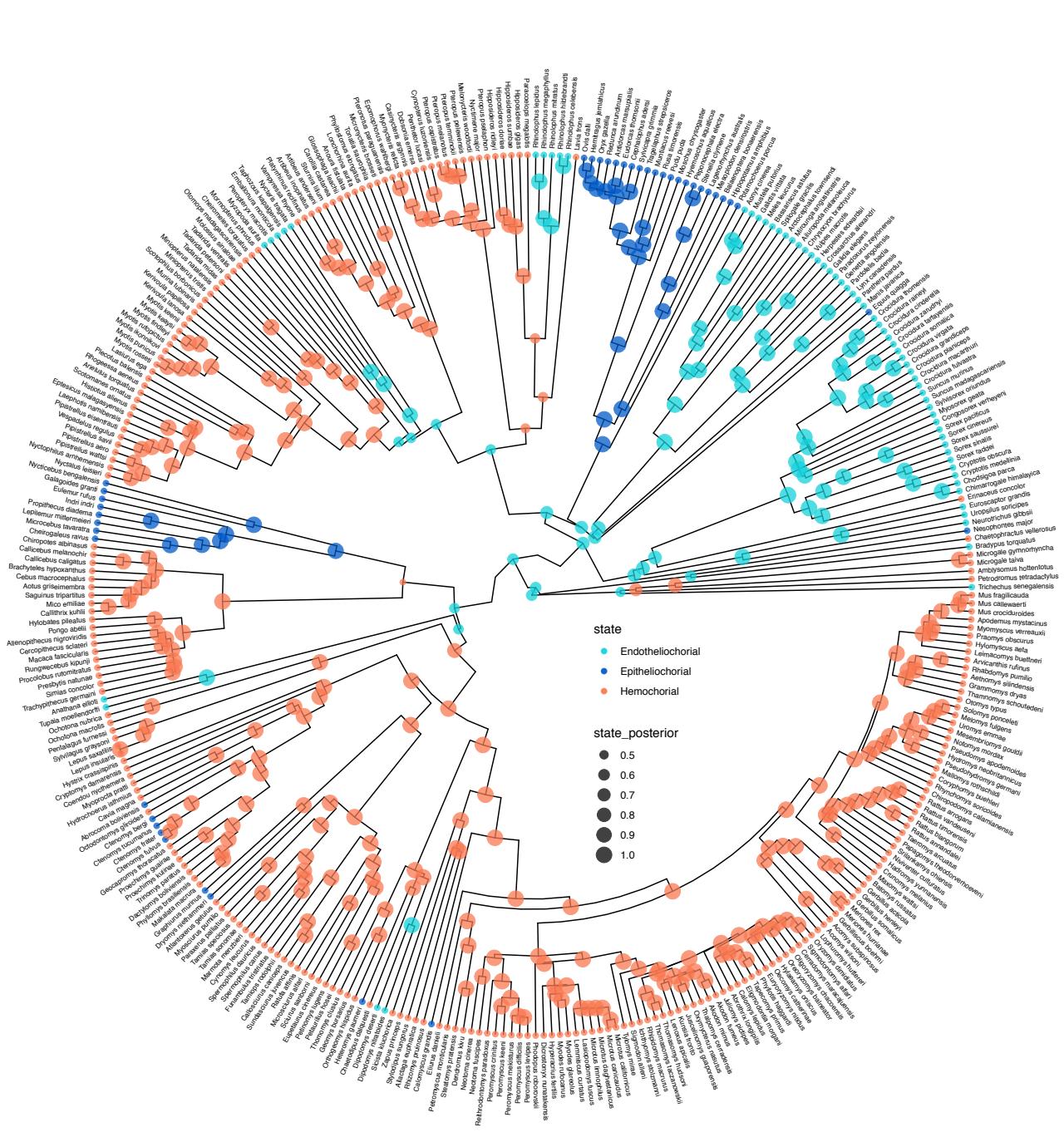
# Phylogenetics

Model relationships between living things

Test hypotheses with statistical models



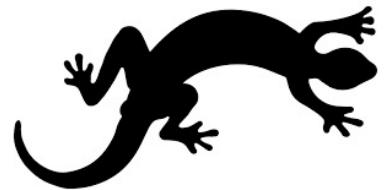
# Phylogenetics

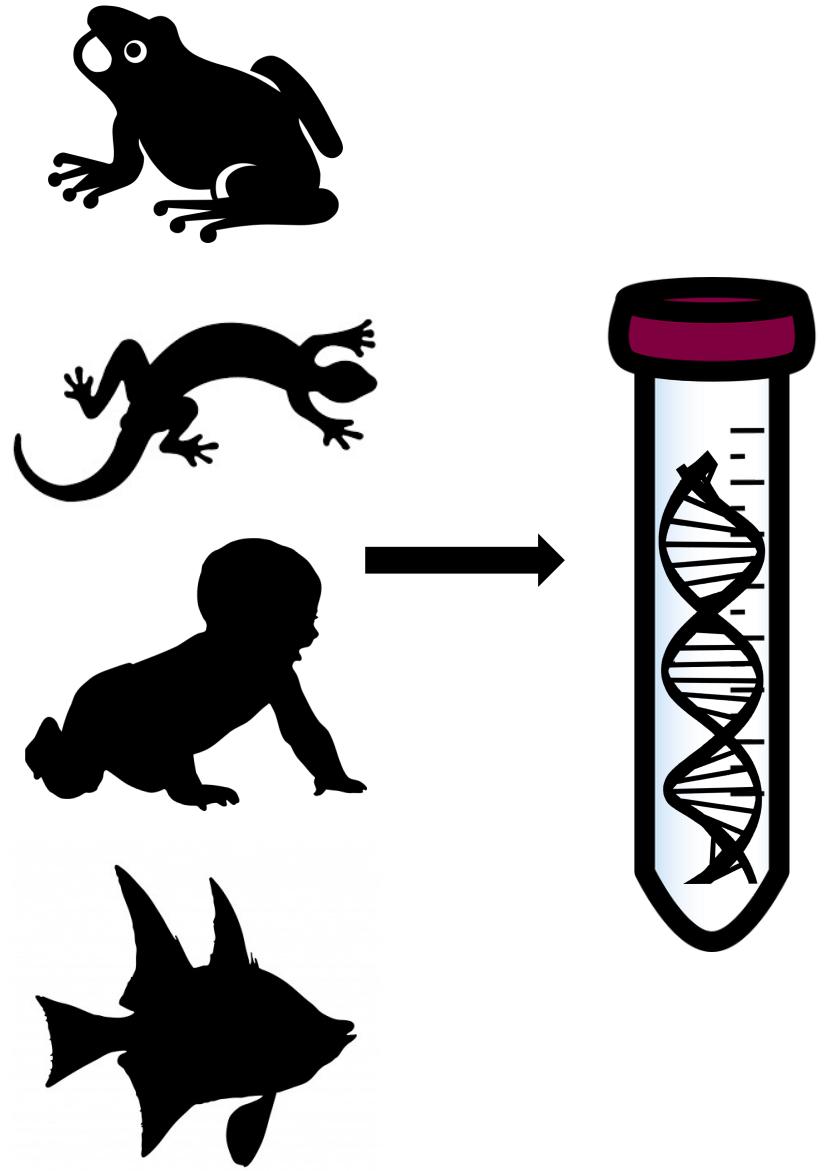


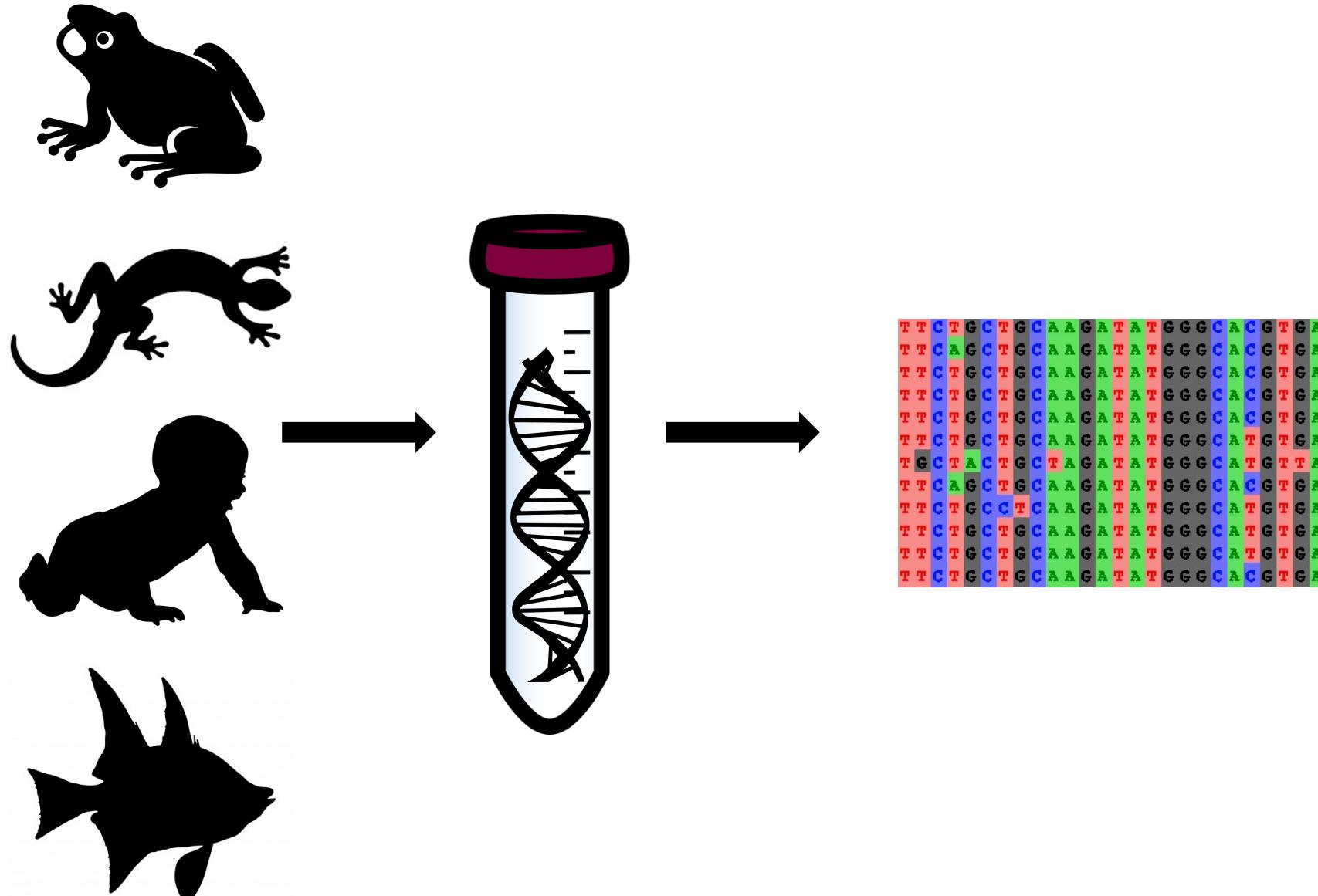
Model relationships between living things

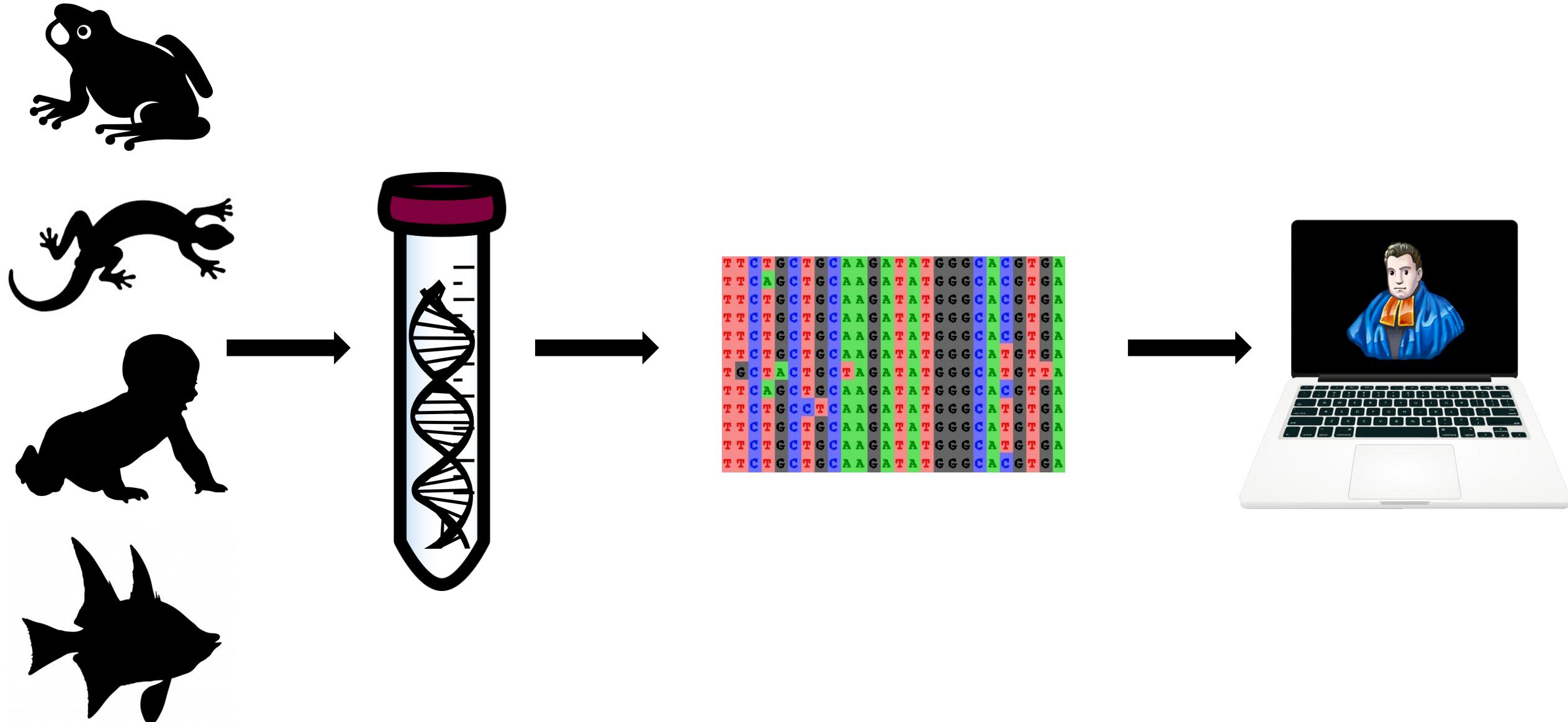
Test hypotheses with statistical models

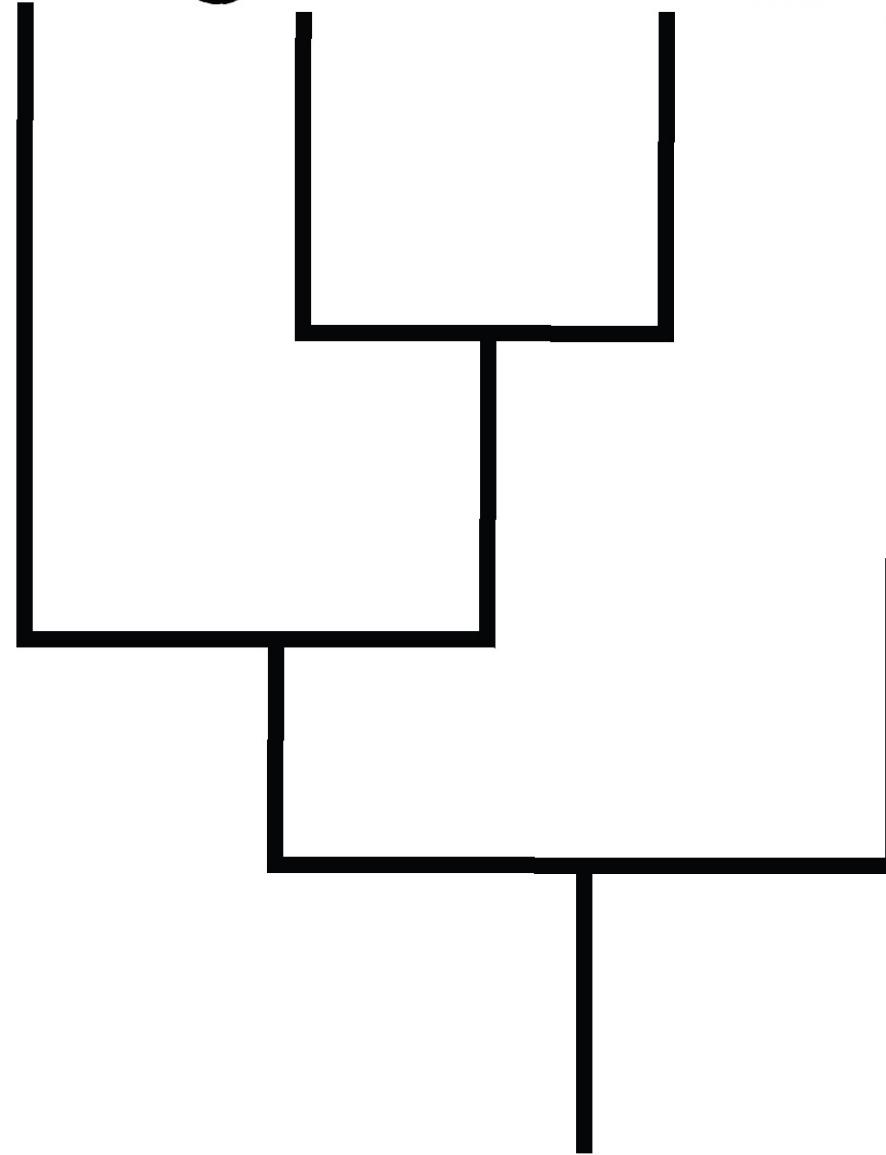
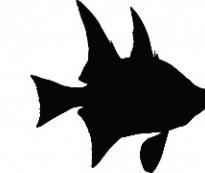
Integrates statistics, computer science, and biology

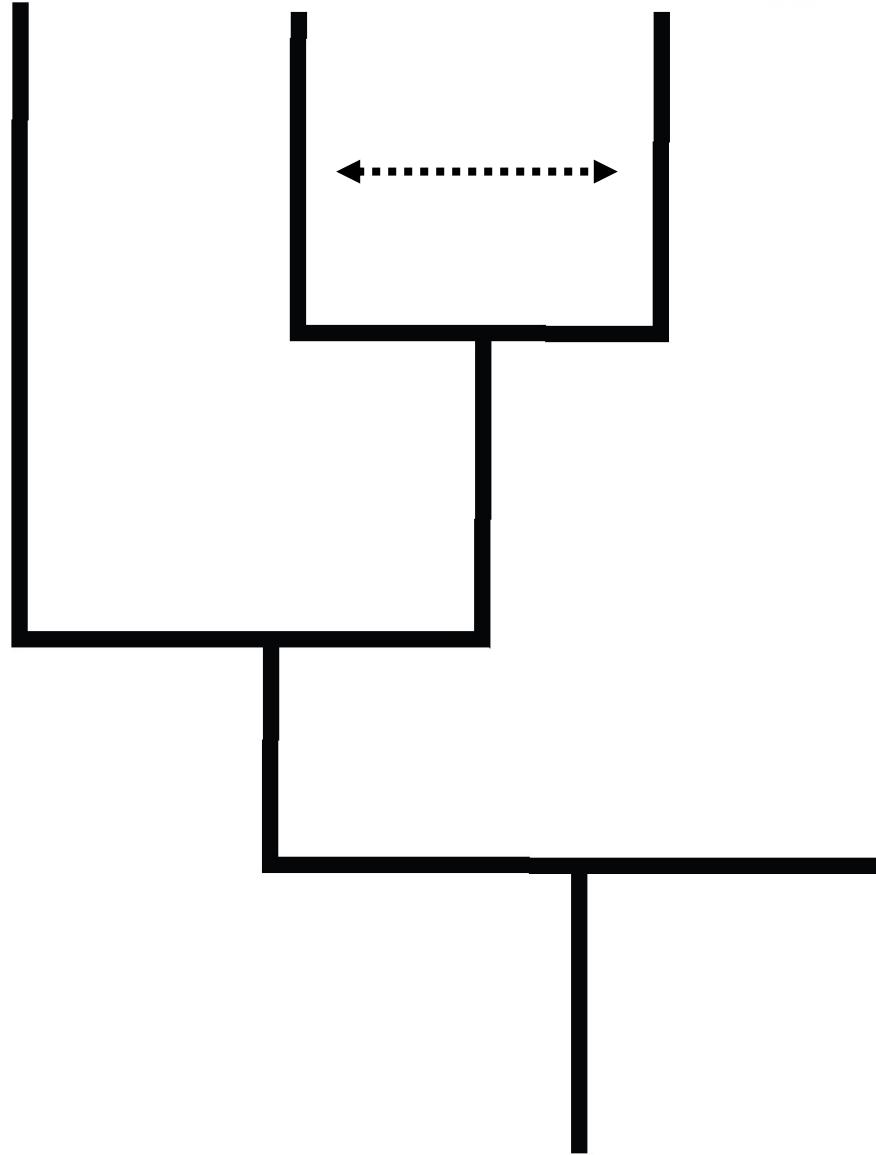
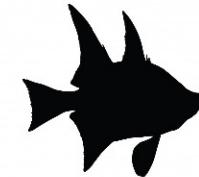


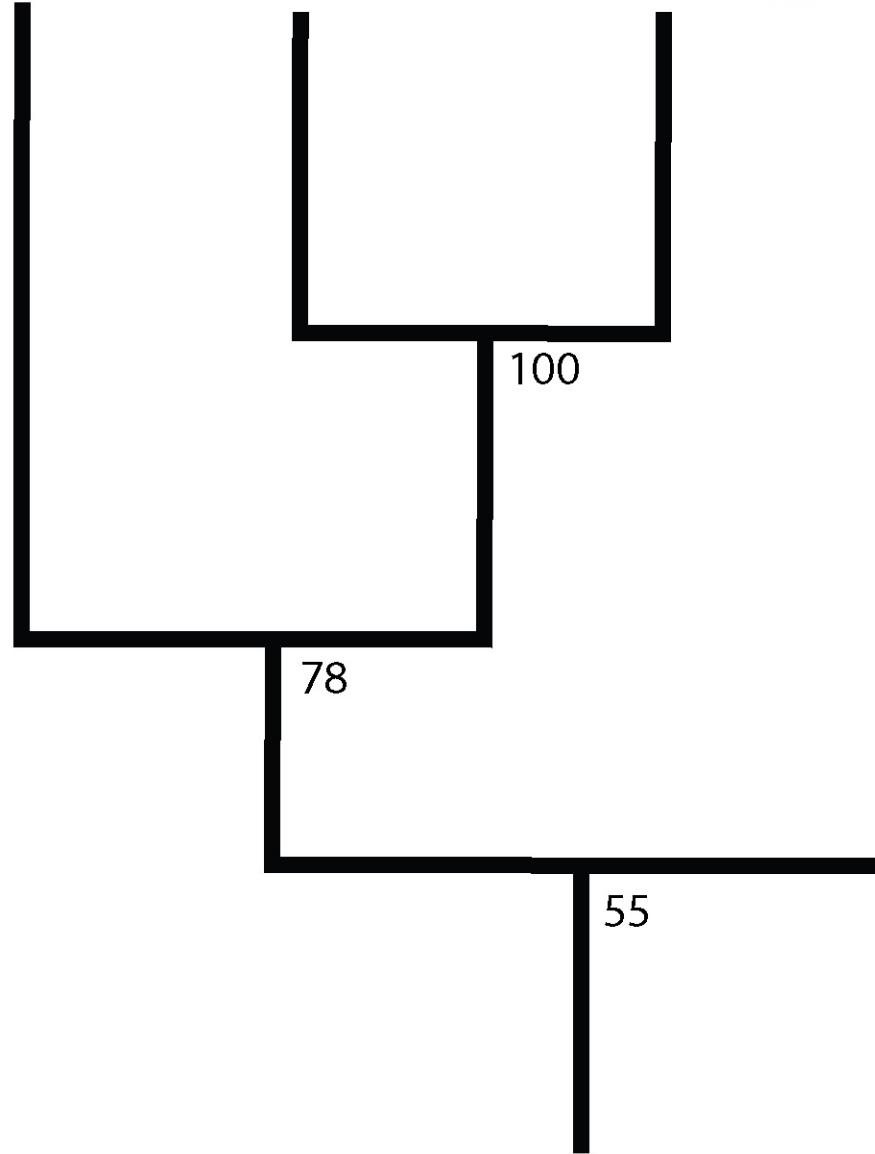
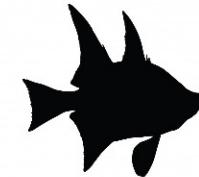


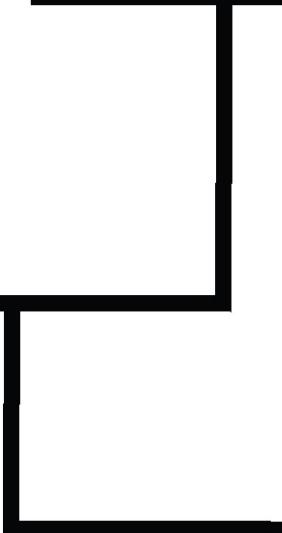
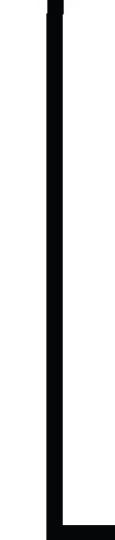
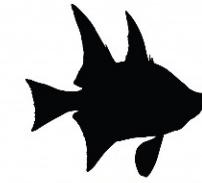


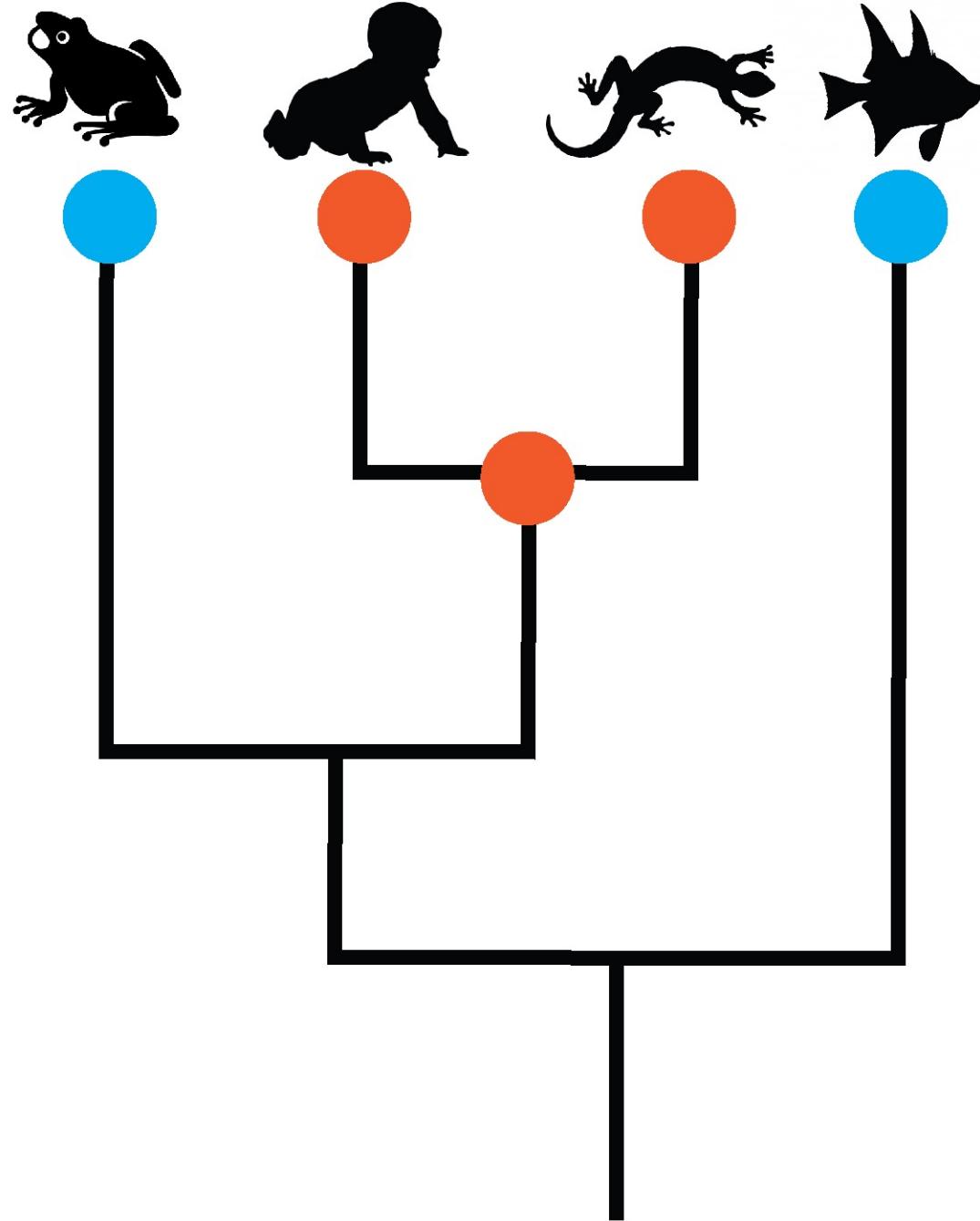


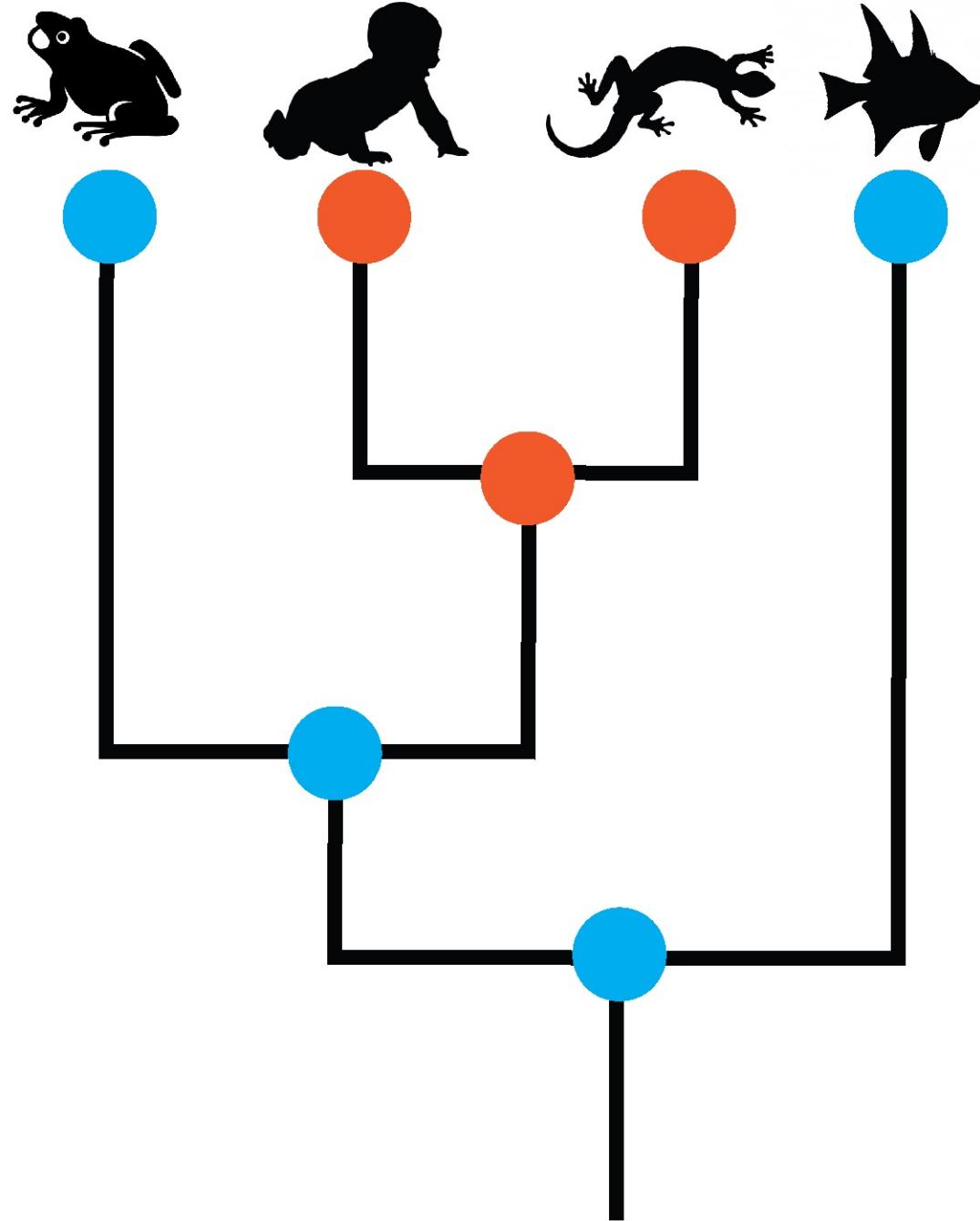


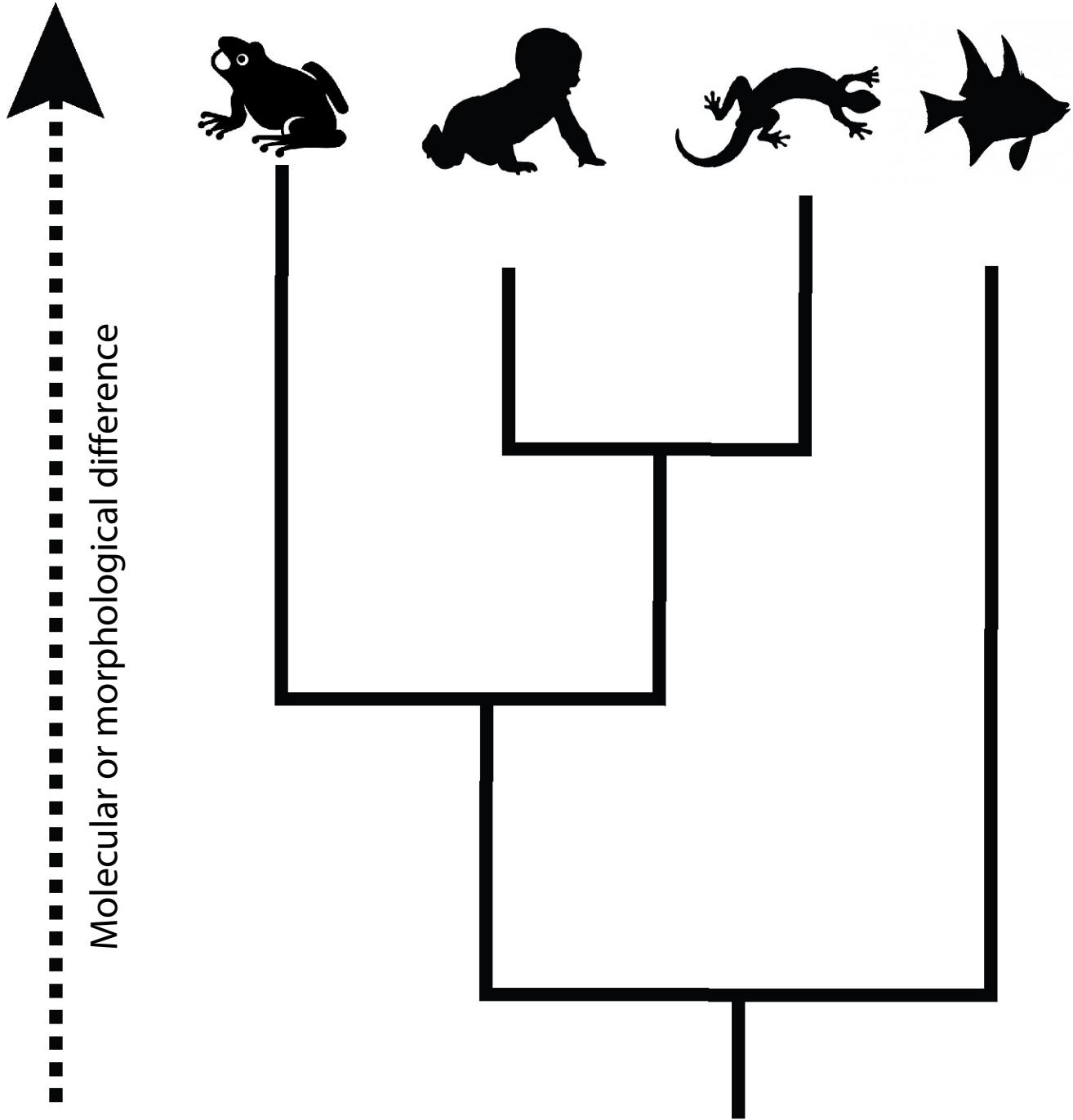


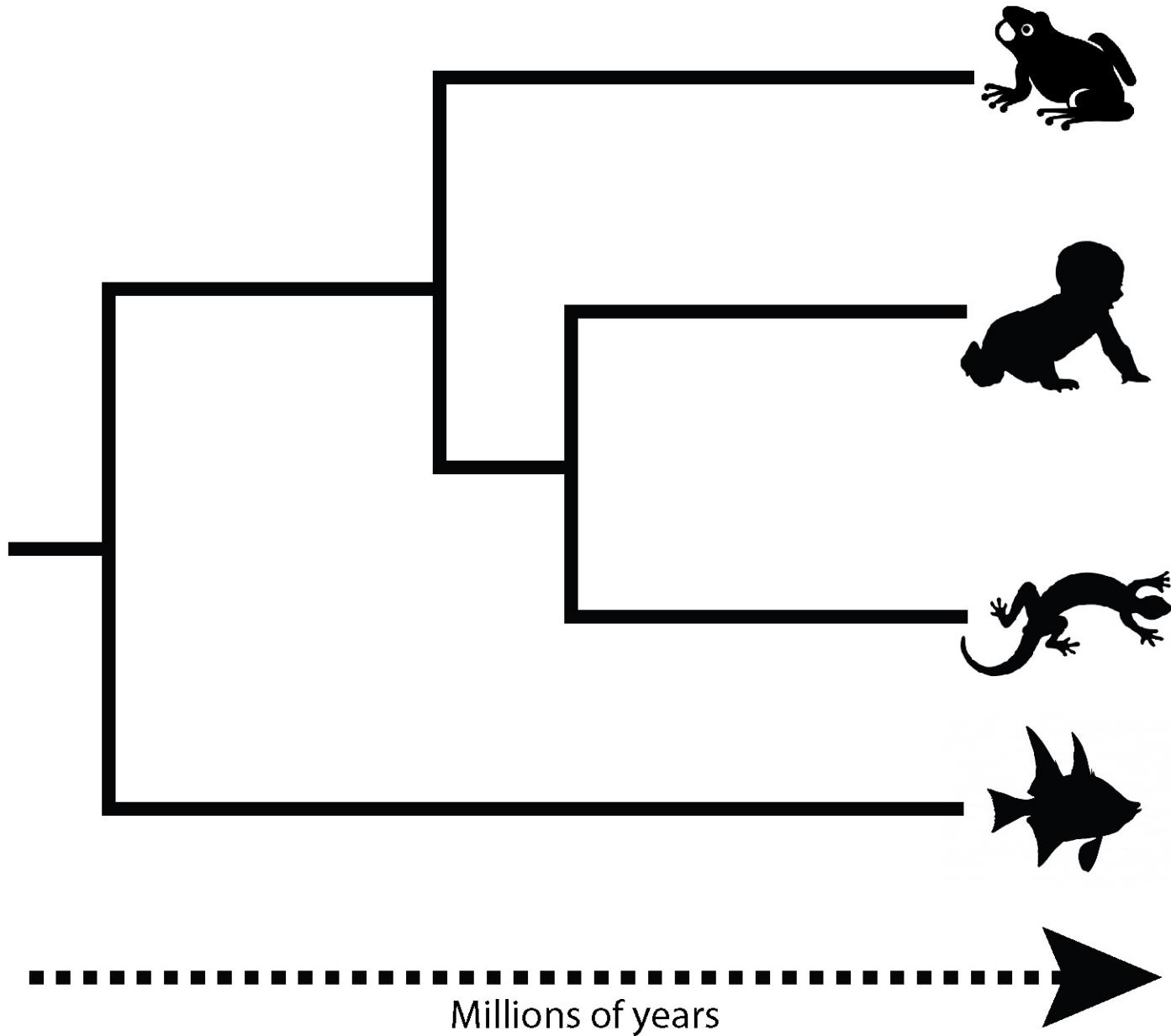




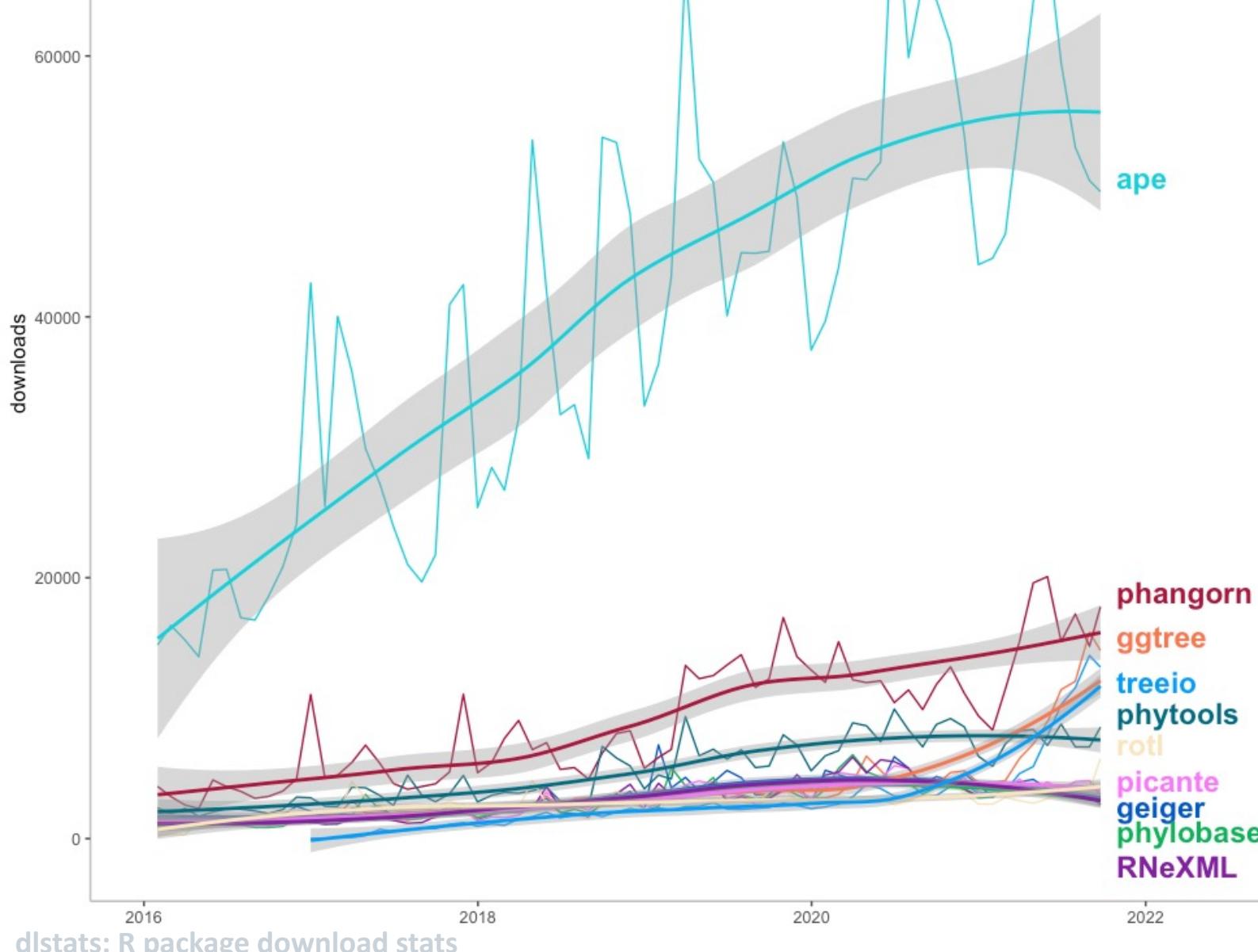




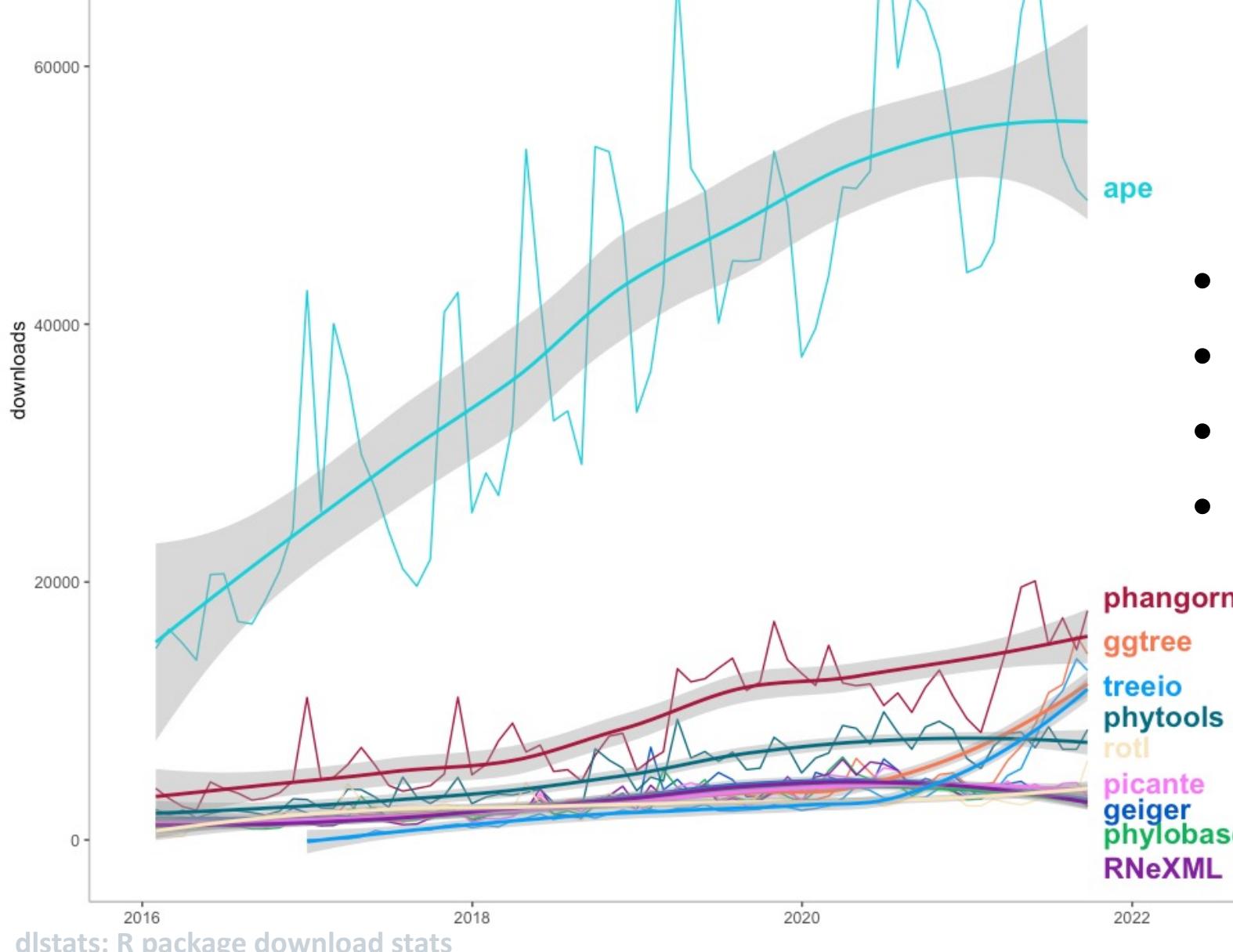




# What do we do with the tree of life in R?

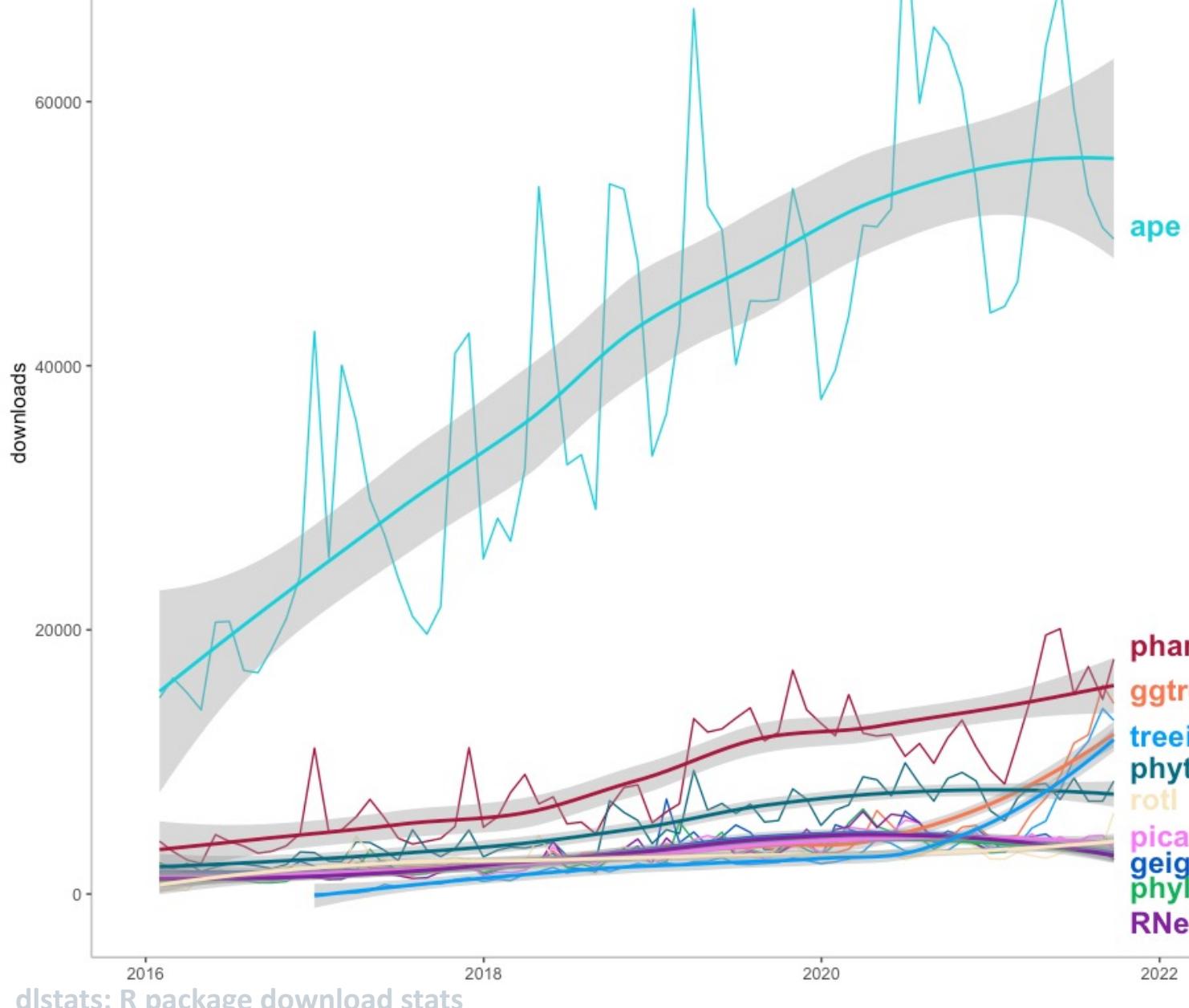


# What do we do with the tree of life in R?



- read and parse tree objects
- build trees
- analyze data on trees
- plot trees and data

# What do we do with the tree of life in R?



Dr. Carrie M. Tribble  
@TribbleTweets ...

Hello phylotweeps! How do you use R in your work?

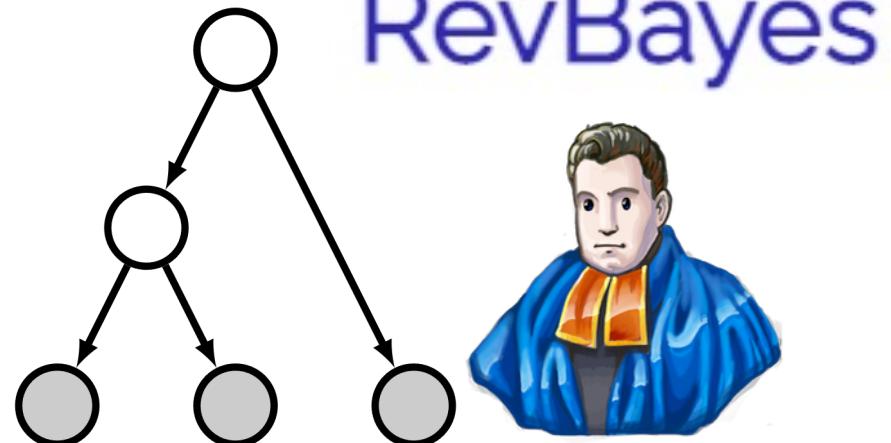
Build phylogenies in R	7.4%
Comparative analyses in R	81.5%
Never use R	11.1%

54 votes · Final results

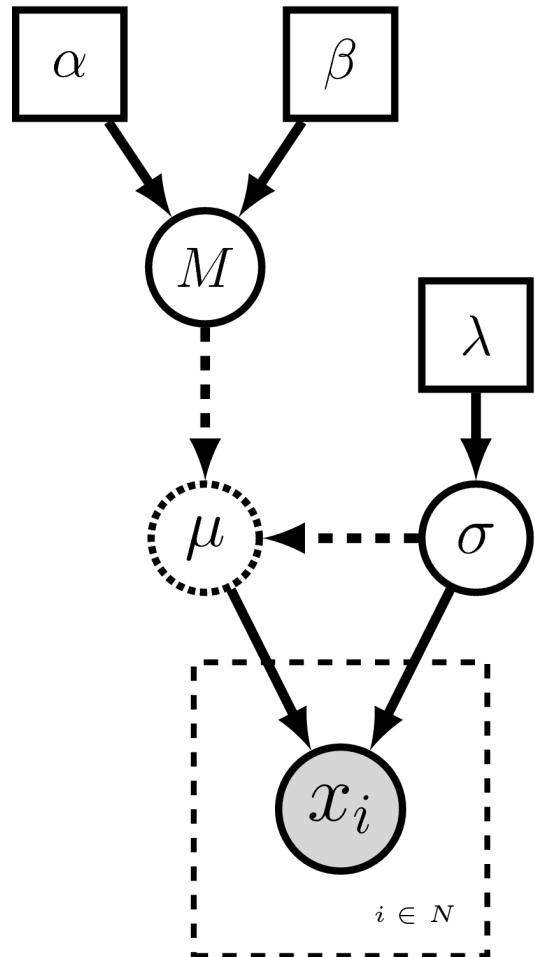




The logo for Julia. The word "julia" is written in a large, bold, black sans-serif font. Above the letter "u", there are four small colored circles: a blue circle on the top left, a red circle on the top right, a green circle on the top center, and a purple circle on the bottom right.

The word "julia" in a large, bold, black sans-serif font. Above the letter "i", there are four small colored circles: blue, red, purple, and green.

# Probabilistic Graphical Models in RevBayes



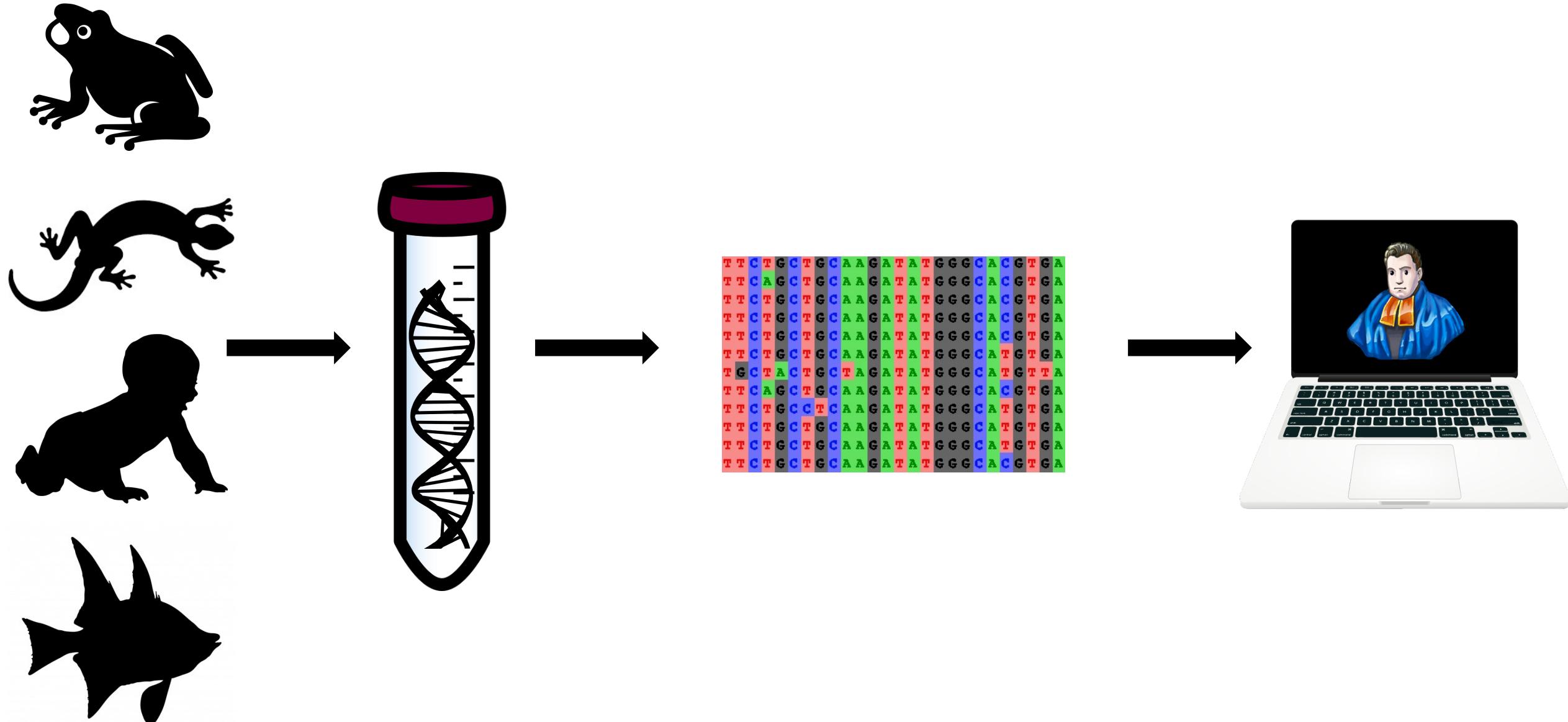
```
observations <- [<your data go here>]

alpha <- 3.0
beta <- 1.0
M ~ dnGamma(alpha, beta)

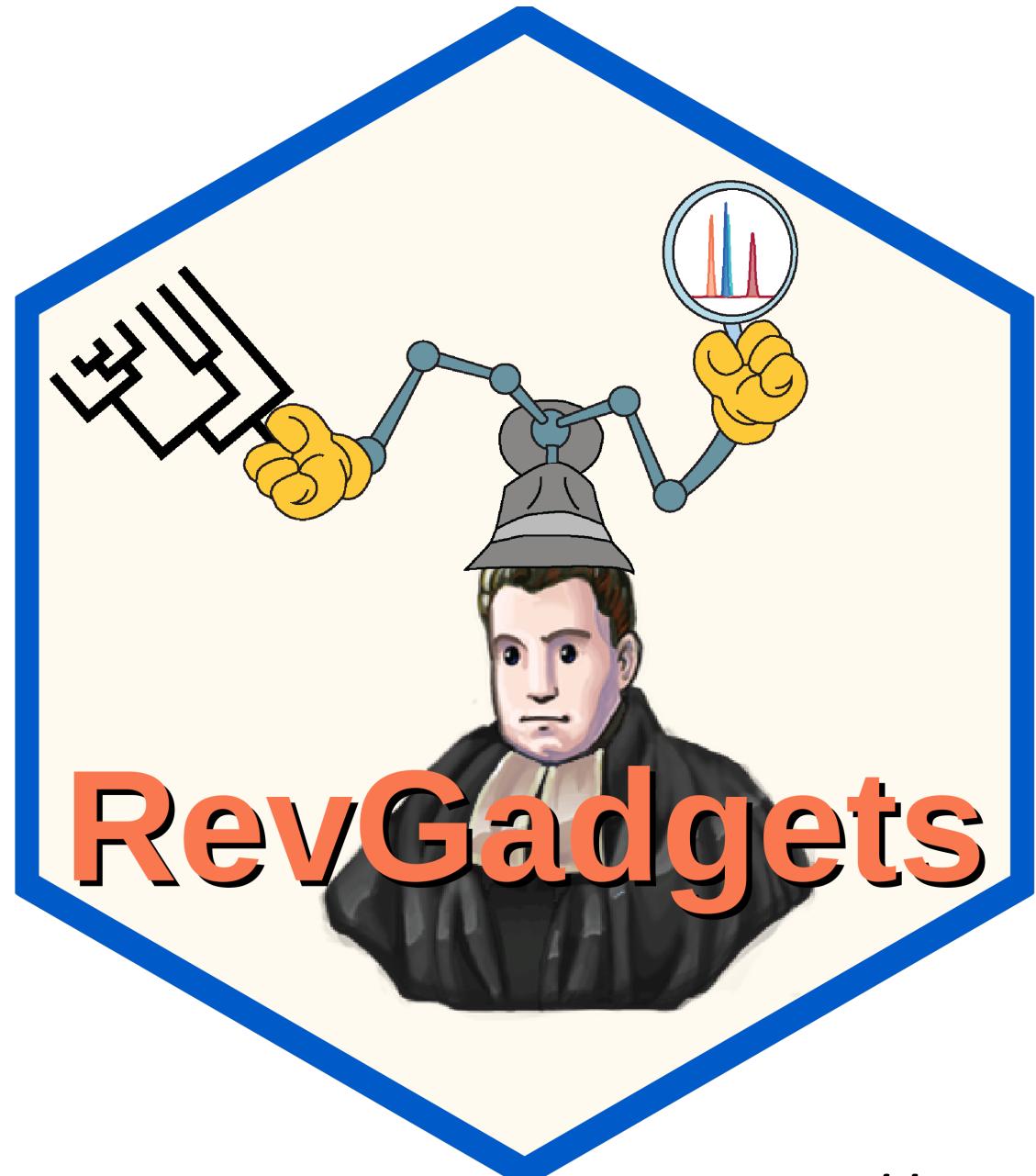
lambda <- 1.0
sigma ~ dnExponential(lambda)

mu := ln(M) - (power(sigma, 2.0) / 2.0)

N <- observations.size()
for( i in 1:N ){
    x[i] ~ dnLnorm(mu, sigma)
    x[i].clamp(observations[i])
}
```







# RevGadgets

an R Package for visualizing  
Bayesian phylogenetic  
analyses from RevBayes

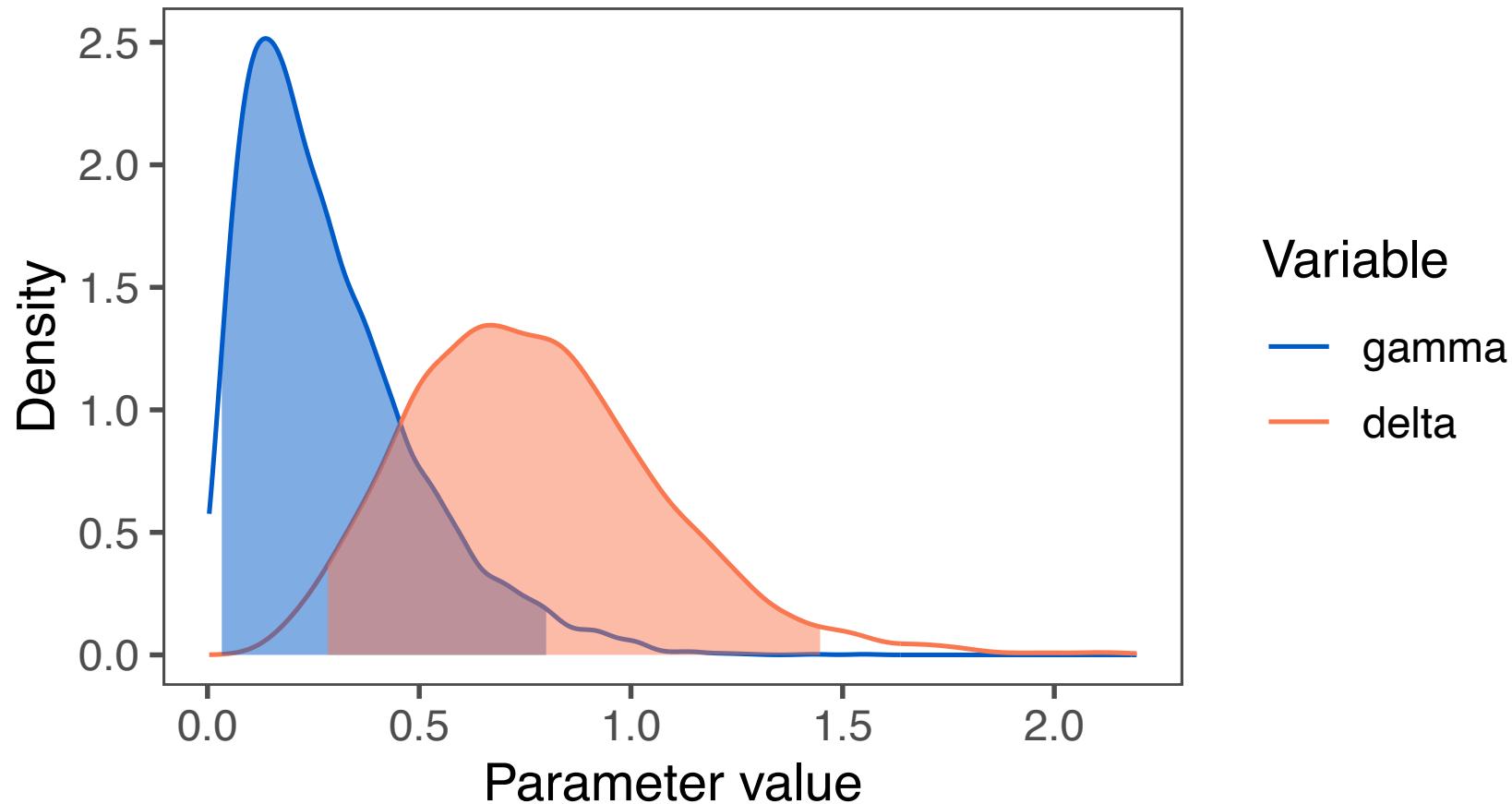
Available on CRAN

[github.com/cmt2/revgadgets](https://github.com/cmt2/revgadgets)

<https://revbayes.github.io/tutorials/intro/revgadgets>

```
# specify the log files with rates of  
# chromosome evolution  
files <- c("chromevol_simple.log")  
  
# read the trace  
trace <- readTrace(path = files)  
  
# plot the posteriors of each parameter  
plotTrace(trace = trace,  
          vars = c("gamma", "delta"))[[1]]
```

Trace 1



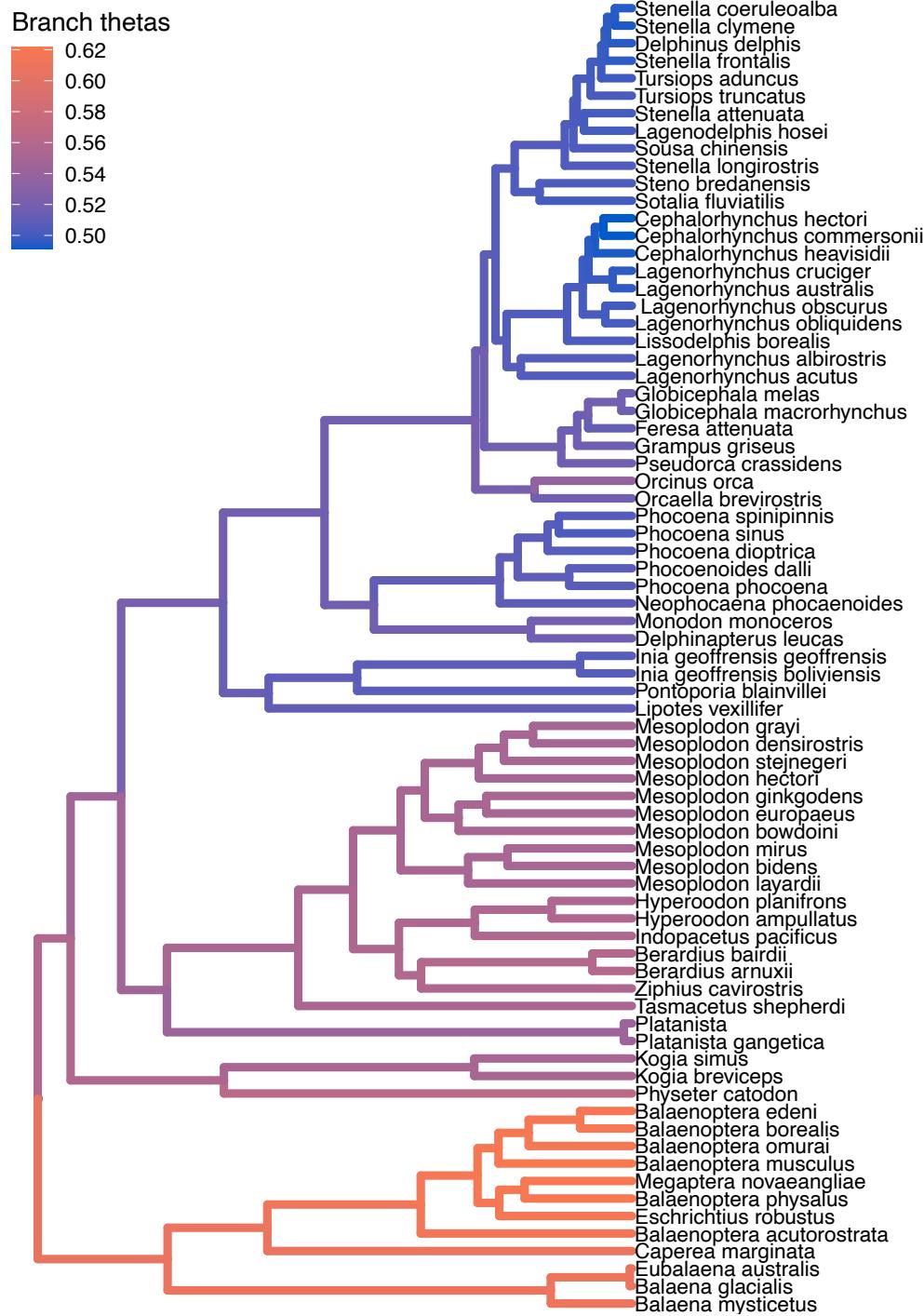
```

# specify the annotated tree file
file <- "relaxed_OU_MAP.tre"

# read the tree
tree <- readTrees(paths = file)

# plot the tree
plotTree(tree = tree,
          tip_labels_italics = FALSE,
          color_branch_by = "branch_thetas",
          line_width = 1.7)

```



```

# specify the log files with diversification
# rates and rate-change times
speciation_time_file <-
  "primates_EBD_speciation_times.log"

speciation_rate_file <-
  "primates_EBD_speciation_rates.log"

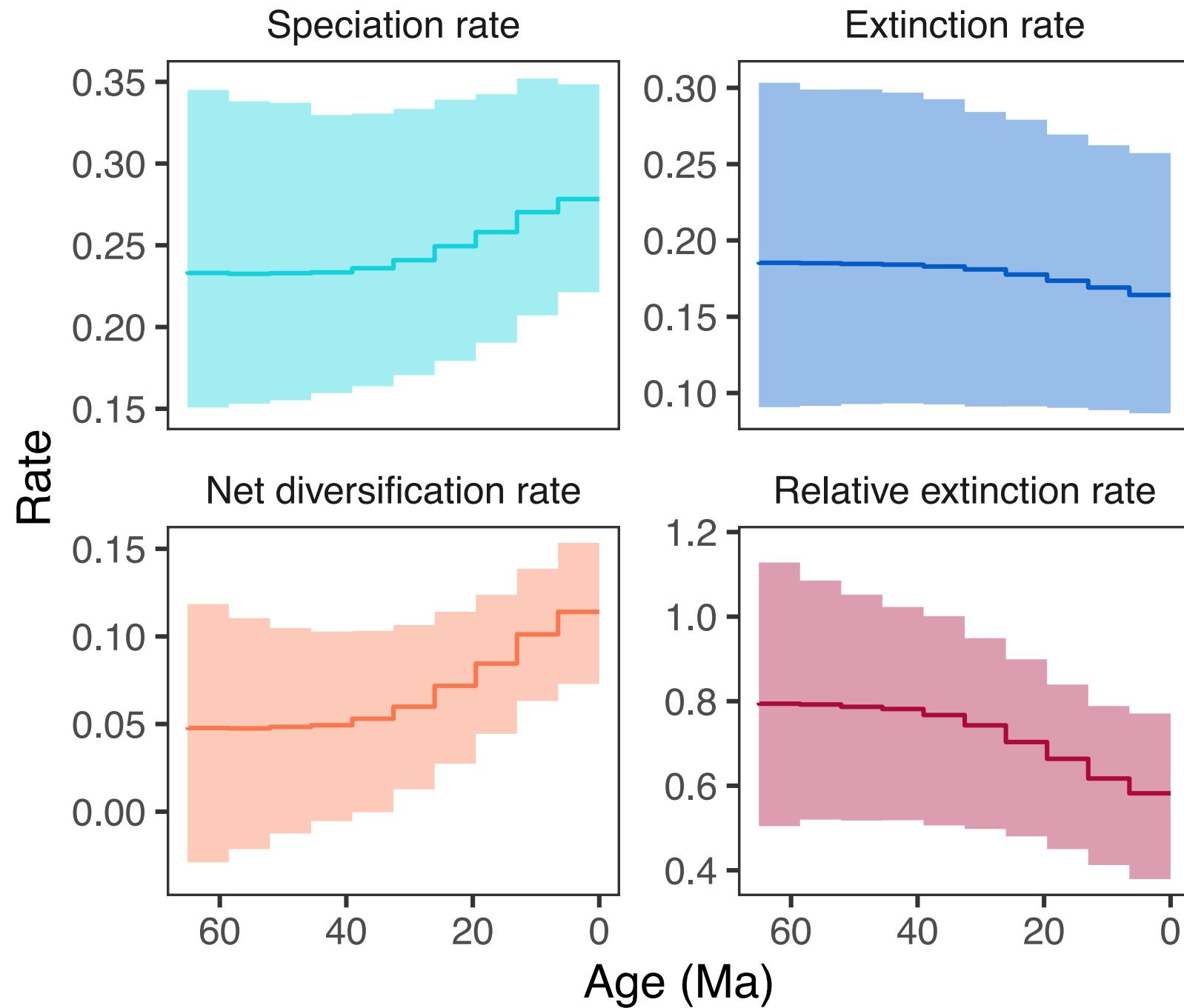
extinction_time_file <-
  "primates_EBD_extinction_times.log"

extinction_rate_file <-
  "primates_EBD_extinction_rates.log"

# read the log files
rates <- processDivRates(
  speciation_time_log =
    speciation_time_file,
  speciation_rate_log =
    speciation_rate_file,
  extinction_time_log =
    extinction_time_file,
  extinction_rate_log =
    extinction_rate_file,
  burnin = 0.25)

# plot the diversification rates
plotDivRates(rates = rates)

```



```

# specify the simulated statistics file
sim <- "simulated_data_pps.csv"

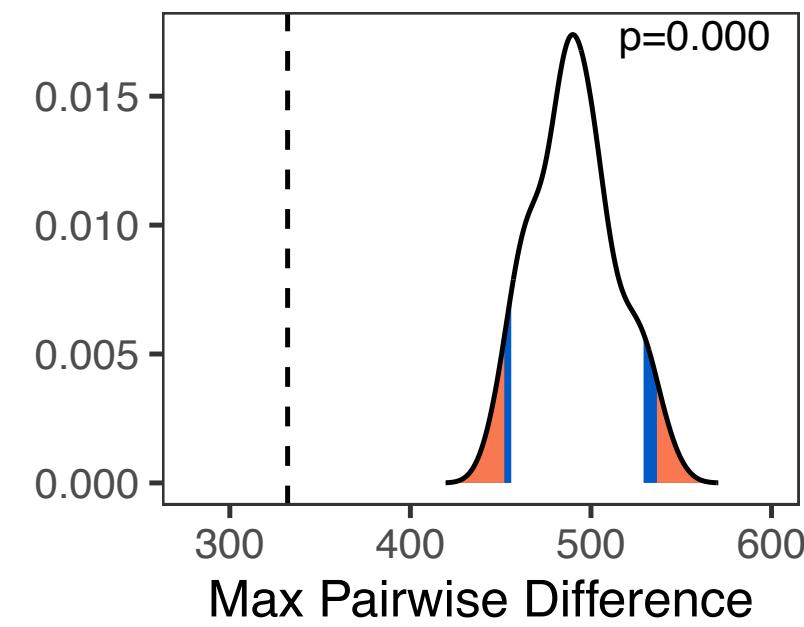
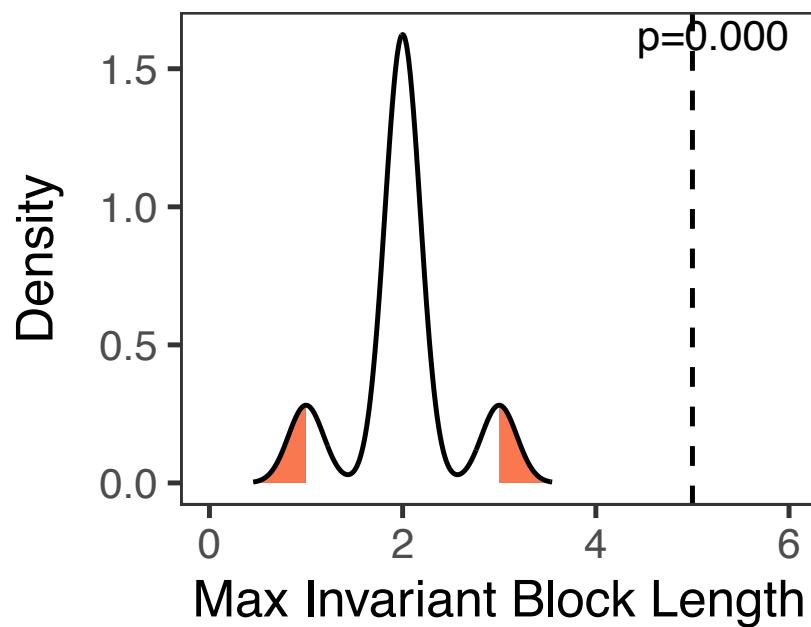
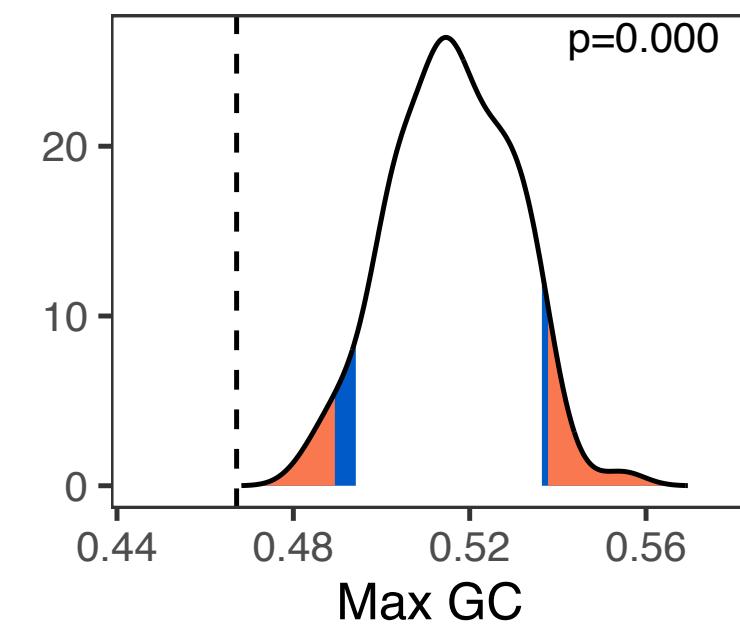
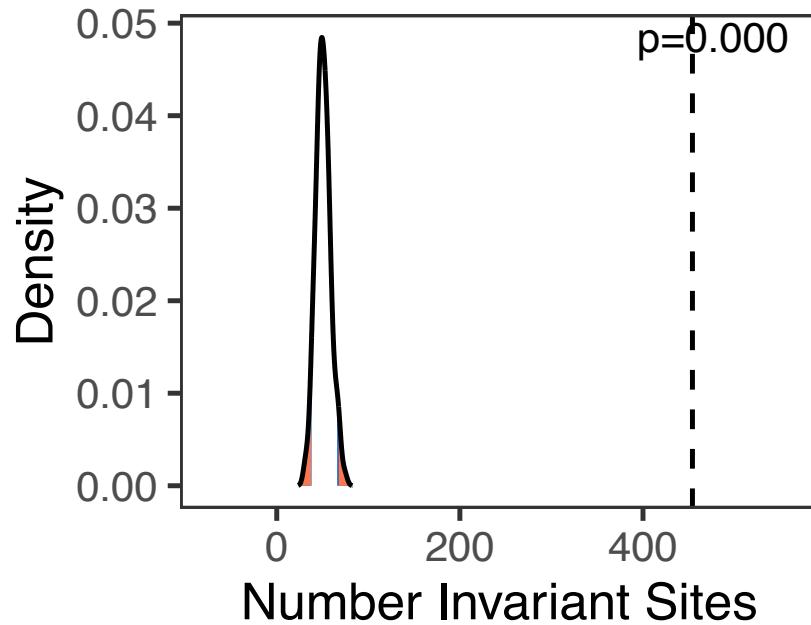
# specify the empirical statistics file
emp <- "empirical_data_pps.csv"

# read the statistics files
stats <- processPostPredStats(path_sim = sim,
                                path_emp = emp)

# create the posterior-predictive plots
plots <- plotPostPredStats(data = stats)

# plot some of the statistics
plots[c(1,3,5,7)]

```



```

# specify the simulated statistics file
sim <- "simulated_data_pps.csv"

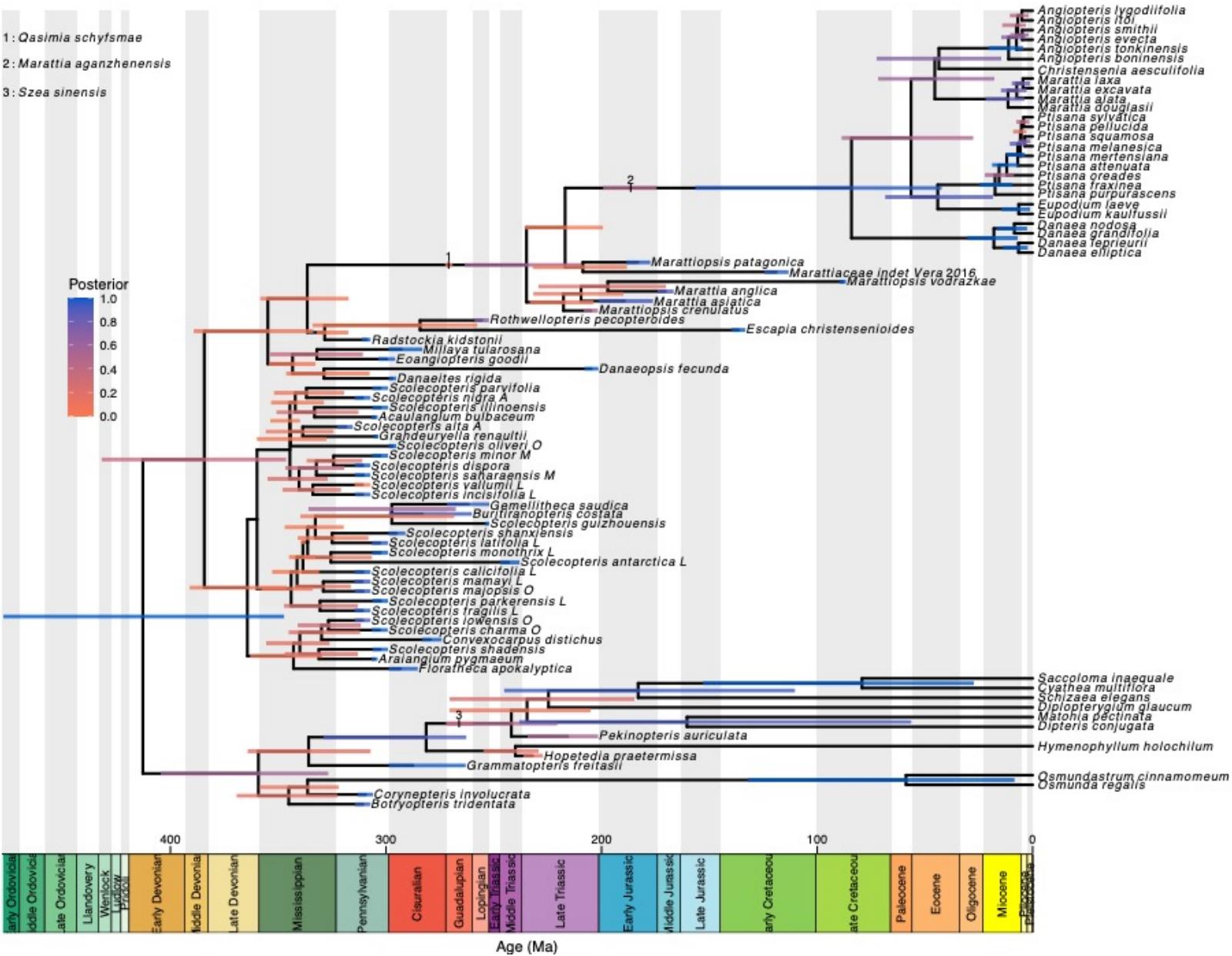
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emp <- "empirical_data_pps.csv"

# read the statistics files
stats <- processPostPredStats(path_sim = sim,
                                path_emp = emp)

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plots <- plotPostPredStats(data = stats)

# plot some of the statistics
plots[c(1,3,5,7)]

```



```

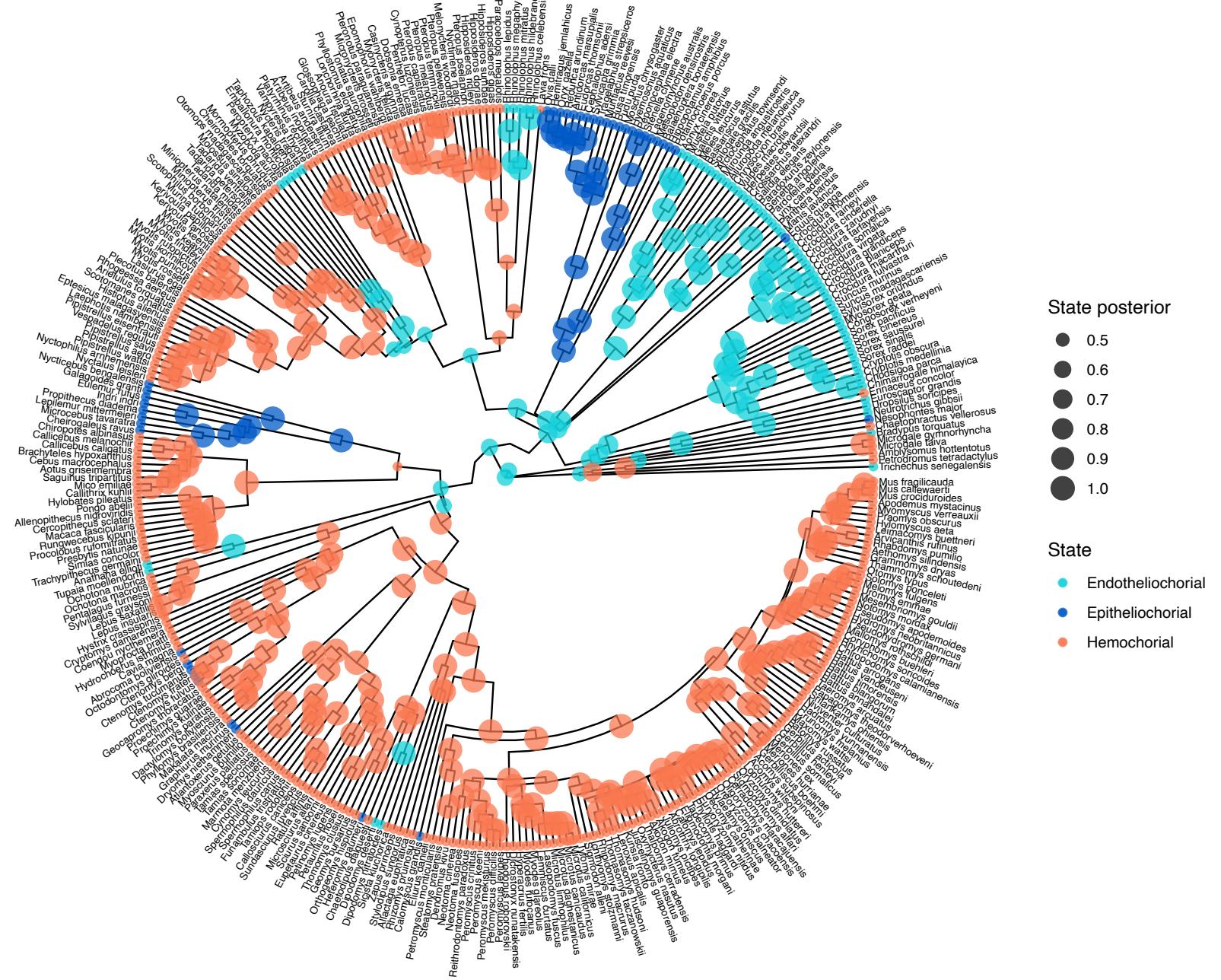
# specify the tree file
file <- "ase_frek.tree"

labs <- c("1" = "Epitheliochorial",
        "2" = "Endotheliochorial",
        "3" = "Hemochorrial")

# read in the tree annotated with ancestral states
freeK <- processAncStates(file,
                           state_labels = labs)

# plot the tree with MAP ancestral states
plotAncStatesMAP(t = freeK,
                  tree_layout = "circular")

```



```

# specify the annotated tree file
file <- "simple_ase.tre"

# define the state labels
labs <- c("1" = "K", "2" = "O",
         "3" = "M", "4" = "H",
         "5" = "KO", "6" = "KM",
         "7" = "OM", "8" = "KH",
         "9" = "OH", "10" = "MH",
         "11" = "KOM", "12" = "KOH",
         "13" = "KMH", "14" = "OMH",
         "15" = "KOMH")

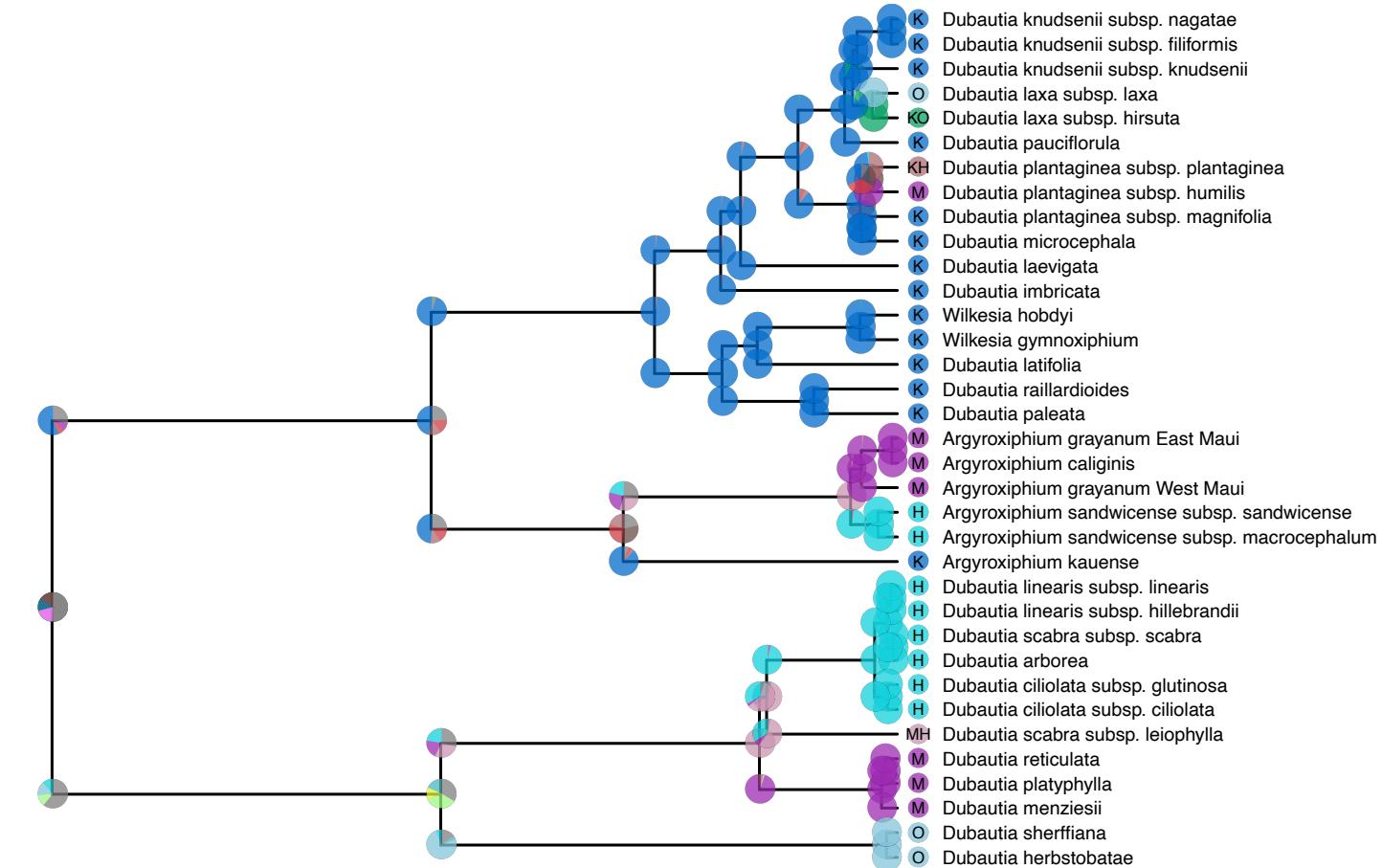
# read the annotated tree file
dec_example <-
  processAncStates(file,
                   state_labels = labs)

# plot the tree with pie charts
plotAncStatesPie(t = dec_example,
                  cladogenetic = TRUE,
                  tip_labels_states = TRUE,
                  tip_labels_offset = 0.2,
                  tip_pie_nudge_x = 0.15,
                  tip_pie_size = 1.0,
                  node_pie_size = 1.5,
                  tip_labels_states_offset = 0.05)

```

State

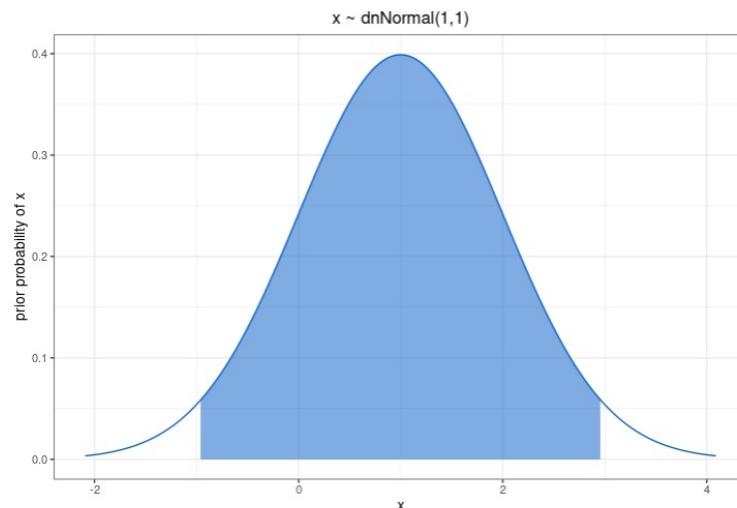
- H
- K
- KH
- KM
- KMH
- KO
- KOH
- KOMH
- M
- MH
- O
- OH
- OM
- OMH
- other



## Prior Distributions

Rev code:

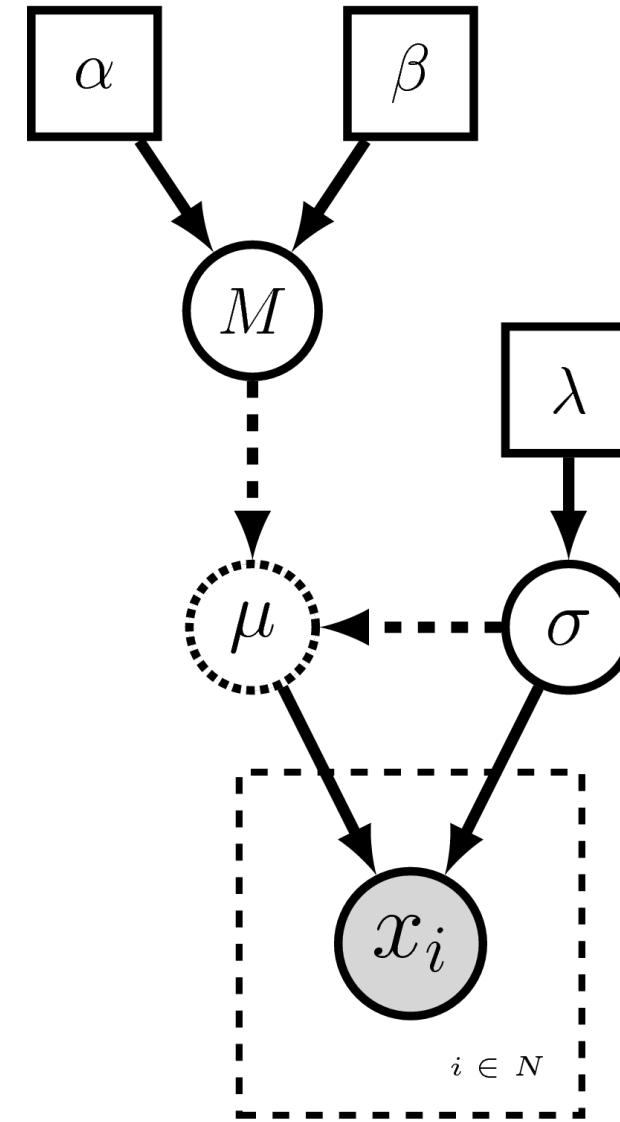
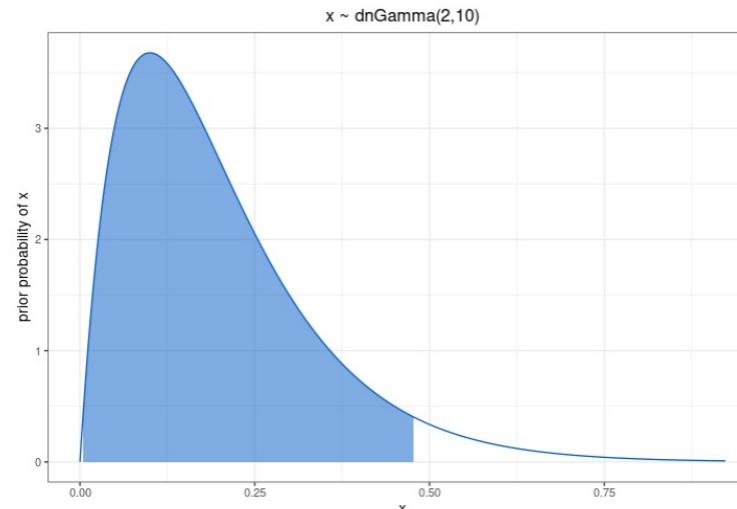
```
x ~ dnNormal(1,1)
```



## Prior Distributions

Rev code:

```
x ~ dnGamma(2,10)
```





Mike May



Jun Ying Lim



Will Freyman



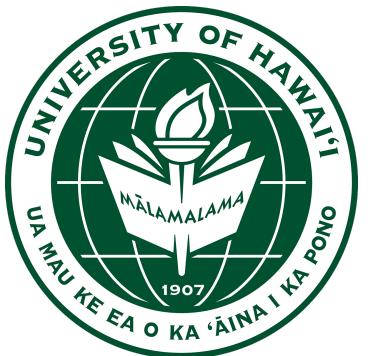
Sebastian Höhna



Joëlle Barido-Sottani



Bjørn Kopperud



@tribbletweets

ape; phangorn; phytools;  
ggplot2; deeptime; dplyr;  
treeplyr; tidytree; reshape;  
ggthemes; tidyR; tibble;  
gginnards; ggimage;  
ggplotify; png; ggpp

