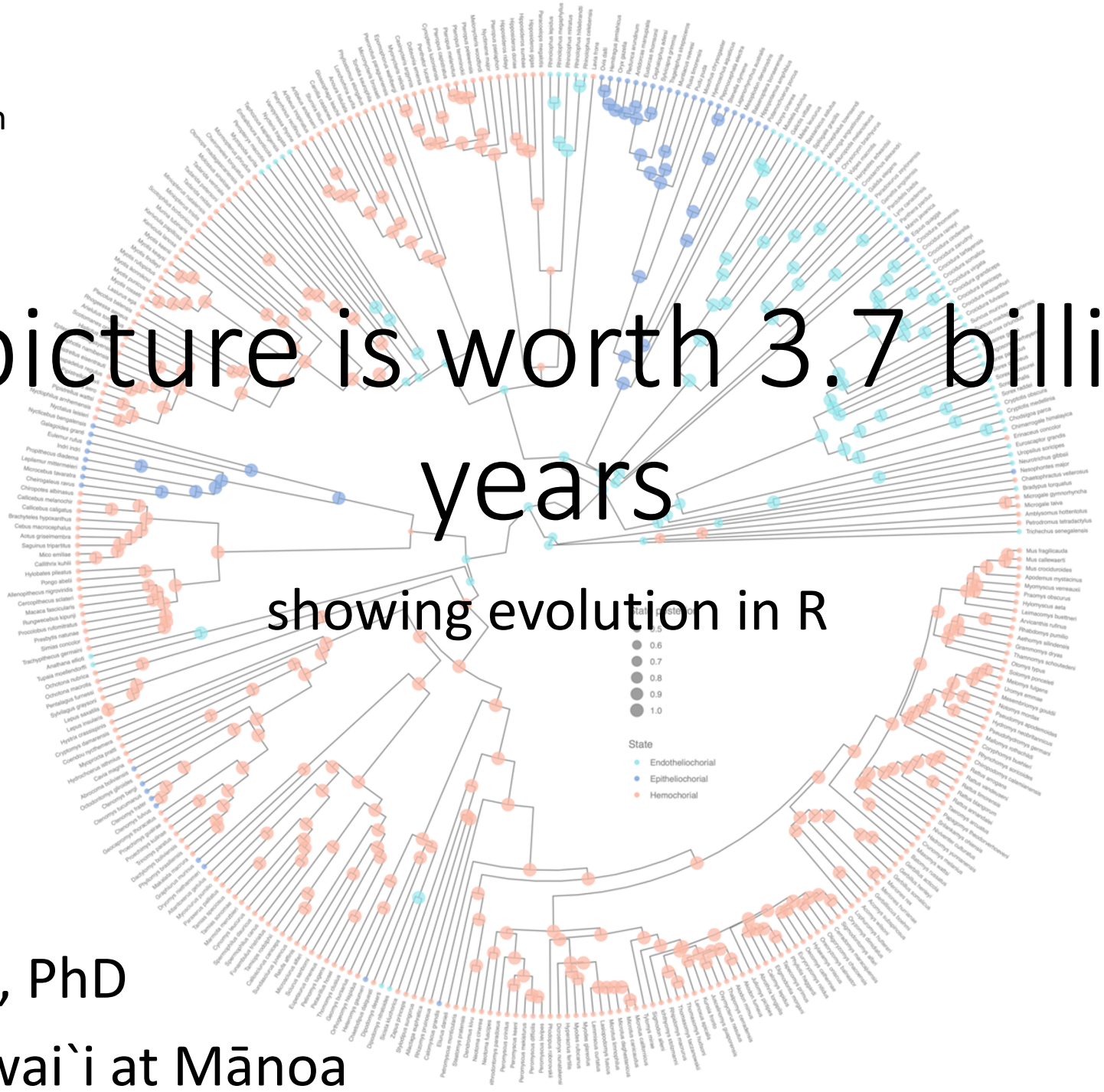
@tribbletweets

ctribble09@gmail.com

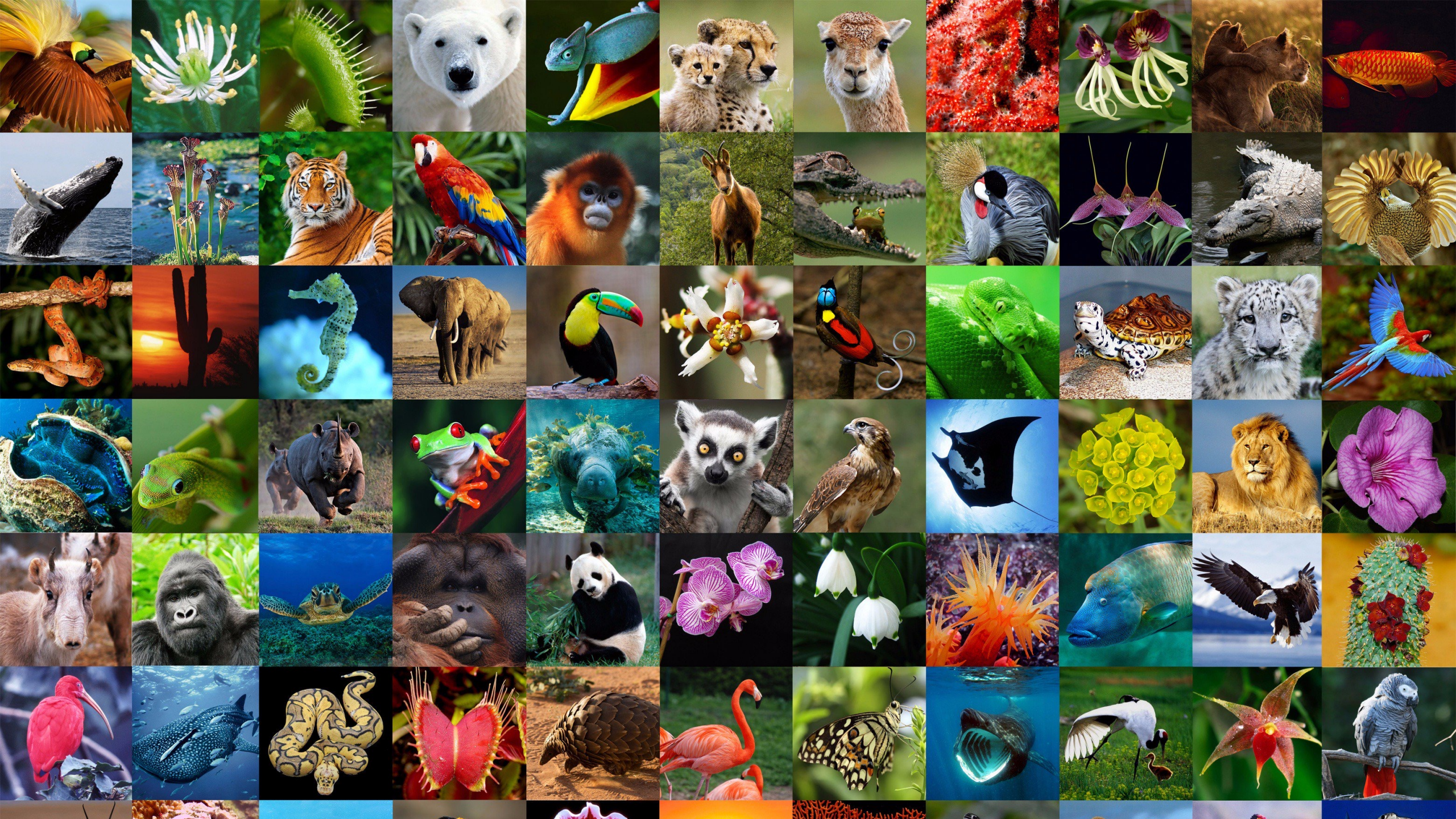
A picture is worth 3.7 billion years

showing evolution in R



Carrie M. Tribble, PhD

University of Hawai`i at Mānoa



David Patte/ U.S. Fish and Wildlife Service

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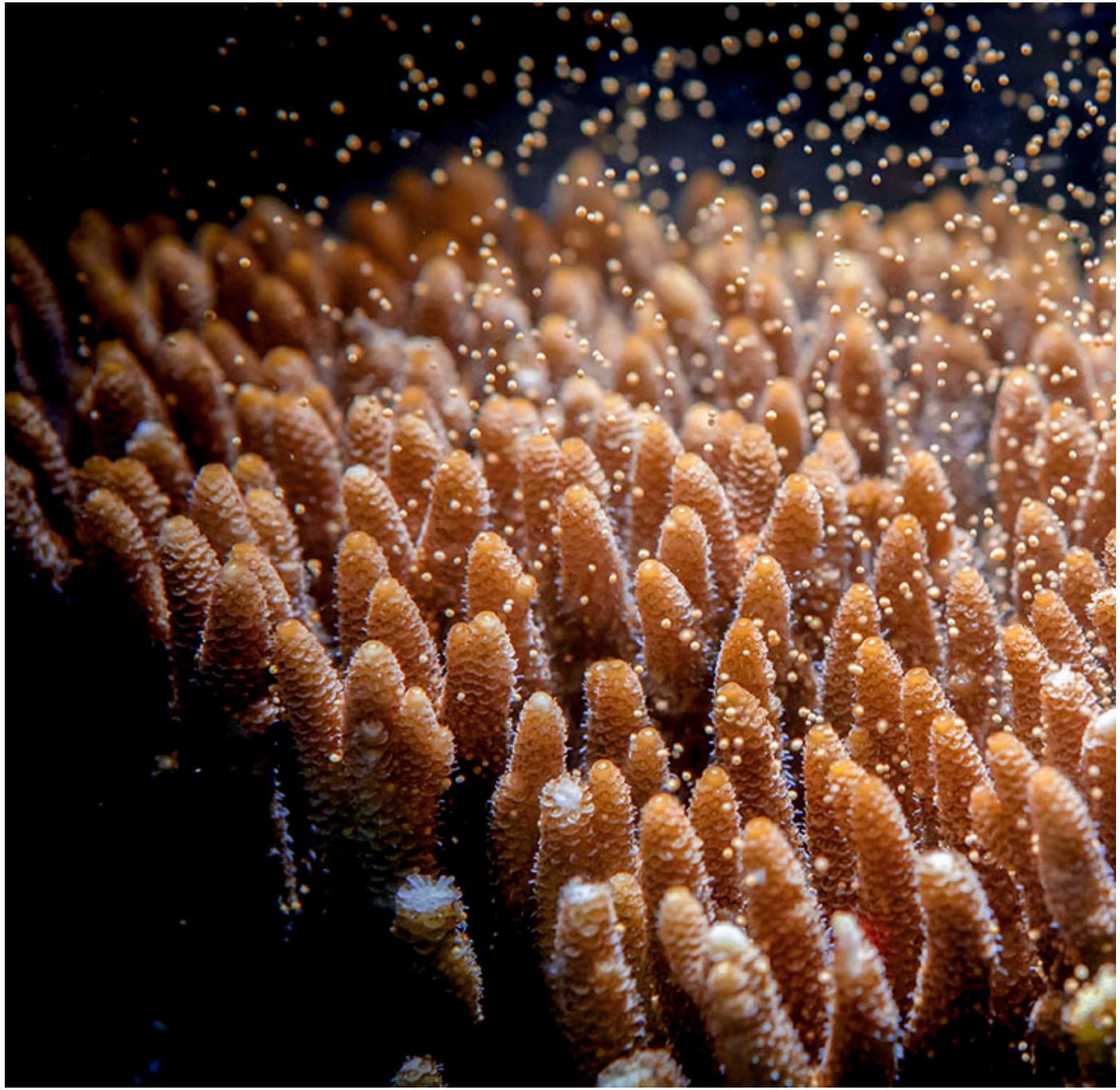
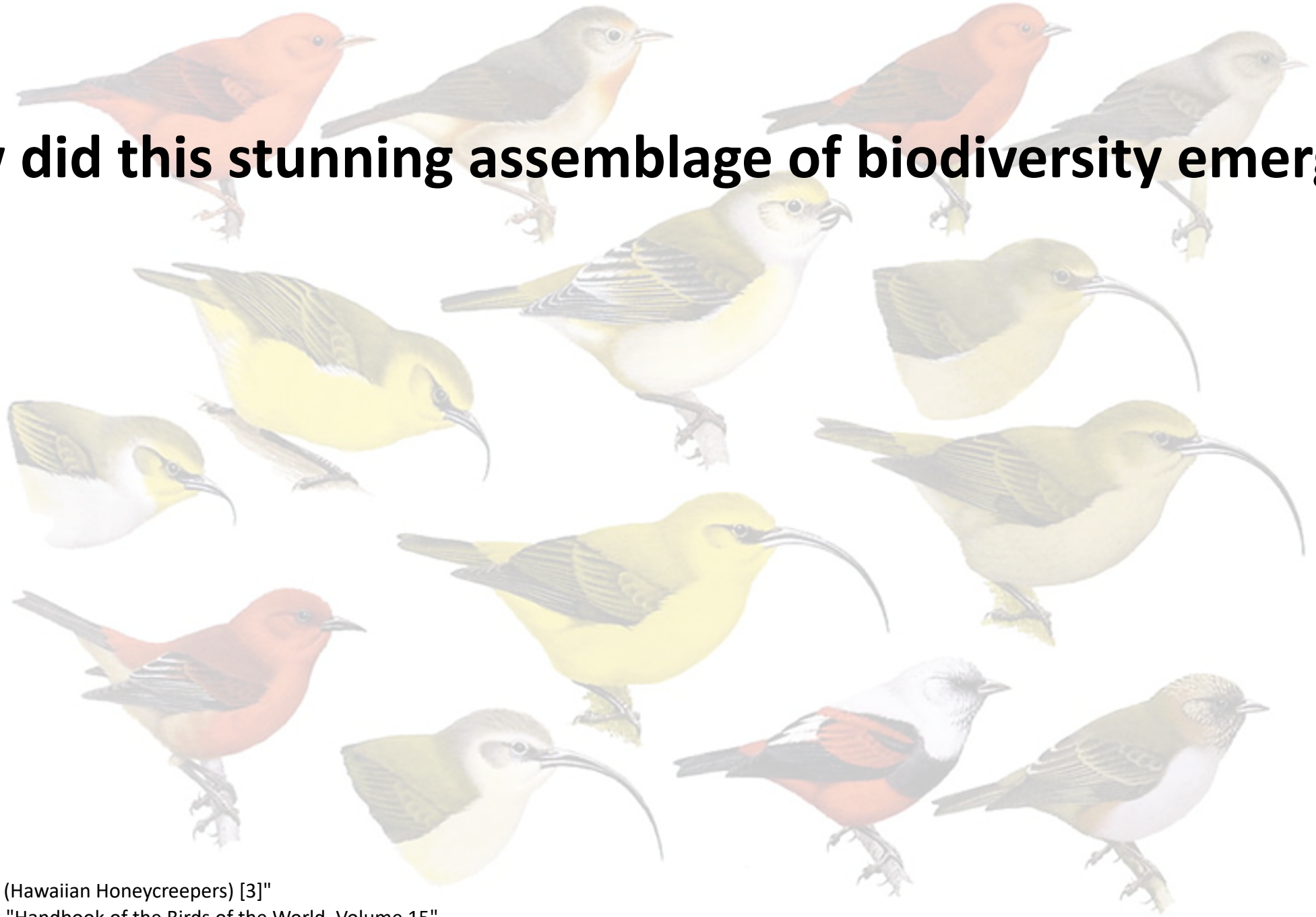


Mikaela Nordborg/ Australian Institute of Marine Science

"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?



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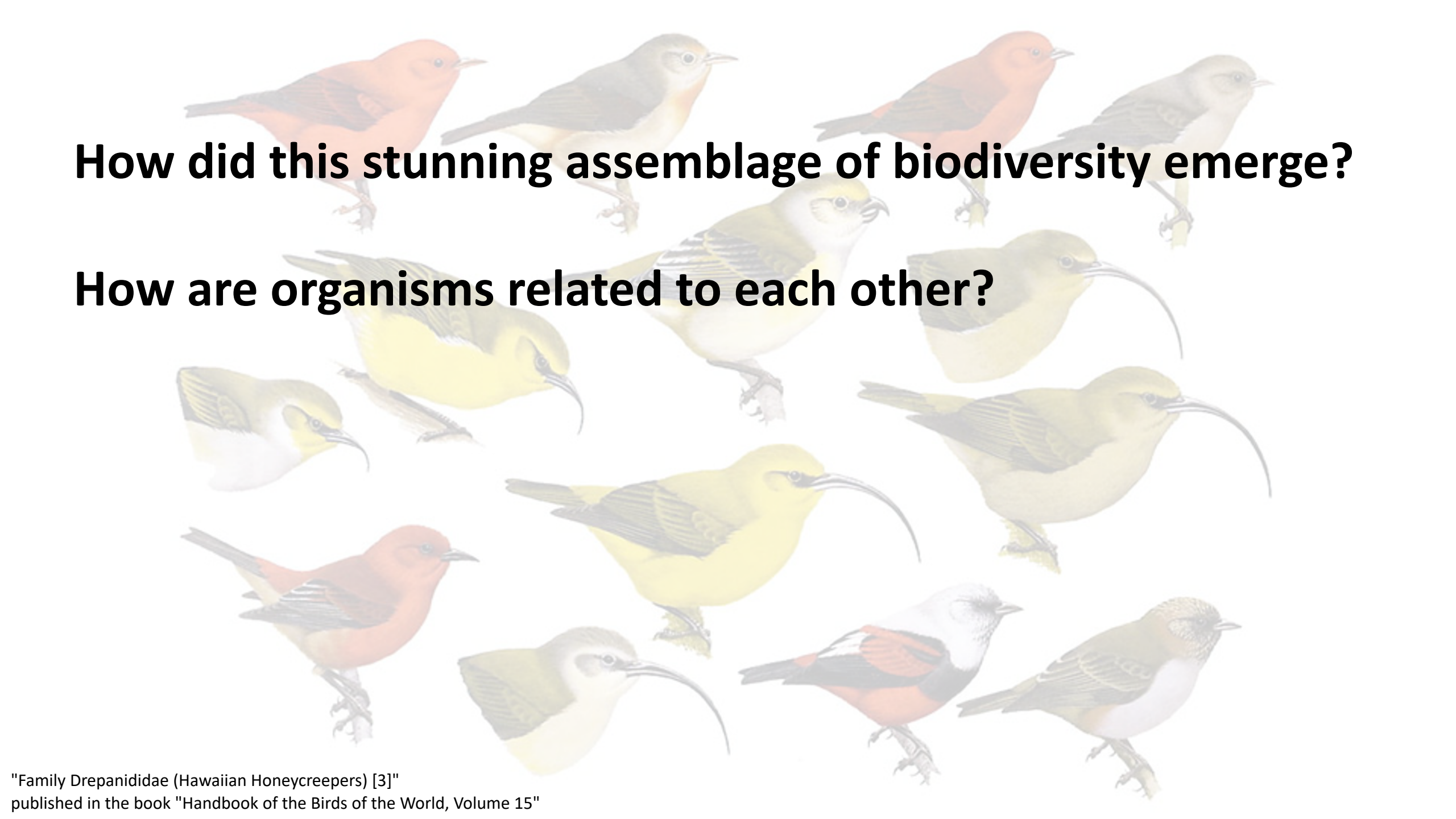

How did this stunning assemblage of biodiversity emerge?

How are organisms related to each other?

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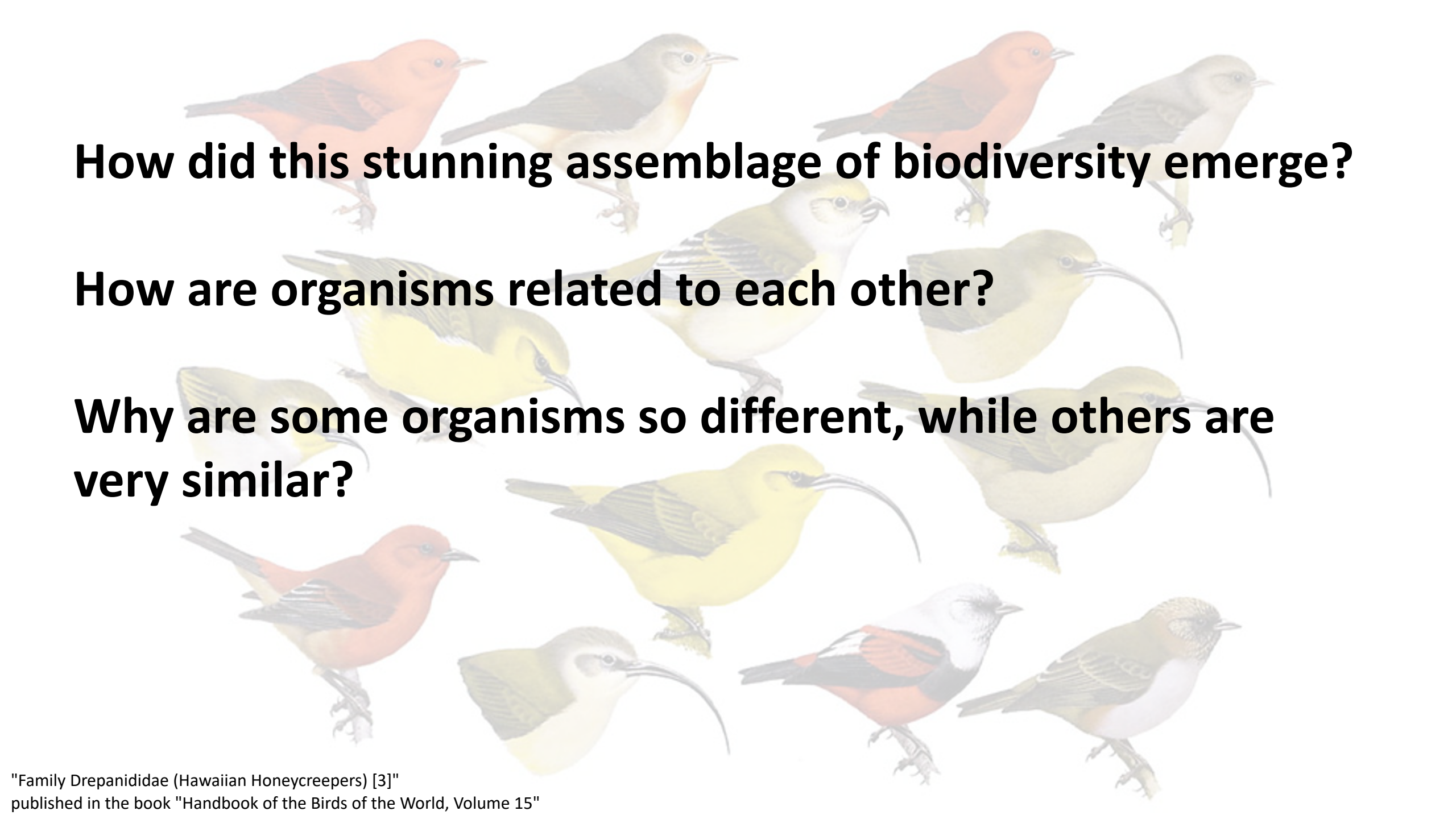

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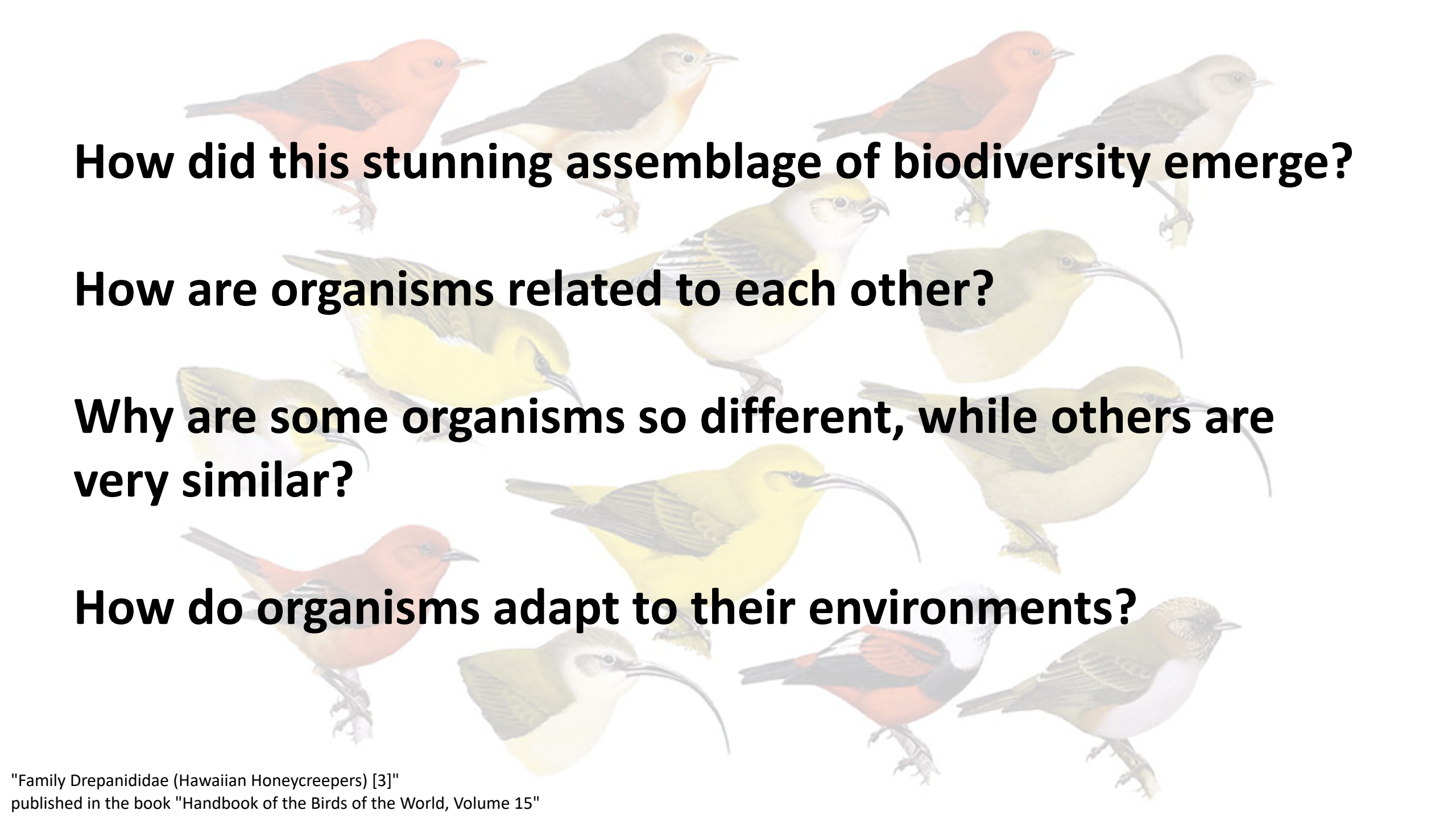

How did this stunning assemblage of biodiversity emerge?

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

How do organisms adapt to their environments?

"Family Drepanididae (Hawaiian Honeycreepers) [3]"
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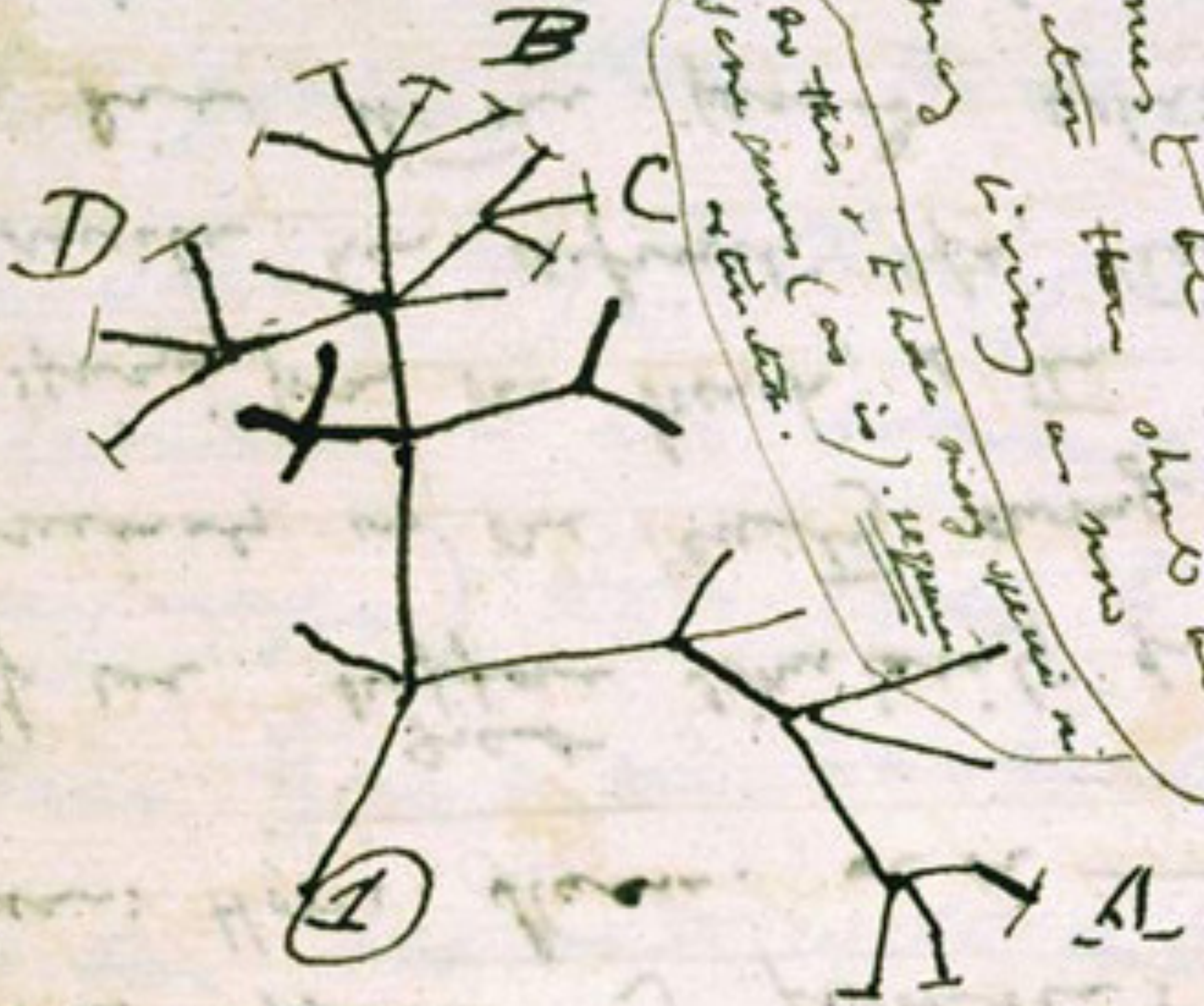
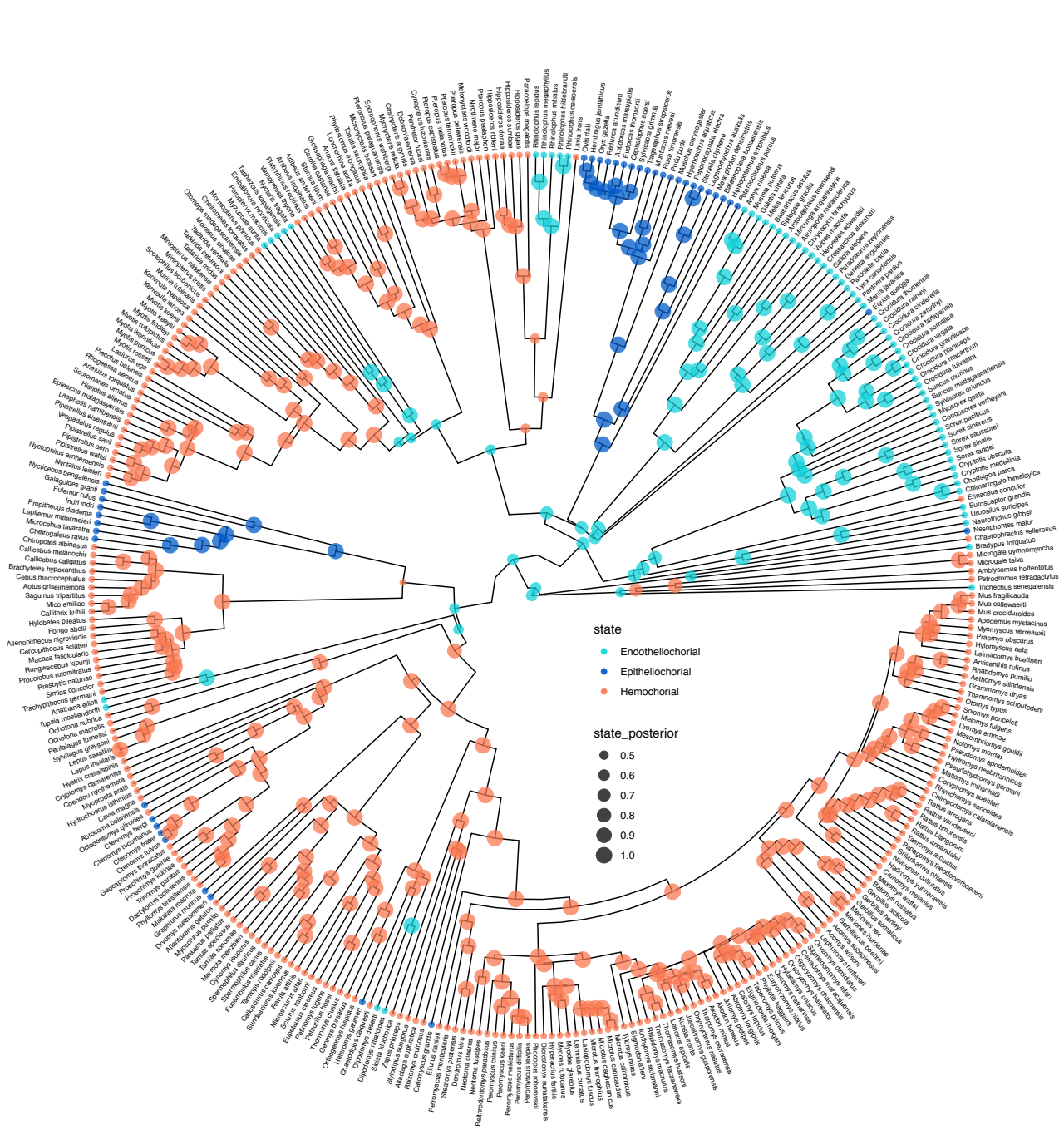
I think

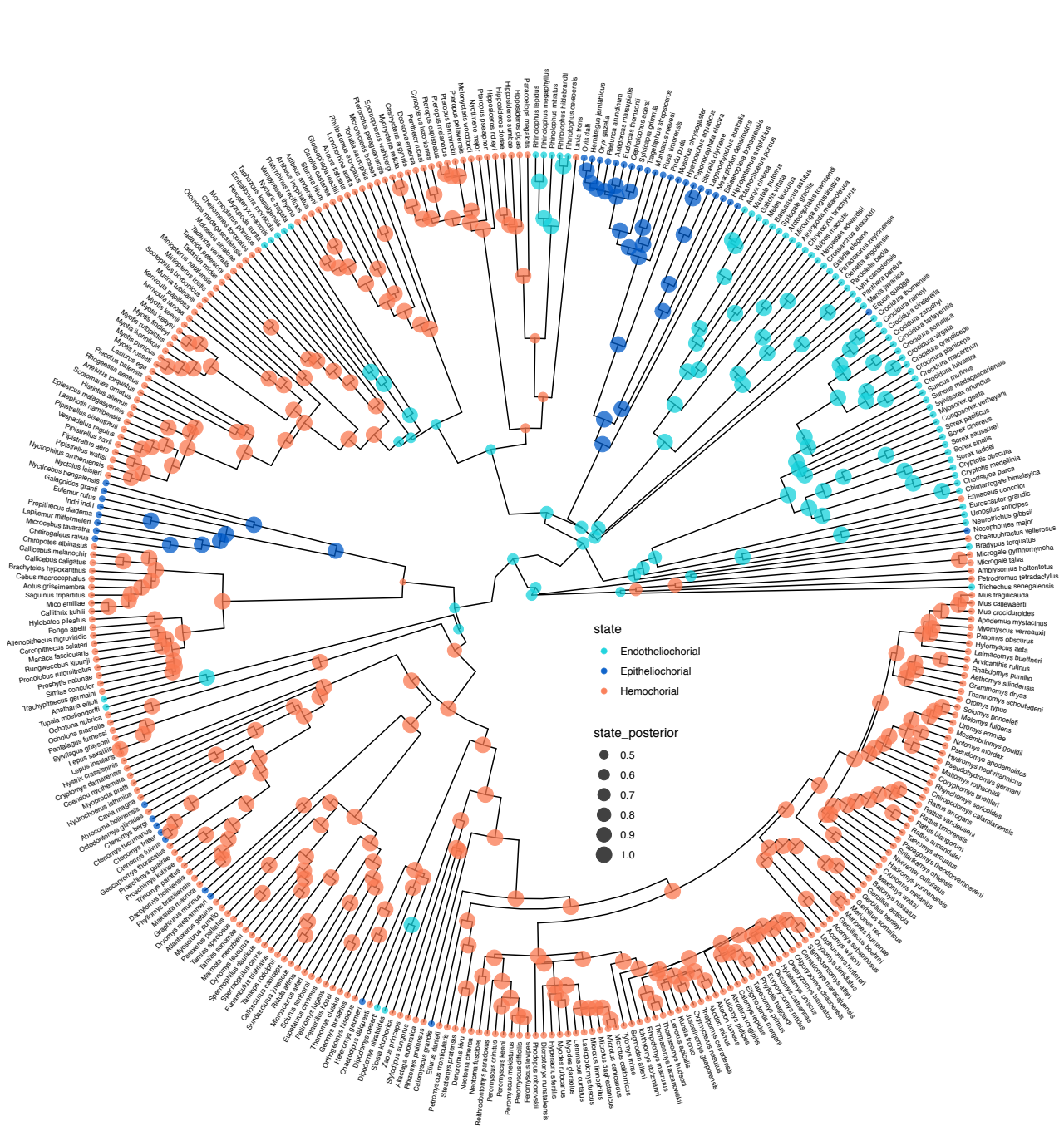


Case must be that one generation then should be as many living as now. To do this & to have many species in same genus (as is). requires extinction.



Phylogenetics

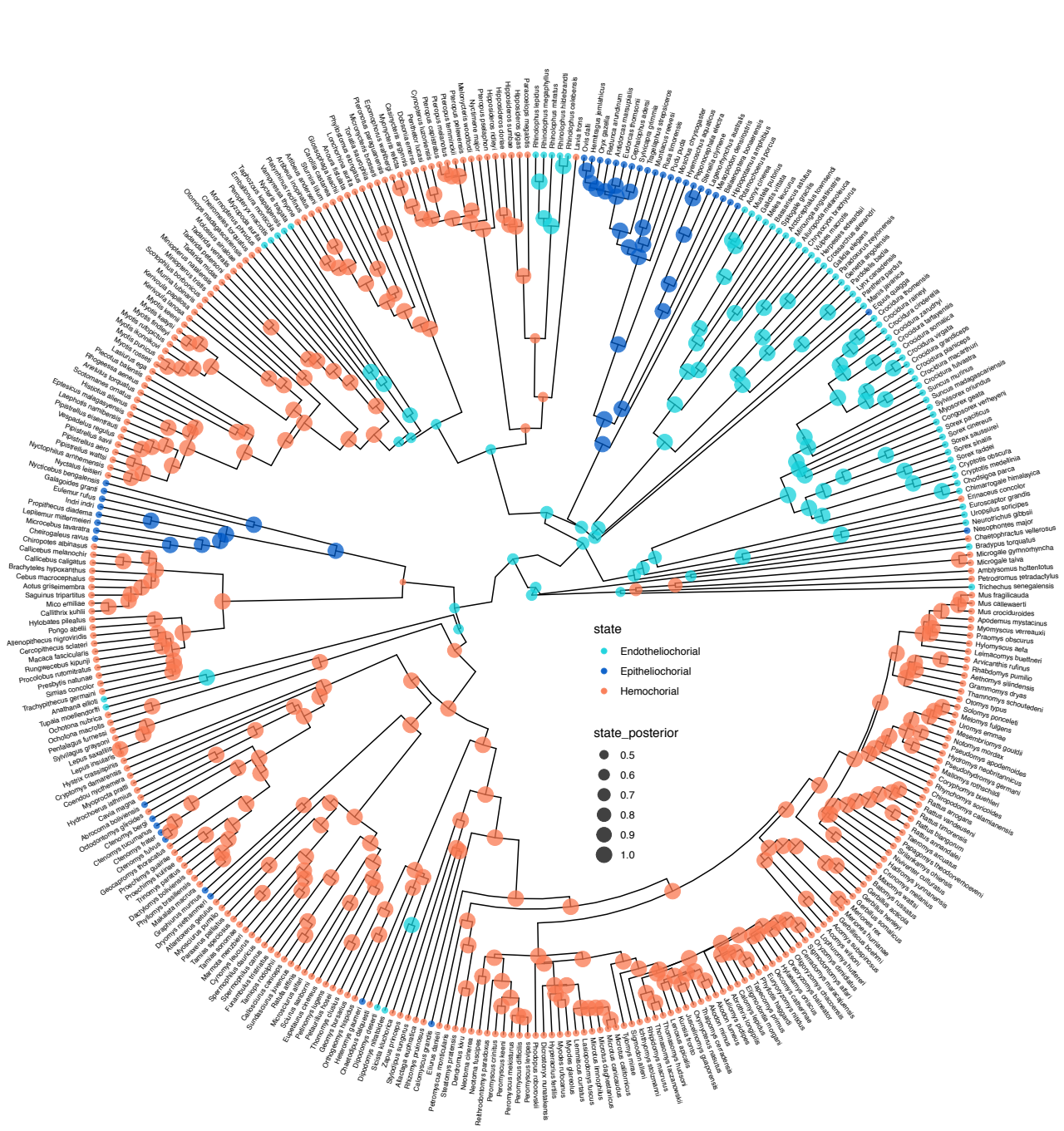
Model relationships between living things



Phylogenetics

Model relationships between living things

Test hypotheses with statistical models

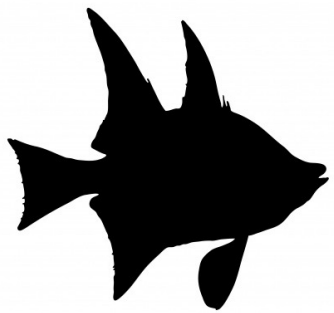


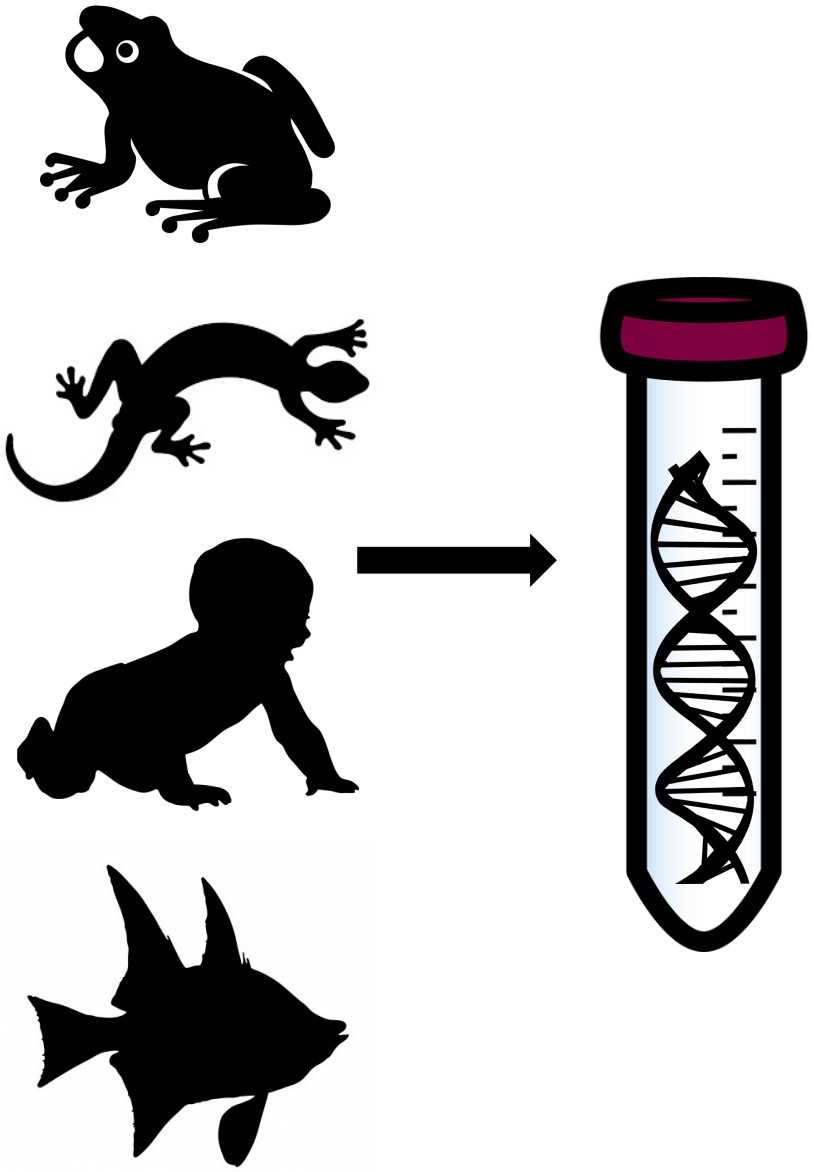
Phylogenetics

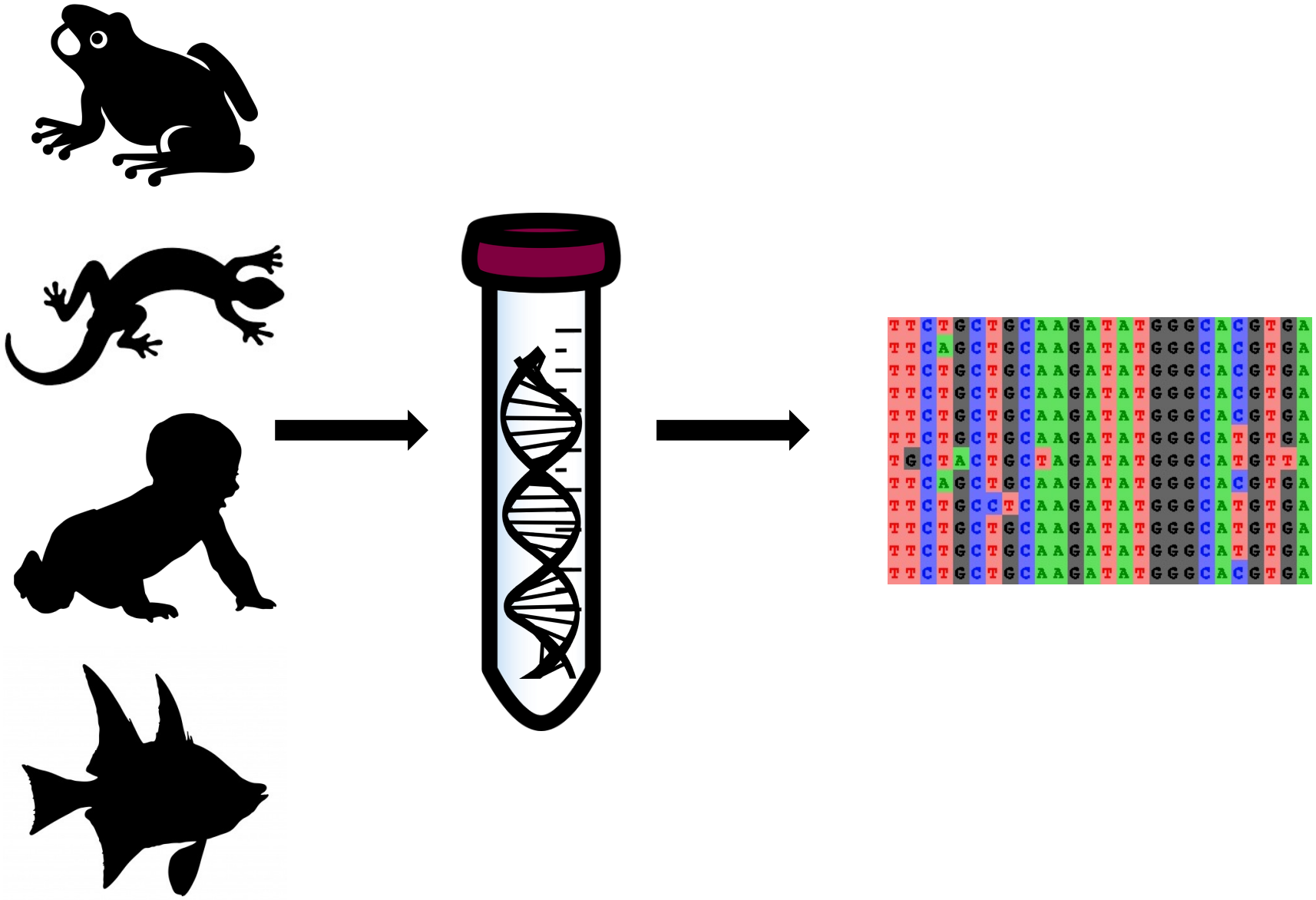
Model relationships between living things

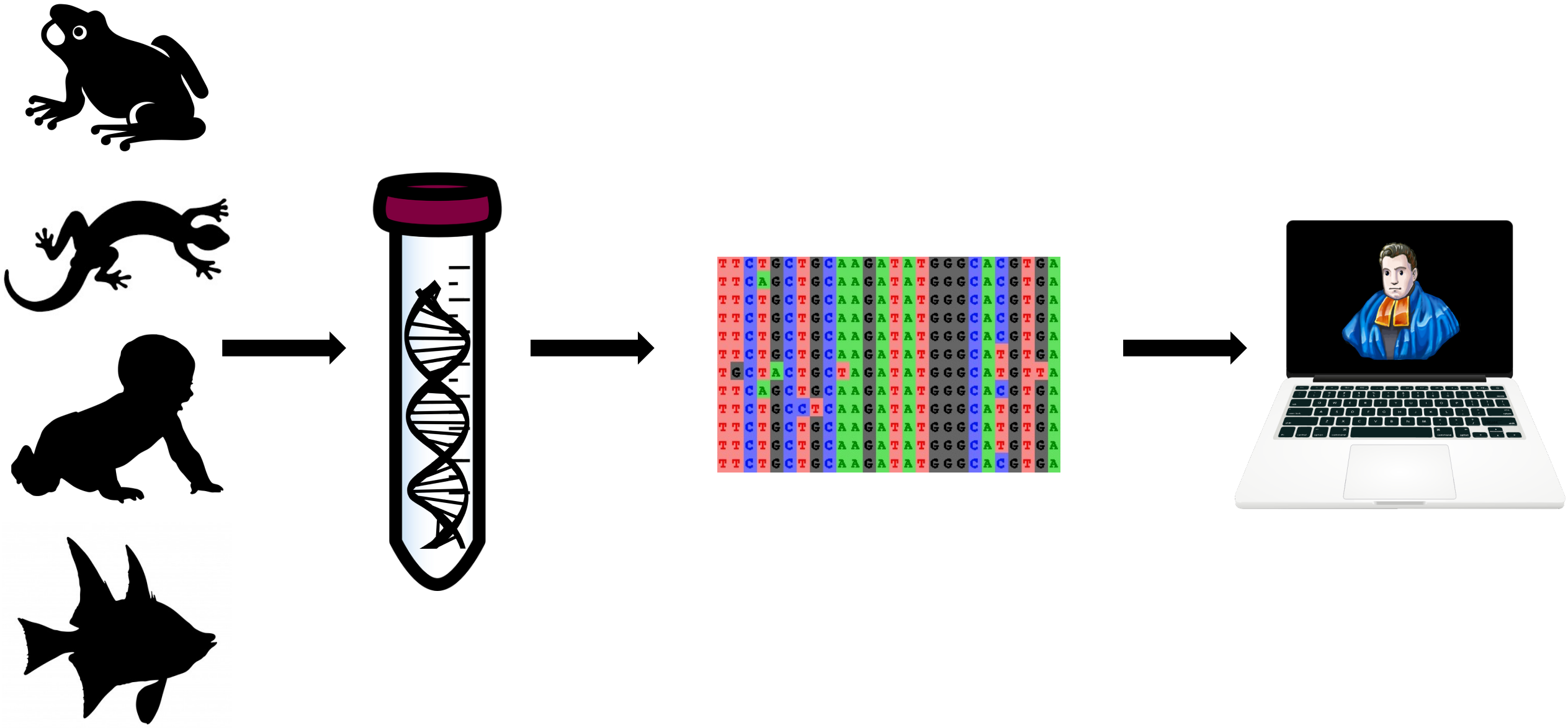
Test hypotheses with statistical models

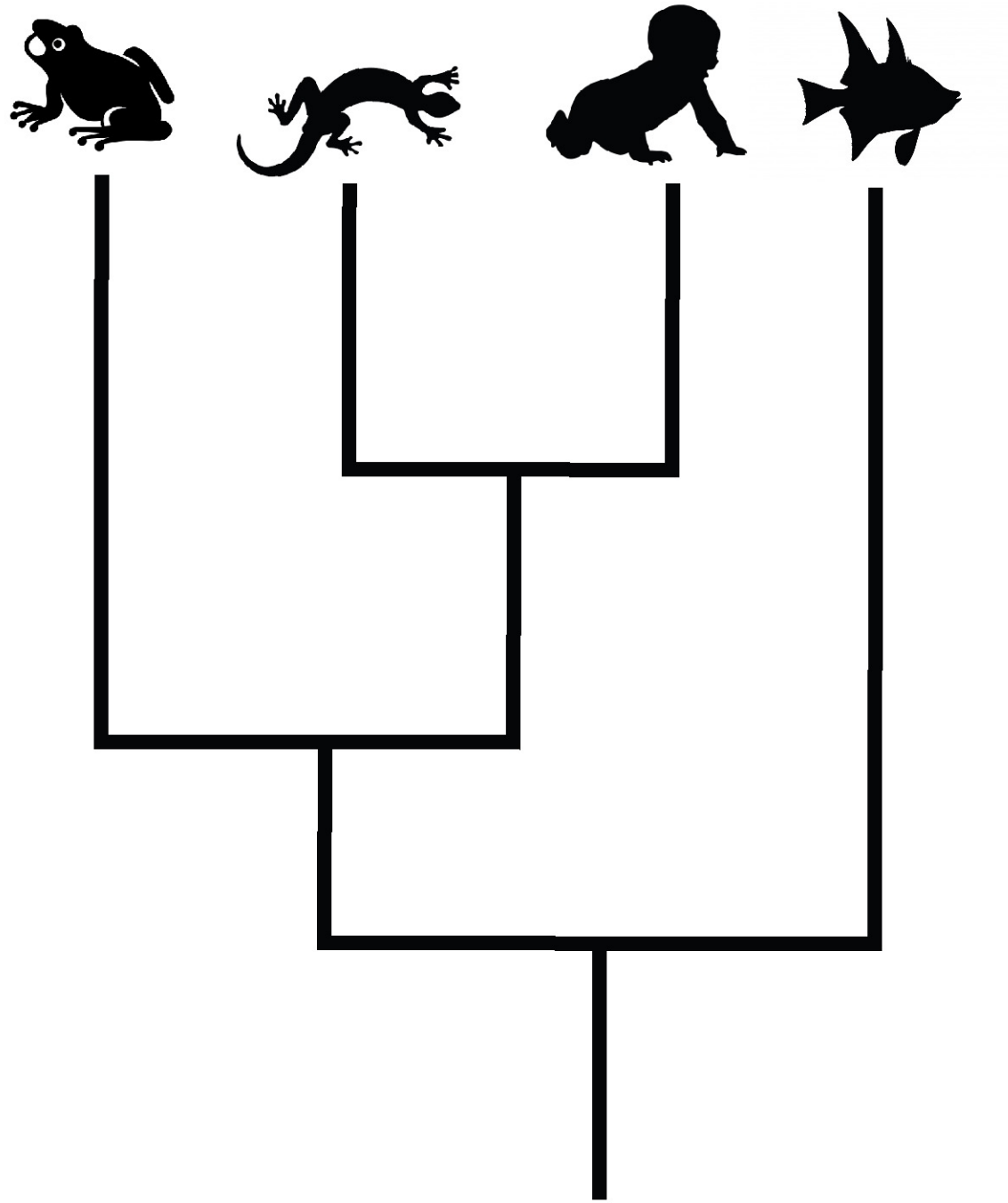
Integrates statistics, computer science, and biology

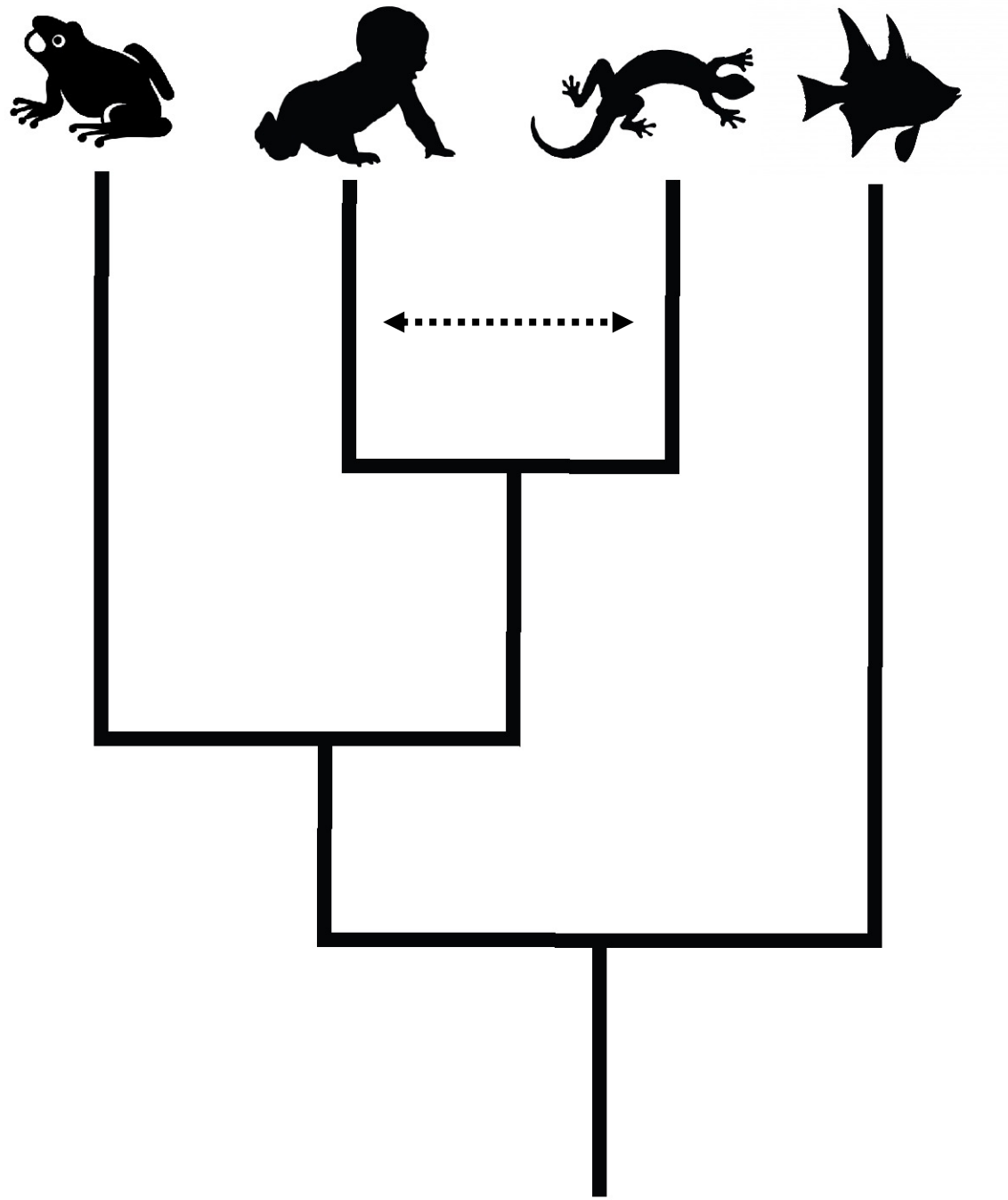


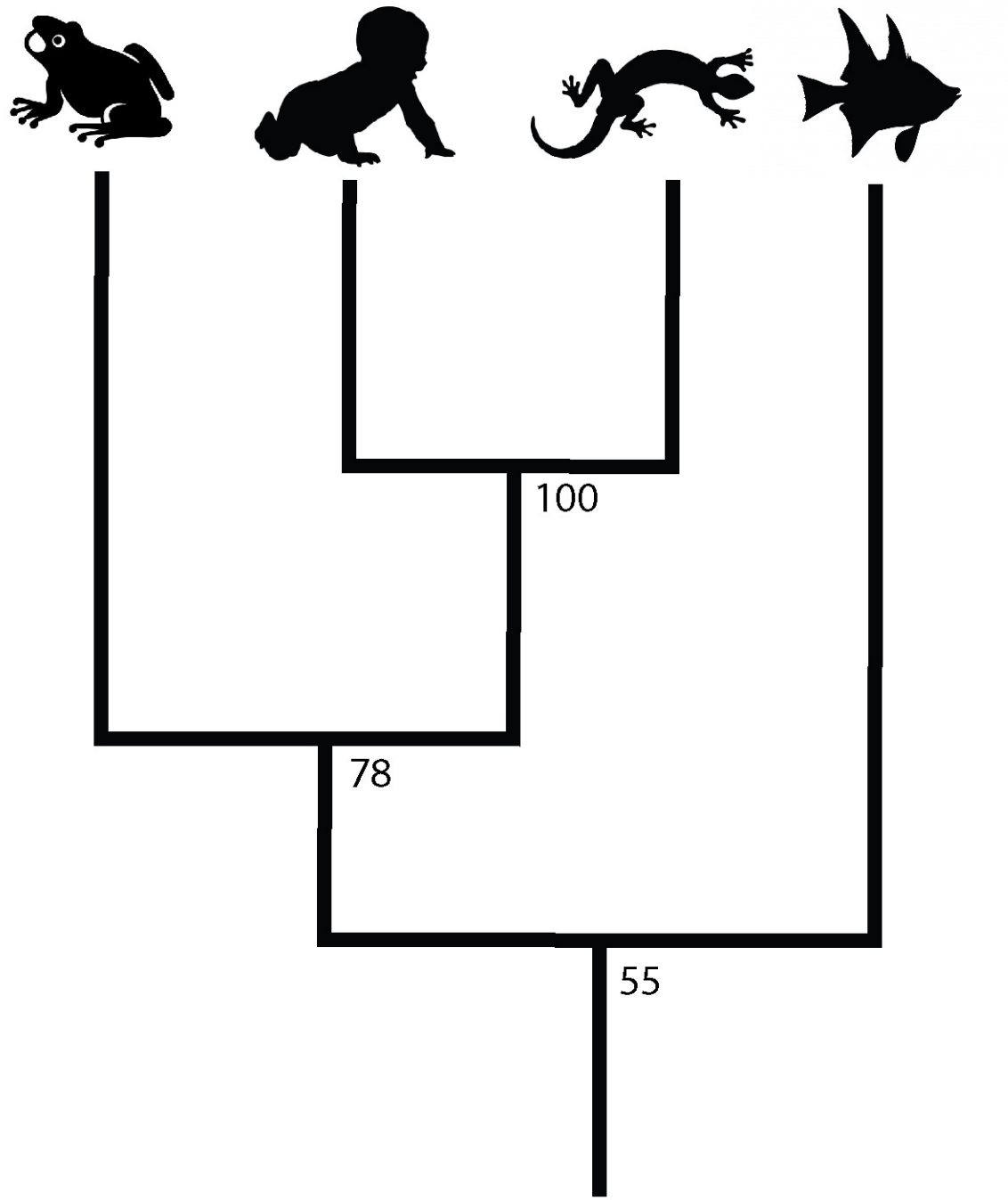








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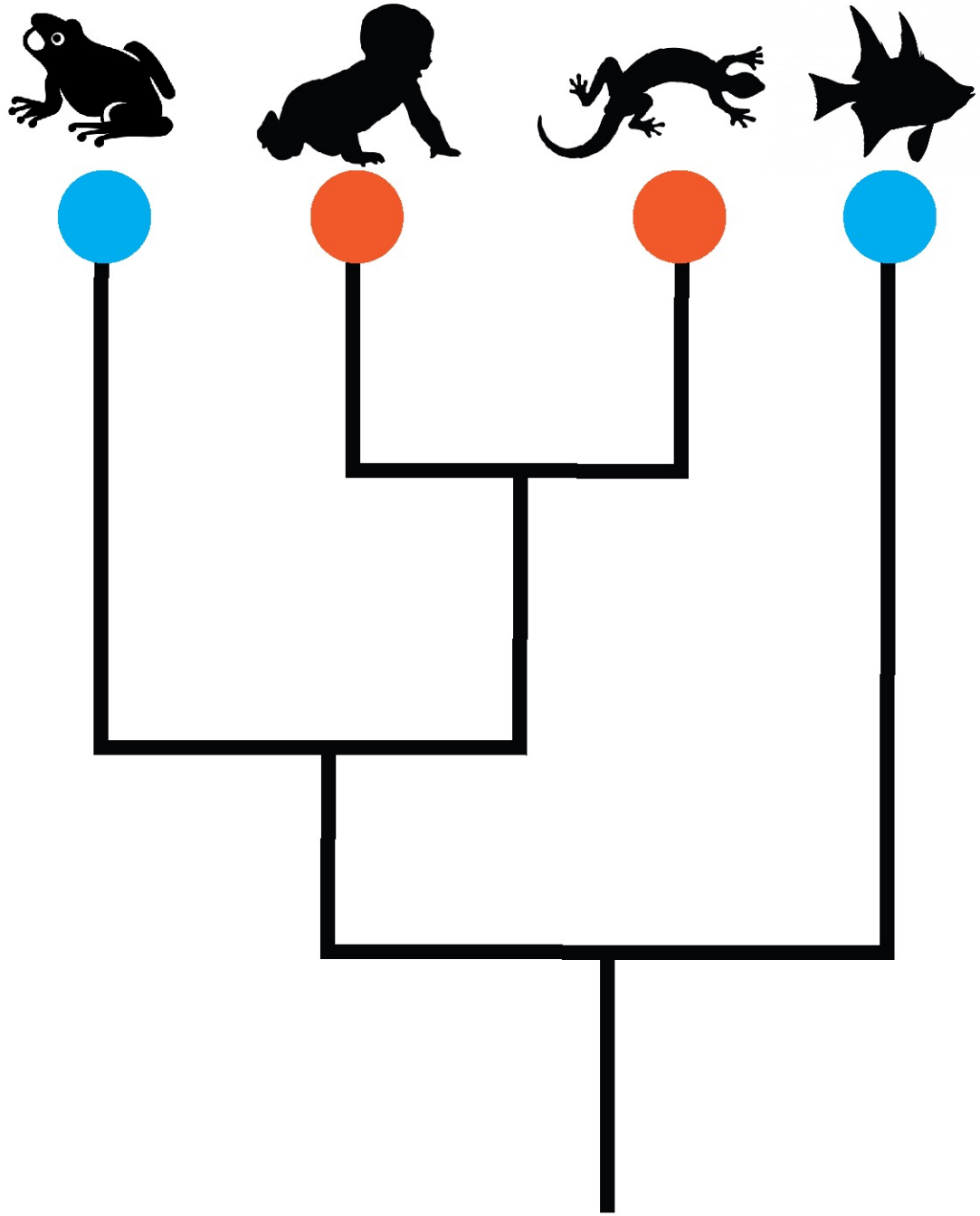
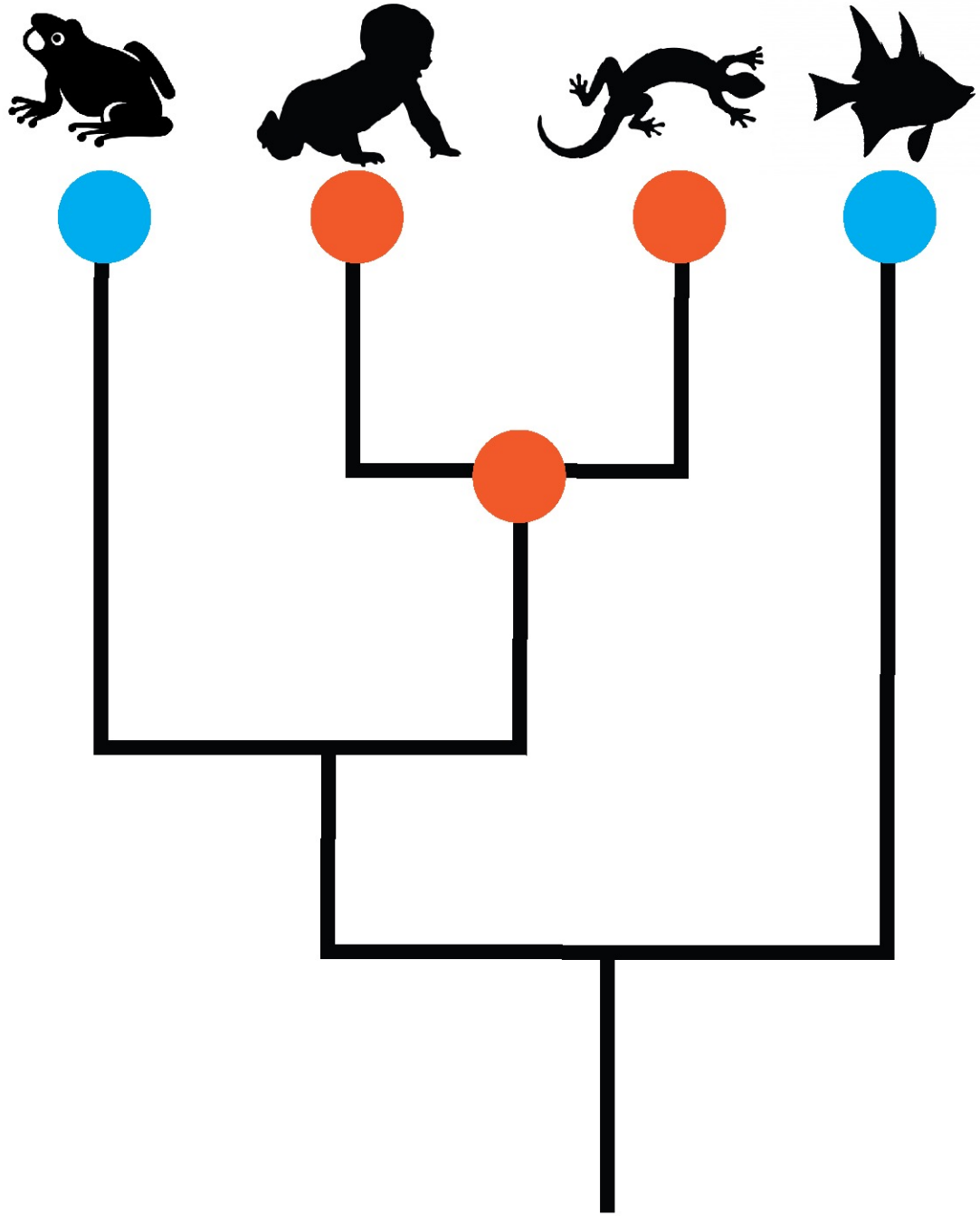
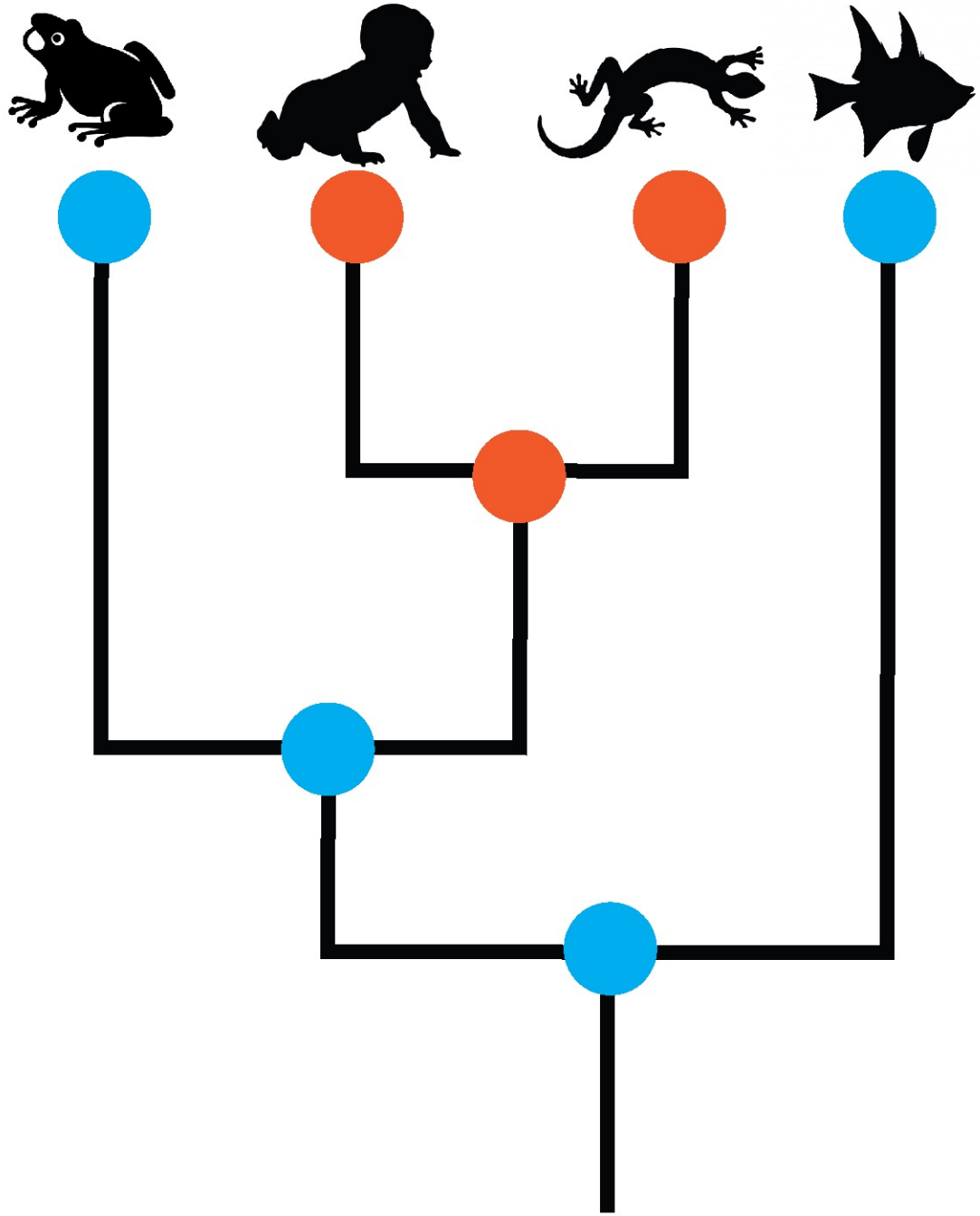
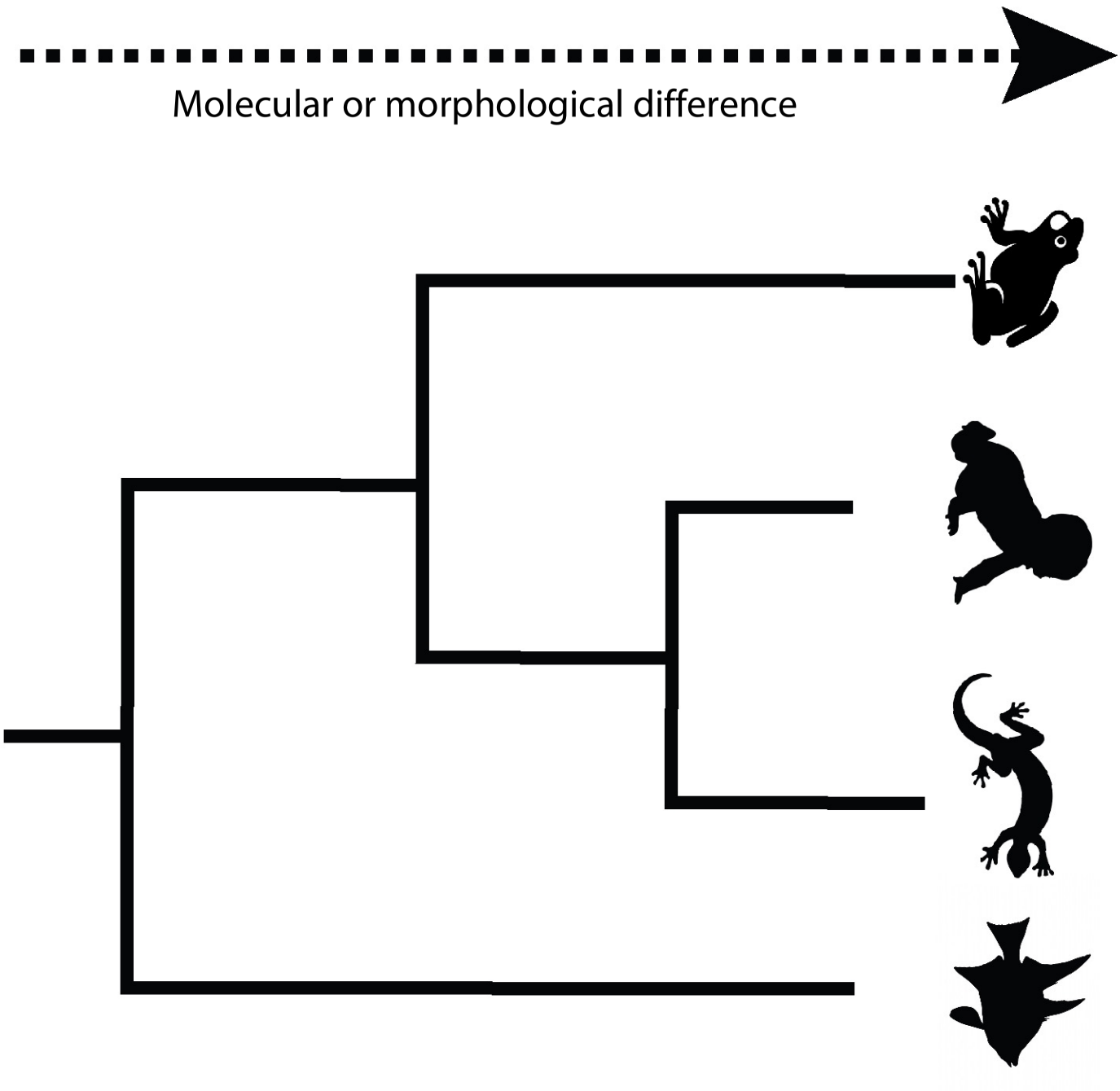
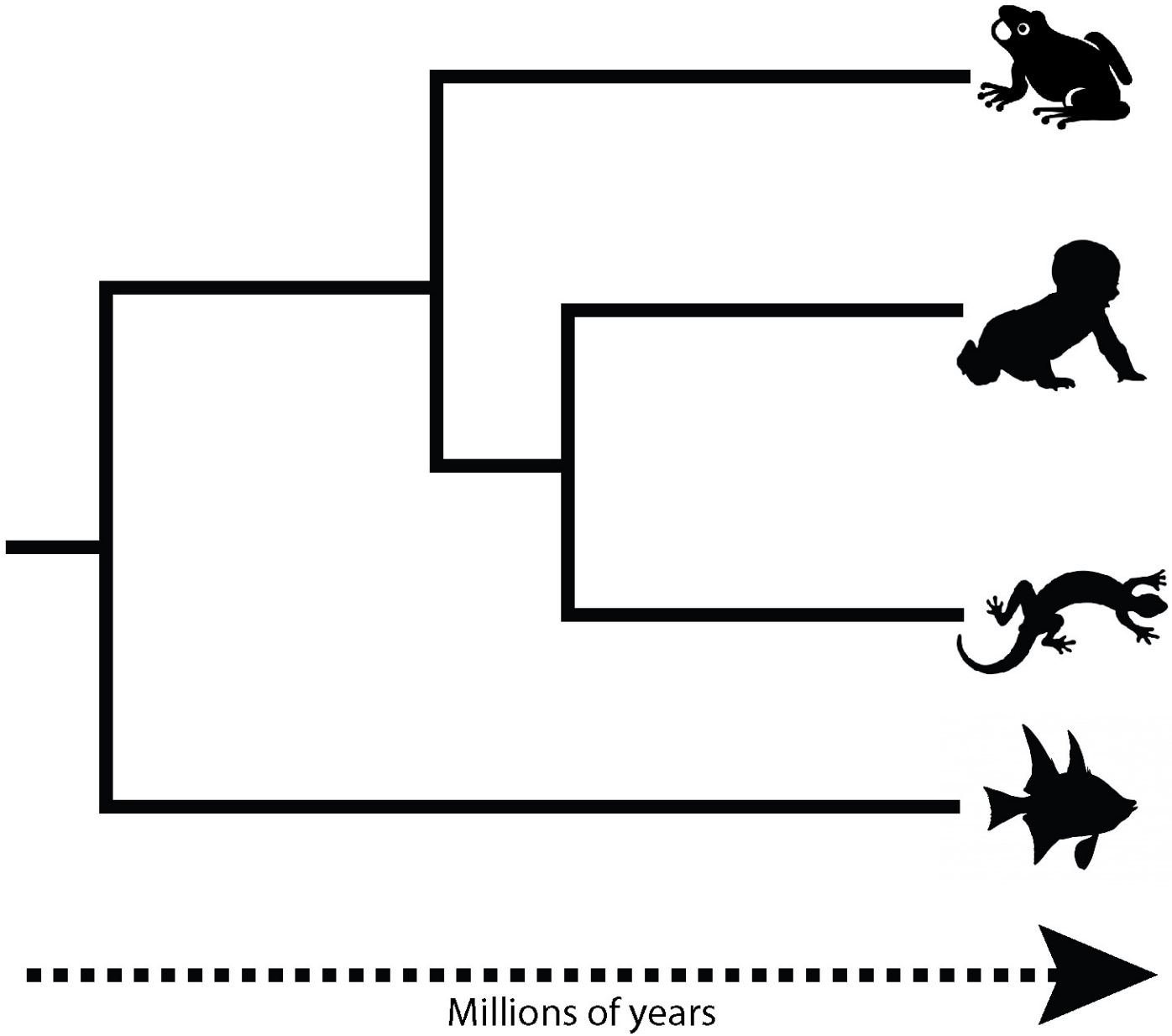
78
55



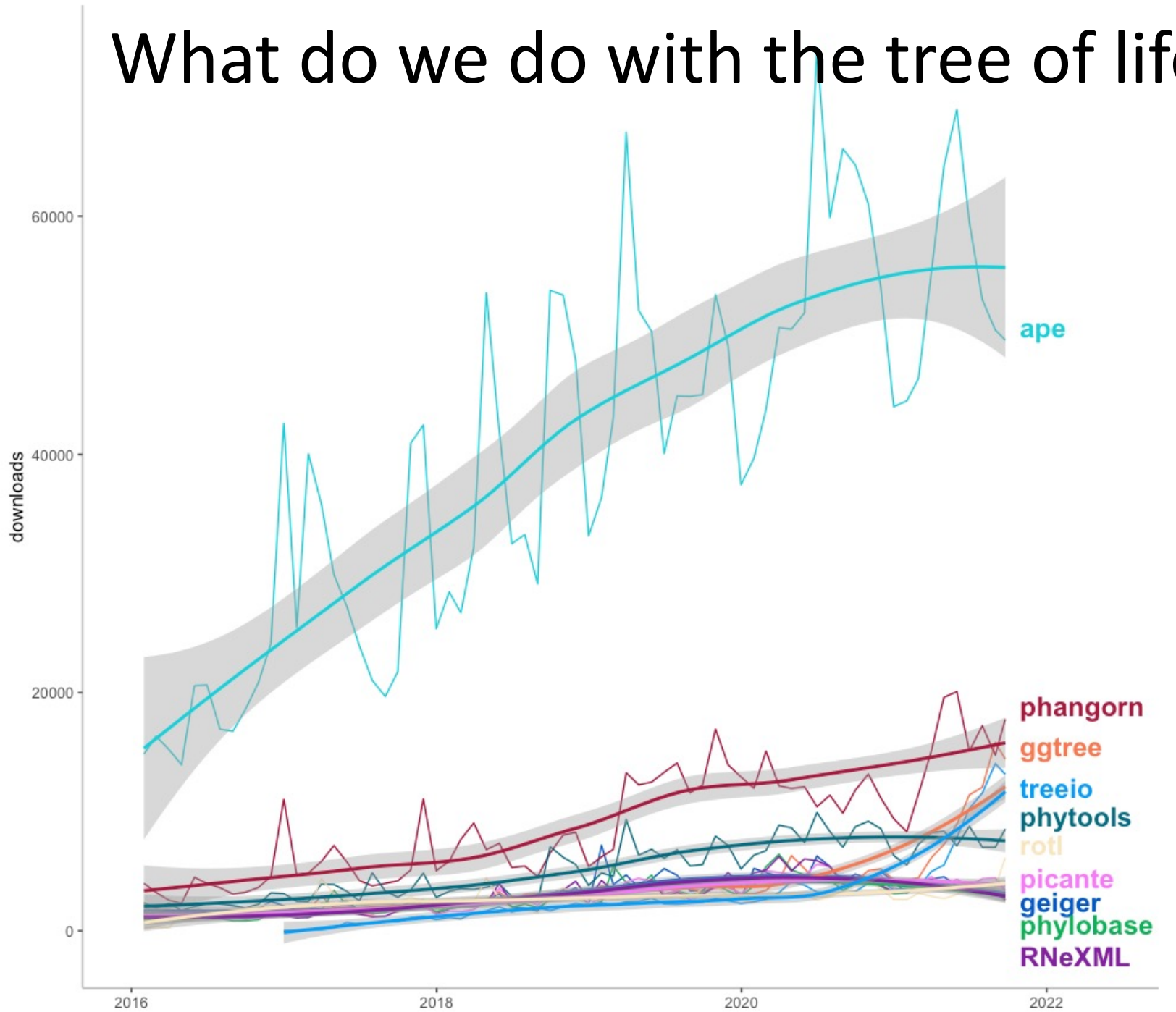





Molecular or morphological difference

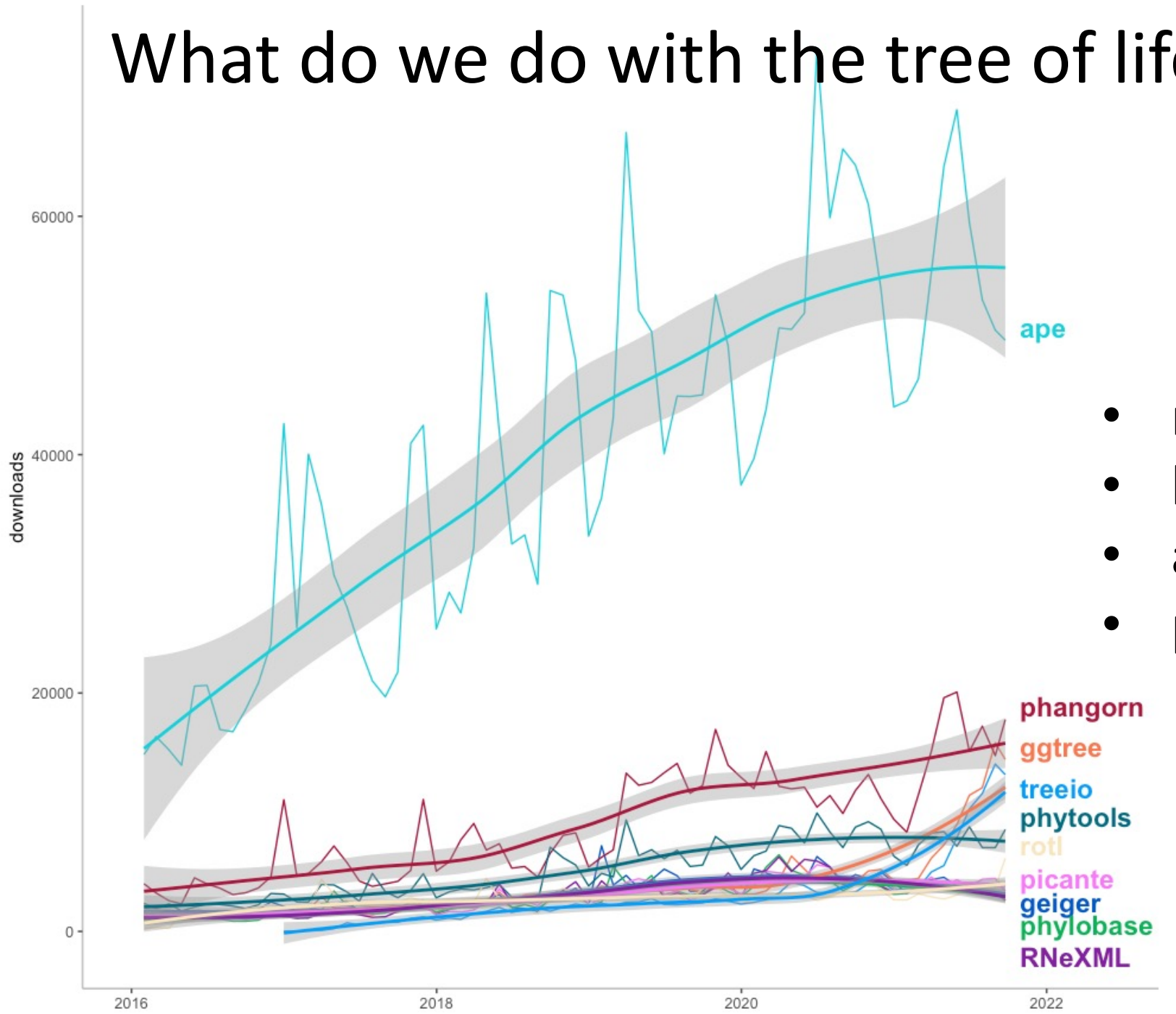

Millions of years

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



dlstats: R package download stats

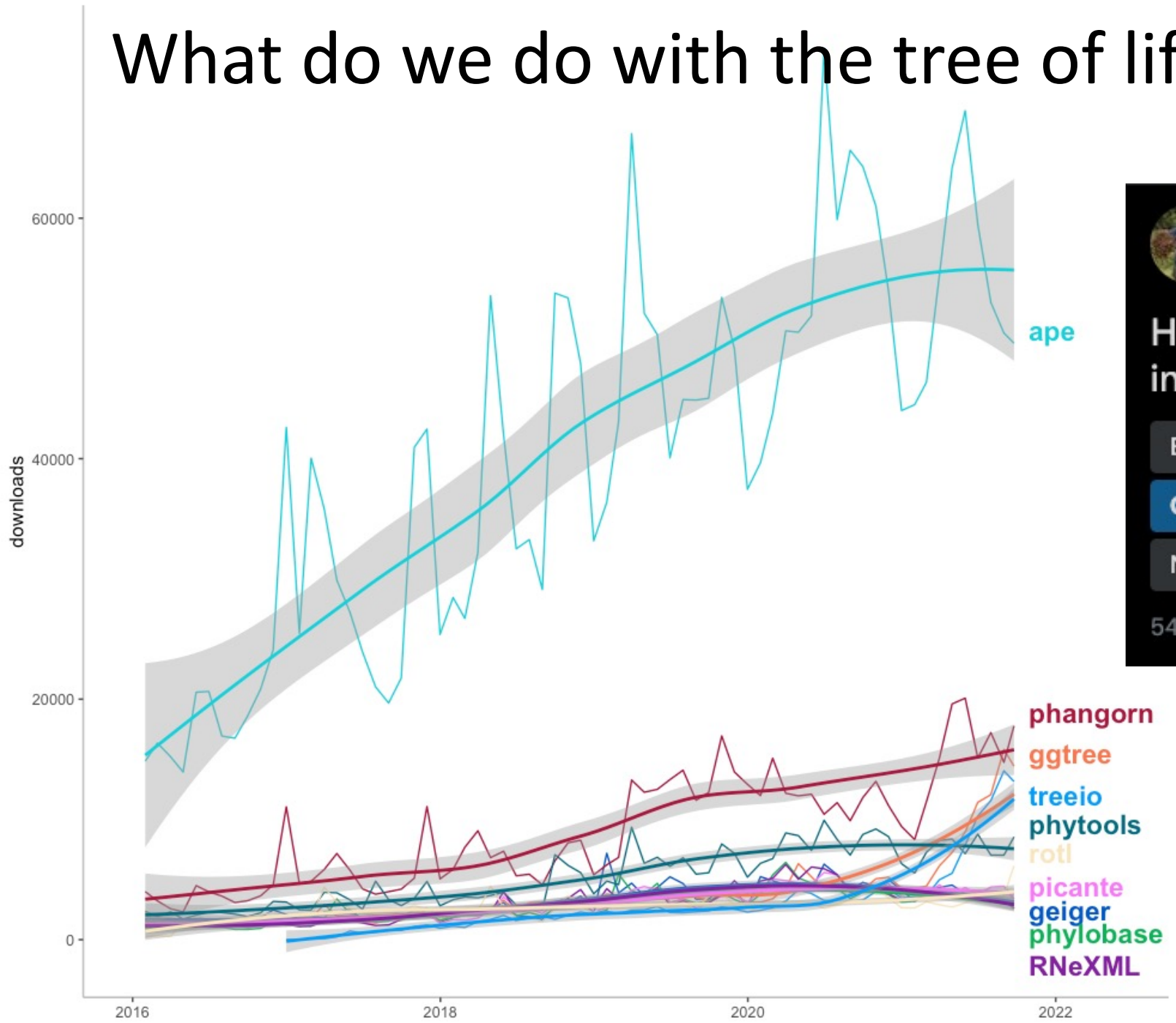
What do we do with the tree of life in R?

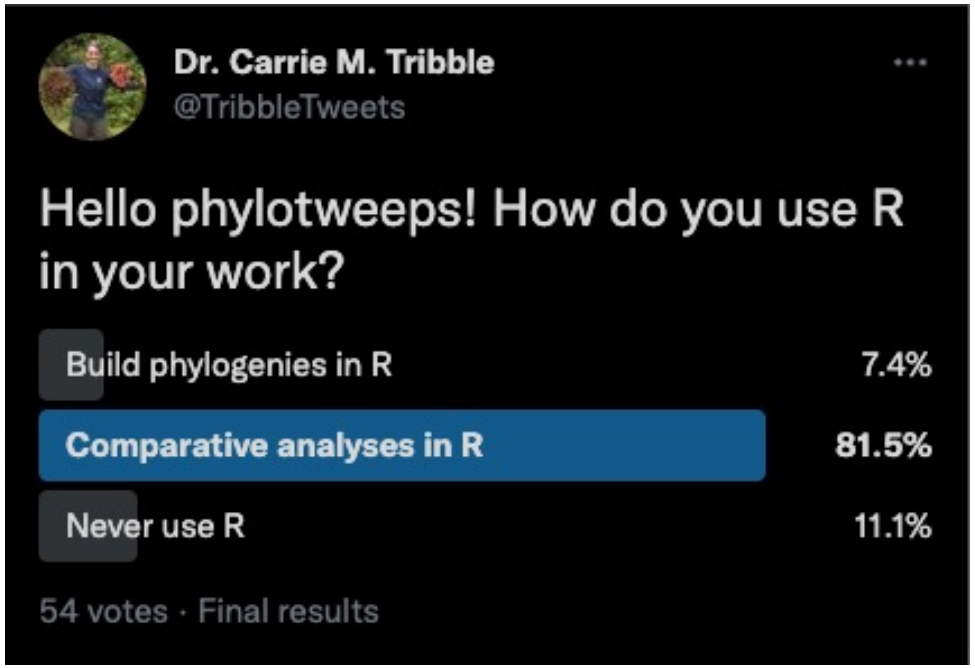


- read and parse tree objects
- build trees
- analyze data on trees
- plot trees and data

dlstats: R package download stats

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





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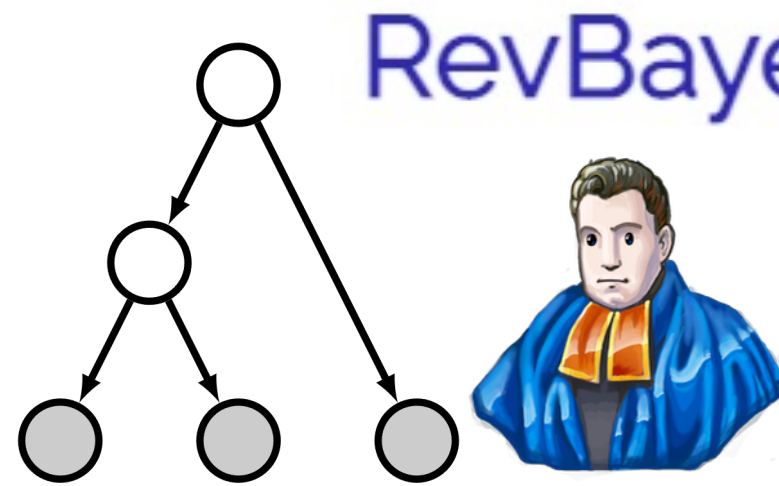
python
δendroPy

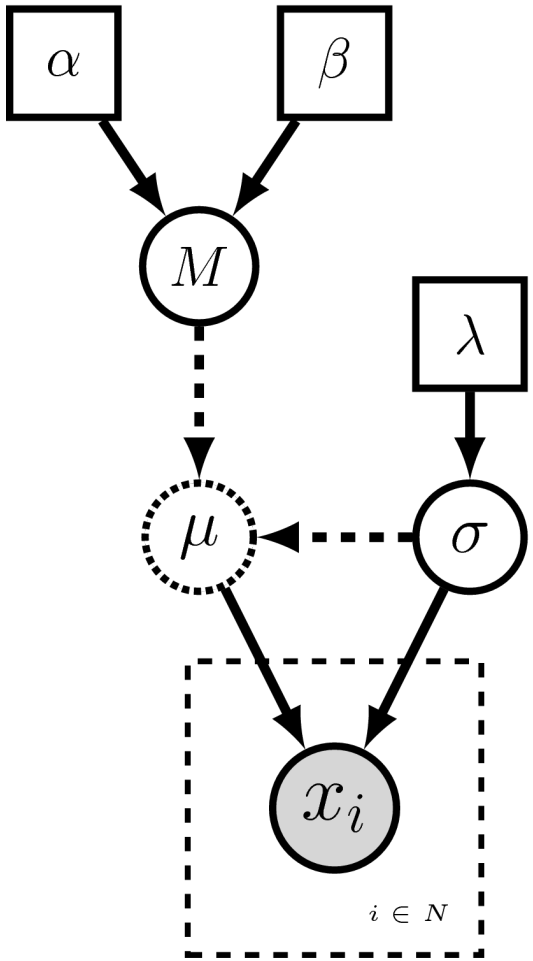

python
δendroPy


julia

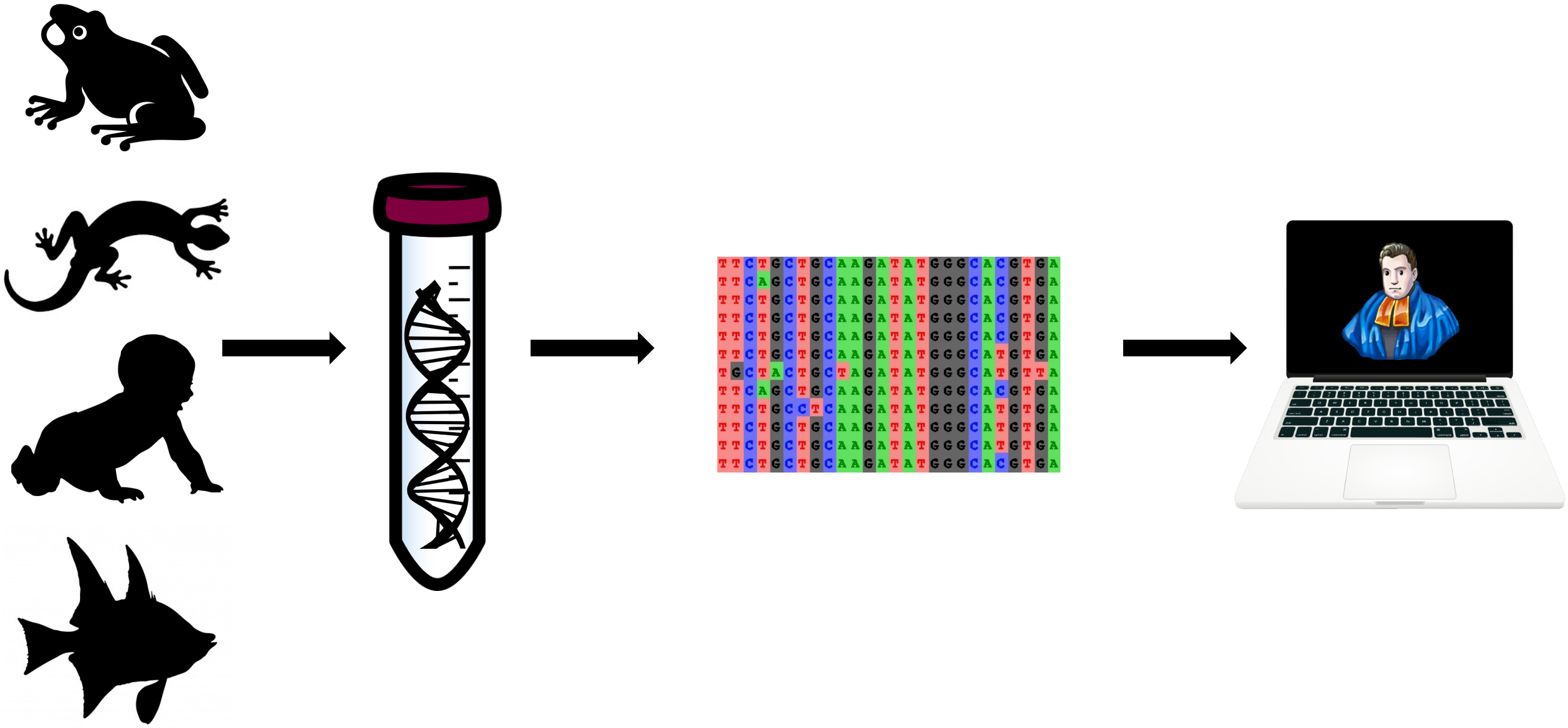
julia



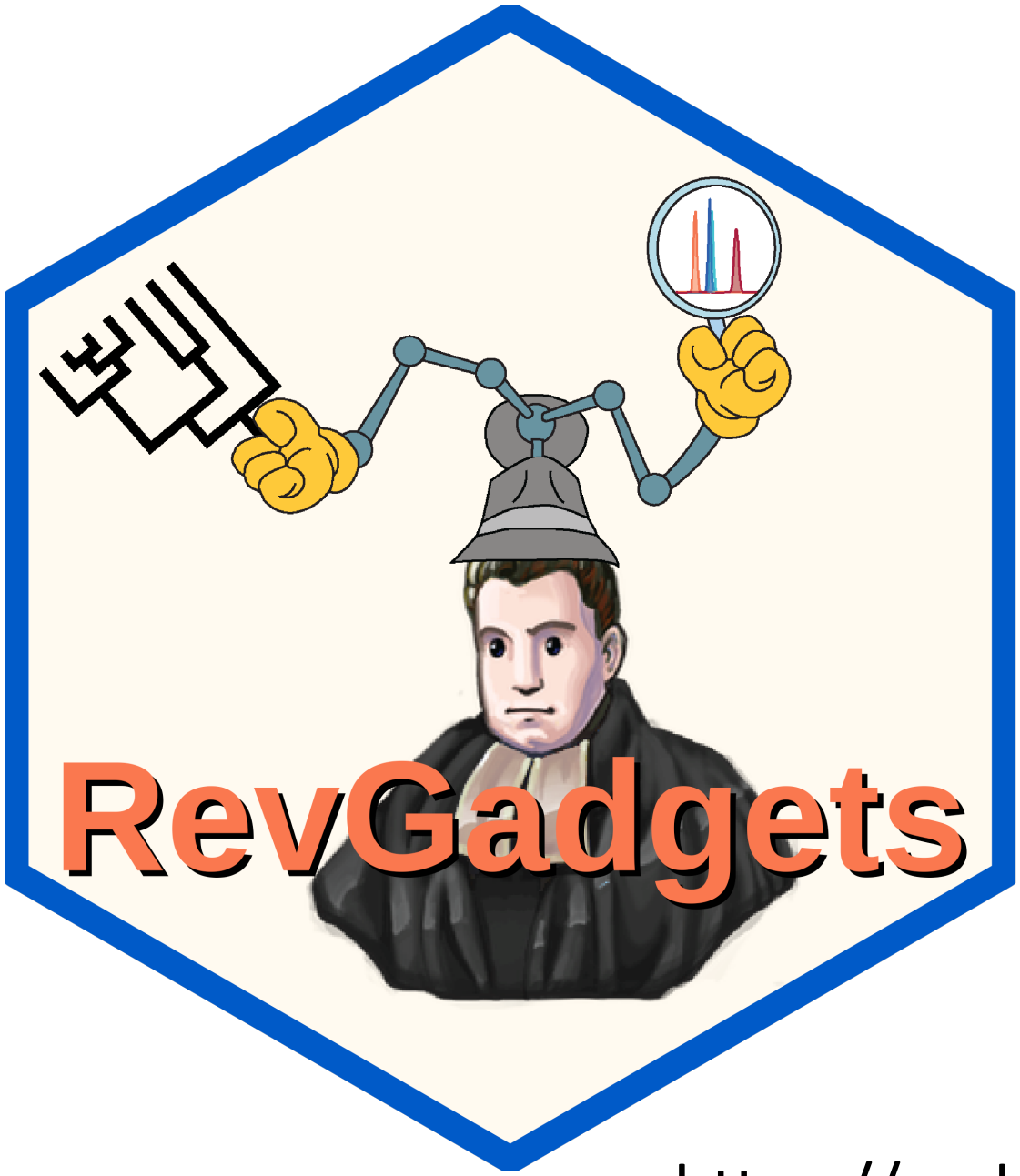
Probabilistic Graphical Models in RevBayes




```
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])
}
```



Iteration	Posterior	Likelihood	Prior	ana_both_dry	ana_both_wet	ana_dry_both	ana_wet_both	anagenetic_change	cladogenetic_change
0	-790.0051	-780.4788	-9.526339	0.4910882	1.596216	1.58578 0.4673842	0.6310142	0.6310142	0.1 0.1 0.1 0 0 0 0 0 0 0
1	-729.6538	-719.2849	-10.36886	0.6712829	1.685157	1.167794	0.210479	0.8923729	0.6755347	0.1011246	0.3402081	0.2879784
2	-727.5051	-718.4702	-9.034909	0.5123734	1.281049	1.126864	0.3394797	0.8410979	0.8162875	0.1248864	0.3402081	0.4008258
3	-718.5638	-710.998	-7.565731	0.4182964	0.9501834	0.4598878	0.08730785	0.1522666	0.4176467	0.1974044	0.2897294	0.4008258
4	-722.7219	-715.9461	-6.775825	0.2414421	0.5492974	0.4495262	0.134788	0.2918582	0.5548939	0.1974044	0.3023111	0.4008258
5	-721.8121	-714.8872	-6.924901	0.328724	0.8307746	0.3654149	0.1695493	0.2754446	0.5787315	0.2758623	0.4153234	0.3638519
6	-718.0725	-711.1212	-6.951355	0.4698872	1.61803 0.5947551	0.24968 0.2094472	0.4592419	0.2758623	0.3262309	0.3502299	-0.1310
7	-721.2581	-714.2359	-7.022151	0.6751901	1.192748	0.3546455	0.1997935	0.1964433	0.4120527	0.2743293	0.3262309	0.406472
8	-720.4758	-713.0597	-7.416037	0.3145424	1.66211 0.6086919	0.2545966	0.1150949	0.4454871	0.412955	0.3770338	0.406472	-0.
9	-718.5269	-711.7979	-6.728935	0.5010305	1.040012	0.5317579	0.2034627	0.2693844	0.3426141	0.1729175	0.3463416	0.406472
10	-719.182	-711.9865	-7.195469	0.4225996	1.997446	0.4648564	0.4199497	0.2419852	0.2881196	0.3564048	0.258123	0.3748067
11	-723.328	-714.3143	-9.013788	0.3615851	1.481187	0.3667703	0.2196757	0.5140708	0.2834111	0.1940831	0.2846637	0.3748067
12	-721.957	-713.1999	-8.757076	0.1665487	1.21655 0.3909736	0.2202226	0.4207509	0.2594803	0.2826962	0.2846637	0.371827	-0.
13	-722.9498	-714.2993	-8.650515	0.4959006	1.665536	0.5864067	0.2726558	0.2589001	0.5266525	0.07181975	0.2846637	0.371827
14	-721.8032	-713.6953	-8.107844	0.2786448	1.531329	0.7979823	0.344397	0.4710328	0.4120893	0.1933432	0.3865736	0.371827
15	-725.8901	-718.3396	-7.55047	0.451597	2.548345	0.4111326	0.4143225	0.5998574	0.2896945	0.3628954	0.3483699	0.371827
16	-724.5507	-716.9219	-7.628821	0.4657509	2.156674	0.5303696	0.2541706	0.3397561	0.2168938	0.472154	0.3483699	0.371827
17	-721.8529	-711.6791	-10.17379	0.2315763	2.281754	0.3770735	0.398082	0.09887553	0.5530886	0.03735246	0.346155	0.371827
18	-724.7855	-713.814	-10.97143	0.1325092	1.067469	0.426021	0.206234	0.3042973	0.7667723	0.04589935	0.346155	0.4171764
19	-719.5225	-712.1667	-7.355722	0.6989711	1.06702 0.4510134	0.1976105	0.4880307	0.4363484	0.164381	0.346155	0.6156627	-0.
20	-720.2135	-709.7951	-10.41842	0.4920336	1.128275	0.6640891	0.1983302	1.454243	0.7708584	0.164381	0.346155	0.6156627
21	-722.0716	-713.1862	-8.885409	0.4507315	1.190263	0.345538	0.2480339	1.106671	0.3479654	0.3973659	0.346155	0.6156627
22	-724.3936	-713.4949	-10.8987	0.4483615	2.583497	0.59515 0.3594397	0.6738285	1.79948 0.3973659	0.3844042	0.6156627	-0.9282
23	-727.0166	-713.468	-13.54853	0.9441742	3.360122	0.739658	0.7323008	0.09227213	1.505489	0.2392712	0.4721602	0.804648
24	-732.5225	-716.5421	-15.98033	1.241862	7.090214	1.58324 1.475692	0.859229	1.104643	0.6030517	0.4721602	0.804648	-0.
25	-731.6697	-714.7947	-16.87498	0.4026313	12.08721	0.5997639	2.366395	0.2750033	0.9742266	0.7408228	0.4454431	0.804648
26	-723.8321	-710.5964	-13.2357	0.3068095	6.378163	0.5867534	1.561742	0.318134	0.9730621	0.5994102	0.5414435	0.804648
27	-725.0139	-715.7289	-9.285069	0.2802539	1.970997	0.6711525	0.4334442	0.2148694	0.6597386	0.2925033	0.5414435	0.9552714
28	-730.4732	-720.5212	-9.951948	0.2891504	1.404327	0.4702493	0.4844559	0.2623072	0.6995813	0.3298186	1.22654 0.9552714	-1.
29	-729.1257	-717.046	-12.0797	0.22282 3.309503	0.7228465	0.6032598	0.8638858	0.7032729	0.3298186	0.2078692	0.9407169	-0.
30	-725.1287	-714.4562	-10.67244	0.4895125	3.076629	0.5311531	0.4007898	0.3308623	0.6416762	0.6585716	0.6315894	0.9407169
31	-729.401	-717.484	-11.91705	0.3820498	1.6875 1.052657	0.430263	0.5253926	0.5692855	0.3564671	1.292466	0.9407169	-1.
32	-728.3187	-715.8004	-12.51822	0.8562141	2.65767 1.021915	0.485031	0.374405	0.4430734	0.7847968	1.292466	0.9407169	-0.
33	-727.155	-714.265	-12.88993	0.4363994	2.508708	0.9099066	0.6521763	0.3411776	0.8389228	0.7847968	1.292466	0.7942005
34	-724.6938	-714.2054	-10.48841	0.4169776	2.322568	0.8384613	0.5362443	0.392203	0.4853335	0.5125453	1.014506	0.8624797
35	-722.2084	-712.507	-9.701355	0.4645472	1.861467	0.7869112	0.3499786	0.6756 0.6116106	0.5125453	0.6559701	0.8624797	-0.
36	-730.8842	-718.2505	-12.6337	0.5275001	6.505948	1.069829	1.058938	0.2858671	0.6365545	0.5125453	0.6559701	0.9467844
37	-727.1167	-713.7086	-13.40807	0.4759459	7.625785	0.8461218	2.210933	0.1390575	0.3863018	0.4599137	0.6559701	0.9467844
38	-730.2559	-715.1198	-15.1361	1.043551	9.491474	1.541917	2.058075	0.349743	0.4480308	0.4599137	0.7010315	0.73908 -0.
39	-733.3809	-719.9594	-13.42152	1.955123	6.461538	1.541917	0.8695607	0.2487574	0.3370976	0.4599137	0.7010315	0.73908 -1.
40	-732.5108	-720.2337	-12.27713	1.33024 5.058632	1.532104	1.011598	0.1025068	0.2878803	0.4599137	0.8810157	0.73908 -0.6278
41	-732.6625	-719.158	-13.50449	2.662438	4.324147	1.972654	0.6860722	0.8619453	0.3367074	0.3550154	0.8810157	0.73908 -0.
42	-727.4229	-715.0868	-12.33602	1.560882	2.301829	2.103341	0.4306147	1.1249 0.6161058	0.303371	0.9709358	0.73908 -1.0358
43	-732.4801	-721.2512	-11.22889	1.524695	2.108399	1.777625	0.5065302	1.214774	0.4237529	0.303371	0.6786291	0.73908 0.0
44	-730.6713	-718.9623	-11.70896	0.647513	2.890947	0.8238042	0.5934201	0.6750525	1.405144	0.6694555	0.3657751	0.73908 -0.
45	-724.1296	-714.5482	-9.581453	0.3135643	2.173557	0.6332301	0.3760491	0.1994618	1.416281	0.2197426	0.3657751	0.73908 -0.
46	-727.4277	-717.7596	-9.668158	0.5571328	2.151761	0.8031183	0.3358018	0.1235847	1.178697	0.2698604	0.4311817	0.7570241
47	-724.2832	-715.1199	-9.163304	1.483818	1.823837	1.645328	0.5080247	0.2229799	0.4708436	0.2887582	0.4212467	0.7570241



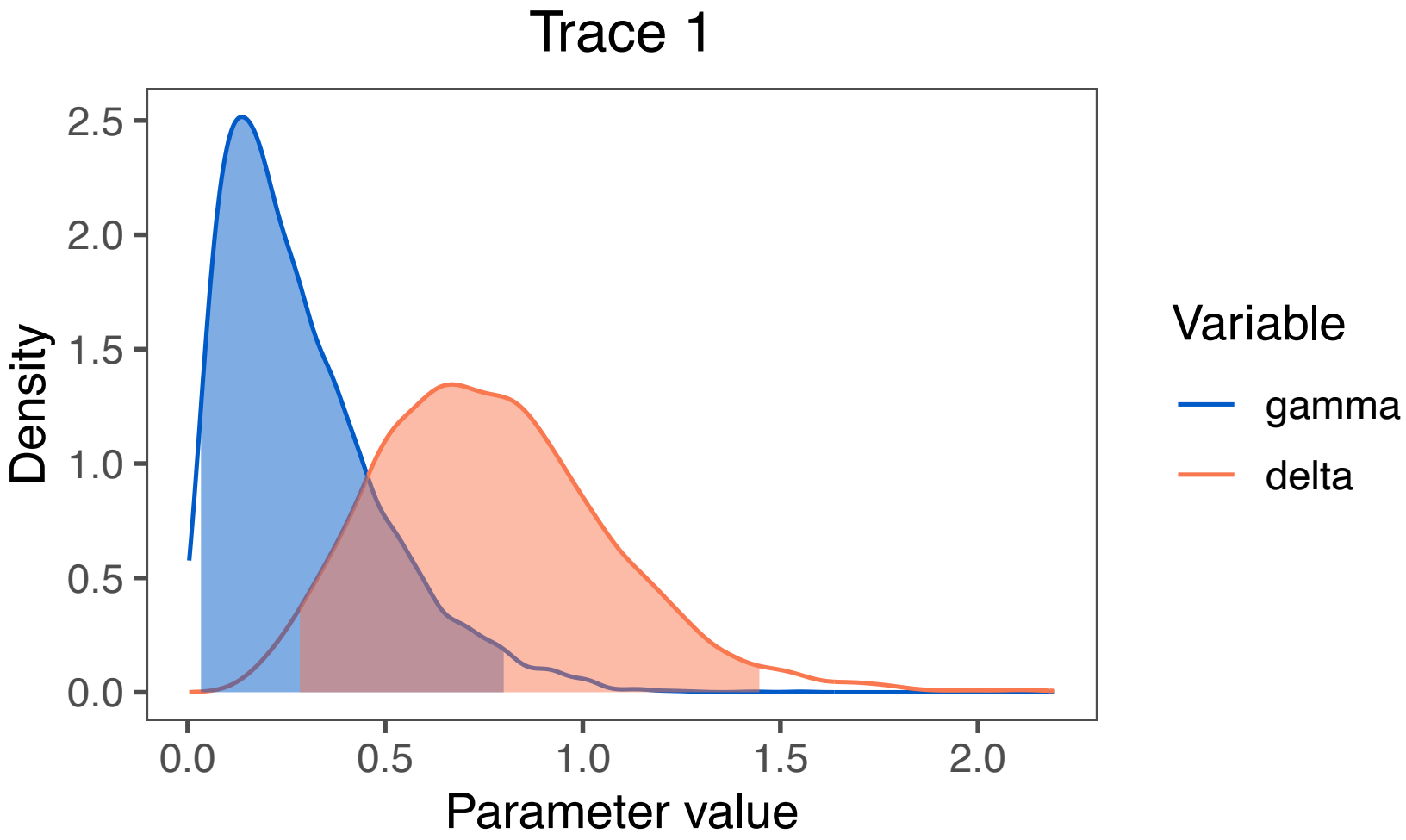
an R Package for visualizing Bayesian phylogenetic analyses from RevBayes

Available on CRAN

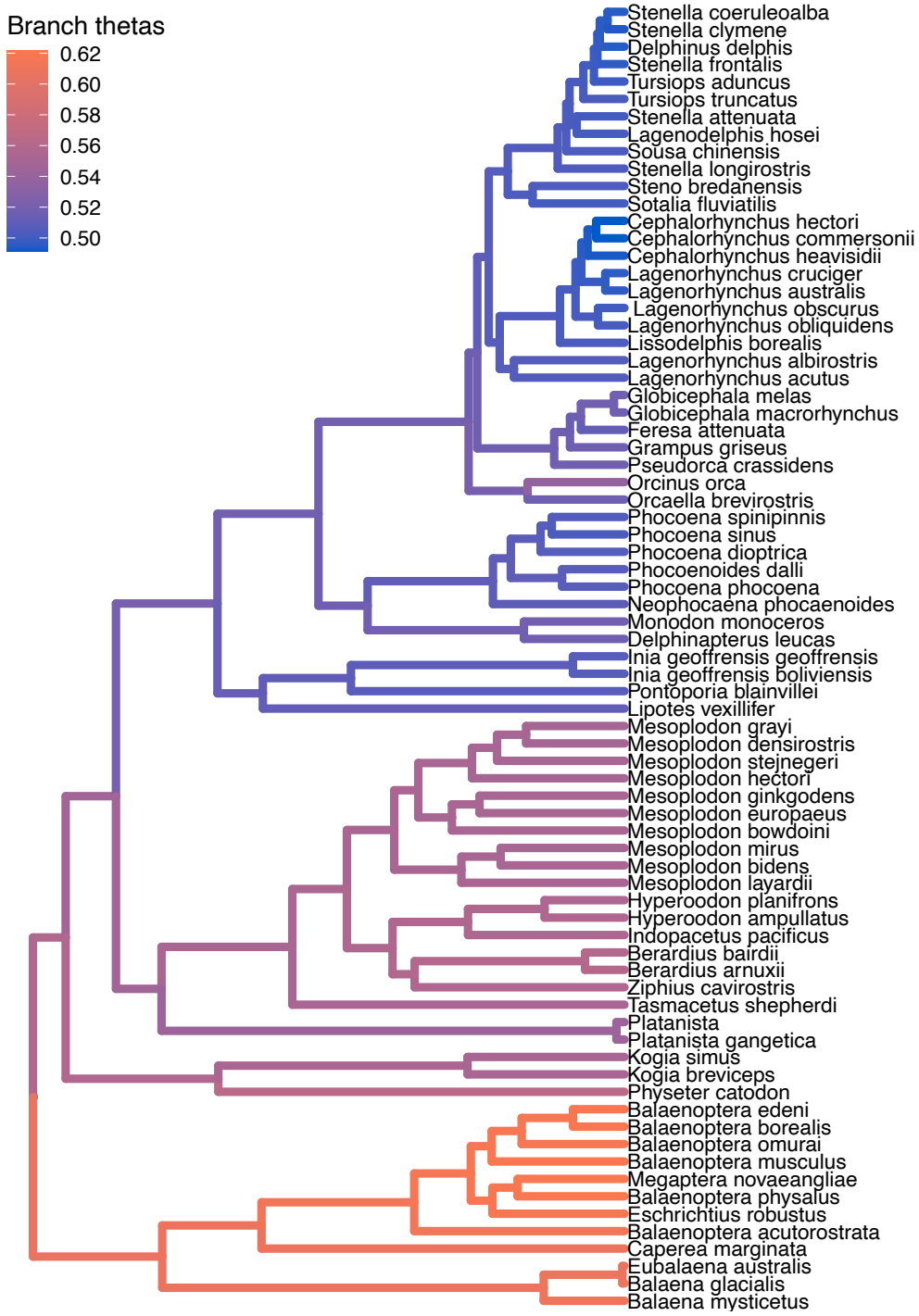
github.com/cmt2/revgadgets

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

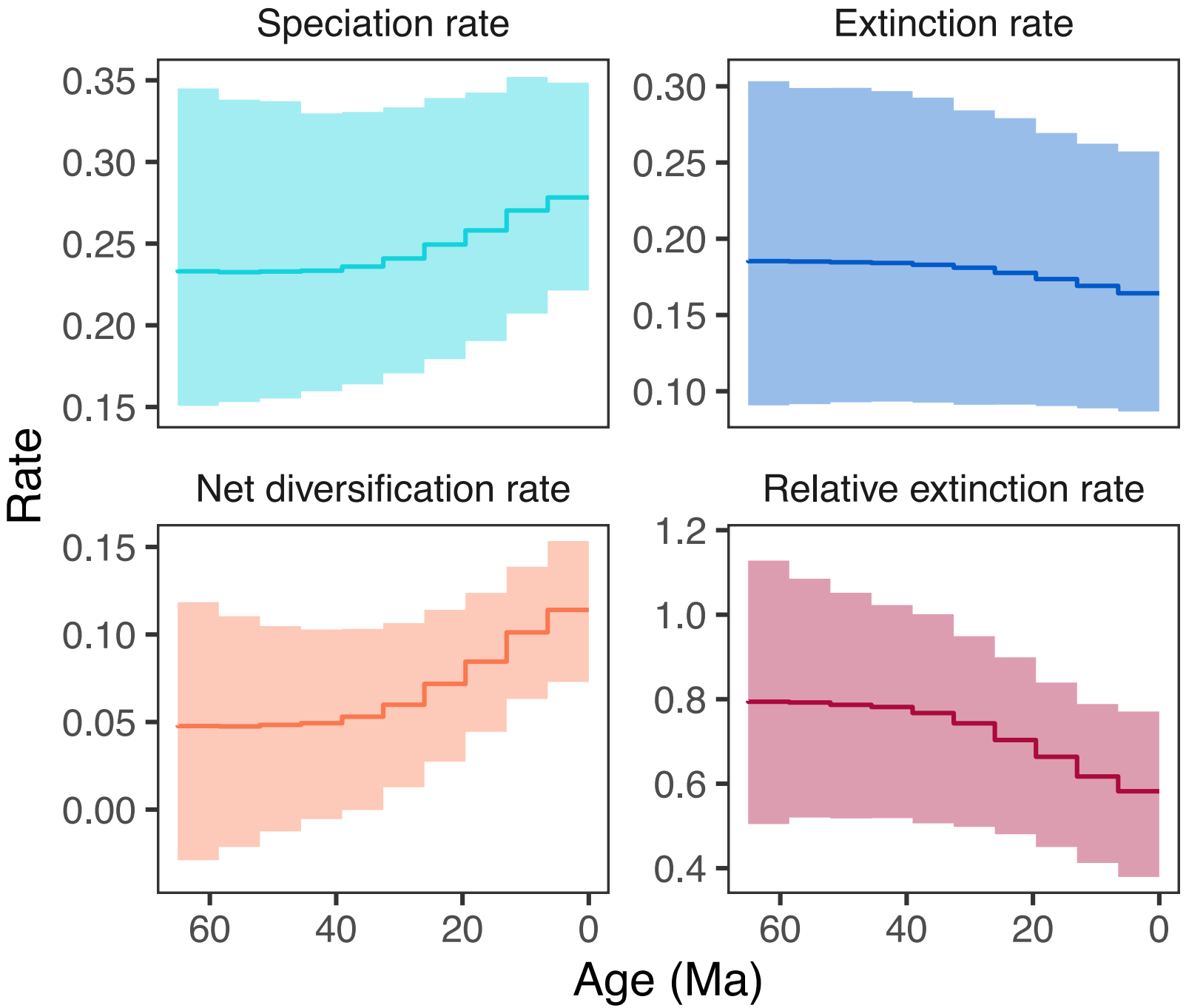
```
# specify the log files with rates of
# chromosome evolution
files <- c("chromevol_simple.log")

# read the trace
trace <- readTrace(path = files)

# plot the posteriors of each parameter
plotTrace(trace = trace,
    vars  = c("gamma", "delta"))[[1]]
```



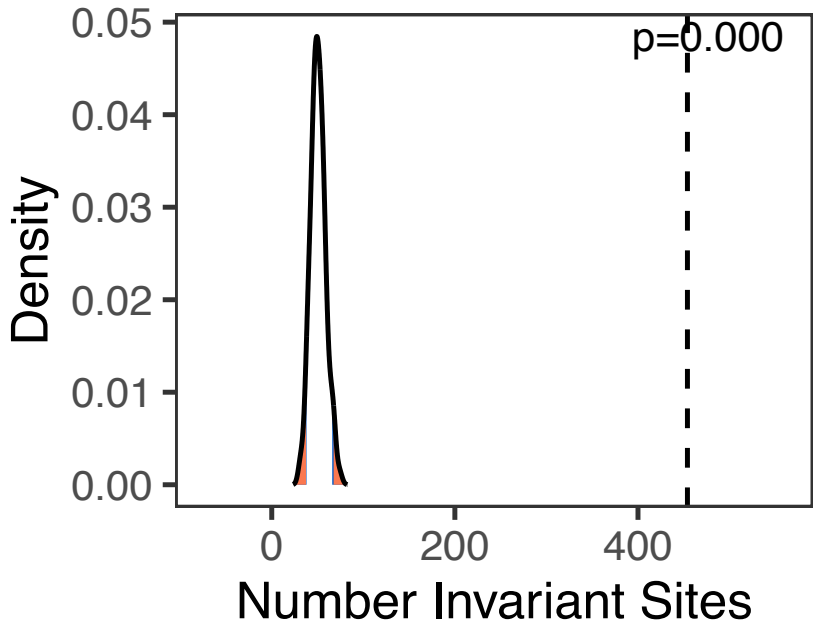
```r
# specify the annotated tree file
file <- "relaxed_OU_MAP.tre"

# 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)
```

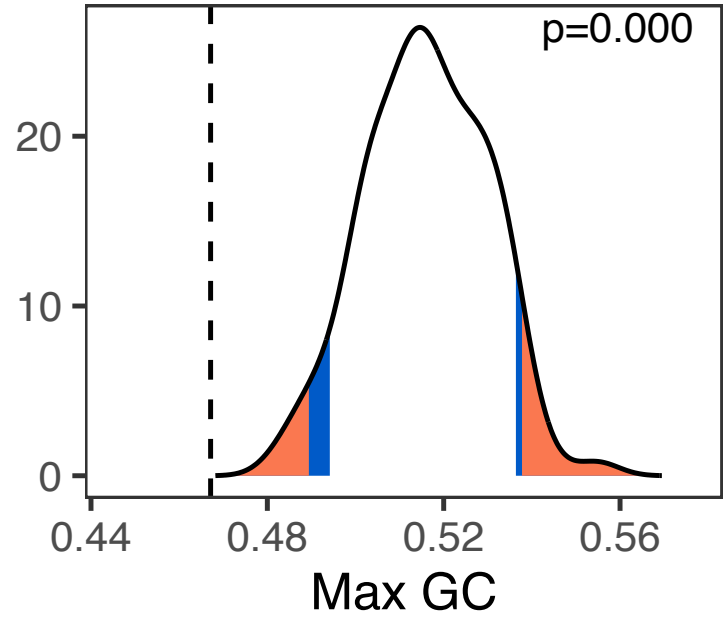


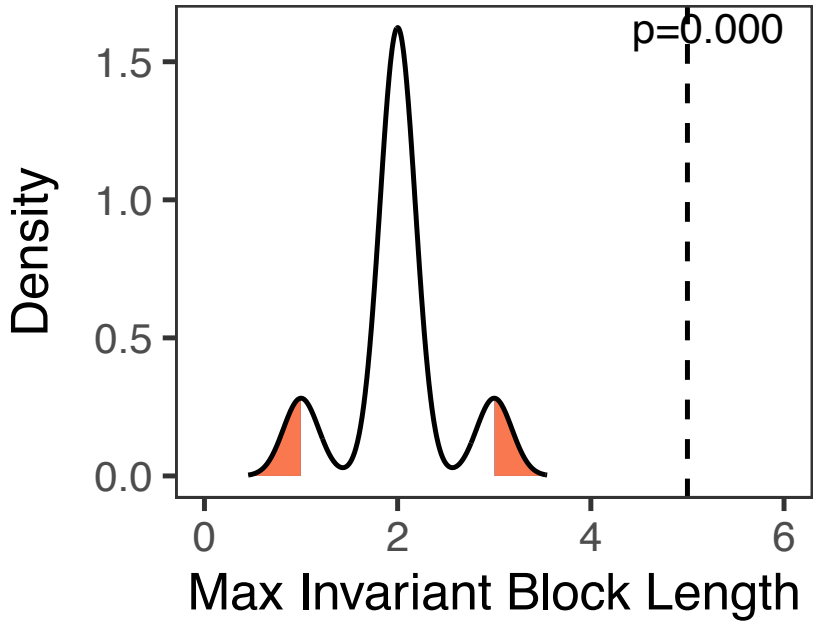
```
# specify the log files with diversification
# rates and rate-change times
speciation_time_file <-
        "primates_EBD_speciation_times.log"

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)
```

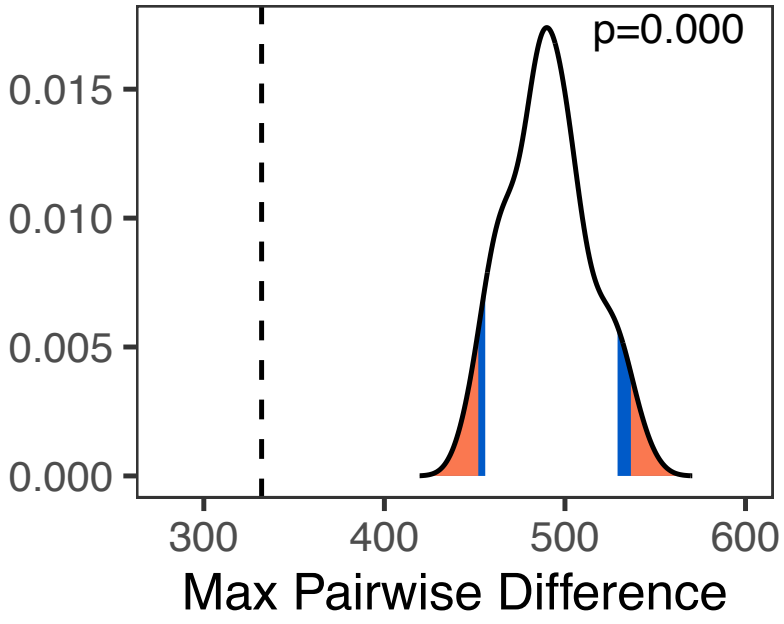


```
# specify the simulated statistics file
sim <- "simulated_data_pps.csv"

# 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)]
```

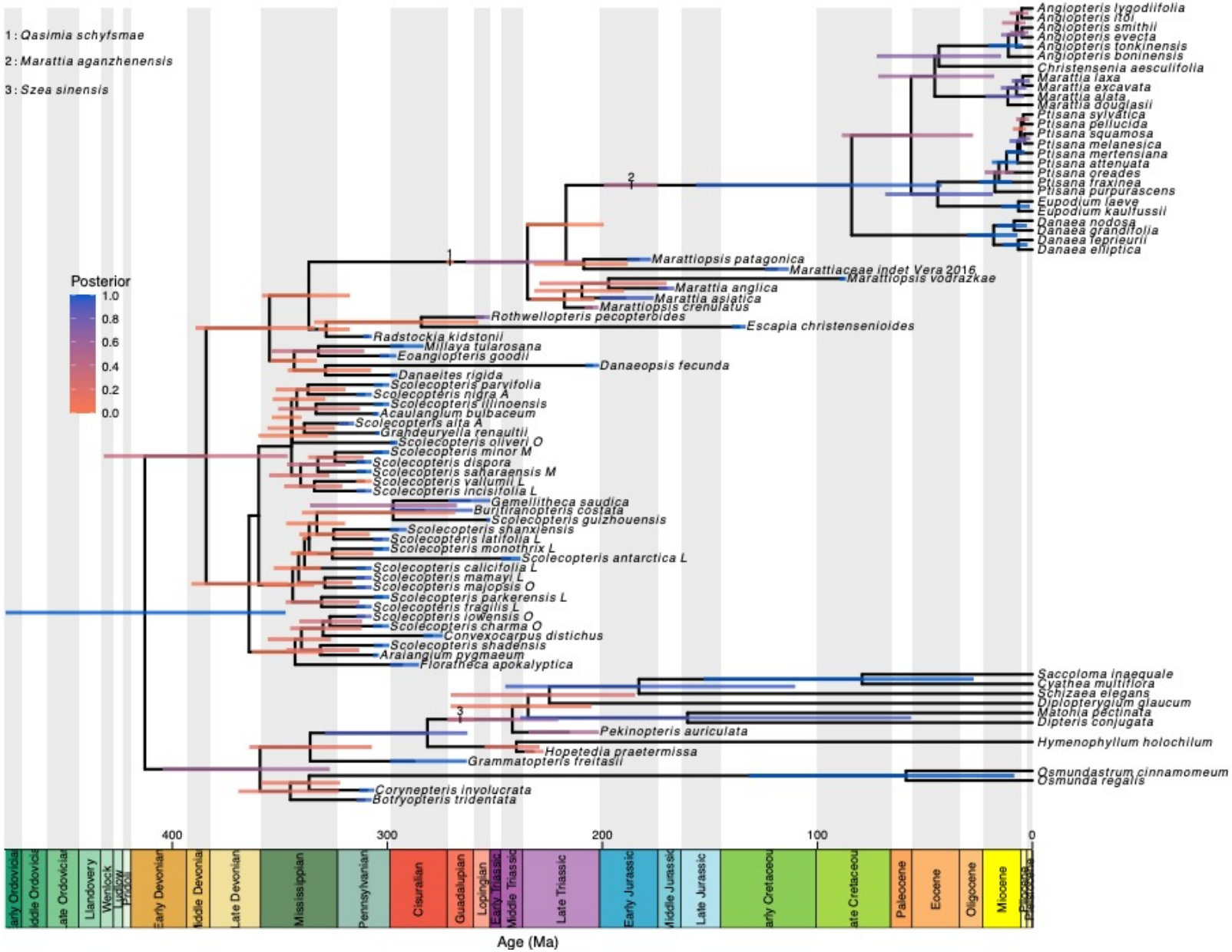




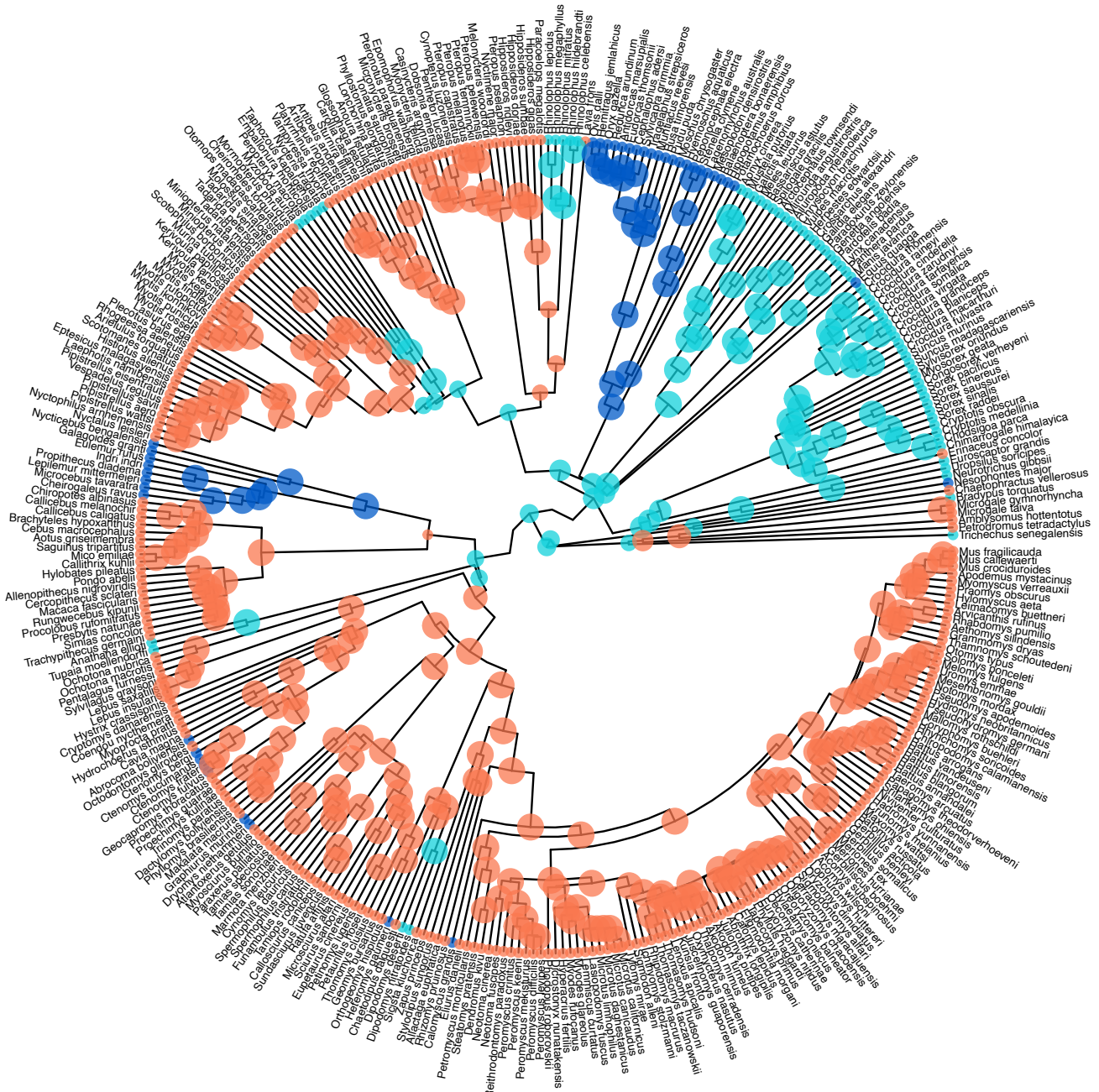




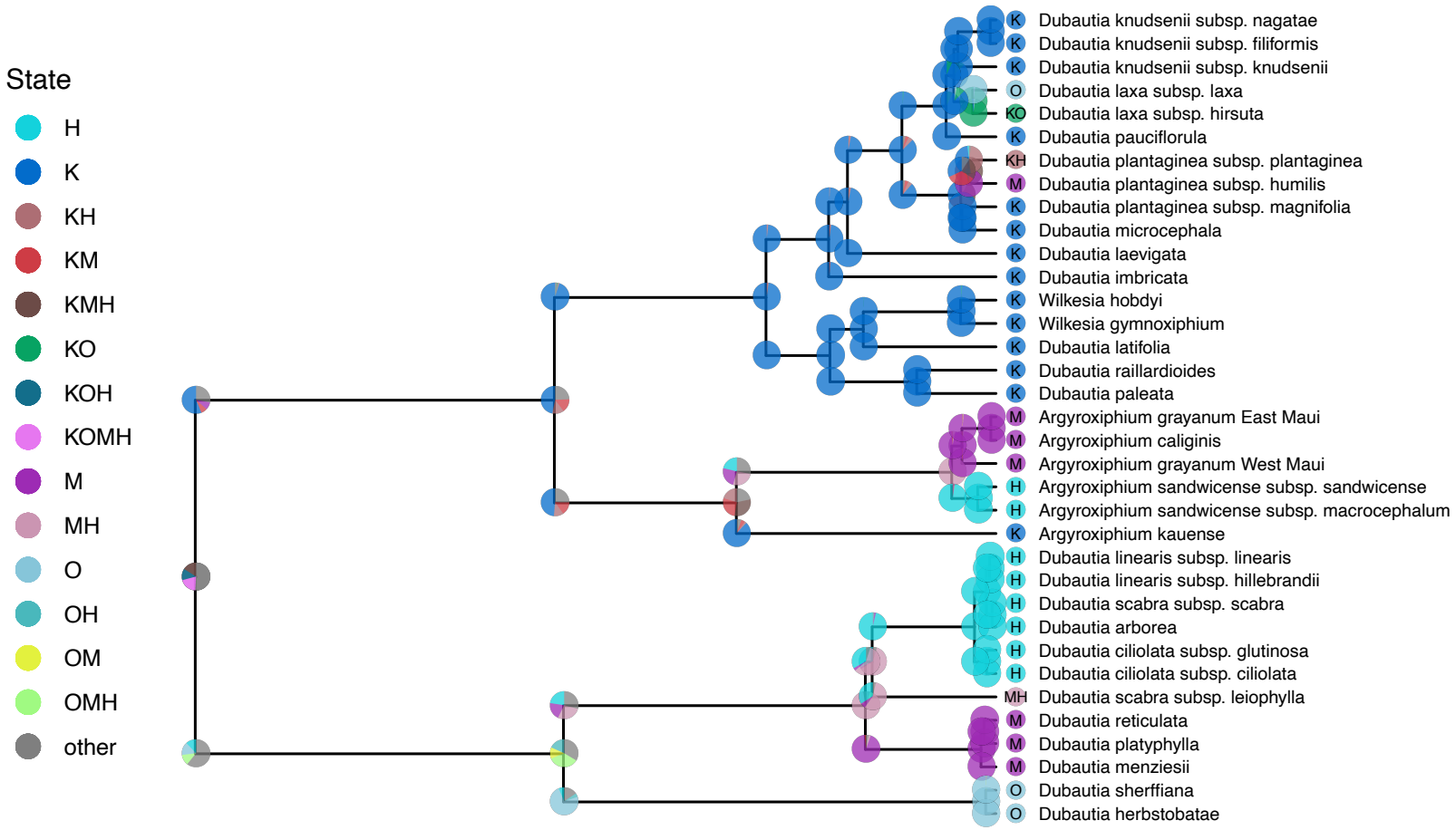
```r
# specify the simulated statistics file
sim <- "simulated_data_pps.csv"

# 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)]
```



```r
# specify the tree file
file <- "ase_freK.tree"

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

# 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")
```



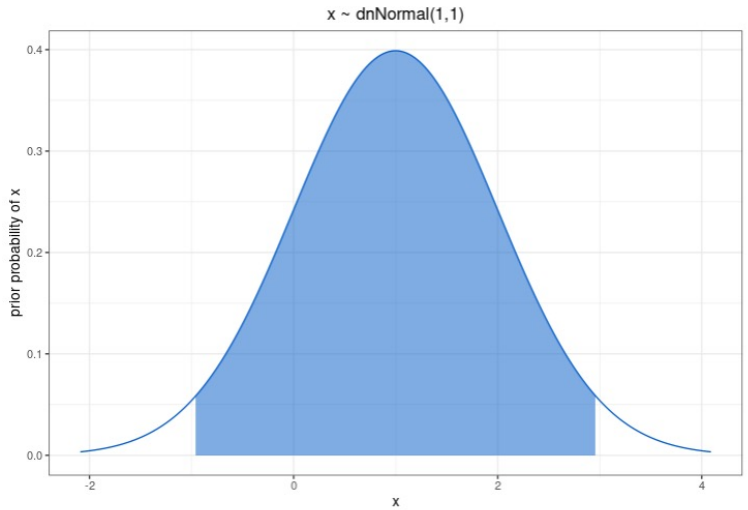
```r
file <- "simple_ase.tre"

# 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)
```



Prior Distributions

Rev code:

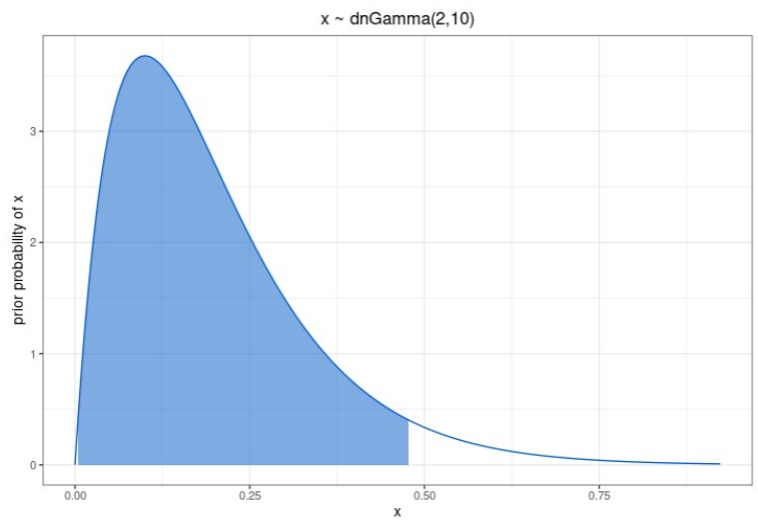
```
x ~ dnNormal(1,1)
```

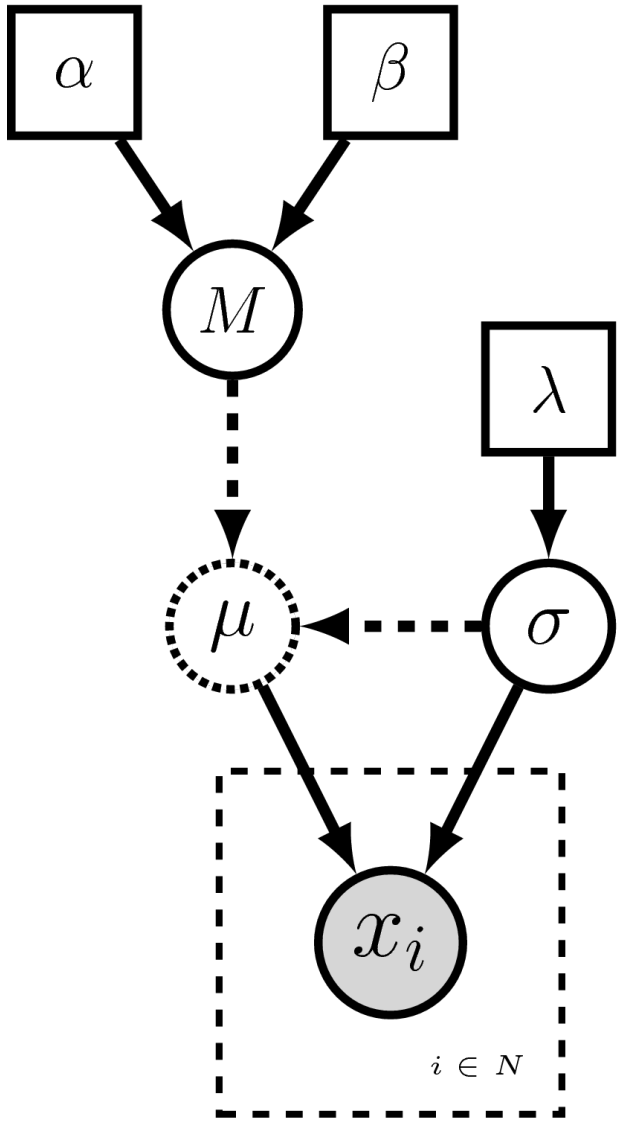


Prior Distributions

Rev code:

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





Mike May

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Sebastian Höhna

Joëlle Barido-Sottani

Bjørn Kopperud

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

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