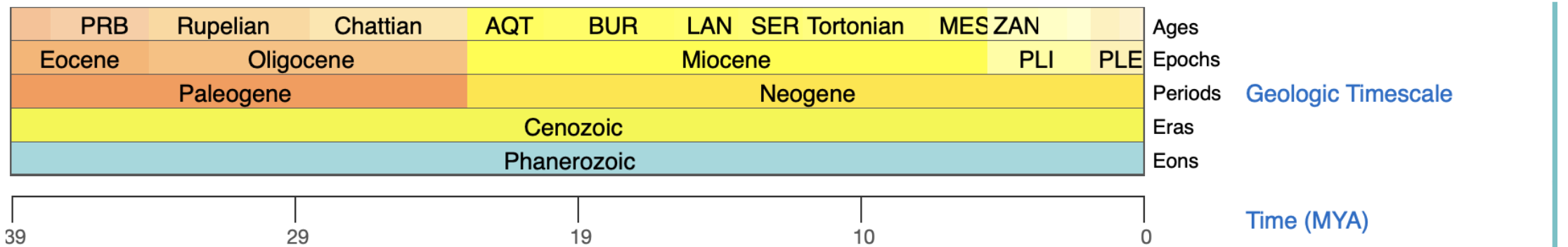
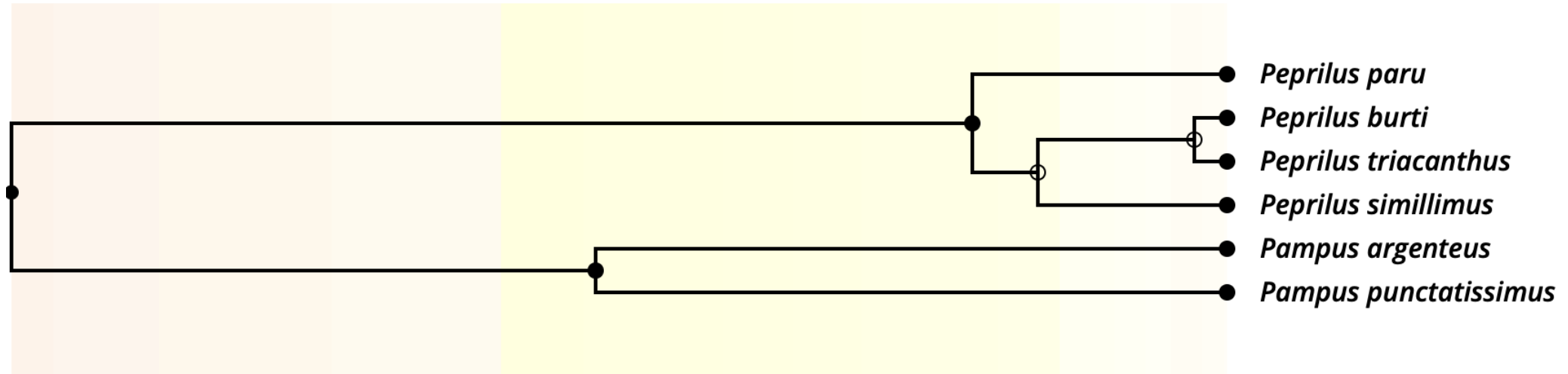


# Time tree



# Time tree

- [Http://timetree.org](http://timetree.org)

3,164 Studies 97,085 Species

**TIMETREE**  
THE TIMESCALE of LIFE

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Search

## TimeTree of Life

TimeTree is a public knowledge-base for information on the evolutionary timescale of life. Data from thousands of published studies are assembled into a searchable tree of life scaled to time. Three search modes are possible:

- **NODE TIME** - to find the divergence time of two species or higher taxa
- **TIMELINE** - to drill back through time and find evolutionary branches from the perspective of a single species
- **TIMETREE** - to build a timetree of a group of species or custom list

**TIMEPANELS** showing events in geological time and astronomical history are provided for comparison with timelines and timetrees. Results can be exported in different formats for additional analyses and publication.

### Search

**NODE TIME** GET DIVERGENCE TIME FOR A PAIR OF TAXA

Specify 2 Taxon Names <sup>?</sup>

Taxon 1:

Taxon 2:


Clear Search

Resolve Ambiguity <sup>?</sup>

Taxon 1:

Taxon 2:

Show Time



# Time tree

- Estimating branch lengths in proportion to time is confounded by the fact that the rate of evolution and time are intrinsically linked when inferring genetic differences between species.
- A model of lineage-specific substitution rate variation must be applied to tease apart rate and time.
- When applied in methods for divergence time estimation, the resulting trees have branch lengths that are proportional to time.
- External node age estimates from the fossil record or other sources are necessary for inferring the real-time (or absolute) ages of lineage divergences.

# Time tree

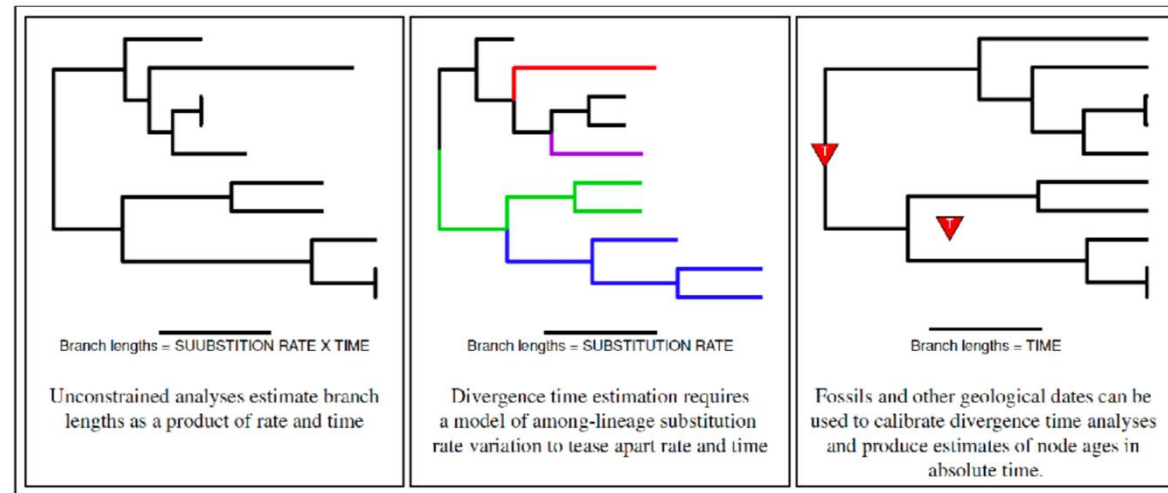


Figure 1: Estimating branch lengths in units of time requires a model of lineage-specific rate variation, a model for describing the distribution of speciation events over time, and external information to calibrate the tree.

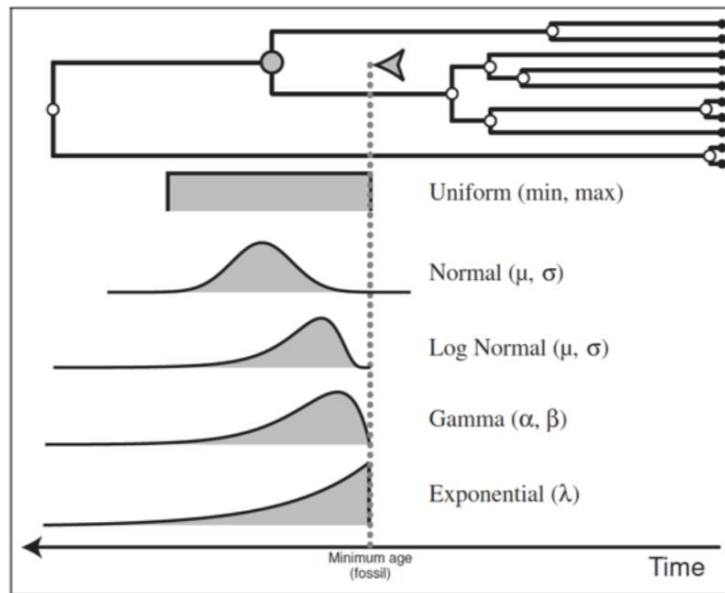


Figure 2: Five different parametric distributions that can be applied as priors on the age of a calibrated node. (figure adapted from [Heath, 2012](#))

# Uniform distribution

- Typically, you must have both maximum and minimum age bounds when applying a uniform calibration prior.
- The minimum bound is provided by the fossil member of the clade.
- The maximum bound may come from a bracketing method or other external source.
- This distribution places equal probability across all ages spanning the interval between the lower and upper bounds.

# Normal distribution

- The normal distribution is not always appropriate for calibrating a node using fossil information (though some methods allow for assigning a truncated normal prior density).
- When applying a biogeographical date or a secondary calibration , the normal distribution can be a useful calibration prior.

# Gamma distribution

- The gamma distribution is commonly used as a prior on scalar variables in Bayesian inference.
- the gamma distribution is the sum of  $\alpha$  independently and identical exponentially distributed random variables with rate  $\lambda$ .
- As  $\alpha$  becomes very large ( $\alpha > 10$ ), this distribution approaches the normal distribution.



# Exponential distribution

- The exponential distribution is a special case of the gamma distribution and is characterized by a single rate parameter ( $\lambda$ ) and is useful for calibration if the fossil age is very close to the age of its ancestral node.

# Log-normal distribution

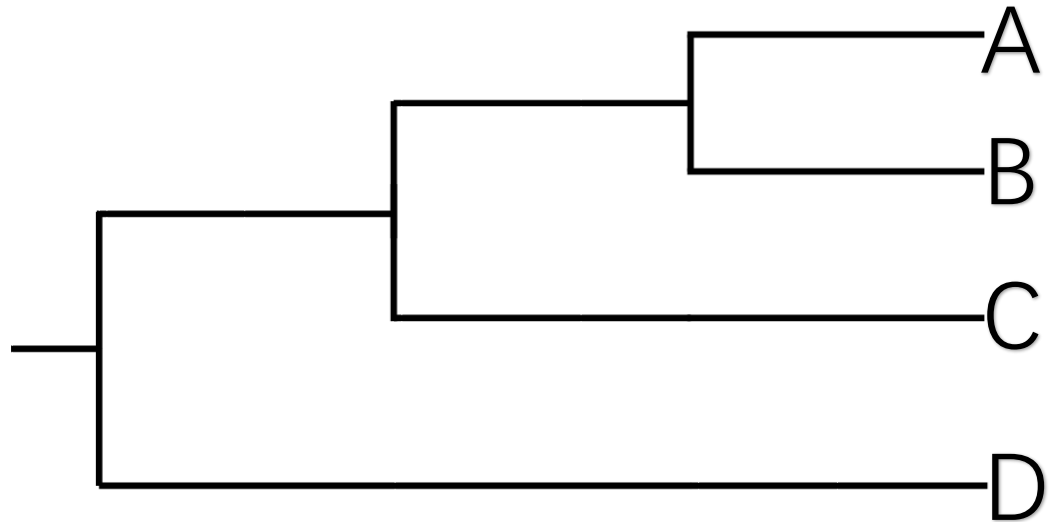
- Log-normal prior on the calibrated node age places the highest probability on ages somewhat older than the fossil, with non-zero probability to  $\infty$ .

# Workflow

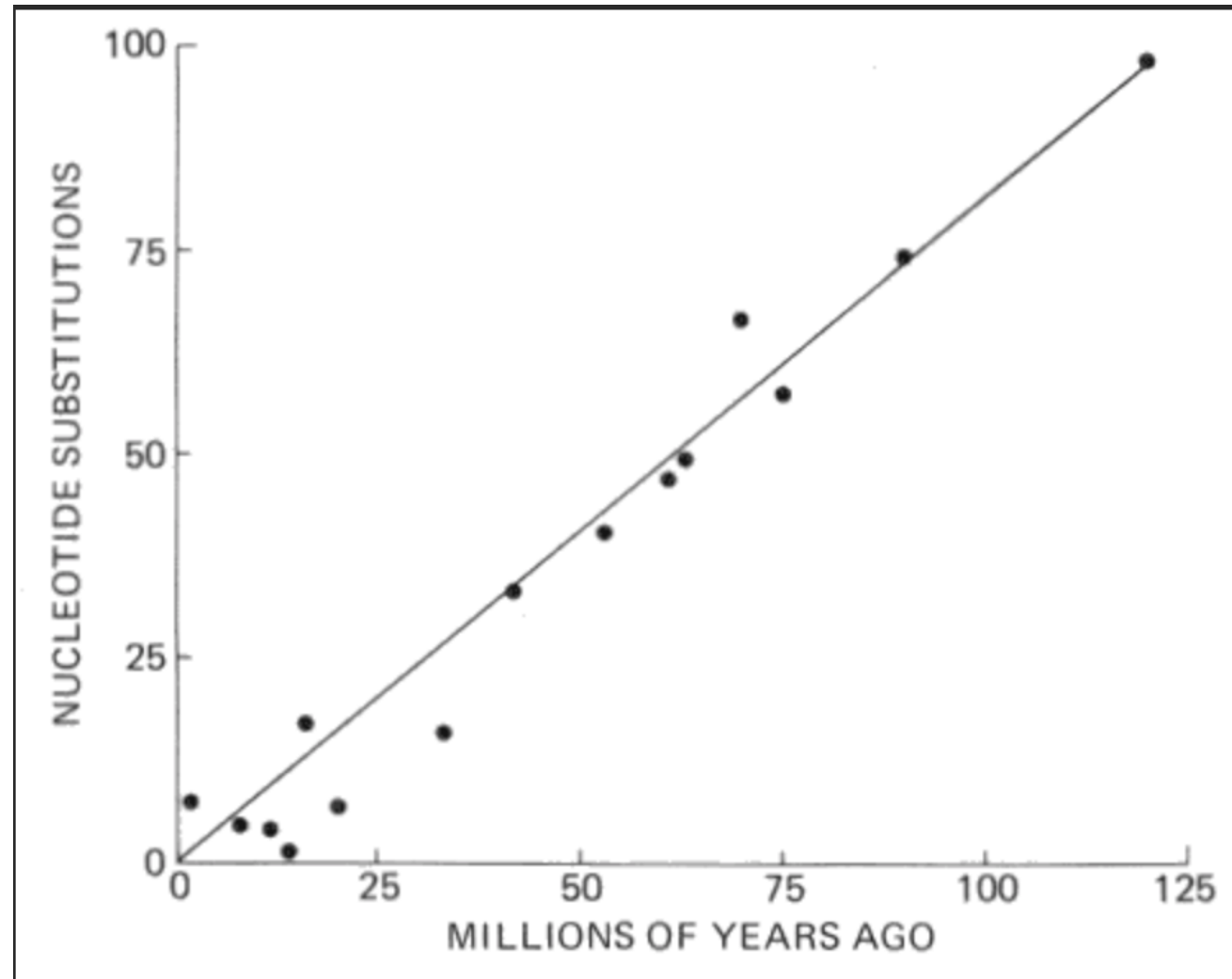
- File of Phylogeny tree
- Fossil calibration points (minimum age, maximum age)
- Add fossil data in phylogeny tree using a R package ape
- Set parameters in Beatui
- Run in beast

# File of phylogeny tree

- Pick 100 gene that fit molecular clock model.
- Reconstruct tree using raxml → `***.nex` file

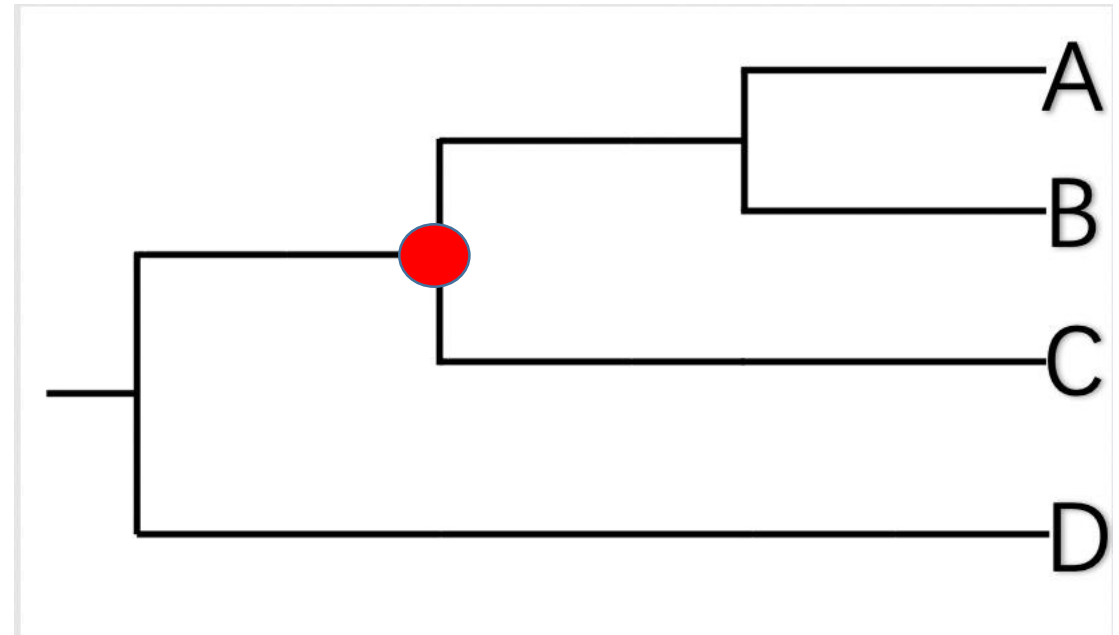


# Molecular clock



# Fossil calibration points

- Earliest time in C's fossil
- Oldest time in D's fossil



# Add fossil data in phylogeny tree using a R package ape

```
#load the necessary library
library(ape)

#read the tree
raxmlTree<-read.tree(file='forstartingtree.nwk')

#plot unrooted tree, show node labels
plot(raxmlTree)
nodelabels()

#root the tree with outgroup node, save over original tree
raxmlTree<-root(raxmlTree, node=25)
plot(raxmlTree)

#have another look at node labels
nodelabels()

#get the node for the MRCA for Rhyacichthys and a goby
mrca(raxmlTree)["01RHAS", "04TYPA"]

# answer: node 48. we will set this to minimum of 52 million years, max of 83

#use penalized likelihood to make a quick time-calibrated tree using our three calibration points.
GobyTree_PL<-chronopl(raxmlTree, lambda=1, age.min=c(47.8), age.max=c(122), node=c(28))

plot(GobyTree_PL)

# save the tree as newick
write.tree(GobyTree_PL, file="0d_StartingTree.nwk")
```

# Setting parameters in Beauti

BEAUti 2: Standard /Users/ygx/Desktop/data\_analysis/化石矫正指南/write\_in\_R\_化石矫正/pampus\_timetree\_F.xml

Partitions Tip Dates Site Model Clock Model Priors MCMC

Link Site Models Unlink Site Models Link Clock Models Unlink Clock Models Link Trees Unlink Trees

Name	File	Taxa	Sites	Data Type	Site Model	Clock Model	Tree	...
timetree_1	timetree	9	4969	nucleotide	timetree_1	divtimeclock	divtimetree	<input type="checkbox"/>
timetree_2	timetree	9	4969	nucleotide	timetree_1	divtimeclock	divtimetree	<input type="checkbox"/>
timetree_3	timetree	9	4969	nucleotide	timetree_1	divtimeclock	divtimetree	<input type="checkbox"/>

+ - r Split



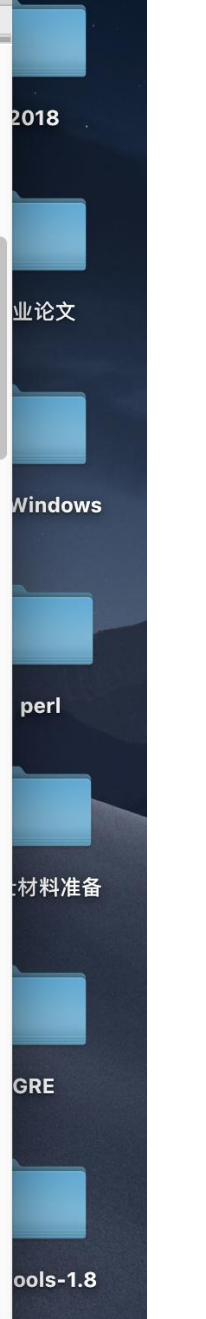
# Change parameters and run in beast

- Add topology information it is the result of R studio
- The weight of four parameters: Birth Death Subtree Slide, Narrow, Wide and Wilson-Balding were set as zero to fix the tree topology

```

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43   </alignment>
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53 <parameter id="gammaShape.s:timetree_1" name="stateNode">1.0</parameter>
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56 <parameter id="birthRate2.t:divtimetree" lower="0.0" name="stateNode" upper="10000.0">1.0</parameter>
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58 <parameter id="uclDMean.c:divtimeclock" name="stateNode">1.0</parameter>
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65
66 <distribution id="posterior" spec="util.CompoundDistribution">
67 <distribution id="prior" spec="util.CompoundDistribution">
68 <distribution id="BirthDeath.t:divtimetree" spec="beast.evolution.speciation.BirthDeathGernhard08Model" birthDiffRate="@birthRate2.t:divtimetree" relativeDeathRate=
69 <prior id="BirthRatePrior.t:divtimetree" name="distribution" x="@birthRate2.t:divtimetree">
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80 <parameter id="RealParameter.02" estimate="false" name="beta">10.0</parameter>
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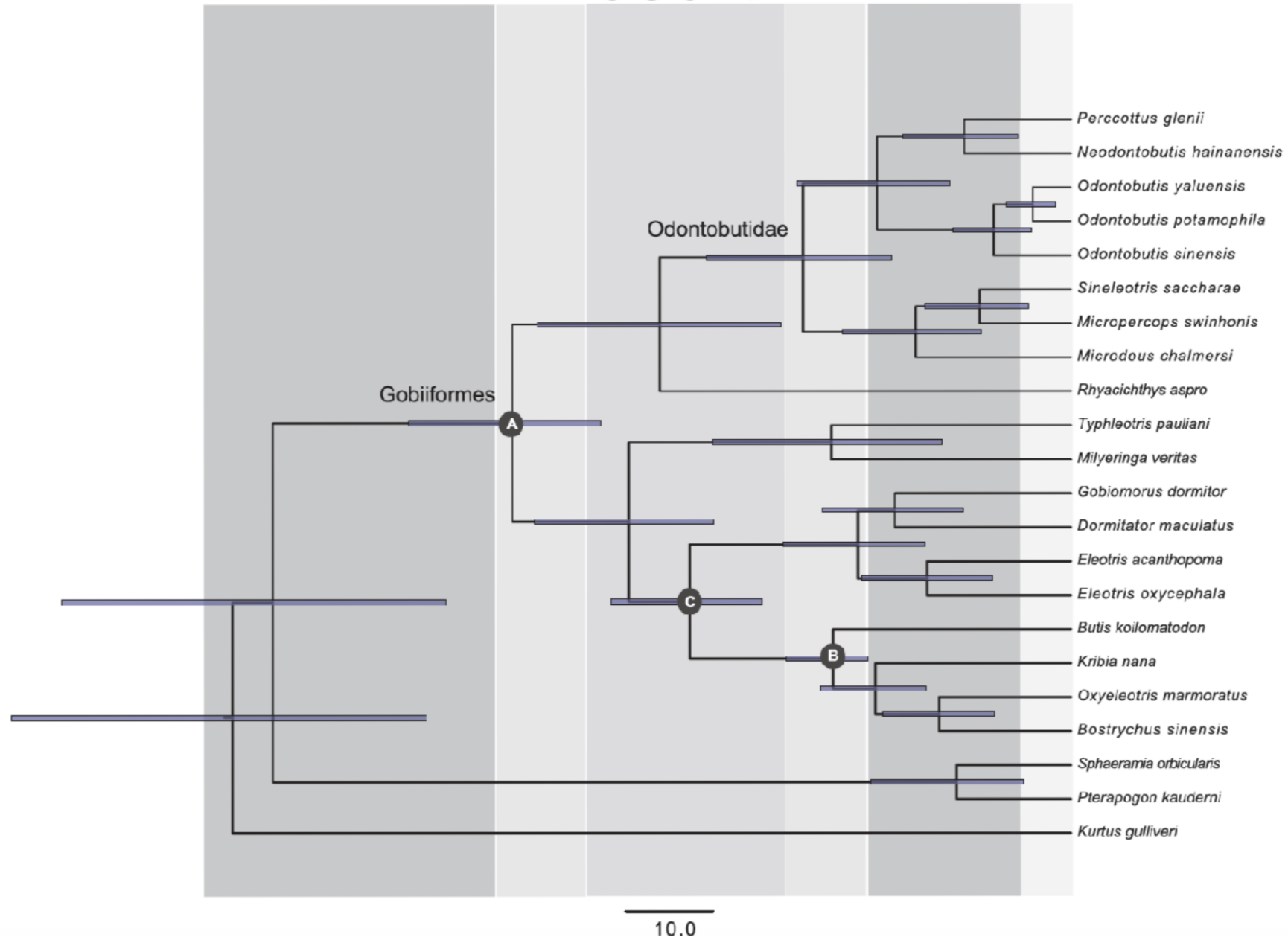
```



```
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212 <operator id="CategoriesSwapOperator.c:divtimeclock" spec="SwapOperator" intparameter="@rateCategories.c:divtimeclock" weight="10.0"/>
213
214 <operator id="CategoriesUniform.c:divtimeclock" spec="UniformOperator" parameter="@rateCategories.c:divtimeclock" weight="10.0"/>
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218 <operator id="BirthDeathTreeRootScaler.t:divtimetree" spec="ScaleOperator" rootOnly="true" scaleFactor="0.5" tree="@Tree.t:divtimetree" weight="3.0"/>
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220 <operator id="BirthDeathUniformOperator.t:divtimetree" spec="Uniform" tree="@Tree.t:divtimetree" weight="30.0"/>
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224 <operator id="BirthDeathNarrow.t:divtimetree" spec="Exchange" tree="@Tree.t:divtimetree" weight="0"/>
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226 <operator id="BirthDeathWide.t:divtimetree" spec="Exchange" isNarrow="false" tree="@Tree.t:divtimetree" weight="0"/>
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243   <log idref="likelihood"/>
244   <log idref="prior"/>
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253   <log idref="rateCG.s:timetree_1"/>
254   <log idref="rateGT.s:timetree_1"/>
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```



# Result



**Thanks for your attention!**