

Tutorial using BEAST v2.7.7

contraband tutorial

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Total-evidence dating and trait-evolution evolutionary inference using phylogenetic multivariate Brownian motion models

1 Background

Bird’s-eye view. This tutorial shows how to use the **contraband** package in **BEAST 2** to model continuous trait evolution along a phylogeny with Brownian motion. Unlike methods that assume a “known”, fixed tree, **contraband** lets you estimate the tempo and mode of trait evolution simultaneously with both species relationships and divergence times.

1.1 What is contraband for

In this tutorial, we will walk you through running a simple analysis with the **contraband** (**continuous traits brownian models**) **BEAST 2** package. As the name suggests, **contraband** implements Brownian motion (BM) models for the evolution of continuous traits on a phylogeny.

To understand how these models can be useful to evolutionary biologists, let’s put our X-ray goggles on and look at the core of the **contraband** package: the probability density function (pdf) of the multivariate Brownian motion model – the same pdf used for a multivariate normal distribution:

$$f(\mathbf{M}|\mathbf{V}, \mathbf{y}_0) = \frac{1}{(2\pi)^{nk/2}|\mathbf{V}|^{1/2}} \exp\left(-\frac{1}{2}(\text{vec}(\mathbf{M}) - \mathbf{y}_0)^T \mathbf{V}^{-1}(\text{vec}(\mathbf{M}) - \mathbf{y}_0)\right), \quad (1)$$

This equation simply gives us the probability of observing our data \mathbf{M} – that is, one or more continuous traits – given two key parameters: (i) the expected value vector (or mean vector), \mathbf{y}_0 , and (ii) the variance-covariance matrix, \mathbf{V} . If you have tried a few of the other Taming the BEAST tutorials, these two parameters are the quantities whose posterior probability distributions we want to approximate via Markov Chain Monte Carlo (MCMC).

In phylogenetics, \mathbf{V} is typically decomposed as $\mathbf{V} = \mathbf{\Sigma} \otimes \mathbf{T}$, where $\mathbf{\Sigma}$ describes the variance and covariance structure of the traits, and \mathbf{T} represents phylogenetic relatedness. In essence, \mathbf{T} captures the phylogeny itself – the shared evolutionary history among species.

In many software tools, especially those implemented in R and using frequentist methods, the phylogeny (\mathbf{T}) is not estimated but instead fixed to a tree point estimate from the literature. The downside of this approach is that the continuous trait data can only inform our estimates of trait evolution parameters, \mathbf{y}_0 and $\mathbf{\Sigma}$ – not the phylogeny itself.

While it is possible to take this approach in **BEAST 2** as well, its hierarchical Bayesian framework allows us to go further: we can co-estimate \mathbf{T} (i.e., the species tree or phylogeny) together with the parameters of trait evolution. This means we can infer trait-evolution parameters **alongside** the species divergence times and phylogenetic relationships captured in \mathbf{T} . In other words, **contraband** is a tool not only for studying how continuous traits evolve, but also for estimating the topology and divergence times of phylogenies.

The estimation of divergence times using multiple types of data – for example, molecular sequences combined with discrete and/or continuous morphological traits – is known as *total-evidence dating* (TED; Ronquist et al. 2012). Among other things, **contraband** is a TED method. It is designed to help evolutionary biologists leverage continuous traits to reconstruct species evolutionary histories, including both divergence times and the tempo and mode of phenotypic evolution.

1.2 A quick peek under the hood

Later in this tutorial, you will be placing prior distributions on a series of parameters, as well as making modeling decisions related to things like the correlation between traits, for example, or the intraspecific variance in trait values. Setting up such an analysis can quickly become overwhelming, so in this section we will introduce a few implementation and statistical details to help you understand what comes next.

While it is possible to directly compute the value of equation (1) via matrix algebra, this is computationally expensive. Instead, **contraband** saves us time by using an alternative mathematical formulation (Mitov et al. 2020) and a dynamic programming algorithm. The details do not matter for this tutorial, but it is important to re-write equation (1) as:

$$f(\mathbf{M}|\mathbf{V}, \mathbf{y}_0) = f(\mathbf{M}|\Phi, \mathbf{y}_0, \mathbf{r}, \boldsymbol{\rho}, c_m, \mathbf{b}_m, \boldsymbol{\theta}) \quad (2)$$

You should recognize some of these terms as they have direct counterparts in models used for molecular evolution, e.g., those involved in the morphological clock model. These are [list the clock parameters here] morphological clock rate (c_m) and morphological relative branch rates (\mathbf{b}_m). This joint posterior probability density gives the posterior distribution of the time-scaled phylogenetic tree (Φ), morphological and molecular relative branch rates ($\mathbf{b}_m, \mathbf{b}_d, \mathbf{b}_s$) and all remaining parameters ($\boldsymbol{\theta}$) – given continuous and discrete morphology data matrices, \mathbf{M} and \mathbf{D} , respectively, and molecular sequence alignment \mathbf{S} .

Other parameters, however, are unique to multivariate Brownian models, like [list those parameters here], and explain them the character values from all characters at the root of Φ (\mathbf{y}_0), a vector containing all relative character-specific evolutionary rates (\mathbf{r}), a matrix containing between-character correlation values ($\boldsymbol{\rho}$). These parameters can in principle be estimated with MCMC, but the accuracy of and uncertainty about our estimates will be a function of our data set size, which include the number of traits as well as the number of species (more details can be found in Zhang et al. 2024), as well as analysis running times.

Among the most challenging parameters to estimate are \mathbf{r} and $\boldsymbol{\rho}$ [list parameters here]. Here, one thing that researchers can do is to ([list pre-analysis procedures, like shrinkage delta estimates]) obtain intraspecific character variation and correlation from multiple characters observed across multiple individuals within a species in the phylogeny, which amounts to ([list pre-analysis procedures, like shrinkage delta estimates]) 1) normalizing each observed character by their corresponding unbiased estimators of intraspecific variance 2) averaging an independent correlation ($\rho = 1$) and an unbiased estimate weighted by the shrinkage parameter. The assumption here is that ([list assumptions]) 1) intraspecific character variation is incremented by constant measurements from multiple individuals from a species 2) character correlations are the same across species and over time, which may be more or less justifiable depending on the data set. This is an assumption we will make in this tutorial.

Given all of the above, here is a list of the parameters we want to estimate, and for which we will need to place prior distributions on:

[add an enumerate list here with all parameters]

- 1) Character evolutionary rates
- 2) Character correlations
- 3) Ancestral state values
- 4) Tree priors
- 5) Clock model priors

In what follows, we will guide you through the explicit steps – including installation of dependencies and post-processing tools – that will (i) set up the analysis for inferring the above parameters, and (ii) help you process and visualize the results.

2 Programs used in this exercise

2.0.1 BEAST2 - Bayesian Evolutionary Analysis Sampling Trees2

BEAST2 (<http://www.beast2.org>) is a free software package for Bayesian evolutionary analysis of molecular sequences using MCMC and strictly oriented toward inference using rooted, time-measured phylogenetic trees. This tutorial is written for BEAST v2.7.7 (Bouckaert et al. 2019).

2.0.2 BEAUti2 - Bayesian Evolutionary Analysis Utility

BEAUti2 is a graphical user interface tool for generating BEAST2 XML configuration files.

Both BEAST2 and BEAUti2 are Java programs, which means that the exact same code runs on all platforms. For us it simply means that the interface will be the same on all platforms. The screenshots used in this tutorial are taken on a Mac OS X computer; however, both programs will have the same layout and functionality on both Windows and Linux. BEAUti2 is provided as a part of the BEAST2 package so you do not need to install it separately.

2.0.3 TreeAnnotator

TreeAnnotator is used to produce a summary tree from the posterior sample of trees using one of the available algorithms. It can also be used to summarise and visualise the posterior estimates of other tree parameters (e.g. node height).

TreeAnnotator is provided as a part of the BEAST2 package so you do not need to install it separately.

2.0.4 Tracer

Tracer (<http://tree.bio.ed.ac.uk/software/tracer>) is used to summarise the posterior estimates of the various parameters sampled by the Markov Chain. This program can be used for visual inspection and to assess convergence. It helps to quickly view median estimates and 95% highest posterior density intervals of the parameters, and calculates the effective sample sizes (ESS) of parameters. It can also be used to investigate potential parameter correlations. We will be using Tracer v1.7.2.

2.0.5 FigTree

FigTree (<http://tree.bio.ed.ac.uk/software/figtree>) is a program for viewing trees and producing publication-quality figures. It can interpret the node-annotations created on the summary trees by TreeAn-

notator, allowing the user to display node-based statistics (e.g. posterior probabilities). We will be using FigTree v1.4.4.

3 Practical Part I: Download and install packages

In this tutorial we will estimate evolutionary rates, trait correlations, ancestral states and phylogenetic trees using the Brownian motion implemented in BEAST2, contraband.

The aim is to:

- Learn how to infer phylogenetic trees with continuous traits/characters
- Get to know how to choose the set-up of such an analysis
- Learn how to read the output of a “contraband” analysis

First, we have to download the package contraband using the BEAUTi package manager. Go to *File >> Manage Packages* and download the package contraband.

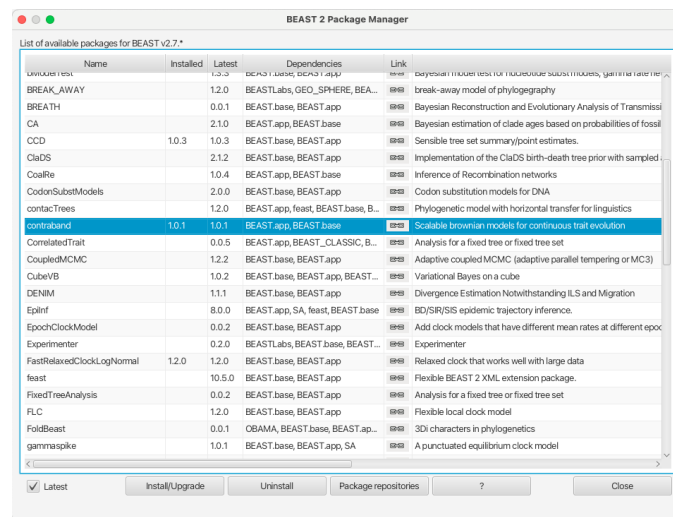


Figure 1: Download the contraband package.

contraband will only be available in BEAUTi once you close and restart the program.

In addition, we will need to install to complete the analyses in this tutorial bdtree, sampled-ancestors, morph-models.

4 Practical Part II: Data preparation

The data sets used in this tutorial include three data types associated with 27 Carnivore species, 11 of which are extinct and 16 of which are extant. The detailed description are introduced below.

4.0.1 Continuous characters

There are 19 species of interest having 3-dimensional cranium landmarks (Álvarez-Carretero et al. 2019), which are considered as 87 continuous traits (carnivora_continuous_27.nex). In particular, it is necessary to have the same dimension of landmarks from 21 *Vulpes vulpes* individuals (vulpes_continuous_data.txt).

4.0.2 Discrete characters

12 species of interest have discrete morphological characters that describe their basicranial, dental, postcranial anatomical features (carnivora_discrete_27.nex) (Barrett et al. 2021). There are 183 features in total and the number of character states ranges from 0 to 3.

4.0.3 Molecular sequences

The molecular sequences of 12 mitochondrial genes for 14 species of interest are collected from NCBI database and are further were concatenated, aligned using MAFFT (carnivora_dna_27.fasta).

5 Practical Part III: Parameter and State inference under Brownian motion model

5.0.1 Loading the Carnivoran Continuous data

The continuous characters can be found in the *data* folder named *carnivora_continuous_27.nex*. It can be either drag and dropped into BEAUti "Partitions" panel or added using BEAUti's menu system via *File >> Load Continuous Data*. Once the character are loaded successfully into BEAUti, the panel will show

5.0.2 Get the fossil ages (Tip Dates)

Since the data set have fossil species, we will need to open the "Tip Dates" panel and then select the "Use tip dates" checkbox to specify the fossil ages. This can be done in multiple ways. In our case, we can obtain the date information from the species names. We can tell BEAUti to use these by clicking the *Auto-configure* button. The fossil ages appear following the second underscore "_" in the species name. To extract these times, select "use everything", then select "after last" from the drop-down box to the right, and input "_" (without the quotes) in the text box immediately to the right, as shown in the figure below [Figure 2](#). Clicking "Ok" should now populate the table with the fossil ages extracted from the species names.

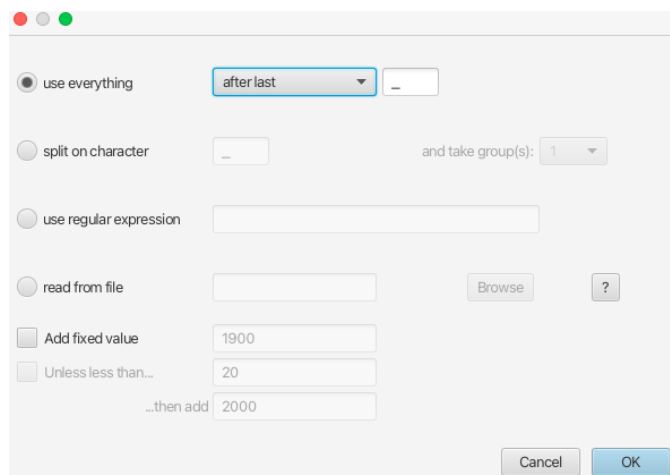


Figure 2: Guess sampling times.

In the populated table, the two columns **Date** and **Height** should now have values between 0.0 and 35.55

in million years [Figure 3](#).

Taxon	Date (raw value)	Age/Height
Aelurodon_ferox_13.13	13.13	13.13
Canis_dirus_0.0285	0.0285	0.0285
Epicyon_haydeni_11.95	11.95	11.95
Hesperocyon_gregarius_35.55	35.55	35.55
Paraenhydrocyon_josephi_25.615	25.615	25.615
Tomarctus_hippophaga_14.785	14.785	14.785
Enhydrocyon_pahinsintewakpa_28.55	28.55	28.55
Cuon_alpinus_0.0	0.0	0.0
Speothos_venaticus_0.0	0.0	0.0
Canis_lupus_0.0	0.0	0.0
Cerdocyon_thous_0.0	0.0	0.0
Otocyon_megalotis_0.0	0.0	0.0
Vulpes_vulpes_0.0	0.0	0.0
Ursus_americanus_0.0	0.0	0.0
Allurus_fulgens_0.0	0.0	0.0
Nandinia_binotata_0.0	0.0	0.0
Paradoxurus_hemaphysalis_0.0	0.0	0.0
Hyaenictitherium_wongli_6.65	6.65	6.65
Smilodon_fatalis_0.0285	0.0285	0.0285
Canis_latrans_0.0	0.0	0.0
Smilodon_populator_0.39	0.39	0.39
Puma_concolor_0.0	0.0	0.0
Protherops_0.0	0.0	0.0

Figure 3: Fossil ages.

5.0.3 Set the Brownian motion Model

As is introduced above, the parameters under the Brownian motion model include trait evolutionary rate (Sigmasq), trait correlations (Correlation) and ancestral states at the root (Root Values). Here we assume that all characters share one evolutionary rate. Therefore, we put a tick in the box in front of the "One Rate Only".

5.0.4 Set the Clock model

We assume the relative branch-specific rates are independently distributed and follow a LogNormal distribution with a fixed mean of 1. Therefore, we specify a relaxed clock model by selecting "Optimised Relaxed Clock" in the drop-down menu, where the mean clock rate represents the global morphological clock rate that will be estimated by default. The detailed description of the model can be found in [Douglas et al. 2021](#).

5.0.5 Specify the priors

In the "Priors" panel, we select "Fossilized Birth Death Model" ([Gavryushkina et al. 2014](#)) as the tree prior and leave the rest of the parameters having their default prior distributions.

5.0.6 Specify the MCMC chain length (MCMC)

Here we can set the length of the MCMC chain and after how many iterations the parameter and trees are logged. For this dataset, 2 million iterations should be sufficient. In order to have enough samples but not create too large files, we can set the logEvery to 2000, so we have 1001 samples overall. Next, we have to

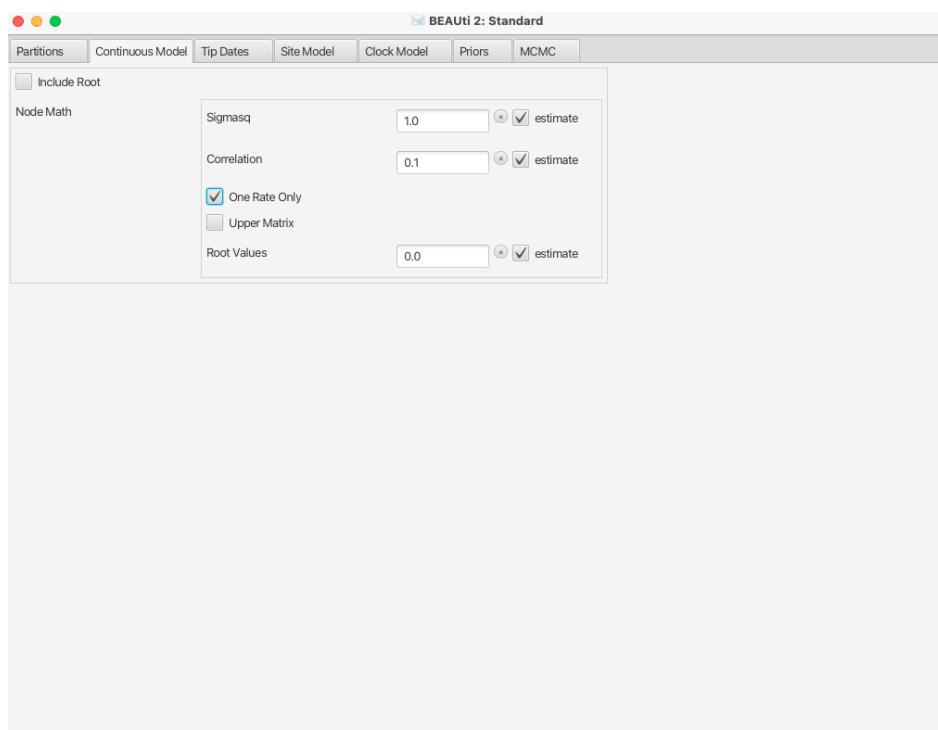


Figure 4: BM model parameter specifications.

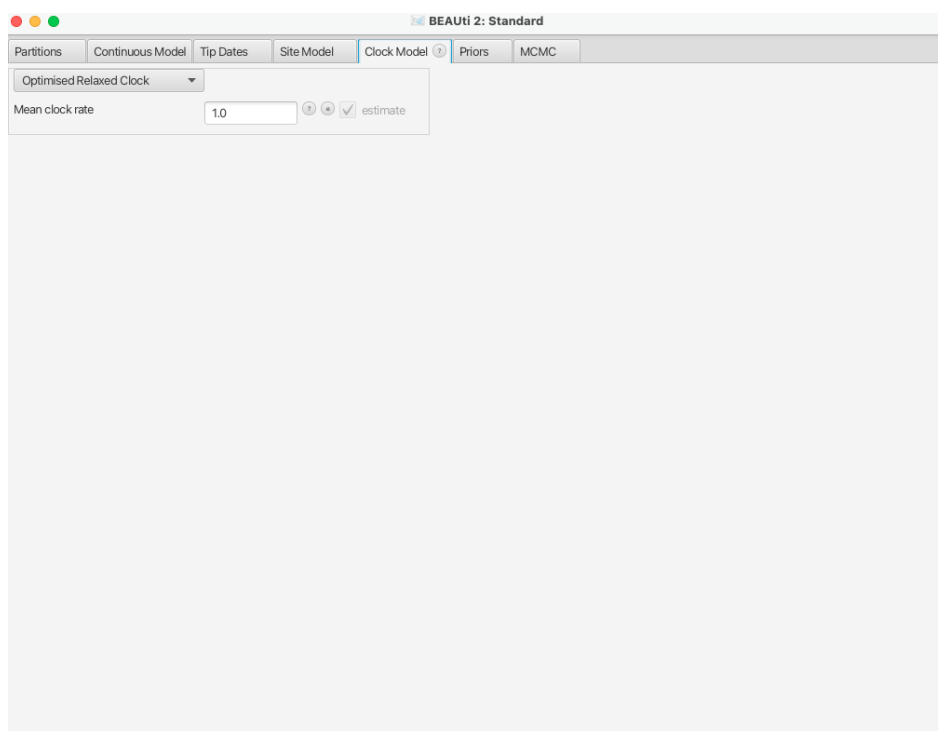


Figure 5: Set the initial clock rate.

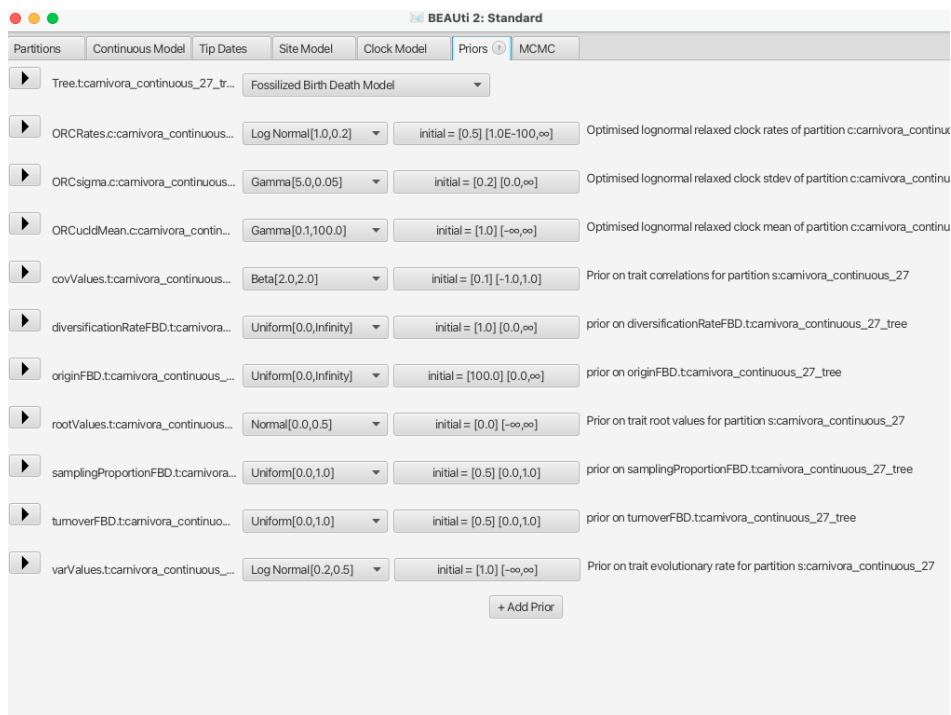


Figure 6: Set the tree model and priors on parameters.

save the *.xml file under *File >> Save as*.

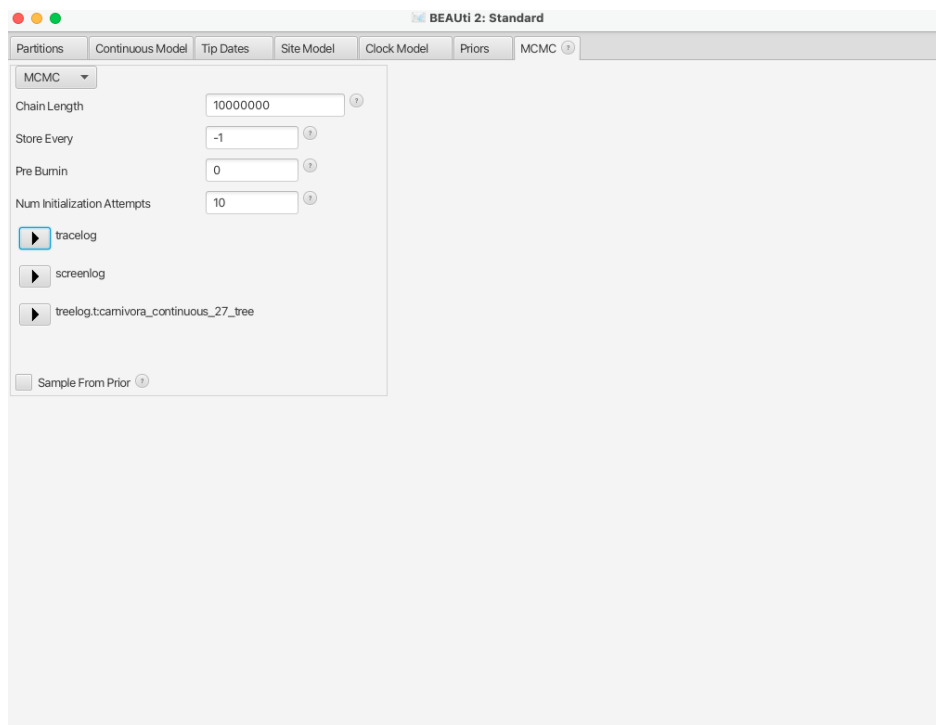


Figure 7: save the *.xml.

5.0.7 Run the Analysis using BEAST2

Run the *.xml using BEAST2 or use finished runs from the *precooked-runs* folder. The analysis should take about 6 to 7 minutes.

5.0.8 Post analysis

- Analyse the log file using Tracer

First, we can open the *.log file in tracer to check if the MCMC has converged. The ESS value should be above 200 for almost all values and especially for the posterior estimates (Figure 8).

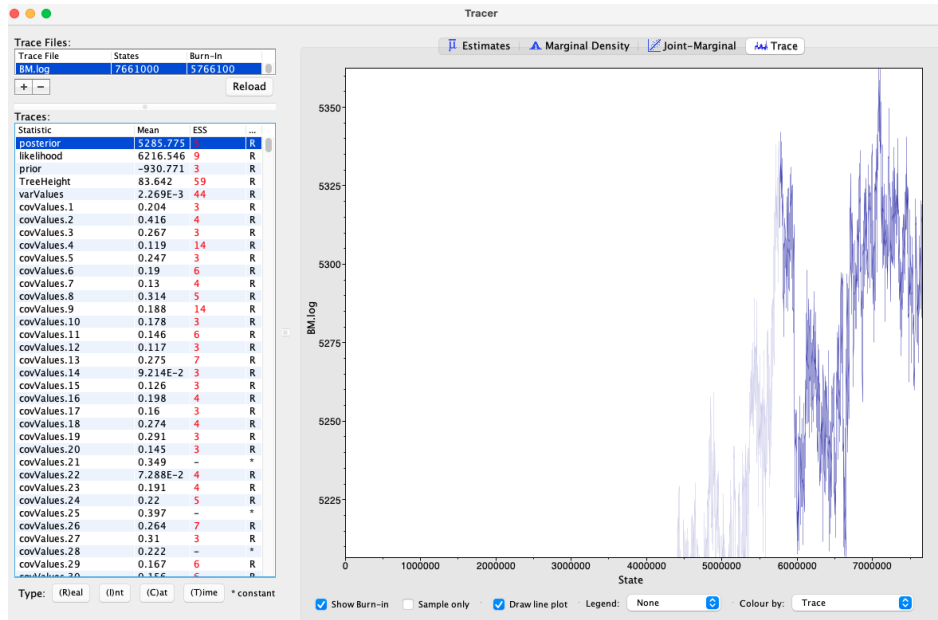


Figure 8: Check if the posterior converged.

- The estimated evolutionary rate (Figure 9)
- The estimated character correlations (Figure 10)
- The estimated ancestral states at the root (Figure 11)
- The inferred morphological clock model (Figure 12)
- Make the summary tree using TreeAnnotator

Open **TreeAnnotator** and then set the options including **Burnin percentage**, **Target tree type**, **Node heights**, **Input Tree File** and the **Output File**. Use the logged trees in the file `carnivora_continuous_27_tree_bm.trees` as **Input Tree File**. Name output file `carnivora_continuous_27_bm_mcc->.tree`. After clicking **Run** the program should summarize the trees.

6 Practical Part IV: Parameter and State inference using combined data with Brownian motion model with shrinkage method

6.0.1 Loading the Carnivoran data sets

We first load the continuous data and parse the fossil ages as is mentioned in previous sections 5.0.1 and 5.0.2. Then, in the "Partitions" panel, we continue to load the Carnivoran molecular sequences via *File >> Import Alignment*. Finally, we add the discrete characters by *File >> Add Morphological Data*. As is

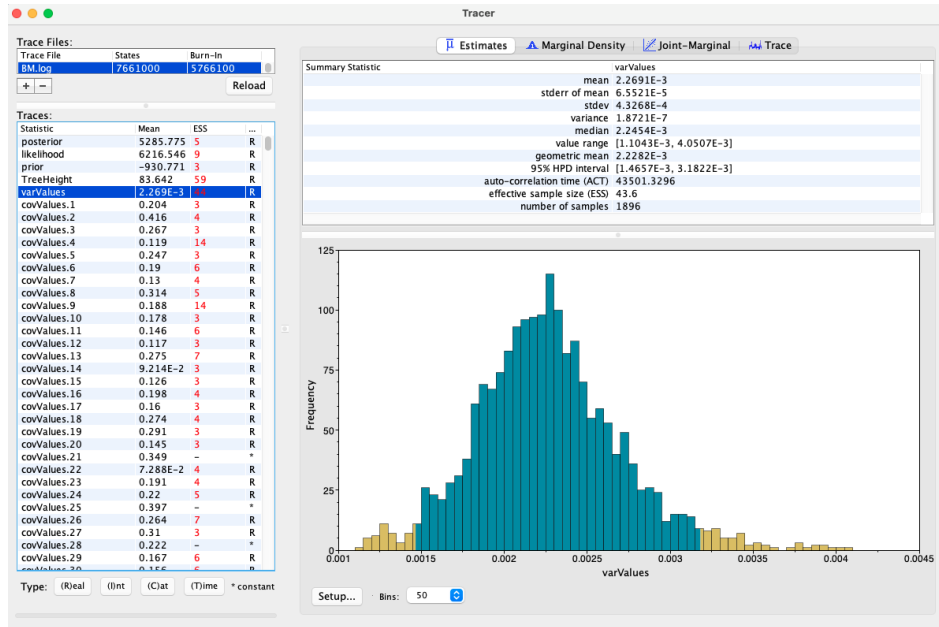


Figure 9: Evolutionary rate shared by 87 characters.

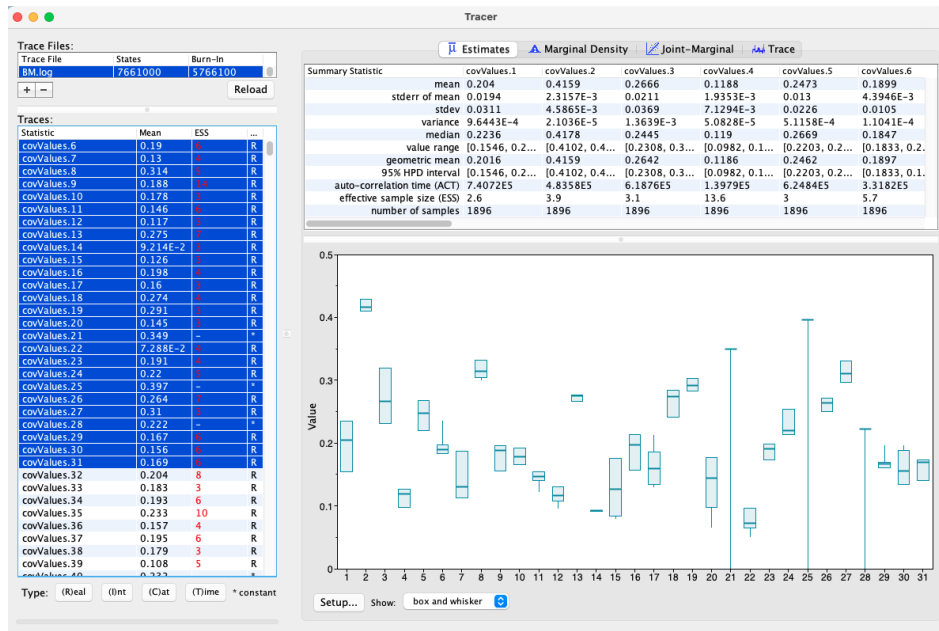


Figure 10: Character correlations among 87 characters.

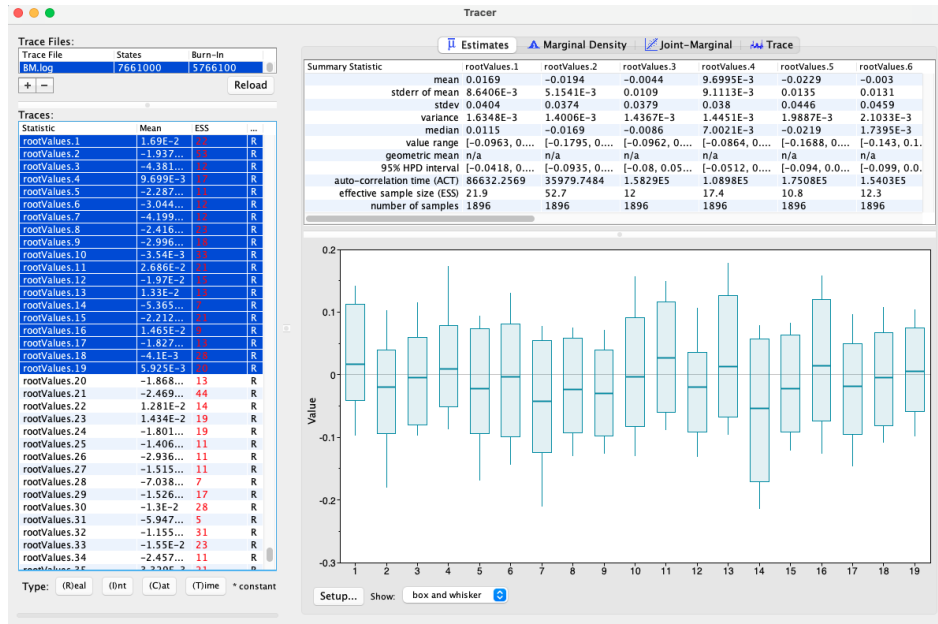


Figure 11: 87 trait values at the root of the tree.

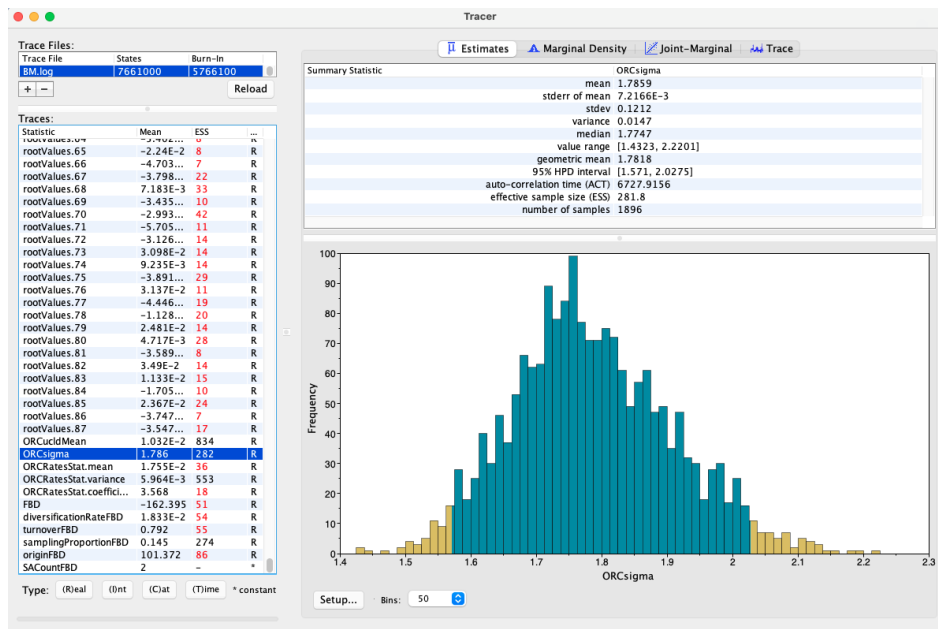


Figure 12: Compare the inferred migration rates.

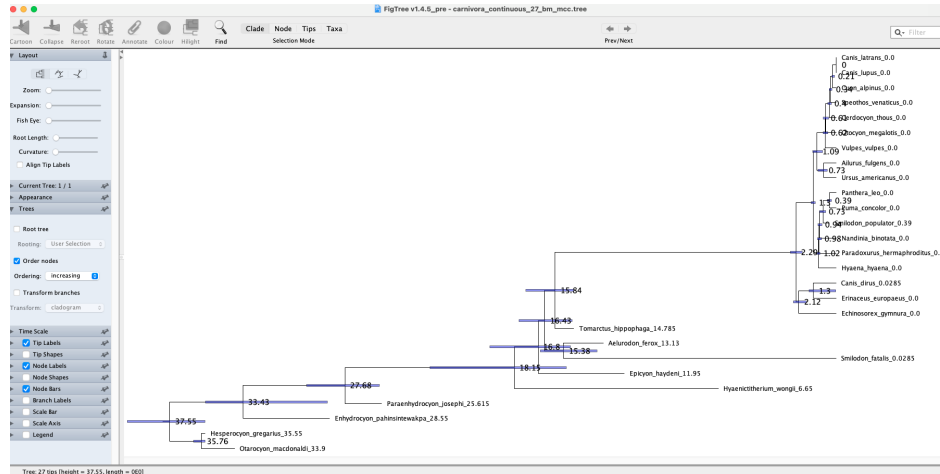


Figure 13: Summarised MCC tree of logged trees under Brownian motion model.

shown in Figure 14,

6.0.2 Set the Shrinkage Model

In the "Shrinkage Model" panel, we will need to fill in three components of the model. First, the shrinkage parameter is given by a constant value in the box to the right of "Delta". Second, the continuous characters from 21 *Vulpes vulpes* individuals are given in the block of "Population Traits". To be more specific, the trait data should be written in one-line data separated by spaces. In addition, the number of trait is given by "Minordimension" and should be consistent with the dimension of the continuous data in "Partitions" panel. Third, the added individual trait values are not only used for estimating correlations, but also normalizing the continuous data of the 19 carnivoran species. Therefore, we put a ✓ in the box in front of "Include Pop Var".

6.0.3 Set the Substitution Model

In the "Site Model" panel, we assume a HKY+Gamma for nucleotide substitutions by specifying 4 categories Figure 1. In addition, we assume Mk models (Lewis 2001) for discrete characters, as is shown in Figure 17.

6.0.4 Set the Clock model

Similar to what is mentioned in section subsection 5.0.4, we assume relaxed clock model for each data partition. The specifications are shown in Figure 18.

6.0.5 Specify the priors

First, we select "Fossilized Birth Death Model" from the drop-down menu and set it as the tree prior. Then we also keep the default priors for the rest of the parameters Figure 19.

6.0.6 Specify the MCMC chain length (MCMC)

Here we can set the length of the MCMC chain and after how many iterations the parameter and trees are logged. For this dataset, 2 million iterations should be sufficient. In order to have enough samples but not create too large files, we can set the logEvery to 2000, so we have 1001 samples overall. Next, we have to

[illegible]

Figure 14: Load continuous characters, molecular sequences and discrete characters.

BEAUTi 2: Standard

Partitions Shrinkage Model Tip Dates Site Model Clock Model Priors MCMC

Delta 0.636349274

☒ Include Pop Var

Delta Var 0.0

Population Traits

0.1201189436: *

Lower

Upper

Value 0.120118943693226 0.0:

Dimension 1827

Minordimension 87

☐ Estimate

Sigmasq 1.0 * ☐ estimate

Figure 15: Set the shrinkage model.

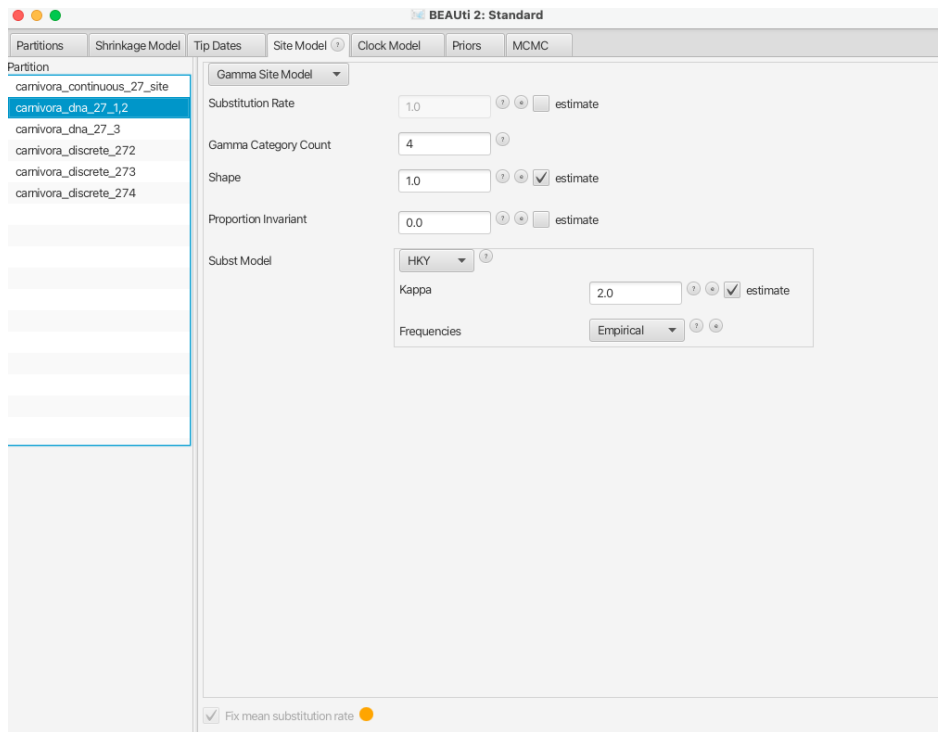


Figure 16: Set site models for molecular sequences and discrete characters.

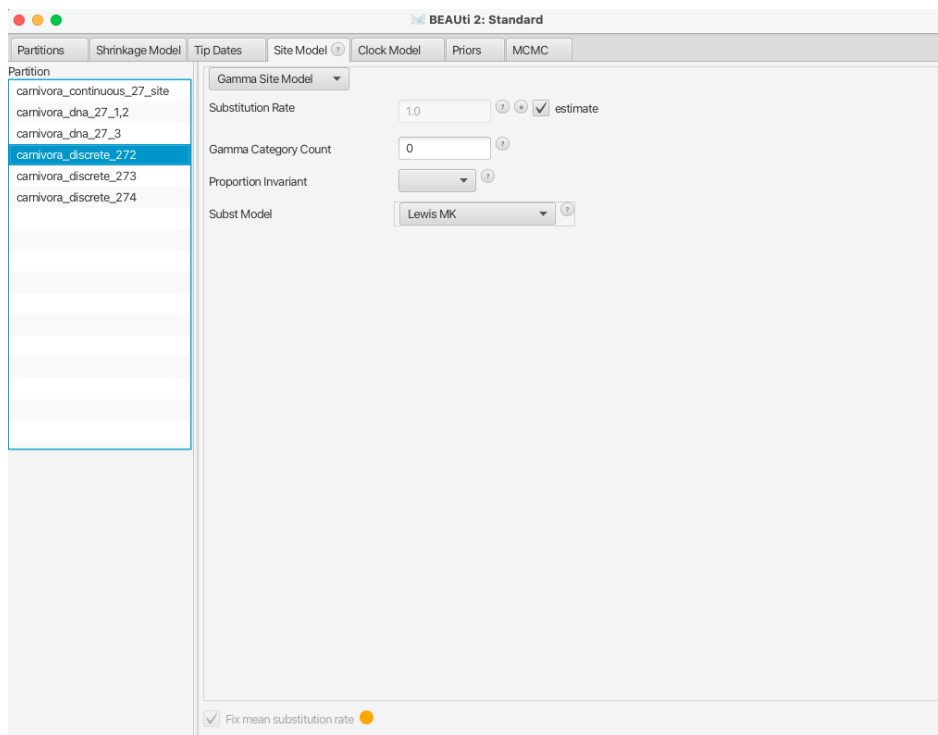


Figure 17: Set site models for molecular sequences and discrete characters.

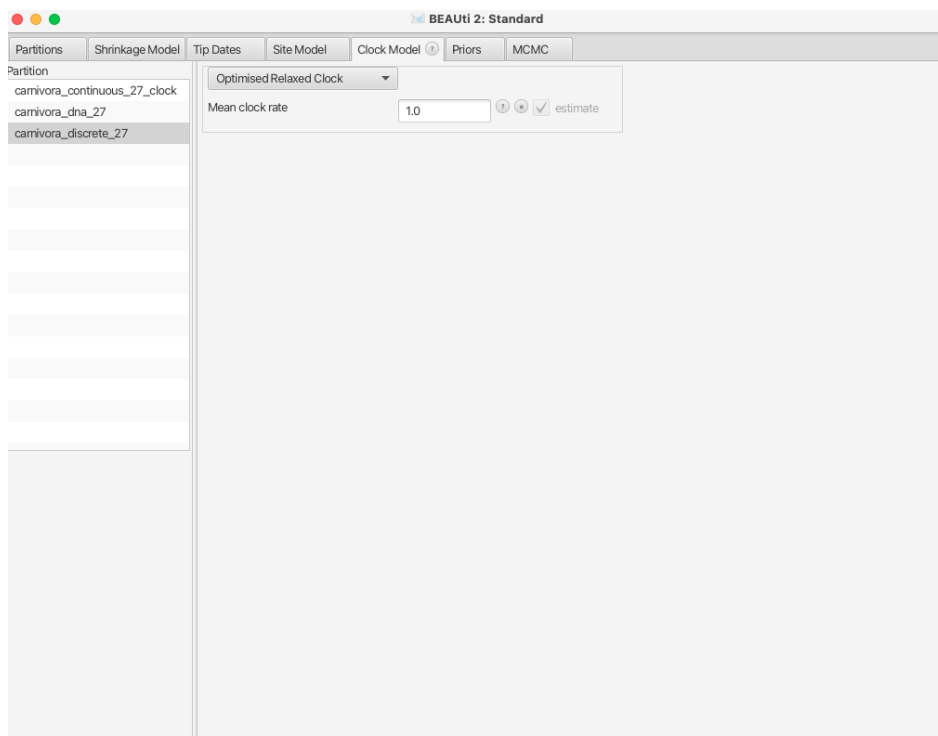


Figure 18: Set the initial clock models for continuous data, molecular data and discrete data.

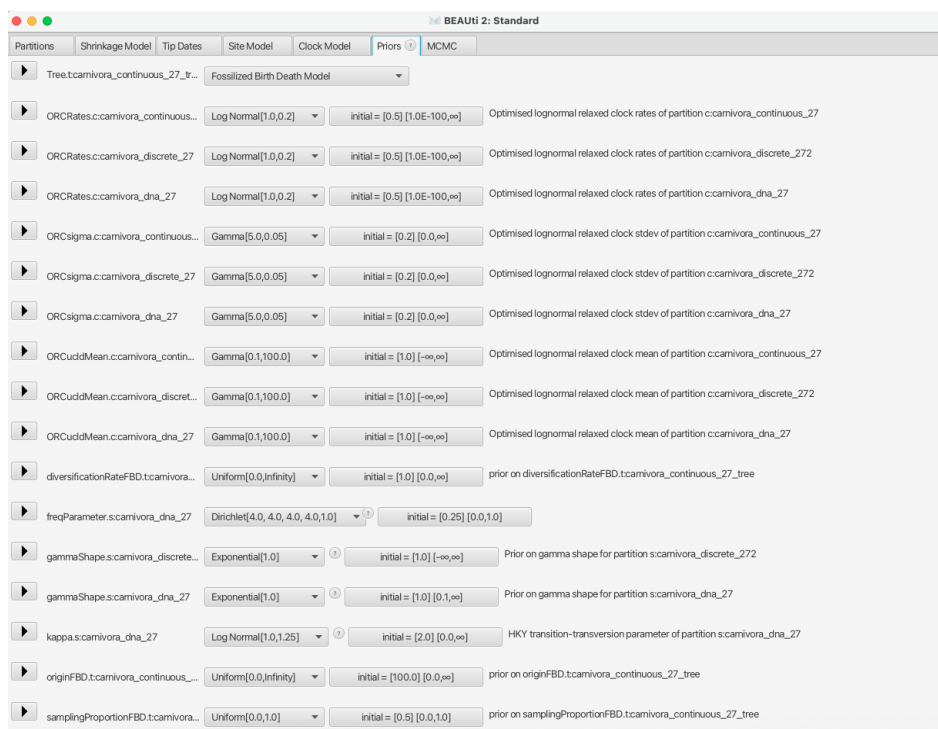


Figure 19: Set up tree model and the prior distributions.

save the *.xml file under *File >> Save as*.

6.0.7 Run the Analysis using BEAST2

Run the *.xml using BEAST2 or use finished runs from the *precooked-runs* folder. The analysis should take about 6 to 7 minutes.

6.0.8 Post analysis

- Inferred clock models for continuous data, discrete data and molecular sequences (Figure 20 and Figure 21)

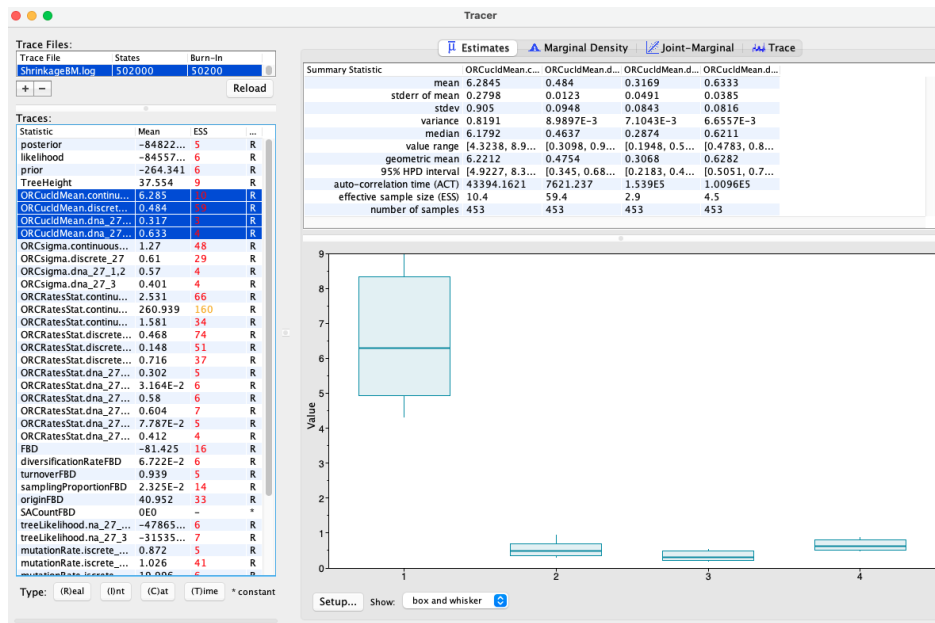


Figure 20: Estimated clock rates.

- Make the summary tree using TreeAnnotator (Figure 22)

7 Errors that can occur (Work in progress)

One of the errors message that can occur regularly is the following: *Infinity likelihood*

Negative branch length

Unequal likelihoods

Version dated: July 9, 2025

Relevant References

Álvarez-Carretero, S, A Goswami, Z Yang, and M dos Reis. 2019. Bayesian estimation of species divergence times using correlated quantitative characters. *Syst. Biol.* 68: 967–986.

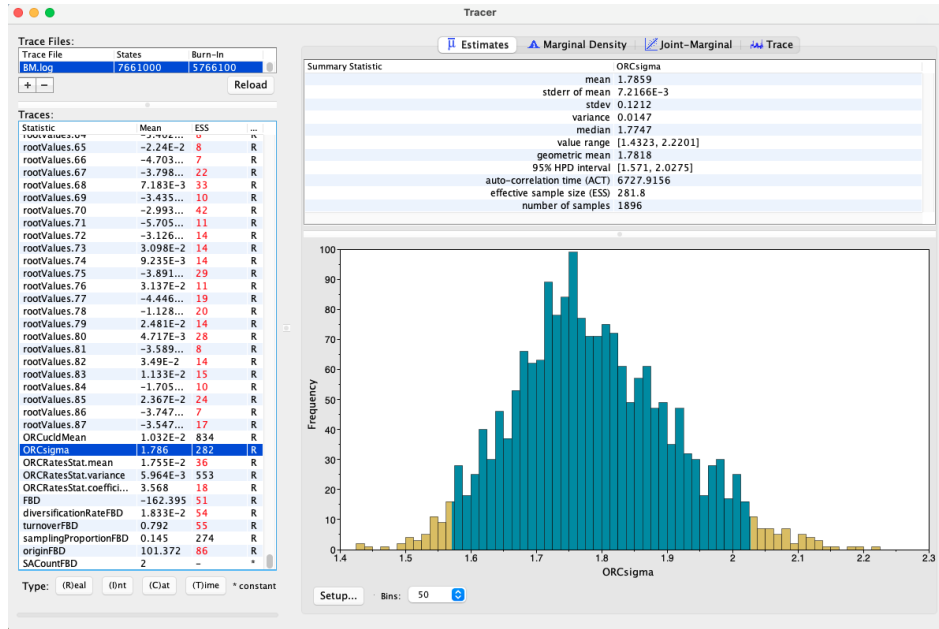


Figure 21: Estimated standard deviations.

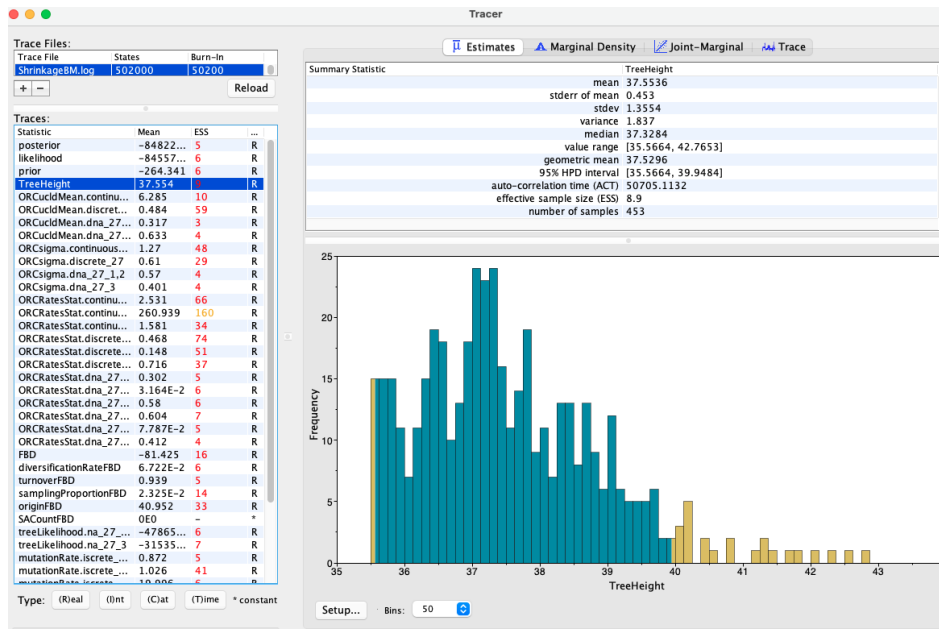


Figure 22: Summarised MCC trees estimated by combined data sets.

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- Zhang, R, AJ Drummond, and FK Mendes. 2024. Fast bayesian inference of phylogenies from multiple continuous characters. *Systematic Biology* 73: 102–124.