

Phylogenetic Inference using RevBayes

Divergence Time Estimation using Relaxed Clocks

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1 Background

Estimating nodes ages (*i.e.*, 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.

$$\text{branch length} = \text{rate} \times \text{time} \tag{1}$$

A model of substitution rate and divergence time 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 (Figure ??).

1.1 Modeling lineage-specific substitution rates

Many factors can influence the rate of substitution in a population such as mutation rate, generation time, and selection. As a result, many models have been proposed that describe how substitution rate may vary across the Tree of Life. The simplest model, the molecular clock, assumes that the rate of substitution remains constant over time (Zuckerkandl and Pauling 1962). However, many studies have shown that molecular data (in general) violate the assumption of a molecular clock and that there exists considerable variation in the rates of substitution among lineages.

Several models have been developed and implemented for inferring divergence times without assuming a strict molecular clock and are commonly applied to empirical data sets. Some models assume that rates are heritable and autocorrelated over the tree, others model rate change as a step-wise process, and others assume that the rates on each branch are independently drawn from a single distribution. Many of these models have been applied as priors using Bayesian inference methods. The implementation of dating methods in a Bayesian framework provides a flexible way to model rate variation and obtain reliable estimates of speciation times, provided the assumptions of the models are adequate. When coupled with numerical methods, such as MCMC, for approximating the posterior probability distribution of parameters, Bayesian methods are extremely powerful for estimating the parameters of a statistical model and are widely used in phylogenetics.

1.1.1 Some models of lineage-specific rate variation:

Global molecular clock: a constant rate of substitution over time (Zuckerkandl and Pauling 1962).

Local molecular clocks: Closely related lineages share the same rate and rates are clustered by subclades (Kishino et al. 1990; Rambaut and Bromham 1998; Yang and Yoder 2003; Drummond and Suchard 2010)

Compound Poisson process: Rate changes occur along lineages according to a point process and at rate-change events, the new rate is a product of the old rate and a Γ -distributed multiplier (Huelsbeck et al. 2000).

Autocorrelated rates: substitution rates evolve gradually over the tree

- *Log-normally distributed rates:* the rate at a node is drawn from a log-normal distribution with a mean equal to the parent rate (Thorne et al. 1998; Kishino et al. 2001; Thorne and Kishino 2002)
- *Cox-Ingersoll-Ross Process:* the rate of the daughter branch is determined by a non-central χ^2 distribution. This process includes a parameter that determines the intensity of the force that drives the process to its stationary distribution (Lepage et al. 2006).

Uncorrelated rates: The rate associated with each branch is drawn from a single underlying parametric distribution such as an exponential or log-normal (Drummond et al. 2006; Rannala and Yang 2007; Lepage et al. 2007).

Mixture model on branch rates: Branches are assigned to distinct rate categories according to a Dirichlet process (Heath et al. 2012).

1.2 Priors on node times

There are many components that make up a Bayesian analysis of divergence time. One that is often overlooked is the prior on node times, often called a tree prior. This model describes how speciation events are distributed over time. When this model is combined with a model for branch rate, Bayesian inference allows you to estimate relative divergence times. Furthermore, because the rate and time are confounded in the branch-length parameter, the prior describing the branching times may have a strong effect on divergence time estimation.

We can separate the priors on node ages into different categories:

Phenomenological: models that make no explicit assumptions about the biological processes that generated the tree. These priors are conditional on the age of the root.

- *Uniform distribution:* This simple model assumes that internal nodes are uniformly distributed between the root and tip nodes (Lepage et al. 2007; Ronquist et al. 2012b).
- *Dirichlet distribution:* A flat Dirichlet distribution describes the placement of internal nodes on every path between the root and tips (Kishino et al. 2001; Thorne and Kishino 2002).

Mechanistic: models that describe the biological processes responsible for generating the pattern of lineage divergences.

- *Population-level processes:* Coalescent processes describe the time, in generations, between coalescent events and allow for the estimation of population-level parameters (Kingman 1982). Furthermore, they describe demographic processes (suitable for describing differences among individuals in the same species/population).
- *Species-level processes:* Birth-death stochastic branching models describe lineage diversification (suitable for describing the timing of divergences between samples from different species) (Kendall 1948; Thompson 1975; Nee et al. 1994; Rannala and Yang 1996; Yang and Rannala 1997; Höhna 2015).

We cover the different process that can be used for tree and divergence time prior distributions in detail in the [RB_DiversificationRate_Tutorial](#) because of their interest in estimating diversification rates and patterns.

1.3 Calibration to absolute time

Without external information to calibrate the tree, divergence time estimation methods can only reliably provide estimates of relative divergence times and not absolute node ages; or if one would know the (average) rate of substitutions. Calibration information can come from a variety of sources including “known” substitution rates (often secondary calibrations estimated from a previous study), dated tip sequences from serially sampled data (time-stamped virus data or ancient DNA), or geological date estimates (fossils or biogeographical data). Age estimates from fossil organisms are the most common form of divergence time calibration information. These data are used as age constraints on their putative ancestral nodes. There are numerous difficulties with incorporating node age estimates from fossil data including disparity in fossilization and sampling, uncertainty in dating, and correct phylogenetic placement of the fossil. Thus, it is critical that careful attention is paid to the paleontological data included in phylogenetic divergence time analyses. With an accurately dated and identified fossil in hand, further consideration is required to determine how to apply the node-age constraint. If the fossil is truly a descendant of the node it calibrates, then it provides a reliable minimum age bound on the ancestral node time. However, maximum bounds are far more difficult to come by.

Bayesian methods provide a way to account for uncertainty in fossil calibrations. Prior distributions reflecting our knowledge (or lack thereof) of the amount of elapsed time from the ancestral node to is calibrating fossil are easily incorporated into these methods. A nice review paper by [Ho and Phillips \(2009\)](#) outlines a number of different parametric distributions appropriate for use as priors on calibrated nodes.

Uniform distribution: Typically, you must have both maximum and minimum age bounds when applying a uniform calibration prior (though some methods are available for applying uniform constraints with soft bounds). 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: When applying a biogeographical date (*e.g.*, the Isthmus of Panama) or a secondary calibration (a node age estimate from a previous study), the normal distribution can be a useful calibration prior. This distribution is always symmetrical and places the greatest prior weight on the mean. Its scale is determined by the standard deviation parameter.

Exponential distribution: The exponential distribution is characterized by a single rate parameter and is useful for calibration if the fossil age is very close to the age of its ancestral node. The expected (mean) age difference under this distribution is equal to the $1/\text{rate}$. Under the exponential distribution, the greatest prior weight is placed on node ages very close to the age of the fossil with diminishing probability to ∞ . As the rate parameter is increased, this prior density becomes strongly informative, whereas very low values of the rate result in a fairly non-informative prior (Figure 3a).

Log-normal distribution: An offset, log-normal prior on the calibrated node age places the highest probability on ages somewhat older than the fossil, with non-zero probability to ∞ .

1.4 Integrating Fossil Occurrence Times in the Speciation Model

Calibrating Bayesian divergence-time estimates using parametric densities (as described in the previous section: Sec. 1.3) are typically applied in a multiplicative manner such that the prior probability of a calibrated node age is the product of the probability coming from the tree-wide speciation model and the probability under the calibration density (Heled and Drummond 2012; Warnock et al. 2012; 2015). However, when using fossil information, it is also possible to account for the fact that the fossils are part of the same diversification process (*i.e.*, birth-death model) that generated the extant species using the fossilized birth-death (FBD) model described in Stadler (2010) and Heath et al. (2014). This model simply treats the fossil observations as part of the prior on node times. The fossilized birth-death process provides a model for the distribution of speciation times, tree topology, and distribution of lineage samples before the present (*i.e.*, non-contemporaneous samples like fossils or viruses). Thus, it provides a reasonable prior distribution for analyses combining morphological or DNA data for both extant and fossil taxa—*i.e.*, the so-called ‘total-evidence’ or ‘tip-dating’ approaches described by Ronquist et al. (2012a) (also see Pyron (2011)). When matrices of discrete morphological characters for both living and fossil species are unavailable, the fossilized birth-death model imposes a time structure on the tree by marginalizing over all possible attachment points for the fossils on the extant tree (Heath et al. 2014), therefore, some prior knowledge of phylogenetic relationships is important, much like for calibration-density approaches.

2 Overview

This tutorial extends on the node and fossil calibration tutorial and focuses on relaxed clock methods. In the first part we will use an uncorrelated lognormal (UCLN) relaxed clock model. All the assumptions will be covered more in detail later in this tutorial.

Requirements

We assume that you have read and hopefully completed the following tutorials:

- RB_Getting_Started
- RB_Basics_Tutorial
- RB_CTMC_Tutorial
- RB_DivergenceTime_Tutorial

Note that the RB_Basics_Tutorial introduces the basic syntax of **Rev** but does not cover any phylogenetic models. You may skip the RB_Basics_Tutorial if you have some familiarity with **R**. We tried to keep this tutorial very basic and introduce all the language concepts on the way. You may only need the RB_Basics_Tutorial for a more in-depth discussion of concepts in **Rev**.

3 Data and files

We provide the data file of DNA sequences required for this tutorial. You may want to use your own data instead.

→ Create a folder called **data** and download the following files:

- [primates_cytb.nex](#): Alignment of the *cytochrome b* subunit from 23 primates representing 14 of the 16 families (*Indriidae* and *Callitrichidae* are missing).

Additionally, we will use the same fossil calibration as in the previous tutorial.

4 Divergence time estimation using uncorrelated, lognormal distributed branch rates

4.1 Getting Started

The first section of this exercise involves: (1) setting up a general time reversible (GTR) substitution model (Tavaré 1986) with gamma distributed rate variation among sites (Yang 1994) for an alignment of the cytochrome b subunit; (2) use node calibrations to date the phylogeny; (3) use a relaxed clock model; (4) approximating the posterior probability of the tree topology and node ages (and all other parameters) using MCMC, and; (5) summarizing the MCMC output by computing the maximum *a posteriori* tree. This analysis is mostly equivalent to the analysis performed in the RB_CTMC_Tutorial.

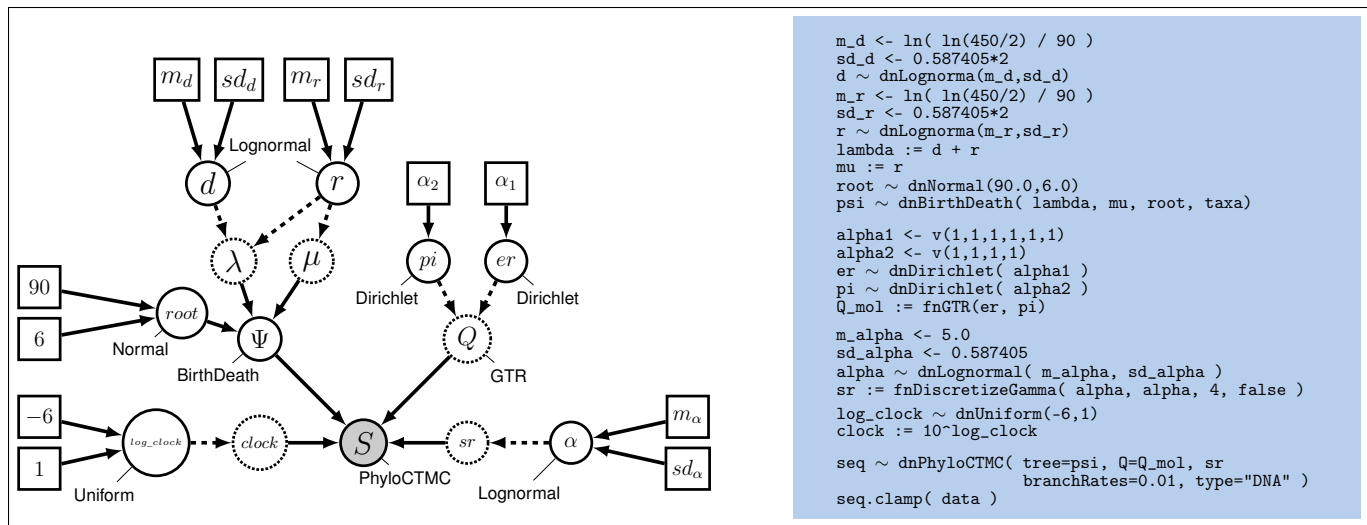


Figure 1: An example phylogenetic model depicted in graphical-model notation (left) and the corresponding specification in the Rev language (right). This example shows the basic outline of the root calibration that we will use in the first exercise.

The general structure of the model is represented in Figure 1. This figure shows the full model graph.

4.2 Loading the Data

- You should have already downloaded the data files in Section 3. Links to additional files, including the scripts to run these analyses can be found on the [RevBayes tutorials website](#). Remember that the data file should be in a directory called **data** that is in your current working directory.

First load in the sequences using the `readDiscreteCharacterData()` function.

```
data <- readDiscreteCharacterData("data/primates_cytb.nex")
```

Executing these lines initializes the data matrix as the respective Rev variable.

Next we will specify some useful variables based on our dataset. The variable **data** has *member functions* that we can use to retrieve information about the dataset. These include the number of species (**n_species**) and the tip labels (**taxa**). Each of these variables will be necessary for setting up different parts of our model (*e.g.*, the birth-death process prior).

```
n_species <- data.ntaxa()
taxa <- data.taxa()
```

Additionally, we set up a counter variable for the number of moves that we already added to our analysis. [Recall that moves are algorithms used to propose new parameter values during the MCMC simulation.] This will make it much easier if we extend the model or analysis to include additional moves or to remove some moves.

```
mvi = 0
```

You may have noticed that we used the `=` operator to create the move index. This simply means that the variable is not part of the model. You will later see that we use this operator more often, *e.g.*, when we create moves and monitors.

With the data loaded, we can now proceed to specify our substitution model.

4.3 General Time Reversible (GTR) Substitution Model

The GTR model requires that we define and specify a prior on the six exchangeability rates, which we will describe using a flat Dirichlet distribution. As we did previously for the Dirichlet prior on base frequencies, we first define a constant node specifying the vector of concentration-parameter values using the **v()** function:

```
er_prior <- v(1,1,1,1,1,1)
```

This node defines the concentration-parameter values of the Dirichlet prior distribution on the exchangeability rates. Now, we can create a stochastic node for the exchangeability rates using the **dnDirichlet()** function, which takes the vector of concentration-parameter values as an argument and the `~` operator. Together, these create a stochastic node named **er**, see Figure 1:

```
er ~ dnDirichlet(er_prior)
```

The Dirichlet prior on our parameter **er** creates a *simplex* of values that sum to 1.

For each stochastic node in our model, we must also specify a proposal mechanism if we wish to estimate that parameter.

```
moves[++mvi] = mvSimplexElementScale(er)
```

We can use the same type of distribution as a prior on the 4 stationary frequencies ($\pi_A, \pi_C, \pi_G, \pi_T$) since these parameters also represent proportions. Specify a flat Dirichlet prior density on the base frequencies:

```
pi_prior <- v(1,1,1,1)
pi ~ dnDirichlet(pi_prior)
```

The node **pi** represents the π node in Figure 1. Now add the simplex scale move on the stationary frequencies to the moves vector:

```
moves[++mvi] = mvSimplexElementScale(pi)
```

We can finish setting up this part of the model by creating a deterministic node for the GTR instantaneous-rate matrix **Q**. The **fnGTR()** function takes a set of exchangeability rates and a set of base frequencies to compute the instantaneous-rate matrix used when calculating the likelihood of our model.

```
Q := fnGTR(er,pi)
```

4.4 Setting up the Gamma Model

Create a constant node called **alpha_prior_mean** and a second constant node called **alpha_prior_sd** for the lognormal prior on the gamma-shape parameter (this is represented as the constant rate parameter in Figure 1):

```
alpha_prior_mean <- 5.0
alpha_prior_sd <- 0.587405
```

Then create a stochastic node called **alpha** with an lognormal prior (this represents the stochastic node for the α -shape parameter in Figure 1):

```
alpha ~ dnLognormal( alpha_prior_mean, alpha_prior_sd )
```

The way the ASRV model is implemented involves discretizing the mean-one gamma distribution into a set number of rate categories, k . To specify this, we need a deterministic node that is a vector that will hold the set of k rates drawn from the gamma distribution with k rate categories. The **fnDiscretizeGamma()** function returns this deterministic node and takes three arguments: the shape and rate of the gamma

distribution and the number of categories. Since we want to discretize a mean-one gamma distribution, we can pass in **alpha** for both the shape and rate.

Initialize the **gamma_rates** deterministic node vector using the **fnDiscretizeGamma()** function with 4 bins:

```
gamma_rates := fnDiscretizeGamma( alpha, alpha, 4 )
```

The random variable that controls the rate variation is the stochastic node **alpha**. We will apply a simple scale move to this parameter.

```
moves[++mvi] = mvScale(alpha, weight=2.0)
```

For more information on ASRV please read the [RB_CTMC_Tutorial](#).

4.5 Tree Prior: Tree Topology and Node Ages

The tree (the topology and node ages) is a stochastic node in our phylogenetic model. In Figure 1, the tree is denoted Ψ . We will assume a constant-rate birth-death process as the prior distribution on the tree. The distribution in RevBayes is **dnBDP()**. For more information on tree priors please read the [RB_DiversificationRate_Tutorial](#).

For the birth-death process we need a speciation rate and extinction rate parameter. Instead of prior distributions on these parameters directly, we will specify lognormal prior distributions on the diversification and turnover rates.

```
diversification_mean <- ln( ln(n_species/2.0) / 90 )
diversification_sd <- 0.587405*2
diversification ~ dnLognormal(mean=diversification_mean,sd=diversification_sd)
moves[++mvi] = mvScale(diversification,lambda=1.0,tune=true,weight=3.0)

turnover_mean <- ln( ln(n_species/2.0) / 90 )
turnover_sd <- 0.587405*2
turnover ~ dnLognormal(mean=turnover_mean,sd=turnover_sd)
moves[++mvi] = mvScale(turnover,lambda=1.0,tune=true,weight=3.0)

### Transform the parameters
birth_rate := diversification + turnover
death_rate := turnover
```

In our reference publication, [Perelman et al. \(2011\)](#) used a normal distribution with mean of 90.0 MYA with stdev = 6.0 as the prior distribution on the root age. The normal distribution itself is defined on the complete real line (*i.e.*, from $-\infty$ to $+\infty$), however, we know that the root age of primates is definitely larger than 0 (it happen before the present) and smaller than, say, 5000 MYA. Thus, we truncate the

normal distribution. This also has the advantage that the type of the variable for the root age is a positive real number, instead of a real number.

```
root_time ~ dnNormal(mean=90.0,sd=6.0,min=0.0,max=5000.0)
moves[++mvi] = mvScale(root_time,weight=2.0)
```

Additionally, we know that we do not have all primate species included in this data set. We only have 23 out of the approximately 450 primate species. Thus, we use a sampling fraction to represent this incomplete taxon sampling (Höhna et al. 2011; Höhna 2014).

```
rho <- n_species/450
```

Next, specify the **tree** stochastic node by passing in the tip labels **taxa** to the **dnBDP()** distribution:

```
psi ~ dnBDP(lambda=birth_rate, mu=death_rate, rho=rho, rootAge=root_time,
  samplingStrategy="uniform", condition="survival", taxa=taxa)
```

Some types of stochastic nodes can be updated by a number of alternative moves. Different moves may explore parameter space in different ways, and it is possible to use multiple different moves for a given parameter to improve mixing (the efficiency of the MCMC simulation). In the case of our rooted tree, for example, we can use both a nearest-neighbor interchange move without and with changing the node ages (**mvNarrow** and **mvNNI**) and a fixed-nodeheight subtree-prune and regrafting move (**mvFNPR**). For overviews about moves on tree see Lakner et al. (2008), Höhna et al. (2008) and Höhna and Drummond (2012). We also need moves that change the ages of the internal nodes; which are for example the **mvSubtreeScale** and **mvNodeTimeSlideUniform**. These moves do not have tuning parameters associated with them, thus you only need to pass in the **psi** node and proposal **weight**.

```
moves[++mvi] = mvNarrow(psi, weight=5.0)
moves[++mvi] = mvNNI(psi, weight=1.0)
moves[++mvi] = mvFNPR(psi, weight=5.0)
moves[++mvi] = mvFNPR(psi, weight=2.0)
moves[++mvi] = mvSubtreeScale(psi, weight=3.0)
moves[++mvi] = mvNodeTimeSlideUniform(psi, weight=15.0)
```

The weight specifies how often the move will be applied either on average per iteration or relative to all other moves. Have a look at the MCMC tutorial for more details about moves and MCMC strategies: <http://revbayes.github.io/tutorials.html>

4.6 Calibrating node ages

In this exercise we use soft-bounded node calibrations (Yang and Rannala 2006). You can also apply different node calibrations if you want.

We start with a deterministic node monitoring the age of the *Catarrhini*. This involves create a clade object. A clade object simply contains a number of species names. Note, the names need to match **exactly**. Then, we use the **tmrca** function which will record the time of the most recent common ancestor of this clade. Once we have this variable, we can use it for our calibration

```
clade_catarrhini = clade("Pan_paniscus", "Macaca_mulatta")
age_catarrhini := tmrca(psi, clade_catarrhini)
min_age_catarrhini <- 20.55
max_age_catarrhini <- 37.3
width_age_prior_catarrhini <- (max_age_catarrhini-min_age_catarrhini)/2.0
mean_age_prior_catarrhini <- min_age_catarrhini + width_age_prior_catarrhini
obs_age_catarrhini ~ dnSoftBoundUniformNormal(min=age_catarrhini -
  width_age_prior_catarrhini, max=age_catarrhini + width_age_prior_catarrhini, sd
  =2.5, p=0.95)
obs_age_catarrhini.clamp( mean_age_prior_catarrhini )
```

Next, a calibration for the *Platyrrhini*:

```
clade_platyrrhini = clade("Alouatta_palliata", "Callicebus_donacophilus")
age_platyrrhini := tmrca(psi, clade_platyrrhini)
min_age_platyrrhini <- 11.8
max_age_platyrrhini <- 37.3
width_age_prior_platyrrhini <- (max_age_platyrrhini-min_age_platyrrhini)/2.0
mean_age_prior_platyrrhini <- min_age_platyrrhini + width_age_prior_platyrrhini
obs_age_platyrrhini ~ dnSoftBoundUniformNormal(min=age_platyrrhini -
  width_age_prior_platyrrhini, max=age_platyrrhini + width_age_prior_platyrrhini, sd
  =2.5, p=0.95)
obs_age_platyrrhini.clamp( mean_age_prior_platyrrhini )
```

Then, a calibration for the *Simiiformes*:

```
clade_simiiformes = clade("Cebus_albifrons", "Macaca_mulatta")
age_simiiformes := tmrca(psi, clade_simiiformes)
min_age_simiiformes <- 28.3
max_age_simiiformes <- 56
width_age_prior_simiiformes <- (max_age_simiiformes-min_age_simiiformes)/2.0
mean_age_prior_simiiformes <- min_age_simiiformes + width_age_prior_simiiformes
obs_age_simiiformes ~ dnSoftBoundUniformNormal(min=age_simiiformes -
  width_age_prior_simiiformes, max=age_simiiformes + width_age_prior_simiiformes, sd
  =2.5, p=0.95)
width_age_prior_simiiformes)
obs_age_simiiformes.clamp( mean_age_prior_simiiformes )
```

And finally, a calibration for the *Lorisiformes*:

```
clade_lorisiformes = clade("Loris_tardigradus", "Galago_senegalensis")
age_lorisiformes := tmrca(psi, clade_lorisiformes)
min_age_lorisiformes <- 37.1
max_age_lorisiformes <- 56
width_age_prior_lorisiformes <- (max_age_lorisiformes-min_age_lorisiformes)/2.0
mean_age_prior_lorisiformes <- min_age_lorisiformes + width_age_prior_lorisiformes
obs_age_lorisiformes ~ dnSoftBoundUniformNormal(min=age_lorisiformes -
  width_age_prior_lorisiformes, max=age_lorisiformes + width_age_prior_lorisiformes,
  sd=2.5, p=0.95)
width_age_prior_lorisiformes)
obs_age_lorisiformes.clamp( mean_age_prior_lorisiformes )
```

4.7 The Uncorrelated Lognormal Relaxed Clock Model

In theory each branch has its own clock rate drawn independently and identically (iid) from a lognormal distribution. However, independent draws from this continuous distribution are problematic because the prior density would converge to ∞ when all rates are equal and the variance is equal to zero. Instead, a discretized version of the chosen prior distribution behaves better and is computationally more efficient. We will thus specify (more or less arbitrarily) the number of rate categories to be 10.

```
NUM_RATE_CATEGORIES = 10
```

You can experiment with the number of rate categories if you want.

The lognormal distribution is parameterized by the log-transformed mean and the standard deviation. As usual, we will say that every magnitude or clock rates between 10^{-6} and 10^1 are equally probably a priori. Additionally, we use an exponential prior distribution on the standard deviation because we want to give the highest prior probability to small values which represent our preference to a more clock-like behavior.

```
ucln_mean ~ dnUnif(1E-6, 10)
ucln_log_mean := ln( ucln_mean )
ucln_sigma ~ dnExponential(10.0)
```

Since both variables are stochastic parameters of the model, and defined for positive real numbers, we apply scaling moves on them.

```
moves[++mvi] = mvScale(ucln_sigma, lambda=0.5, weight=5.0)
```

In the next step we use the function **fnDiscretizeDistribution** to compute the quantiles deterministically of the lognormal distribution. The **fnDiscretizeDistribution** function can be applied to discretize any distribution (*e.g.*, the exponential or gamma distribution) we

```
rate_categories := fnDiscretizeDistribution(dnLnorm(ucln_log_mean, ucln_sigma),
  NUM_RATE_CATEGORIES)
```

```
rate_probs <- simplex(rep(1, NUM_RATE_CATEGORIES))
```

```
for (j in 1:n_branches) {
  # for each branch pull from one of the rate categories
  branch_rates[j] ~ dnMixture(rate_categories, rate_probs)
  moves[++mvi] = mvMixtureAllocation(branch_rates[j], weight=2.0)
}
```

```
mean_rt := mean(branch_rates)
```

4.8 Putting it All Together

We have fully specified all of the parameters of our phylogenetic model—the tree topology with branch lengths, and the substitution model that describes how the sequence data evolved over the tree with branch lengths. Collectively, these parameters comprise a distribution called the *phylogenetic continuous-time Markov chain*, and we use the **PhyloCTMC** constructor function to create this node. This distribution requires several input arguments: (1) the **tree** with branch lengths; (2) the instantaneous-rate matrix **Q**; (3) the branch-specific clock rates, and; (4) the **type** of character data.

Build the random variable for the character data (sequence alignment).

```
# the sequence evolution model
seq ~ dnPhyloCTMC(tree=psi, Q=Q, branchRates=branch_rates, siteRates=gamma_rates, type
  ="DNA")
```

Once the **PhyloCTMC** model has been created, we can attach our sequence data to the tip nodes in the tree.

```
seq.clamp(data)
```

Finally, we wrap the entire model to provide convenient access to the DAG. To do this, we only need to give the **model()** function a single node. With this node, the **model()** function can find all of the other nodes by following the arrows in the graphical model:

```
mymodel = model(Q)
```

4.9 Performing an MCMC Analysis Under the Global Clock Model

In this section, will describe how to set up the MCMC sampler and summarize the resulting posterior distribution of trees.

4.9.1 Specifying Monitors

For our MCMC analysis, we set up a vector of *monitors* to record the states of our Markov chain. First, we will initialize the model monitor using the **mnModel** function. This creates a new monitor variable that will output the states for all model parameters when passed into a MCMC function.

```
monitors[++mni] = mnModel(filename="output/primates_cytb_UCLN.log", printgen=10,  
    separator = TAB)
```

The **mnFile** monitor will record the states for only the parameters passed in as arguments. We use this monitor to specify the output for our sampled trees.

```
monitors[++mni] = mnFile(filename="output/primates_cytb_UCLN.trees", printgen=10,  
    separator = TAB, psi)
```

Finally, create a screen monitor that will report the states of specified variables to the screen with **mnScreen**:

```
monitors[++mni] = mnScreen(printgen=1000, mean_rt, root_time, age_simiiformes)
```

4.9.2 Initializing and Running the MCMC Simulation

With a fully specified model, a set of monitors, and a set of moves, we can now set up the MCMC algorithm that will sample parameter values in proportion to their posterior probability. The **mcmc()** function will create our MCMC object:

```
mymcmc = mcmc(mymodel, monitors, moves)
```

We may wish to run the **.burnin()** member function.

```
mymcmc.burnin(generations=10000,tuningInterval=250)
```

Now, run the MCMC:

```
mymcmc.run(generations=30000)
```

When the analysis is complete, you will have the monitored files in your output directory.

→ Look at the file called `output/primates_cytb_UCLN.log` in Tracer.

4.10 Exercise 1

Again, we are interested in the divergence time estimate between *Simiiformes*, *Platyrrhini*, *Catarrhini*, *Lorisiformes* and all primates.

- Specify your model using the UCLN relaxed clock as outlined above.
- Run the MCMC analysis.
- Look at the output in Tracer.
- Do the node-ages fall into the calibration intervals?
- Fill in the Table 1.
- * Repeat the analysis using an exponential distribution for the branch rates.

To obtain an estimate of the divergence time we read in the tree trace and build the annotated maximum *a posteriori* tree.

```
treetrace = readTreeTrace("output/primates_cytb_UCLN.trees",
                        treetype="clock")
mapTree(treetrace,"output/primates_cytb_UCLN.tree")
```

→ Look at the file called `output/primates_cytb_UCLN.tree` in FigTree.

Table 1: Estimated divergence times in our primates example*.

Clock Model	Primates		Simiiformes		Platyrrhini		Catarrhini		Lorisiformes	
	Mean Estimate	Credible interval	Mean Estimate	Credible interval	Mean Estimate	Credible interval	Mean Estimate	Credible interval	Mean Estimate	Credible interval
4 UCLN										
?? UCE										

*you can edit this table

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