

Phylogenetic Inference using RevBayes

State-Dependent Diversification Rate Estimation

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Estimating Character State-Dependent Speciation & Extinction Rates

Introduction

This tutorial describes how to specify character state-dependent branching process models in **RevBayes**. Frequently referred to as state-dependent speciation and extinction (SSE) models, these models are a birth-death process where the diversification rates are dependent on the state of an evolving character. The original model of this type considered a binary character (a trait with two discrete state values; called BiSSE, [Maddison et al. 2007](#)). Several variants have also been developed for other types of traits ([FitzJohn 2010](#); [Goldberg et al. 2011](#); [Goldberg and Igić 2012](#); [Magnuson-Ford and Otto 2012](#); [FitzJohn 2012](#); [Beaulieu and O’Meara 2016](#); [Freyman and Höhna 2017](#)).

We will outline the theory behind this method, and then you will fit it to data using Markov chain Monte Carlo (MCMC). **RevBayes** is a powerful tool for SSE analyses. After working through this tutorial you should be able to set up custom SSE models and use them to infer character-dependent diversification rates and ancestral states. We also provide examples of how to plot the results using the **RevGadgets** R package.

Contents

The State-Dependent Speciation and Extinction tutorial contains several sections:

- Section 1: Introduction to diversification rate estimation
- Section 2: Theory behind diversification rate models
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- Section 5: Running a HiSSE analysis in **RevBayes**
- Section 6: Running a ClaSSE analysis in **RevBayes**

Requirements

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

- [Getting started](#)

- [Rev basics](#)
- [Basic Diversification Rate Estimation](#)

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

Data and files

We provide the data files which we will use in this tutorial. You may want to use your own data instead. In the `data` folder, you will find the following files:

- [primates_tree.nex](#): Dated primate phylogeny including 233 out of 367 species. (This tree is from [Magnuson-Ford and Otto 2012](#), who took it from [Vos and Mooers 2006](#) and then randomly resolved the polytomies using the method of [Kuhn et al. 2011](#).)
- [primates_morph.nex](#): A set of several discrete-valued characters. The characters are described in the file [primates_morph_description.txt](#).
- [primates_biogeo.tre](#): A dated phylogeny of the 23 primate species.
- [primates_biogeo.tsv](#): Biogeographic range data for 23 primate species.

→ Open the tree files `primates_tree.nex` and `primates_biogeo.tre` in FigTree.

→ Open the character data files `primates_morph.nex` and `primates_biogeo.tsv` in a text editor.

Overview: Diversification Rate Estimation

Models of speciation and extinction are fundamental to any phylogenetic analysis of macroevolutionary processes (*e.g.*, divergence time estimation, diversification rate estimation, continuous and discrete trait evolution, and historical biogeography). First, a prior model describing the distribution of speciation events over time is critical to estimating phylogenies with branch lengths proportional to time. Second, stochastic branching models allow for inference of speciation and extinction rates. These inferences allow us to investigate key questions in evolutionary biology.

Diversification-rate parameters may be included as nuisance parameters of other phylogenetic models—*i.e.*, where these diversification-rate parameters are not of direct interest. For example, many methods for estimating species divergence times—such as BEAST (Drummond et al. 2012), MrBayes (Ronquist et al. 2012), and RevBayes (Höhna et al. 2016)—implement ‘relaxed-clock models’ that include a constant-rate birth-death branching process as a prior model on the distribution of tree topologies and node ages. Although the parameters of these ‘tree priors’ are not typically of direct interest, they are nevertheless estimated as part of the joint posterior probability distribution of the relaxed-clock model, and so can be estimated simply by querying the corresponding marginal posterior probability densities. In fact, this may provide more robust estimates of the diversification-rate parameters, as they accommodate uncertainty in the other phylogenetic-model parameters (including the tree topology, divergence-time estimates, and the other relaxed-clock model parameters). More recent work, *e.g.*, Heath et al. (2014), uses macroevolutionary models (the fossilized birth-death process) to calibrate phylogenies and thus to infer dated trees.

In these tutorials we focus on the different types of macroevolutionary models to study diversification processes and thus the diversification-rate parameters themselves. Nevertheless, these macroevolutionary models should be used for other evolutionary questions, when an appropriate prior distribution on the tree and divergence times is needed.

Types of Hypotheses for Estimating Diversification Rates

Many evolutionary phenomena entail differential rates of diversification (speciation – extinction); *e.g.*, adaptive radiation, diversity-dependent diversification, key innovations, and mass extinction. The specific study questions regarding lineage diversification may be classified within three fundamental categories of inference problems. Admittedly, this classification scheme is somewhat arbitrary, but it is nevertheless useful, as it allows users to navigate the ever-increasing number of available phylogenetic methods. Below, we describe each of the fundamental questions regarding diversification rates.

(1) Diversification-rate through time estimation *What is the (constant) rate of diversification in my study group?* The most basic models estimate parameters of the stochastic-branching process (*i.e.*, rates of speciation and extinction, or composite parameters such as net-diversification and relative-extinction rates) under the assumption that rates have remained constant across lineages and through time; *i.e.*, under a constant-rate birth-death stochastic-branching process model (Nee et al. 1994). Extensions to the (basic) constant-rate models include diversification-rate variation through time (Stadler 2011; Höhna 2015). First, we might ask whether there is evidence of an episodic, tree-wide increase in diversification rates (associated with a sudden increase in speciation rate and/or decrease in extinction rate), as might occur during an episode of adaptive radiation. A second question asks whether there is evidence of a continuous/gradual decrease in diversification rates through time (associated with decreasing speciation rates and/or increasing extinction rates), as might occur because of diversity-dependent diversification (*i.e.*, where competitive ecological interactions among the species of a growing tree decrease the opportunities for

speciation and/or increase the probability of extinction, *e.g.*, Höhna (2014)). Third, we can ask whether changes in diversification rates are correlated with environmental factors, such as environmental CO₂ or temperature (Condamine et al. 2013). A final question in this category asks whether our study tree was impacted by a mass-extinction event (where a large fraction of the standing species diversity is suddenly lost, *e.g.*, May et al. (2016)). The common theme of these studies is that the diversification process is tree-wide, that is, all lineages of the study group have the exact same rates at a given time.

(2) Diversification-rate variation across branches estimation *Is there evidence that diversification rates have varied significantly across the branches of my study group?* Models have been developed to detect departures from rate constancy across lineages; these tests are analogous to methods that test for departures from a molecular clock—*i.e.*, to assess whether substitution rates vary significantly across lineages (Alfaro et al. 2009; Rabosky 2014). These models are important for assessing whether a given tree violates the assumptions of rate homogeneity among lineages. Furthermore, these models are important to answer questions such as: *What are the branch-specific diversification rates?*; and *Have there been significant diversification-rate shifts along branches in my study group, and if so, how many shifts, what magnitude of rate-shifts and along which branches?*

(3) Character-dependent diversification-rate estimation *Are diversification rates correlated with some variable in my study group?* Character-dependent diversification-rate models aim to identify overall correlations between diversification rates and organismal features (binary and multi-state discrete morphological traits, continuous morphological traits, geographic range, etc.). For example, one can hypothesize that a binary character, say if an organism is herbivorous/carnivorous or self-compatible/self-incompatible, impact the diversification rates. Then, if the organism is in state 0 (*e.g.*, is herbivorous) it has a lower (or higher) diversification rate than if the organism is in state 1 (*e.g.*, carnivorous) (Maddison et al. 2007).

Diversification Rate Models

We begin this section with a general introduction to the stochastic birth-death branching process that underlies inference of diversification rates in RevBayes. This primer will provide some details on the relevant theory of stochastic-branching process models. We appreciate that some readers may want to skip this somewhat technical primer; however, we believe that a better understanding of the relevant theory provides a foundation for performing better inferences. We then discuss a variety of specific birth-death models, but emphasize that these examples represent only a tiny fraction of the possible diversification-rate models that can be specified in RevBayes.

The birth-death branching process

Our approach is based on the *reconstructed evolutionary process* described by Nee et al. (1994); a birth-death process in which only sampled, extant lineages are observed. Let $N(t)$ denote the number of species at time t . Assume the process starts at time t_1 (the ‘crown’ age of the most recent common ancestor of the study group, t_{MRCA}) when there are two species. Thus, the process is initiated with two species, $N(t_1) = 2$. We condition the process on sampling at least one descendant from each of these initial two lineages; otherwise t_1 would not correspond to the t_{MRCA} of our study group. Each lineage evolves independently of all other lineages, giving rise to exactly one new lineage with rate $b(t)$ and losing one existing lineage with rate $d(t)$ (Figure 1 and Figure 2). Note that although each lineage evolves independently, all lineages share both a common (tree-wide) speciation rate $b(t)$ and a common extinction rate $d(t)$ (Nee et al. 1994; Höhna 2015). Additionally, at certain times, t_{M} , a mass-extinction event occurs and each species existing at that time has the same probability, ρ , of survival. Finally, all extinct lineages are pruned and only the reconstructed

tree remains (Figure 1).

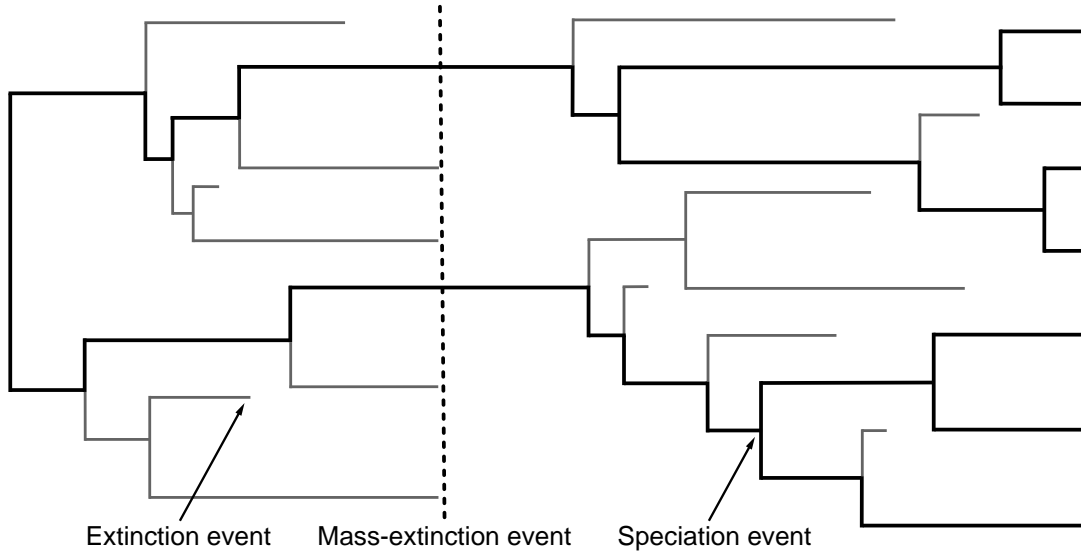


Figure 1: A realization of the birth-death process with mass extinction. Lineages that have no extant or sampled descendant are shown in gray and surviving lineages are shown in a thicker black line.

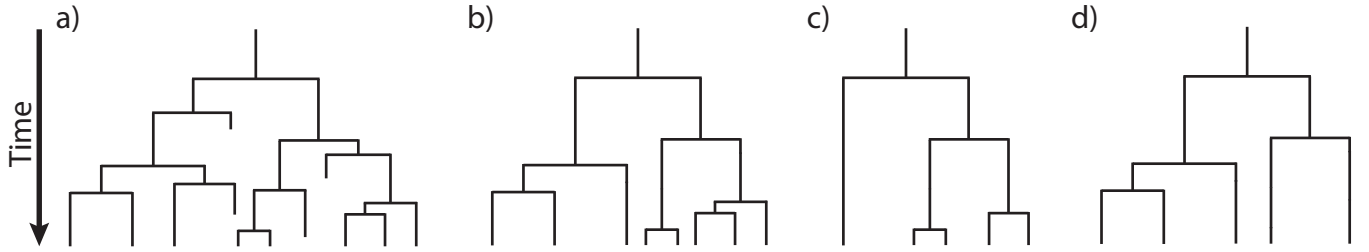


Figure 2: **Examples of trees produced under a birth-death process.** The process is initiated at the first speciation event (the ‘crown-age’ of the MRCA) when there are two initial lineages. At each speciation event the ancestral lineage is replaced by two descendant lineages. At an extinction event one lineage simply terminates. (A) A complete tree including extinct lineages. (B) The reconstructed tree of tree from A with extinct lineages pruned away. (C) A *uniform* subsample of the tree from B, where each species was sampled with equal probability, ρ . (D) A *diversified* subsample of the tree from B, where the species were selected so as to maximize diversity.

To condition the probability of observing the branching times on the survival of both lineages that descend from the root, we divide by $P(N(T) > 0 | N(0) = 1)^2$. Then, the probability density of the branching times, \mathbb{T} , becomes

$$P(\mathbb{T}) = \frac{\overbrace{P(N(T) = 1 | N(0) = 1)^2}^{\text{both initial lineages have one descendant}}}{\underbrace{P(N(T) > 0 | N(0) = 1)^2}_{\text{both initial lineages survive}}} \times \prod_{i=2}^{n-1} \overbrace{i \times b(t_i)}^{\text{speciation rate}} \times \overbrace{P(N(T) = 1 | N(t_i) = 1)}^{\text{lineage has one descendant}},$$

and the probability density of the reconstructed tree (topology and branching times) is then

$$P(\Psi) = \frac{2^{n-1}}{n!(n-1)!} \times \left(\frac{P(N(T) = 1 \mid N(0) = 1)}{P(N(T) > 0 \mid N(0) = 1)} \right)^2 \times \prod_{i=2}^{n-1} i \times b(t_i) \times P(N(T) = 1 \mid N(t_i) = 1) \quad (1)$$

We can expand Equation (1) by substituting $P(N(T) > 0 \mid N(t) = 1)^2 \exp(r(t, T))$ for $P(N(T) = 1 \mid N(t) = 1)$, where $r(u, v) = \int_u^v d(t) - b(t)dt$; the above equation becomes

$$\begin{aligned} P(\Psi) &= \frac{2^{n-1}}{n!(n-1)!} \times \left(\frac{P(N(T) > 0 \mid N(0) = 1)^2 \exp(r(0, T))}{P(N(T) > 0 \mid N(0) = 1)} \right)^2 \\ &\quad \times \prod_{i=2}^{n-1} i \times b(t_i) \times P(N(T) > 0 \mid N(t_i) = 1)^2 \exp(r(t_i, T)) \\ &= \frac{2^{n-1}}{n!} \times \left(P(N(T) > 0 \mid N(0) = 1) \exp(r(0, T)) \right)^2 \\ &\quad \times \prod_{i=2}^{n-1} b(t_i) \times P(N(T) > 0 \mid N(t_i) = 1)^2 \exp(r(t_i, T)). \end{aligned} \quad (2)$$

For a detailed description of this substitution, see [Höhna \(2015\)](#). Additional information regarding the underlying birth-death process can be found in ([Thompson 1975](#); Equation 3.4.6) and [Nee et al. \(1994\)](#) for constant rates and [Höhna \(2013; 2014; 2015\)](#) for arbitrary rate functions.

To compute the equation above we need to know the rate function, $r(t, s) = \int_t^s d(x) - b(x)dx$, and the probability of survival, $P(N(T) > 0 \mid N(t) = 1)$. [Yule \(1925\)](#) and later [Kendall \(1948\)](#) derived the probability that a process survives ($N(T) > 0$) and the probability of obtaining exactly n species at time T ($N(T) = n$) when the process started at time t with one species. Kendall's results were summarized in Equation (3) and Equation (24) in [Nee et al. \(1994\)](#)

$$P(N(T) > 0 \mid N(t) = 1) = \left(1 + \int_t^T \left(\mu(s) \exp(r(t, s)) \right) ds \right)^{-1} \quad (3)$$

$$\begin{aligned} P(N(T) = n \mid N(t) = 1) &= (1 - P(N(T) > 0 \mid N(t) = 1) \exp(r(t, T)))^{n-1} \\ &\quad \times P(N(T) > 0 \mid N(t) = 1)^2 \exp(r(t, T)) \end{aligned} \quad (4)$$

An overview for different diversification models is given in [Höhna \(2015\)](#).

Sidebar: Phylogenetic trees as observations

The branching processes used here describe probability distributions on phylogenetic trees. This probability distribution can be used to infer diversification rates given an “observed” phylogenetic tree. In reality we never observe a phylogenetic tree itself. Instead, phylogenetic trees themselves are estimated from actual observations, such as DNA sequences. These phylogenetic tree estimates, especially the divergence times, can have considerable uncertainty associated with them. Thus, the correct approach for estimating diversification rates is to include the uncertainty in the phylogeny by, for example, jointly

estimating the phylogeny and diversification rates. For the simplicity of the following tutorials, we take a shortcut and assume that we know the phylogeny without error. For publication quality analysis you should always estimate the diversification rates jointly with the phylogeny and divergence times.

Theory behind state-dependent diversification models

The Binary State Speciation and Extinction model (BiSSE; [Maddison et al. 2007](#)) was introduced because of two problems identified by [Maddison \(2006\)](#). First, inferences about character state transitions based on simple transition models (like [Pagel 1999](#)) can be thrown off if the character affects rates of speciation or extinction. Second, inferences about whether a character affects lineage diversification based on sister clade comparisons ([Mitter et al. 1988](#)) can be thrown off if the transition rates are asymmetric. BiSSE and related models are now mostly used to assess if the states of a character are associated with different rates of speciation or extinction.

RevBayes implements the extension of BiSSE to any number of discrete states (i.e., the MuSSE model in [diversitree](#); [FitzJohn 2012](#)). We will first describe the general theory about the model; you may skip over this section if you are not interested in the math behind the model. Then we will show how to run an analysis in RevBayes.

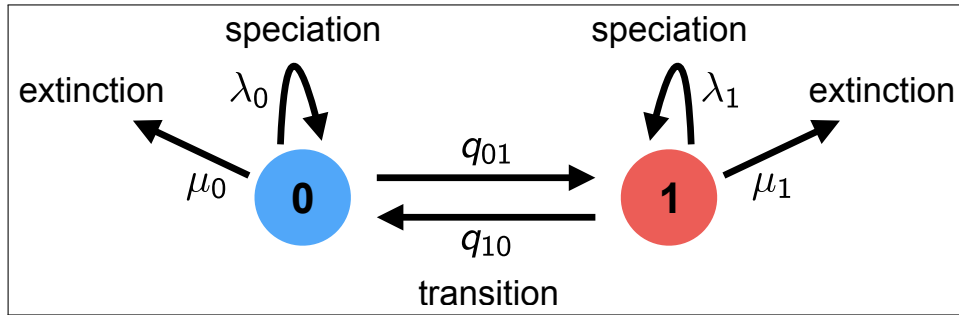


Figure 3: A schematic overview of the BiSSE model. Each lineage has a binary trait associated with it, so it is either in state 0 (blue) or state 1 (red). When a lineage is in state 0, it can either (a) speciate with rate λ_0 which results into two descendant lineage both being in state 0; (b) go extinct with rate μ_0 ; or (c) transition to state 1 with rate q_{01} . The same types of events are possible when a lineage is in state 1 but with rates λ_1 , μ_1 , and q_{10} , respectively.

General approach

The BiSSE model assumes two discrete states (i.e., a binary character), and that the state of each extant species is known (i.e., the discrete-valued character is observed). The general approach adopted by BiSSE and related models is to derive a set of ordinary differential equations (ODEs) that describe how the probability of observing a descendant clade changes along a branch in the observed phylogeny. Each equation in this set describes how the probability of observing a clade changes through time if it is in a particular state over that time period; collectively, these equations are called $\frac{dD_{N,i}(t)}{dt}$, where i is the state of a lineage at time t and N is the clade descended from that lineage.

Computing the likelihood proceeds by establishing an initial value problem. We initialize the procedure by observing the character states of some lineages, generally the tip states. Then starting from those probabilities (e.g., species X has state 0 with probability 1 at the present), we describe how those probabilities change over time (described by the ODEs), working our way back until we have computed the probabilities of observing that collection of lineages at some earlier time (e.g., the root).

As we integrate from the tips to the root, we need to deal with branches coming together at nodes. Assuming that the parent and daughter lineages have the same state, we multiply together the probabilities that the daughters are state i and the instantaneous speciation rate λ_i to get the initial value for the ancestral branch subtending that node.

Proceeding in this way down the tree results in a set of k probabilities at the root; these k probabilities represent the probability of observing the phylogeny conditional on the root being in each of the states (*i.e.*, the i^{th} conditional probability is the probability of observing the tree given that the root is in state i). The overall likelihood of the tree is a weighted average of the k probabilities at the root, where the weighting scheme represents the assumed probability that the root was in each of the k states.

As with all birth-death process models, special care must be taken to account for the possibility of extinction. Specifically, the above ODEs must accommodate lineages that may arise along each branch in the tree that subsequently go extinct before the present (and so are unobserved). This requires a second set of k ODEs, $\frac{dE_i(t)}{dt}$, which define how the probability of eventual extinction from state i changes over time. These ODEs must be solved to compute the differential equations $\frac{dD_{N,i}(t)}{dt}$. We will derive both sets of equations in the following sections.

Derivation for the binary state birth-death process

The derivation here follows the original description in Maddison et al. (2007). Consider a (time-independent) birth-death process with two possible states (a binary character), with diversification rates $\{\lambda_0, \mu_0\}$ and $\{\lambda_1, \mu_1\}$.

Clade probabilities, $D_{N,i}$

We define $D_{N,0}(t)$ as the probability of observing lineage N descending from a particular branch at time t , given that the lineage at that time is in state 0. To compute the probability of observing the lineage at some earlier time point, $D_{N,0}(t + \Delta t)$, we enumerate all possible events that could occur within the interval Δt . Assuming that Δt is small—so that the probability of more than one event occurring in the interval is negligible—there are four possible scenarios within the time interval (Fig. 4):

1. nothing happens;
2. a transition occurs, so the state changes $0 \rightarrow 1$;
3. a speciation event occurs, and the right descendant subsequently goes extinct before the present, or;
4. a speciation event occurs and the left descendant subsequently goes extinct before the present.

We are describing events within a branch of the tree (not at a node), so for (3) and (4), we require that one of the descendant lineages go extinct before the present because we do not observe a node in the tree between t and $t + \Delta t$.

We can thus compute $D_{N,0}(t + \Delta t)$ as:

$$\begin{aligned}
 D_{N,0}(t + \Delta t) = & (1 - \mu_0 \Delta t) \times && \text{in all cases, no extinction of the observed lineage} \\
 & [(1 - q_{01} \Delta t)(1 - \lambda_0 \Delta t) D_{N,0}(t) && \text{case (1) nothing happens} \\
 & + (q_{01} \Delta t)(1 - \lambda_0 \Delta t) D_{N,1}(t) && \text{case (2) state change but no speciation} \\
 & + (1 - q_{01} \Delta t)(\lambda_0 \Delta t) E_0(t) D_{N,0}(t) && \text{case (3) no state change, speciation, extinction} \\
 & + (1 - q_{01} \Delta t)(\lambda_0 \Delta t) E_0(t) D_{N,0}(t)] && \text{case (4) no state change, speciation, extinction}
 \end{aligned}$$

A matching equation can be written down for $D_{N,1}(t + \Delta t)$.

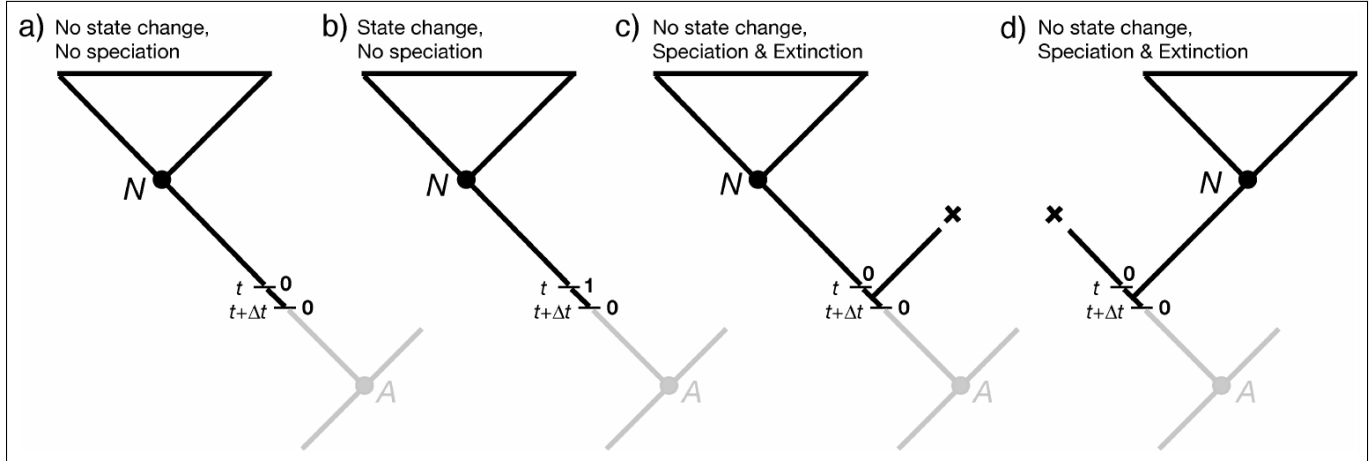


Figure 4: Possible events along a branch in the BiSSE model, used for deriving $D_{N,0}(t + \Delta t)$. This is Figure 2 in [Maddison et al. \(2007\)](#).

To convert these difference equations into differential equations, we take the limit $\Delta t \rightarrow 0$. With the notation that i can be either state 0 or state 1, and j is the other state, this yields:

$$\frac{dD_{N,i}(t)}{dt} = -(\lambda_i + \mu_i + q_{ij}) D_{N,i}(t) + q_{ij} D_{N,j}(t) + 2\lambda_i E_i(t) D_{N,i}(t) \quad (5)$$

Extinction probabilities, E_i

To solve the above equations for $D_{N,i}$, we see that we need the extinction probabilities. Define $E_0(t)$ as the probability that a lineage in state 0 at time t goes extinct before the present. To determine the extinction probability at an earlier point, $E_0(t + \Delta t)$, we can again enumerate all the possible events in the interval Δt (Fig. 5):

1. the lineage goes extinct within the interval;
2. the lineage neither goes extinct nor speciates, resulting in a single lineage that must eventually go extinct before the present;
3. the lineage neither goes extinct nor speciates, but there is a state change, resulting in a single lineage that must go extinct before the present, or;
4. the lineage speciates in the interval, resulting in *two* lineages that must eventually go extinct before the present.

$$\begin{aligned}
 E_0(t + \Delta t) = & \mu_0 \Delta t + && \text{case (1) extinction in the interval} \\
 & (1 - \mu_0 \Delta t) \times && \text{no extinction in the interval and ...} \\
 & [(1 - q_{01} \Delta t)(1 - \lambda_0 \Delta t) E_0(t) && \text{case (2) nothing happens, but subsequent extinction} \\
 & + (q_{01} \Delta t)(1 - \lambda_0 \Delta t) E_1(t) && \text{case (3) state change and subsequent extinction} \\
 & + (1 - q_{01} \Delta t)(\lambda_0 \Delta t) E_0(t)^2] && \text{case (4) speciation and subsequent extinctions}
 \end{aligned}$$

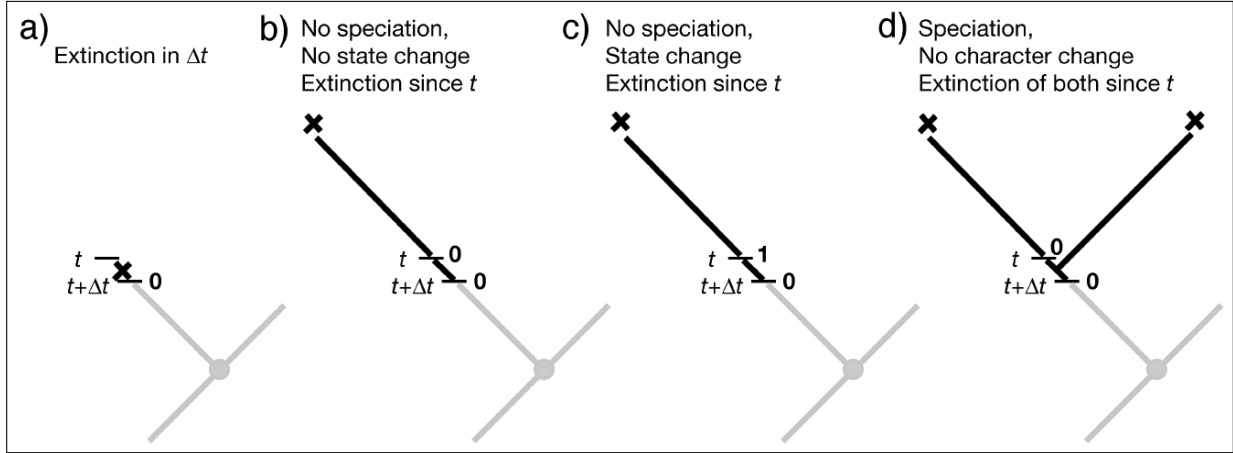


Figure 5: Possible events along a branch in the BiSSE model, used for deriving $E_0(t + \Delta t)$. This is Figure 3 in [Maddison et al. \(2007\)](#).

Again, a matching equation for $E_1(t + \Delta t)$ can be written down.

To convert these difference equations into differential equations, we again take the limit $\Delta t \rightarrow 0$:

$$\frac{dE_i(t)}{dt} = \mu_i - (\lambda_i + \mu_i + q_{ij}) E_i(t) + q_{ij} E_j(t) + \lambda_i E_i(t)^2 \quad (6)$$

Initial values: tips and sampling

The equations above describe how to get the answer at time $t + \Delta t$ assuming we already have the answer at time t . How do we start this process? The answer is with our character state observations, which are generally the tip state values. If species s has state i , then $D_{s,i}(0) = 1$ (probability is 1 at time 0 [the present] because we observed it for sure) and $E_i(0) = 0$ (probability 0 of being extinct at the present). For all states other than i , $D_{s,j}(0) = 0$ and $E_j(0) = 1$.

We can adjust these initial conditions to allow for incomplete sampling. If a proportion ρ of species are included on the tree, we would instead set $D_{s,i}(0) = \rho$ (probability of having state s and of being on the tree) and $E_i(0) = 1 - \rho$ (probability of absent, due to sampling rather than extinction). This simple form of incomplete sampling assumes that any species is equally likely to be on the tree ([FitzJohn et al. 2009](#)).

At nodes

Equations (5) and (6) are the BiSSE ODEs, describing probabilities along the branches of a phylogeny. We also need to specify what happens with the clade probabilities (the D s) at the nodes of the tree. BiSSE assumes the ancestor (called A) and descendants (called N and M) have the same state (*i.e.*, there is no cladogenetic character change). The initial value for the ancestral branch going into a node (at time t_A) is then the product of the final values for each of the daughter branches coming out of that node, times the instantaneous speciation rate (to account for the observed speciation event):

$$D_{A,i}(t_A) = D_{N,i}(t_A) D_{M,i}(t_A) \lambda_i \quad (7)$$

At the root

After we integrate Equations (5) and (6) from the tips to the root, dealing with nodes along the way via Equation (7), we arrive at the root with the D values (called $D_{R,i}$), one for each state. These need to be combined somehow to get the overall likelihood of the data:

$$\text{Likelihood}(\text{tree, tip states} \mid \text{model}) = \sum_i D_{R,i} p_{R,i}$$

What probability weighting, $p_{R,i}$ should be used for the possible root states? Sometimes a fixed approach is used, assuming that the prior root state probabilities are either all equal, or are the same as the observed tip state frequencies, or are the equilibrium state frequencies under the model parameters. These assumptions do not have a real basis, however (unless there is some external data that supports them), and they can cause trouble (Goldberg and Igić 2008). An alternative is to use the BiSSE probabilities themselves to determine the root state weightings, essentially adjusting the weightings to be most consistent with the data and BiSSE parameters (FitzJohn et al. 2009). Perhaps better is to treat the weightings as unknown parameters to be estimated. These estimates are usually quite uncertain, but in a Bayesian framework, one can treat the $p_{R,i}$ as nuisance parameters and integrate over them.

Table 1: **BiSSE model parameters and their interpretation**

Parameter	Interpretation
Ψ	Phylogenetic tree with divergence times
T	Root age
q_{01}	Rate of transitions from 0 to 1
q_{10}	Rate of transitions from 1 to 0
λ_0	Speciation rate for state 0
μ_0	Extinction rate for state 0
λ_1	Speciation rate for state 1
μ_1	Extinction rate for state 1

Equations for the multi-state birth-death process

The entire derivation above can easily be expanded to accommodate an arbitrary number of states (FitzJohn 2012). The only extra piece is summing over all the possible state transitions. The resulting differential equations within the branches are:

$$\begin{aligned} \frac{dD_{N,i}(t)}{dt} &= - \left(\lambda_i + \mu_i + \sum_{j \neq i}^k q_{ij} \right) D_{N,i}(t) + \sum_{j \neq i}^k q_{ij} D_{N,j}(t) + 2\lambda_i E_i(t) D_{N,i}(t) \\ \frac{dE_i(t)}{dt} &= \mu_i - \left(\lambda_i + \mu_i + \sum_{j \neq i}^k q_{ij} \right) E_i(t) + \sum_{j \neq i}^k q_{ij} E_j(t) + \lambda_i E_i(t)^2 \end{aligned}$$

Using state-dependent diversification models with RevBayes: the BiSSE model

Now let's start to analyze an example in RevBayes using the BiSSE model. In RevBayes, it's called "CDBDP," meaning Character Dependent Birth Death Process.

Read in the data

Begin by reading in the observed tree and the character state data. We have both stored in separate nexus files.

```
observed_phylogeny <- readTrees("data/primates_tree.nex")[1]
data <- readCharacterData("data/primates_activity_period.nex")
```

Note, the character-dependent birth-death process currently uses always the first character/site in the alignment file. We have therefore split the character dataset into several small files that include only one character each.

It will be convenient to pull out the list of tip names from the tree:

```
taxa <- observed_phylogeny.taxa()
```

Our vectors of moves and monitors will be defined later, but here we initialize iterator variables for them:

```
mvi = 0
mni = 0
```

Finally, we create a helper variable that specifies the number of states that the observed character has:

```
NUM_STATES = 2
```

Using this variable we can easily change our script to use a different character with a different number of states, essentially changing out model from BiSSE to MuSSE. (This will also be handy in our later example with the hidden-state speciation and extinction model.)

Specify the model

The basic idea behind the model in this example is that speciation and extinction rates are dependent on a binary character, and the character transitions between its two possible states ([Maddison et al. 2007](#)).

Priors on the rates

We start by specifying prior distributions on the diversification rates. We will assume here an identical prior distribution on each of the speciation and extinction rates. Furthermore, we will use a normal distribution as the prior distribution on the log of each speciation and extinction rate. Hence, we will use a mean of $\ln(\frac{\#Taxa}{2})/\text{tree-age}$ which is the expected net diversification rate.

```
rate_mean <- ln( ln(367.0/2.0) / observed_phylogeny.rootAge() )
rate_sd <- 2.0
```

Now we can specify our character-specific speciation and extinction rate parameters. Because we will use the same prior for each rate, it's easy to specify them all in a **for**-loop. We set up moves at the same time; a sliding move is good for a log-transformed variable.

```
for (i in 1:NUM_STATES) {

  ### Create a lognormal distributed variable for the diversification rate
  log_speciation[i] ~ dnNormal(mean=rate_mean,sd=rate_sd)
  speciation[i] := exp( log_speciation[i] )
  moves[++mvi] = mvSlide(log_speciation[i],delta=0.20,tune=true,weight=3.0)

  ### Create a lognormal distributed variable for the turnover rate
  log_extinction[i] ~ dnNormal(mean=rate_mean,sd=rate_sd)
  extinction[i] := exp( log_extinction[i] )
  moves[++mvi] = mvSlide(log_extinction[i],delta=0.20,tune=true,weight=3.0)

}
```

Next we specify the transition rates between the states 0 and 1, q_{01} and q_{10} . As a prior, we choose that each transition rate is drawn from an exponential distribution with a mean of 10 character state transitions over the entire tree. This is reasonable because we use this kind of model for traits that transition not-infrequently, and it leaves a fair bit of uncertainty. (You may want to compare the posterior to the prior and/or check the resulting posterior estimates for different choices of the prior.)

```
rate_pr := observed_phylogeny.treeLength() / 10
rate_12 ~ dnExponential(rate_pr)
rate_21 ~ dnExponential(rate_pr)
```

For both transition rate variables we specify a scaling move.

```
moves[++mvi] = mvScale( rate_12, weight=2 )
moves[++mvi] = mvScale( rate_21, weight=2 )
```

Finally, we put the rates into a matrix, because this is what's needed by the function for the state-dependent birth-death process.

```
rate_matrix := fnFreeBinary( [rate_12, rate_21 ], rescaled=false)
```

Note that we do not “rescale” the rate matrix. Rate matrices for molecular evolution are rescaled to have an average rate of 1.0, but for this model we want estimates of the transition rates with the same time scale as the diversification rates.

Prior on the root state

Create a variable with the prior probabilities of each rate category at the root. We are using a flat Dirichlet distribution as the prior on each state. In this case we are actually estimating the prior frequencies of the root states. There has been some discussion about this in [FitzJohn et al. \(2009\)](#). You could also fix the prior probabilities for the root states to be equal (generally not recommended), or use empirical state frequencies.

```
rate_category_prior ~ dnDirichlet( rep(1,NUM_STATES) )
moves[+mvi] = mvDirichletSimplex(rate_category_prior,tune=true,weight=2)
```

Incomplete taxon sampling

We know that we have sampled 233 out of 367 living primate species. To account for this we can set the sampling parameter as a constant node with a value of 233/367.

```
rho <- observed_phylogeny.ntips()/367
```

Root age

The birth-death process requires a parameter for the root age. In this exercise we use a fixed tree and thus we know the age of the tree.

```
root <- observed_phylogeny.rootAge()
```

The time tree

Now we have all of the parameters we need to specify the full character state-dependent birth-death model. We initialize the stochastic node representing the time tree.

```
timetree ~ dnCDBDP( rootAge      = root,
                    speciationRates = speciation,
```

```
extinctionRates = extinction,  
Q               = rate_matrix,  
pi              = rate_category_prior,  
delta           = 1.0,  
rho             = rho,  
condition       = "survival",  
taxa            = taxa )
```

And then we attach data to it.

```
timetree.clamp( observed_phylogeny )  
timetree.clampCharData( data )
```

Finally, we create a workspace object of our whole model. The `model()` function traverses all of the connections and finds all of the nodes we specified.

```
mymodel = model(rate_matrix)
```

Running an MCMC analysis

Specifying monitors

For our MCMC analysis, we set up a vector of *monitors* to record the states of our Markov chain. The first monitor will model all numerical variables; we are particularly interested in the rates of speciation, extinction, and transition.

```
monitors[++mni] = mnModel(filename="output/primates_BiSSE.log", printgen=1)
```

The second monitor is a new type of monitor: an joint-ancestral-states monitor. This monitor takes a draw from the joint posterior distribution of the ancestral states. Thus, with this output file we will be able to make a nice plot with ancestral states.

```
monitors[++mni] = mnJointConditionalAncestralState(tree=timetree, cdbdp=timetree, type  
  = "Standard", printgen=1, withTips=true, withStartStates=false, filename="output/  
  anc_states_primates_BiSSE.log")
```

(Note that this is a bit different than the marginal ancestral state reconstructions commonly produced by, e.g., Mesquite or various R packages. These joint draws are a self-consistent set of states across all nodes. [Pagel \(1999\)](#) discusses the differences.)

Finally, we add a screen monitor showing some updates during the MCMC run.


```
monitors[++mni] = mnScreen(printgen=10, rate_12, rate_21, speciation, extinction)
```

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)
```

First, we will run a pre-burnin to tune the moves and to obtain starting values from the posterior distribution.

```
mymcmc.burnin(generations=5000,tuningInterval=200)
```

Now, run the MCMC:

```
mymcmc.run(generations=20000)
```

Summarizing ancestral states

After our MCMC run has finished, we read-in again our samples from the joint-ancestral-state posterior distribution.

```
anc_states = readAncestralStateTrace("output/anc_states_primates_BiSSE.log")
```

Then we can use this trace and our fixed tree to compute the posterior probabilities of the ancestral states and prepare the output for plotting. We will use the function called `ancestralStateTree` which stores the tree with ancestral states automatically in a file.

```
anc_tree = ancestralStateTree(tree=observed_phylogeny, ancestral_state_trace_vector=
  anc_states, include_start_states=false, file="output/
  anc_states_primates_BiSSE_results.tree", burnin=0, summary_statistic="MAP", site=0)
```

Plotting ancestral states

Let us first plot the ancestral states mapped on the phylogeny. We will use R and the package `RevGadgets`. Execute the following code in R.

```
library(RevGadgets)

tree_file = "output/anc_states_primates_BiSSE_results.tree"

plot_ancestral_states(tree_file, summary_statistic="MAP",
                      tip_label_size=0,
                      xlim_visible=NULL,
                      node_label_size=0,
                      show_posterior_legend=TRUE,
                      node_size_range=c(2, 6),
                      alpha=0.75)

output_file = "RevBayes_Anc_States_BiSSE.pdf"
ggsave(output_file, width = 11, height = 9)
```

The resulting plot is shown in Figure 6. We see both the maximum *a posteriori* (MAP) estimate for each node as well as the posterior probability of the states represented by the size of the dots.

Plotting diversification rates

Now let us plot the diversification rate estimates. Again, we are going to use R for our plotting. Specifically, we will use the package `ggplot2` but you can also use any other package that you prefer. We are only taking advantage of reading in the tab-delimited file as a table and plot the different diversification rate parameters. Note that we also rely on another provided R script for plotting multiple plots in one file.

```
library(ggplot2)
source("scripts/multiplot.R")

data <- read.table("output/primates_BiSSE.log",header=TRUE)

dat_ext <- data.frame(dens = c(data$extinction.1, data$extinction.2), Type = rep(c(
  "1", "2"), each = length(data$extinction.1)))
dat_spec <- data.frame(dens = c(data$speciation.1, data$speciation.2), Type = rep(c(
  "1", "2"), each = length(data$extinction.1)))
dat_div <- data.frame(dens = c(data$speciation.1-data$extinction.1, data$speciation.2-
  data$extinction.2), Type = rep(c("1", "2"), each = length(data$extinction.1)))
dat_rel <- data.frame(dens = c(data$extinction.1/data$speciation.1, data$extinction.2/
  data$speciation.2), Type = rep(c("1", "2"), each = length(data$extinction.1)))

pdf("RevBayes_BiSSE_Results.pdf")

p1 <- ggplot(dat_spec, aes(x = dens, fill = Type)) + labs(title = "Speciation", x="
  Rate", y="Posterior Density") + geom_density(alpha = 0.5)
p2 <- ggplot(dat_ext, aes(x = dens, fill = Type)) + labs(title = "Extinction", x="Rate
  ", y="Posterior Density") + geom_density(alpha = 0.5)
```

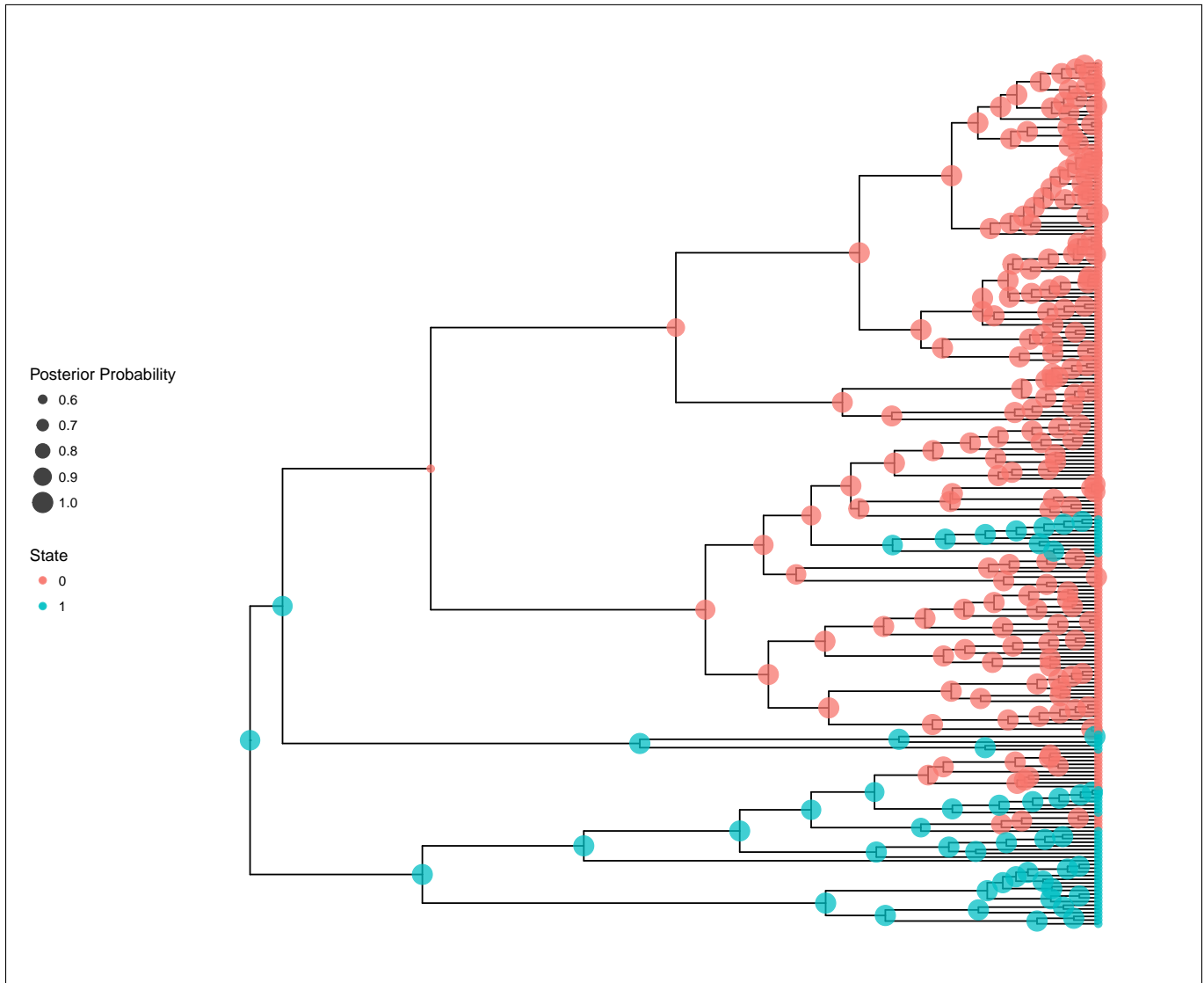


Figure 6: Estimated ancestral states for the activity period of primates.

```
p3 <- ggplot(dat_div, aes(x = dens, fill = Type)) + labs(title = "Net-Diversification", x="Rate", y="Posterior Density") + geom_density(alpha = 0.5)
p4 <- ggplot(dat_rel, aes(x = dens, fill = Type)) + labs(title = "Relative Extinction", x="Rate", y="Posterior Density") + geom_density(alpha = 0.5)

multiplot(p1, p2, p3, p4)
dev.off()
```

Exercise

1. Run an MCMC simulation to estimate the posterior distribution of the speciation rate and extinction rate.

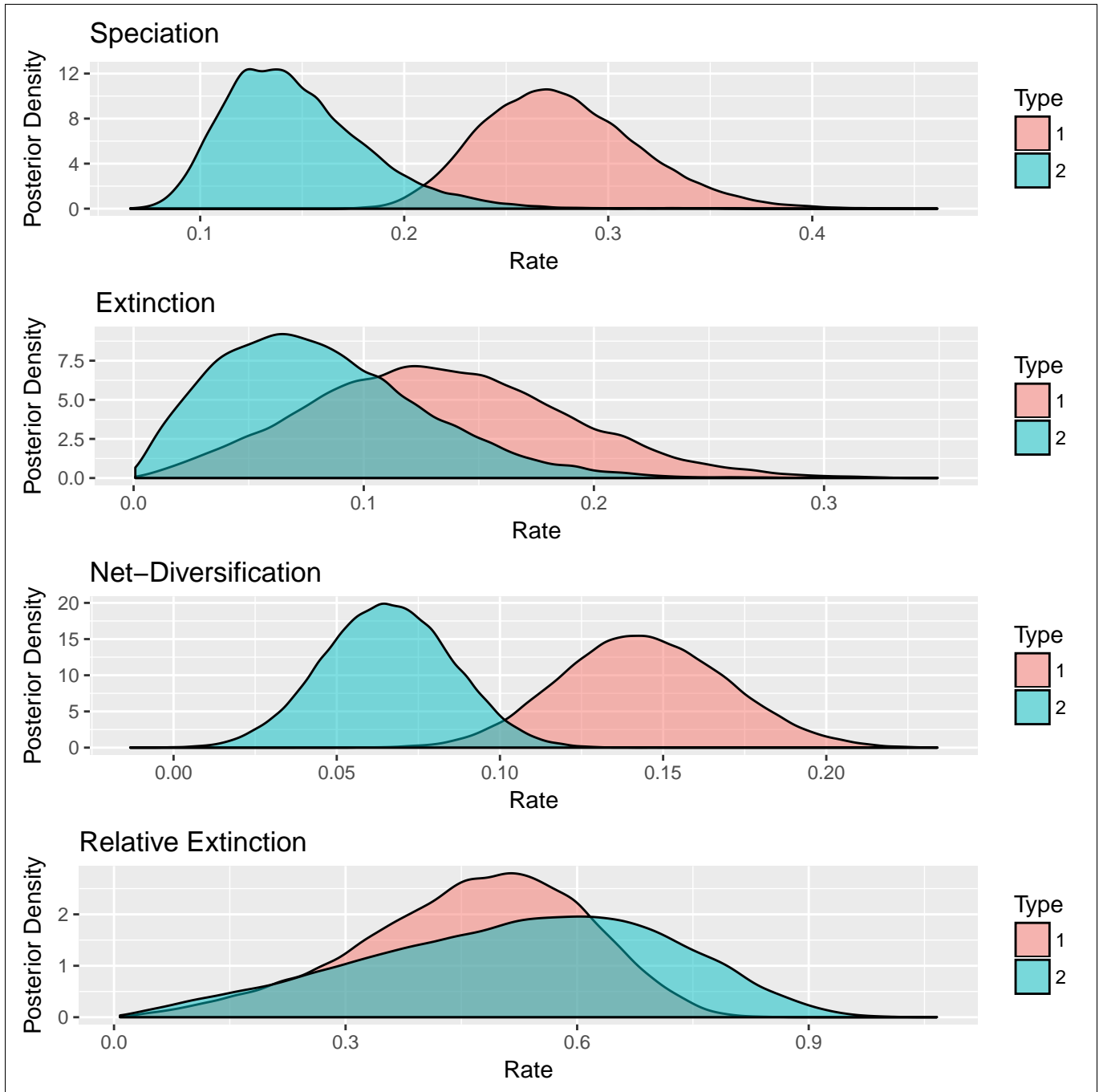


Figure 7: Estimated diversification rate for activity period (state 1 = Diurnal and state 2 = Nocturnal). We see that there is a noticeable difference in the estimated speciation rates but only little difference in the estimated extinction rates.

2. Visualize the state-specific diversification rates using R.
3. Do you see evidence for rate differences between the two states?
4. Repeat this analysis for a different binary character.

Accommodating uncorrelated diversification rate changes: the HiSSE model

BiSSE and MuSSE are powerful approaches for testing the association of a character with diversification rate heterogeneity. However, BiSSE has been shown to be prone to falsely identifying a positive association when diversification rate shifts are correlated with a character *not* included in the model (Maddison and FitzJohn 2015; Rabosky and Goldberg 2015). One approach to reduce the possibility of falsely associating a character with diversification rate heterogeneity is to incorporate a second, unobserved character into the model (i.e. a Hidden State-Dependent Speciation and Extinction (HiSSE) model; Beaulieu and O'Meara 2016). The changes in the unobserved character's state represent background diversification rate changes that are not correlated with the observed character. See Figure 8 for a schematic overview of the HiSSE model, and Table 2 for an explanation of the HiSSE model parameters. Now let's set up and run a HiSSE analysis in RevBayes.

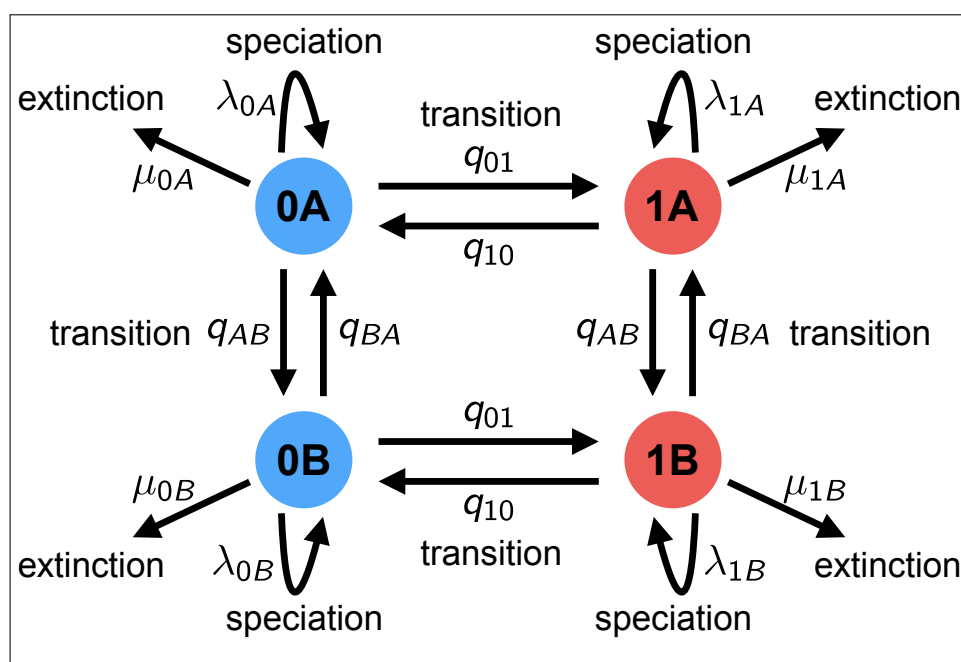


Figure 8: A schematic overview of the HiSSE model. Each lineage has an observed binary state associated to it: state 0 (blue) or state 1 (red). Furthermore, there is a second, unobserved (hidden), binary character with states A or B. The HiSSE model describes jointly the evolution of both of these two characters; a lineage must be in one of four different states: 0A, 0B, 1A, or 1B. We estimate separate speciation and extinction rates for each of these four states. Note that just like BiSSE can easily be extended to MuSSE, RevBayes allows you to extend HiSSE models beyond binary observed and unobserved characters.

Setting up the analysis

Reading in the data

Begin by reading in the observed tree and the character data. We have both stored in separate nexus files.

```
observed_phylogeny <- readTrees("data/primates_tree.nex")[1]
data <- readCharacterData("data/primates_activity_period.nex")
```

Table 2: HiSSE model parameters and their interpretation

Parameter	Interpretation
Ψ	Phylogenetic tree with divergence times.
T	The root age.
q_{01}	The rate of shifts between observed states 0 to 1.
q_{10}	The rate of shifts between observed states 1 to 0.
q_{AB}	The rate of shifts between hidden states A to B.
q_{BA}	The rate of shifts between hidden states B to A.
λ_{0A}	Speciation rate for state 0A.
μ_{0A}	Extinction rate for state 0A.
λ_{1A}	Speciation rate for state 1A.
μ_{1A}	Extinction rate for state 1A.
λ_{0B}	Speciation rate for state 0B.
μ_{0B}	Extinction rate for state 0B.
λ_{1B}	Speciation rate for state 1B.
μ_{1B}	Extinction rate for state 1B.

Note, the character-dependent birth-death process currently uses always the first character/site in the alignment file. We have therefore split the character dataset into several small files that include only one character each.

From the tree, we can get some helpful variables:

```
taxa <- observed_phylogeny.taxa()
```

Additionally, we can initialize an iterator variable for our vector of moves and monitors:

```
mvi = 0
mni = 0
```

Finally, we create a helper variable that specifies the number of states that the character has.

```
NUM_STATES = 2
NUM_HIDDEN = 2
NUM_RATES = NUM_STATES * NUM_HIDDEN
```

Using this variable we can easily change our script to use a different character with a different number of states. We will also use this variable in our second example on hidden-state speciation and extinction model.

Priors on rates

We start by specifying prior distributions on the diversification rates. We will assume here an identical prior distribution on the speciation and extinction rate. Furthermore, we will use a normal distribution as the prior distribution on the log of the speciation and extinction rate. Hence, we will use a mean of $\frac{\ln(\frac{\#Taxa}{2})}{tree-age}$ which is the expected net-diversification rate.

```
rate_mean <- ln( ln(367.0/2.0) / observed_phylogeny.rootAge() )
rate_sd <- 2.0
```

Now we can specify our character-specific speciation and extinction rate parameters. As we just said before, we are going to use normal distributions for the prior on the log-speciation and log-extinction rate. Here we will use a **for**-loop to specify speciation and extinction parameters for each character, *e.g.*, two in a binary state case.

```
for (i in 1:NUM_STATES) {

  ### Create a lognormal distributed variable for the diversification rate
  log_speciation[i] ~ dnNormal(mean=rate_mean,sd=rate_sd)
  speciation[i] := exp( log_speciation[i] )
  moves[++mvi] = mvSlide(log_speciation[i],delta=0.20,tune=true,weight=3.0)

  ### Create a lognormal distributed variable for the turnover rate
  log_extinction[i] ~ dnNormal(mean=rate_mean,sd=rate_sd)
  extinction[i] := exp( log_extinction[i] )
  moves[++mvi] = mvSlide(log_extinction[i],delta=0.20,tune=true,weight=3.0)

}
```

Now we need to create the variable for the hidden states.

```
for (i in 1:(NUM_HIDDEN-1)) {

  ### Create an exponential distributed variable for the diversification rate
  speciation_beta[i] ~ dnExp(1.0)
  moves[++mvi] = mvScale(speciation_beta[i],lambda=0.20,tune=true,weight=2.0)

  ### Create an normal distributed variable for the turnover rate
  extinction_beta[i] ~ dnNormal(0.0,1.0)
  moves[++mvi] = mvSlide(extinction_beta[i],delta=0.20,tune=true,weight=2.0)

}
```

Finally, we match the rates to all possible —hidden and observed— states.

```
for (j in 1:NUM_HIDDEN) {
  for (i in 1:NUM_STATES) {
    if ( j == 1) {
      speciation[i] := exp( speciation_alpha[i] )
      extinction[i] := exp( extinction_alpha[i] )
    } else {
      index = i+(j*NUM_STATES)-NUM_STATES
      speciation[index] := speciation[index-NUM_STATES] * exp( speciation_beta[j-1] )
      extinction[index] := exp( extinction_alpha[i] + extinction_beta[j-1] )
    }
  }
}
```

As before, we specify a rate prior.

```
rate_pr := observed_phylogeny.treeLength() / 10
rate_12 ~ dnExponential(rate_pr)
rate_21 ~ dnExponential(rate_pr)
```

For both rate variable we specify a scaling move.

```
moves[++mvi] = mvScale( rate_12, weight=2 )
moves[++mvi] = mvScale( rate_21, weight=2 )
```

Finally, we build a rate matrix for the relative-rate of change between categories. This is because we need a rate matrix in our state-dependent birth-death process.

```
Q := [ rate_12, rate_21 ]
```

Set up the transition rate matrix for hidden states. We assume the transitions among the hidden states are all equal and drawn from an exponential distribution.

```
hidden_rate ~ dnExponential(rate_pr)
moves[++mvi] = mvScale(hidden_rate, lambda=0.2, tune=true, weight=5)

for (i in 1:(NUM_HIDDEN * (NUM_HIDDEN - 1))) {
  R[i] := hidden_rate
}
```


Create the rate matrix for the combined observed and hidden states

```
rate_matrix := fnHiddenStateRateMatrix(Q, R, rescaled=false)
```

A specific note here is that we do not rescale the rate matrix. This is very important because otherwise rate matrices, as used for molecular evolution, are always rescaled to have an average rate of 1.0. If such a rescaled rate matrix was used, then you need to provide an overall rate scalar δ .

Prior on the root state

Create a variable with the prior probabilities of each rate category at the root. We are using a flat Dirichlet distribution as the prior on each state. In this case we are actually estimating the prior frequencies of the root states.

```
rate_category_prior ~ dnDirichlet( rep(1,NUM_STATES) )
moves[+mv] = mvDirichletSimplex(rate_category_prior,tune=true,weight=2)
```

Incomplete Taxon Sampling

We know that we have sampled 233 out of 367 living primate species. To account for this we can set the sampling parameter as a constant node with a value of 233/367

```
rho <- observed_phylogeny.ntips()/367
```

Root age

The birth-death process requires a parameter for the root age. In this exercise we use a fix tree and thus we know the age of the tree. Hence, we can get the value for the root from the [Magnuson-Ford and Otto \(2012\)](#) tree.

```
root <- observed_phylogeny.rootAge()
```

The time tree

Now we have all of the parameters we need to specify the full state-dependent birth-death model. We initialize the stochastic node representing the time tree.

```
timetree ~ dnCDBDP( rootAge      = root,
                    speciationRates = speciation,
                    extinctionRates = extinction,
                    Q              = rate_matrix,
```

```
pi          = rate_category_prior,  
delta       = 1.0,  
rho         = rho,  
condition   = "survival",  
taxa        = taxa )
```

And then we attach data to it.

```
timetree.clamp( observed_phylogeny )  
timetree.clampCharData( data )
```

Finally, we create a workspace object of our whole model using the `model()` function.

```
mymodel = model(rate_matrix)
```

The `model()` function traversed all of the connections and found all of the nodes we specified.

Running an MCMC analysis

Specifying Monitors

For our MCMC analysis, we set up a vector of *monitors* to record the states of our Markov chain. For more details

```
monitors[++mni] = mnModel(filename="output/primates_HiSSE.log", printgen=1)  
monitors[++mni] = mnJointConditionalAncestralState(tree=timetree, cdbdp=timetree, type  
    ="NaturalNumbers", printgen=1, withTips=true, withStartStates=false, filename="  
    output/anc_states_primates_HiSSE.log")  
monitors[++mni] = mnScreen(printgen=100, Q, R)
```

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)
```

First, we will run a pre-burnin to tune the moves and to obtain starting values from the posterior distribution.

```
mymcmc.burnin(generations=5000,tuningInterval=200)
```

Now, run the MCMC:

```
mymcmc.run(generations=20000)
```

Summarizing ancestral states

After the MCMC run we summarize and estimate the joint-ancestral-state estimates.

```
anc_states = readAncestralStateTrace("output/anc_states_primates_HiSSE.log")
anc_tree = ancestralStateTree(tree=observed_phylogeny, ancestral_state_trace_vector=
  anc_states, include_start_states=false, file="output/
  anc_states_primates_HiSSE_results.tree", burnin=0, summary_statistic="MAP", site=0)
```

Plotting diversification rates

Again, we plot the diversification rate as before.

```
library(ggplot2)
source("scripts/multiplot.R")

data <- read.table("output/primates_HiSSE.log",header=TRUE)

start <- round(0.5*length(data$extinction.1))
end <- length(data$extinction.1)

HiSSE_types <- rep(c("1A", "2A", "1B", "2B"), each = length(data$extinction.1[start:
  end]))
dat_ext <- data.frame(dens = c(data$extinction.1[start:end], data$extinction.2[start:
  end], data$extinction.3[start:end], data$extinction.4[start:end]), Type =
  HiSSE_types)
dat_spec <- data.frame(dens = c(data$speciation.1[start:end], data$speciation.2[start:
  end], data$speciation.3[start:end], data$speciation.4[start:end]), Type =
  HiSSE_types)
dat_div <- data.frame(dens = c(data$speciation.1[start:end]-data$extinction.1[start:
  end], data$speciation.2[start:end]-data$extinction.2[start:end], data$speciation.3[
  start:end]-data$extinction.3[start:end], data$speciation.4[start:end]-
  data$extinction.4[start:end]), Type = HiSSE_types)
dat_rel <- data.frame(dens = c(data$extinction.1[start:end]/data$speciation.1[start:
  end], data$extinction.2[start:end]/data$speciation.2[start:end], data$extinction.3[
  start:end]/data$speciation.3[start:end], data$extinction.4[start:end]/
  data$speciation.4[start:end]), Type = HiSSE_types)
```

```
pdf("RevBayes_HiSSE_Results.pdf")

p1 <- ggplot(dat_spec, aes(x = dens, fill = Type)) + labs(title = "Speciation", x="
  Rate", y="Posterior Density") + geom_density(alpha = 0.5) + guides(fill=
  guide_legend(ncol=2,byrow=TRUE))
p2 <- ggplot(dat_ext, aes(x = dens, fill = Type)) + labs(title = "Extinction", x="Rate
  ", y="Posterior Density") + geom_density(alpha = 0.5) + guides(fill=guide_legend(
  ncol=2,byrow=TRUE))
p3 <- ggplot(dat_div, aes(x = dens, fill = Type)) + labs(title = "Net-Diversification
  ", x="Rate", y="Posterior Density") + geom_density(alpha = 0.5) + guides(fill=
  guide_legend(ncol=2,byrow=TRUE))
p4 <- ggplot(dat_rel, aes(x = dens, fill = Type)) + labs(title = "Relative Extinction
  ", x="Rate", y="Posterior Density") + geom_density(alpha = 0.5) + guides(fill=
  guide_legend(ncol=2,byrow=TRUE))

multiplot(p1, p2, p3, p4)
dev.off()

$
```

Exercise

1. Run an MCMC simulation to estimate the posterior distribution of the speciation rate and extinction rate.
2. Visualize the state-specific diversification rates using R.
3. Do you see evidence for rate differences between the two states?
4. Do you see differences to the previous BiSSE estimates?
5. Repeat this analysis for a different binary character.

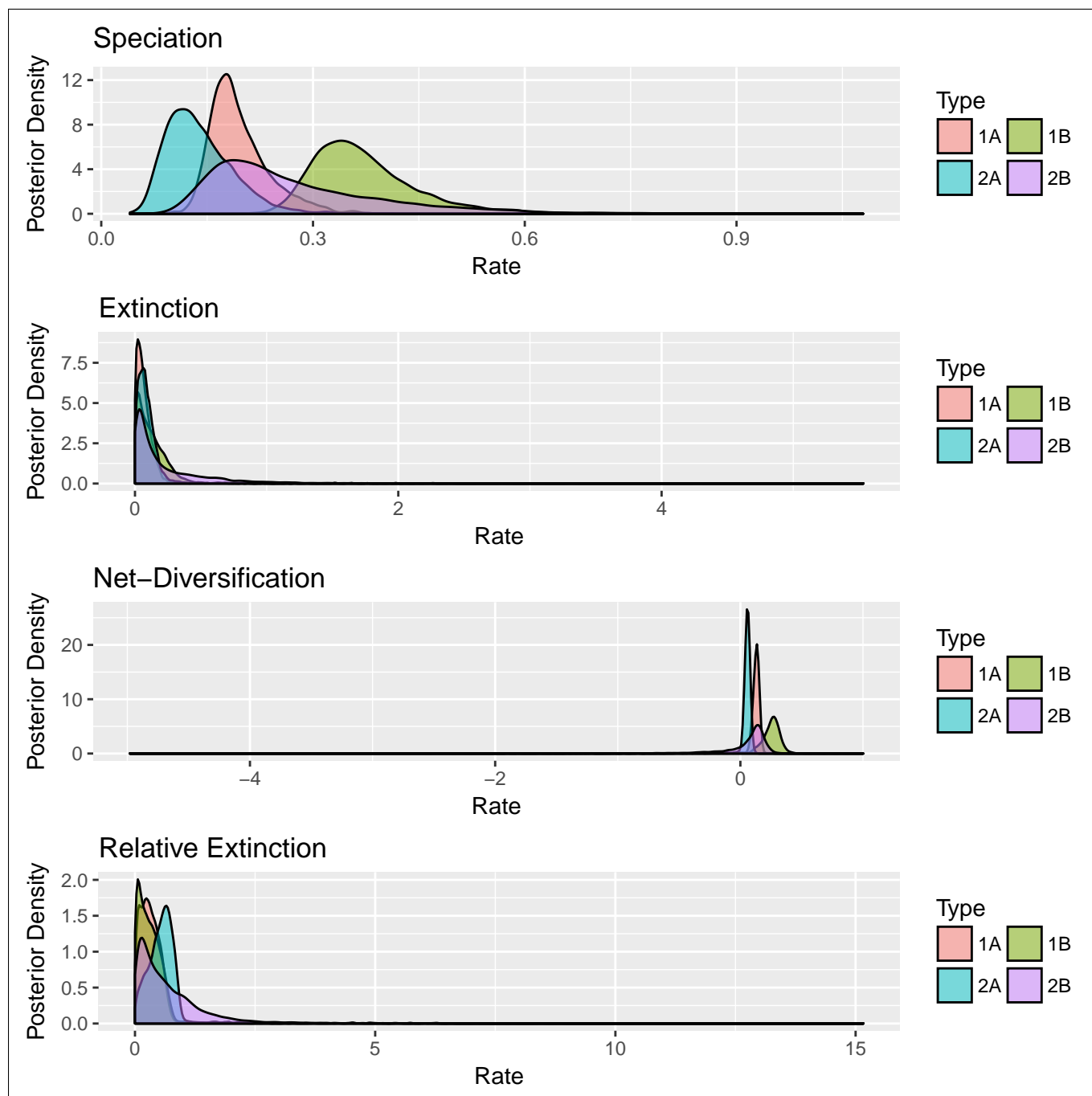


Figure 9: Estimated diversification rate for activity period (state 1 = Diurnal and state 2 = Nocturnal).

Accommodating both cladogenetic and anagenetic changes: the ClaSSE model

In the previous examples we have modeled all character state transitions as anagenetic changes. Anagenetic changes occur along the branches of a phylogeny, within a lineage. Cladogenetic changes, on the other hand, occur at speciation events. They represent changes in a character state that may be associated with

speciation events due to increased reproductive isolation, for example colonizing a new geographic area or a shift in chromosome number. Note that it can be quite tricky to determine if a character state shift is a cause or a consequence of speciation, but we can at least test if state changes tend to occur in the same time window as speciation events.

A major challenge for all phylogenetic models of cladogenetic character change is accounting for unobserved speciation events due to lineages going extinct and not leaving any extant descendants (Bokma 2002), or due to incomplete sampling of lineages in the present. Teasing apart the phylogenetic signal for cladogenetic and anagenetic processes given unobserved speciation events is a major difficulty. Commonly used biographic models like the dispersal-extinction-cladogenesis (DEC; Ree and Smith 2008) simply ignore unobserved speciation events and so result in biased estimates of cladogenetic versus anagenetic change.

This bias can be avoided by using the Cladogenetic State change Speciation and Extinction (ClaSSE) model (Goldberg and Igić 2012), which accounts for unobserved speciation events by jointly modeling both character evolution and the phylogenetic birth-death process. ClaSSE models extend other SSE models by incorporating both cladogenetic and anagenetic character evolution. This approach has been used to model biogeographic range evolution (Goldberg et al. 2011) and chromosome number evolution (Freyman and Höhna 2017).

Here we will use RevBayes to examine biogeographic range evolution in the primates. We will model biogeographic range evolution similar to a DEC model, however we will use ClaSSE to account for speciation events unobserved due to extinction or incomplete sampling.

Setting up the analysis

Reading in the data

Begin by reading in the observed tree.

```
observed_phylogeny <- readTrees("data/primates_biogeo.tre")[1]
```

Get the taxa in the tree. We'll need this later on.

```
taxa = observed_phylogeny.taxa()
```

Now let's read in the biogeographic range data. The areas are represented as the following character states:

- 0 = 00 = the null state with no range
- 1 = 01 = New World only
- 2 = 10 = Old World only
- 3 = 11 = both New and Old World

For consistency, we have chosen to use the same representation of biogeographic ranges used in the RevBayes biogeography/DEC tutorial. Each range is represented as both a natural number (0, 1, 2, 3) and a

corresponding bitset (00, 01, 10, 11). The null state (state 0) is used in DEC models to represent a lineage that has no biogeographic range and is therefore extinct. Our model will include this null state as well, however, we will explicitly model extinction as part of the birth-death process so our character will never enter state 0.

```
data_biogeo = readCharacterDataDelimited("data/primates_biogeo.tsv", stateLabels
  ="0123", type="NaturalNumbers", delimiter="\t", headers=TRUE)
```

Also we need to set the move and monitor indices.

```
mvi = 0
mni = 0
```

Set up the extinction rates

We are going to draw both anagenetic transition rates and diversification rates from a lognormal distribution. The mean of the prior distribution will be $\ln(\frac{\#Taxa}{2})/\text{tree-age}$ which is the expected net diversification rate, and the SD will be 1.0 so the 95% prior interval ranges well over 2 orders of magnitude.

```
num_species <- 424 # approximate total number of primate species
rate_mean <- ln( ln(num_species/2.0) / observed_phylogeny.rootAge() )
rate_sd <- 1.0
```

The extinction rates will be stored in a vector where each element represents the extinction rate for the corresponding character state. We have chosen to allow a lineage to go extinct in both the New and Old World at the same time (like a global extinction event). As an alternative, you could restrict the model so that a lineage can only go extinct if it's range is limited to one area.

```
extinction_rates[1] <- 0.0 # the null state (state 0)
extinction_rates[2] ~ dnLognormal(rate_mean, rate_sd) # extinction when the lineage is
  in New World (state 1)
extinction_rates[3] ~ dnLognormal(rate_mean, rate_sd) # extinction when the lineage is
  in Old World (state 2)
extinction_rates[4] ~ dnLognormal(rate_mean, rate_sd) # extinction when in both (state
  3)
```

Note Rev vectors are indexed starting with 1, yet our character states start at 0. So `extinction_rate[1]` will represent the extinction rate for character state 0.

Add MCMC moves for each extinction rate.

```
moves[++mvi] = mvSlide( extinction_rates[2], weight=4 )
moves[++mvi] = mvSlide( extinction_rates[3], weight=4 )
moves[++mvi] = mvSlide( extinction_rates[4], weight=4 )
```

Let's also create a deterministic variable to monitor the overall extinction rate.

```
total_extinction := sum(extinction_rates)
```

Set up the anagenetic transition rate matrix

First, let's create the rates of anagenetic dispersal:

```
anagenetic_dispersal_13 ~ dnLognormal(rate_mean, rate_sd) # disperse from New to Old
                    World 01 -> 11
anagenetic_dispersal_23 ~ dnLognormal(rate_mean, rate_sd) # disperse from Old to New
                    World 10 -> 11
```

Now add MCMC moves for each anagenetic dispersal rate.

```
moves[++mvi] = mvSlide( anagenetic_dispersal_13, weight=4 )
moves[++mvi] = mvSlide( anagenetic_dispersal_23, weight=4 )
```

The anagenetic transitions will be stored in a 4 by 4 instantaneous rate matrix. We will construct this by first creating a vector of vectors. Let's begin by initializing all rates to 0.0:

```
for (i in 1:4) {
  for (j in 1:4) {
    r[i][j] <- 0.0
  }
}
```

Now we can populate non-zero rates into the anagenetic transition rate matrix:

```
r[2][4] := anagenetic_dispersal_13
r[3][4] := anagenetic_dispersal_23
r[4][2] := extinction_rates[3]
r[4][3] := extinction_rates[2]
```


Note that we have modeled the rate of $11 \rightarrow 01$ ($3 \rightarrow 1$) as being the rate of going extinct in area 2, and the rate of $11 \rightarrow 10$ ($3 \rightarrow 2$) as being the rate of going extinct in area 1.

Now we pass our vector of vectors into the **fnFreeK** function to create the instantaneous rate matrix.

```
ana_rate_matrix := fnFreeK(r, rescaled=false)
```

Set up the cladogenetic speciation rate matrix

Here we need to define each cladogenetic event type in the form [ancestor_state, daughter1_state, daughter2_state] and assign each cladogenetic event type a corresponding speciation rate.

The first type of cladogenetic event we'll specify is widespread sympatry. Widespread sympatric cladogenesis is where the biogeographic range does not change; that is the daughter lineages inherit the same range as the ancestor. In this example we are not going to allow the speciation events like $11 \rightarrow 11$, 11 , as it seems biologically implausible. However if you wanted you could add this to your model.

Define the speciation rate for widespread sympatric cladogenesis events:

```
speciation_wide_sympatry ~ dnLognormal(rate_mean, rate_sd)
moves[+mvi] = mvSlide( speciation_wide_sympatry, weight=4 )
```

Define the widespread sympatric cladogenetic events:

```
clado_events[1] = [1, 1, 1] # 01 -> 01, 01
clado_events[2] = [2, 2, 2] # 10 -> 10, 10
```

and assign each the same speciation rate:

```
speciation_rates[1] := speciation_wide_sympatry/2
speciation_rates[2] := speciation_wide_sympatry/2
```

Subset sympatry is where one daughter lineage inherits the full ancestral range but the other lineage inherits only a single region.

```
speciation_sub_sympatry ~ dnLognormal(rate_mean, rate_sd)
moves[+mvi] = mvSlide( speciation_sub_sympatry, weight=4 )
```

Define the subset sympatry events and assign each a speciation rate:

```

clado_events[3] = [3, 3, 1] # 11 -> 11, 01
clado_events[4] = [3, 1, 3] # 11 -> 01, 11
clado_events[5] = [3, 3, 2] # 11 -> 11, 10
clado_events[6] = [3, 2, 3] # 11 -> 10, 11
speciation_rates[3] := speciation_sub_sympatry/4
speciation_rates[4] := speciation_sub_sympatry/4
speciation_rates[5] := speciation_sub_sympatry/4
speciation_rates[6] := speciation_sub_sympatry/4

```

Allopatric cladogenesis is when the two daughter lineages split the ancestral range:

```

speciation_allopatry ~ dnLognormal(rate_mean, rate_sd)
moves[++mvi] = mvSlide( speciation_allopatry, weight=4 )

```

Define the allopatric events:

```

clado_events[7] = [3, 1, 2] # 11 -> 01, 10
clado_events[8] = [3, 2, 1] # 11 -> 10, 01
speciation_rates[7] := speciation_allopatry/2
speciation_rates[8] := speciation_allopatry/2

```

Now let's create a deterministic variable to monitor the overall speciation rate:

```

total_speciation := sum(speciation_rates)

```

Finally, we construct the cladogenetic speciation rate matrix from the cladogenetic event types and the speciation rates.

```

clado_matrix := fnCladogeneticSpeciationRateMatrix(clado_events, speciation_rates, 4)

```

Let's view the cladogenetic matrix to see if we have set it up correctly:

```

clado_matrix

```

Set up the cladogenetic character state-dependent birth-death process

For simplicity we will fix the root frequencies to be equal except for the null state which has probability of 0.

```
root_frequencies <- simplex([0, 1, 1, 1])
```

ρ is the probability of sampling species at the present:

```
rho <- observed_phylogeny.ntips()/num_species
```

Now we construct a stochastic variable drawn from the cladogenetic character state-dependent birth-death process.

```
classe ~ dnCDCladoBDP( rootAge      = observed_phylogeny.rootAge(),
                       cladoEventMap = clado_matrix,
                       extinctionRates = extinction_rates,
                       Q              = ana_rate_matrix,
                       delta           = 1.0,
                       pi              = root_frequencies,
                       rho             = rho,
                       condition       = "time",
                       taxa            = taxa )
```

Clamp the model with the observed data.

```
classe.clamp( observed_phylogeny )
classe.clampCharData( data_biogeo )
```

Finalize the model

Just like before, we must create a workspace model object.

```
mymodel = model(classe)
```

Set up and run the MCMC

First, set up the monitors that will output parameter values to file and screen.

```
monitors[++mni] = mnModel(filename="output/primates_ClaSSE.log", printgen=1)
monitors[++mni] = mnJointConditionalAncestralState(tree=observed_phylogeny, cdbdp=
  classe, type="NaturalNumbers", printgen=1, withTips=true, withStartStates=true,
  filename="output/anc_states_primates_ClaSSE.log")
monitors[++mni] = mnScreen(printgen=1, speciation_wide_sympatry,
  speciation_sub_sympatry, speciation_allopatry, extinction_rates)
```

Now define our workspace MCMC object.

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

We will perform a pre-burnin to tune the proposals and then run the MCMC. Note that for a real analysis you would want to run the MCMC for many more iterations.

```
mymcmc.burnin(generations=200,tuningInterval=5)
mymcmc.run(generations=1000)
```

Summarize ancestral states

When the analysis has completed you now summarize the ancestral states. The ancestral states are estimated both for the “beginning” and “end” state of each branch, so that the cladogenetic changes that occurred at speciation events are distinguished from the changes that occurred anagenetically along branches. Make sure the `include_start_states` argument is set to `true`.

```
anc_states = readAncestralStateTrace("output/anc_states_primates_ClaSSE.log")
anc_tree = ancestralStateTree(tree=observed_phylogeny, ancestral_state_trace_vector=
  anc_states, include_start_states=true, file="output/
  anc_states_primates_ClaSSE_results.tree", burnin=0, summary_statistic="MAP", site
  =0)
```

Plotting ancestral states

Like before, we’ll plot the ancestral states using the `RevGadgets` R package. Execute the script `plot_anc_states_ClaSSE.R` in R. The results can be seen in Figure 10. The maximum *a posteriori* (MAP) estimate for each node is shown as well as the posterior probability of the states represented by the size of the dots.

```
library(RevGadgets)

tree_file = "output/anc_states_primates_ClaSSE_results.tree"

plot_ancestral_states(tree_file, summary_statistic="MAPRange",
  tip_label_size=3,
  tip_label_offset=1,
  xlim_visible=c(0,100),
  node_label_size=0,
  shoulder_label_size=0,
  include_start_states=TRUE,
  show_posterior_legend=TRUE,
```

```
node_size_range=c(4, 7),
alpha=0.75)

output_file = "RevBayes_Anc_States_ClaSSE.pdf"
ggsave(output_file, width = 11, height = 9)
```

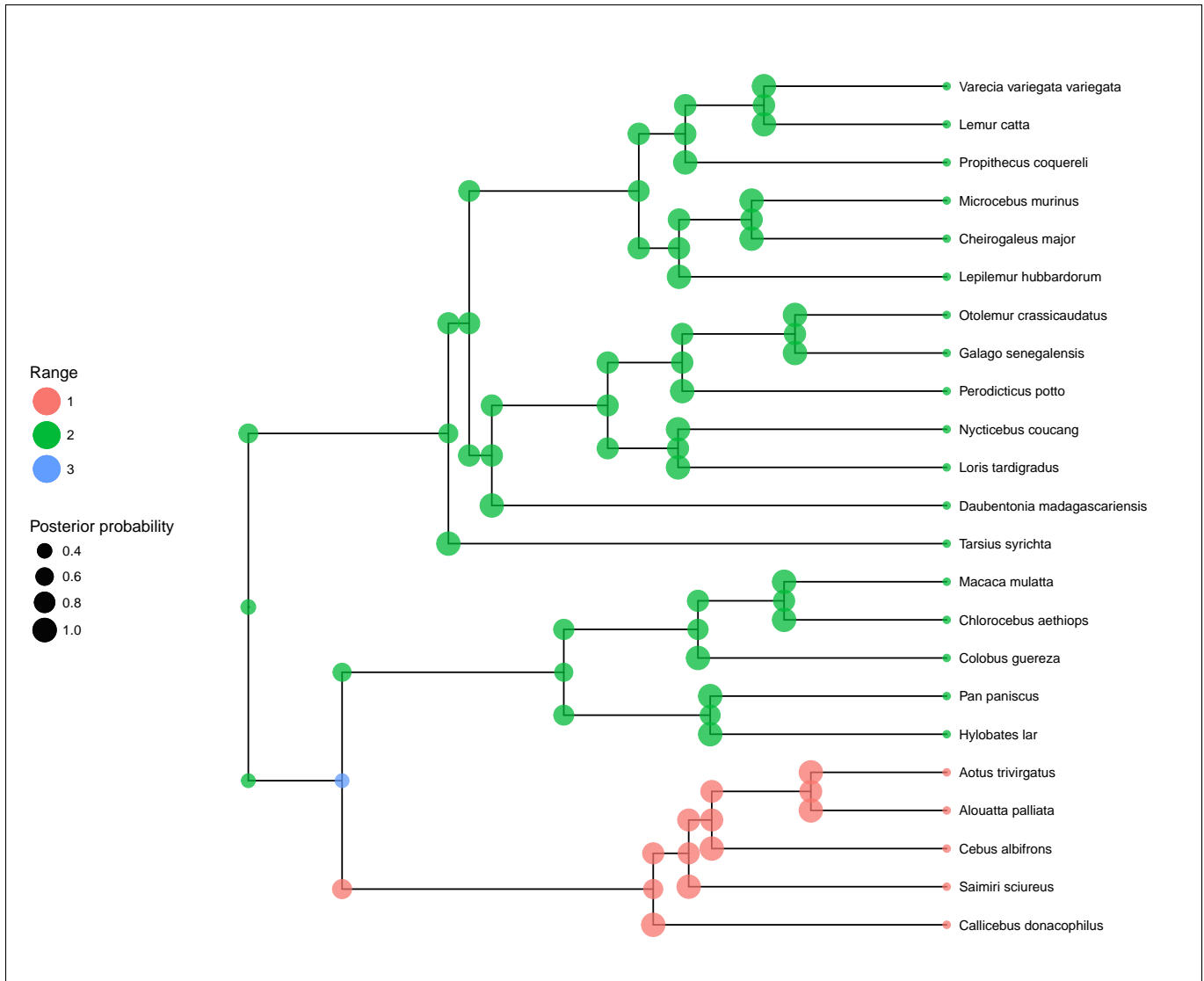


Figure 10: Maximum a posteriori estimate of biogeographic range evolution of the primates. The most recent common ancestor of the primates is inferred to be in the Old World (green). According to this reconstruction, approximately 70 Mya one lineage dispersed to be in both New and Old World (blue). This widespread lineage underwent allopatric cladogenesis, resulting in one daughter lineage in the Old World and one in the New World (green).

Exercise

- Using either R or Tracer, visualize the posterior estimates for different types of cladogenetic events. What kind of speciation events are most common?

2. As we have specified the model, we did not allow cladogenetic long distance (jump) dispersal, for example $01 \rightarrow 01, 10$. Modify this script to include cladogenetic long distance dispersal and calculate Bayes factors to see which model fits the data better. How does this affect the ancestral state estimate?

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Version dated: August 9, 2017