LOCALLY ADAPTIVE BAYESIAN BIRTH-DEATH MODEL SUCCESSFULLY DETECTS SLOW AND RAPID RATE SHIFTS

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Abstract

Birth-death processes have given biologists a model-based framework to answer questions about changes in the birth and death rates of lineages in a phylogenetic tree. Therefore birth-death models are central to macroevolutionary as well as phylodynamic analyses. Early approaches to studying temporal variation in birth and death rates using birth-death models faced difficulties due to the restrictive choices of birth and death rate curves through time. Sufficiently flexible time-varying birth-death models are still lacking. We use a piecewise-constant birth-death model, combined with both Gaussian Markov random field (GMRF) and horseshoe Markov random field (HSMRF) prior distributions, to approximate arbitrary changes in birth rate through time. We implement these models in the widely used statistical phylogenetic software platform `RevBayes`, allowing us to jointly estimate birth-death process parameters, phylogeny, and nuisance parameters in a Bayesian framework. We test both GMRF-based and HSMRF-based models on a variety of simulated diversification scenarios, and then apply them to both a macroevolutionary and an epidemiological dataset. We find that both models are capable of inferring variable birth rates and correctly rejecting variable models in favor of effectively constant models. In general the HSMRF-based model has higher precision than its GMRF counterpart, with little to no loss of accuracy. Applied to a macroevolutionary dataset of the Australian gecko family Pygopodidae (where birth rates are interpretable as speciation rates), the GMRF-based model detects a slow decrease whereas the HSMRF-based model detects a rapid speciation-rate decrease in the last 12 million years. Applied to an infectious disease phylodynamic dataset of sequences from HIV subtype A in Russia and Ukraine (where birth rates are interpretable as the rate of accumulation of new infections), our models detect a strongly elevated rate of infection in the 1990s.

Introduction

Studying variation in the rates of speciation and extinction enables researchers to examine the patterns and processes that shape the diversity of life on earth. Birth-death processes have given biologists a model-based framework in which questions about the birth rate, death rate, or diversification (birth minus death) rate of species can be studied [1]. For example, the question, "are nectar spurs a key innovation in plant evolution leading to a rapid radiation?" can be rephrased as, "is the rate of diversification higher in plant lineages with nectar spurs than in lineages without them?" In infectious disease phylodynamics, the question "was this intervention effective in containing disease spread?" can be rephrased as, "after the intervention, did the birth rate (effective reproduction number) decrease?" Questions involving variation in diversification rates can generally be broken down into two categories. The first class of questions, including the question about nectar spurs, concerns variation in diversification rates across lineages. In these scenarios, models are built that allow the birth and death rates to vary across the branches of the phylogenetic tree [2, 3]. The second class of questions, including the question about intervention efficacy, concerns temporal variation in diversification rates shared by all lineages [4, 5, 6]. In these scenarios, the birth and death rates are modeled as functions of time, but at any instant in time all branches of the tree share a common birth rate and a death rate. This second class of questions and models is our focus in this paper. Our aim is to develop flexible Bayesian nonparametric methods for accurately estimating changes of birth and death rates over time without sacrificing precision.

Birth-death models [7, 8] define a probability distribution on time-calibrated phylogenies—phylogenetic trees where branch lengths are measured in time rather than in evolutionary distances. Early approaches to inferring variability of birth and/or death rates required the use of a time-calibrated phylogeny as data. This involved estimating parameters of birth-death models and then either statistically testing for violations of constant birth and death rates [9] or choosing the best functional form (*e.g.*, two-piece piecewise constant or exponential curves) for birth and death rate trajectories from a set of candidate models via likelihood-ratio tests or the AIC [10, 11]. These early methods had the downside of not accounting explicitly for missing taxa, requiring the use of Monte Carlo simulation in order to determine if the rejection of a constant-rate (or other) model in favor of a more complex model was an artifact of incomplete sampling of phylogenetic lineages [12, 13, 14]. However, the underlying theory and likelihood function for arbitrary functions of birth and death rates including unsampled taxa was already introduced by Nee *et al.* (1994) [8]. Later, the introduction of the piecewise-constant, or episodic, birth-death model (EBD) [15] enabled biologists to perform likelihood-based comparison of birth and death rates' functional forms while accounting for incomplete taxon sampling (see Höhna (2015) for a review of the EBD and comparison to the work by Nee *et al.* (1994) [16, 8]). The EBD model was extended to work in contexts with serial samples (*e.g.*, fossils) and possibly sampled ancestors [17, 18].

The EBD model divides time into a finite number of intervals and assigns each interval its own set of birth and death rates. The first uses of the EBD model assumed that *a priori* birth and death rates in each interval are independent and identically distributed (iid) [17, 18]. This assumption means that the number of intervals (or epochs) needs to be kept small to keep estimation reasonably precise and to avoid overfitting. Further work on Bayesian modeling using the EBD employed temporally autocorrelated models derived from discretizing Ornstein-Uhlenbeck and Brownian motion processes [19, 20, 21], which

provides smoothing and allows the number of episodic intervals to be larger. May *et al.* (2016) propose another EBD model, where birth and death rates change at an unknown, Poisson distributed number of change-points [22]. Wu (2014) uses a similar change-point model [23]. These random change-point models drastically increase the dimensionality of the parameter space and make it variable, requiring complicated reversible-jump Markov chain Monte Carlo (MCMC) [24] algorithms to sample from the posterior distribution of the number of change-points. However, many other Bayesian nonparametric approaches for estimating functional forms have not been applied to EBD modeling.

Parametric and nonparametric estimation of functional forms is not unique to birth-death processes. For example, population genetics researchers have developed a rich toolbox of Bayesian nonparametric approaches to estimate changes of the effective population size in a neighboring class of coalescent models [25]. In fact, EBD models closely resemble piecewise constant effective population size coalescent models [26, 27, 28]. However, EBD models still lack Bayesian regularization approaches that control the potentially high number of model parameters. For coalescent models, such Bayesian regularization is accomplished by Gaussian Markov random field (GMRF) prior distributions, which underly the skyride [27] and skygrid [28] methods, and by their recently developed analog, the horseshoe Markov random field (HSMRF) [29]. These models provide a rich framework for building more complicated models with covariates [30] and are amenable to computationally efficient MCMC sampling techniques. Our goal is to bring GMRF and HSMRF prior distributions to EBD models and to test their performance.

We implement birth-death models that use GMRF and HSMRF prior distributions for the birth and/or death rates in the statistical phylogenetic software platform `RevBayes` [31]. This implementation allows us to jointly estimate birth-death parameters, phylogeny, and other (nuisance) parameters in a Bayesian framework. We develop an efficient, tuning-parameter-free MCMC algorithm for sampling high dimensional parameter vectors associated with GMRF- and HSMRF-based models. We also devise a framework for setting the global scale parameter—the key parameter controlling the degree of parameter regularization (also called shrinkage)—for both models in terms of the implied prior on the number of "effective" rate shifts. We note that our GMRF-based model is closely related to the work of Duplessis (2016), Condamine *et al.* (2018), and Silvestro *et al.*, who use prior distributions that fall into the class of GMRF distributions, but our work differs from these approaches in important computational and statistical details [19, 20, 21]. Namely, we develop a tuning-parameter free MCMC algorithm that enables efficient exploration of the high dimensional parameter vectors associated with GMRF- and HSMRF-based models and introduce a framework for setting the key hyperprior in an interpretable manner. To the best of our knowledge, this is the first instance of applying HSMRF prior distributions to birth-death processes. We test both GMRF-based and HSMRF-based models on a variety of simulated diversification scenarios, and then apply them to a species-level and an epidemiological dataset. We find that both models are capable of inferring variable diversification rates and correctly rejecting variable models in favor of effectively constant models. In general, in line with previous analyses of HSMRF prior distributions [32, 29], we see that the HSMRF-based model has higher precision than its GMRF counterpart, with little to no loss of accuracy. In empirical applications, we show that these models are useful for detecting a speciation-rate decline in the Australian gecko clade Pygopodidae and a complex pattern of variation in the rate of infection of HIV subtype A in Russia and Ukraine.

Methods

Our data, $\mathbf{D}$, take the form of a multiple sequence alignment. We assume that the alignment $\mathbf{D}$ has come from the following probabilistic model. First, a tree is generated from a time-varying birth-death process governed by time varying birth rate $\lambda(t)$, death rate $\mu(t)$, serial sampling rate $\phi(t)$, conditional probability of death upon sampling $r(t)$ (primarily for phylodynamic applications to represent becoming noninfectious when diagnosed and/or treated), and vector of sampling probabilities $\boldsymbol{\Phi}$ (with associated sampling times $\boldsymbol{t_\Phi}$, we refer to these as event sampling times). Time starts at 0 at the most recent event (or serial) sampling time and increases into the past, such that the oldest bifurcation in the tree is t_o, the time of origin (here also the time of the most recent common ancestor) [8]. We call the resulting reconstructed tree T, and it consists only of lineages whose descendants were sampled. On each branch of T, evolution proceeds at a rate governed by a molecular clock model [33, 34, 35]. Columns in the sequence alignment evolve independently under a continuous-time Markov chain (CTMC) model, which commonly is referred to as the substitution model. We use the generalized time reversible substitution model [36] with discretized gamma-distributed rate variation across sites (GTR+G) [37]. For notational simplicity we refer to the vector of substitution and clock model parameters as $\boldsymbol{\theta}$, and we discuss the specifics of these models on a case-by-case basis. We can write the phylogenetic likelihood—probability of the alignment under the CTMC substitution model—as $\Pr(\boldsymbol{D} \mid \boldsymbol{\theta}, T)$. All major statistical phylogenetic software platforms can efficiently compute phylogenetic likelihood via a dynamic programming algorithm, known as the Felsenstein pruning algorithm [38]. We will use the `RevBayes` implementation of this algorithm [31].

In Bayesian inference we need prior distributions for $\lambda(t)$, $\mu(t)$, $\phi(t)$, $r(t)$, $\boldsymbol{\Phi}$, and t_o, as well as prior distributions on $\boldsymbol{\theta}$. We assume that $\boldsymbol{t_\Phi}$ is fixed *a priori* by the user. For our purposes there will only be one time at which event sampling may occur: the present day, making $\boldsymbol{t_\Phi}$ a scalar $t_\Phi = 0$. Notice that the prior on T conditional on $\lambda(t)$, $\mu(t)$, $\phi(t)$, $\boldsymbol{\Phi}$, and t_o is already specified by the birth-death process. The choice of $\Pr(t_o)$ depends on the particular group of taxa studied, and the form of $\Pr(\boldsymbol{\theta})$ on the specifics of the group and the data, so we discuss these on a case-by-case basis. The posterior distribution takes the following form:

$$\begin{aligned}\Pr(\boldsymbol{\theta}, T, t_o, \lambda(t), \mu(t), \phi(t), r(t), \boldsymbol{\Phi} \mid \boldsymbol{D}) \propto\ & \Pr(\boldsymbol{D} \mid \boldsymbol{\theta}, T)\ \Pr(\boldsymbol{\theta})\ \Pr(t_o) \\ & \times\ \Pr(T \mid \lambda(t), \mu(t), \phi(t), r(t), \boldsymbol{\Phi}, \boldsymbol{t_\Phi}, t_o) \\ & \times\ \Pr(\lambda(t))\ \Pr(\mu(t))\ \Pr(\phi(t))\ \Pr(r(t))\ \Pr(\boldsymbol{\Phi}).\end{aligned}$$

In macroevolutionary analyses including extant species, there is a single event sampling at the present ($t = 0$) with known probability Φ_0 [39]. In phylodynamic analyses, there may be no event-sampling, thus we set $\Phi_0 = 0$. We make the simplifying assumptions that the serial sampling rate is a constant, $\phi(t) = \phi$, and that the conditional probability of becoming noninfectious upon sampling is a known constant, $r(t) = r$. For any macroevolutionary dataset $r = 0$, and in our phylodynamic application we assume $r = 1$. Additionally, in our macroevolutionary example there are no serial samples, hence $\phi = 0$ (in which case r is not a parameter of the simplified the model). In all analyses we make the additional simplifying assumption that the death rate is a constant $\mu(t) = \mu$, and place a mean-0.1 exponential prior on μ. In phylodynamic applications, there is often prior information that enables the

use of informative prior distributions on ϕ and μ, which we discuss in a later section. The remaining piece of the puzzle, and our contribution in this paper, is in the specification of $\Pr(\lambda(t))$, for which we use Markov random field models. (Note that our implementation and theory of the GMRF and HSMRF can be applied to all time-varying rates; we focused on the birth rate only for simplicity.) Our simplified posterior distribution takes the following form:

$$\begin{aligned}\Pr(\boldsymbol{\theta}, T, t_o, \lambda(t), \mu, \phi, r, \mid \boldsymbol{D}) \propto\ & \Pr(\boldsymbol{D} \mid \boldsymbol{\theta}, T)\ \Pr(\boldsymbol{\theta}) \\ & \times\ \Pr(T \mid \lambda(t), \mu, \phi, r, \Phi_0, t_o) \\ & \times\ \Pr(\lambda(t))\ \Pr(\mu)\ \Pr(\phi)\ \Pr(r)\ \Pr(t_o).\end{aligned}$$

We note that historically Φ_0 has been called ρ, and $\boldsymbol{\Phi}$ has sometimes been called $\boldsymbol{\rho}$. However, $\boldsymbol{\rho}$ has been used to refer to both sampling probabilities [18] and mass extinction probabilities [15, 16, 22], which creates room for confusion.

Horseshoe Markov random field prior. We define the birth rate on the log scale, $\lambda^*(t) = \ln(\lambda(t))$. Following Stadler (2011), we discretize time into n intervals and assume that $\lambda^*(t) = \lambda_i^*$ when t is in the ith time interval, using the parameterization $\boldsymbol{\lambda^*} = (\lambda_1^*, ..., \lambda_n^*)$ [15]. An HSMRF is a model in which $\lambda_{i+1}^* \mid (\lambda_i^*, \gamma) \sim \text{Horseshoe}(\lambda_i^*, \gamma)$, where γ is a global scale parameter that controls the smoothness of the overall field. The horseshoe is a distribution used as a shrinkage prior, a statistical tool designed to discern signal from noise [40]. In our case, the HSMRF exerts strong prior belief that $\lambda_{i+1}^* \approx \lambda_i^*$; in other words, we do not expect much change in the birth rate between adjacent intervals. However, the horseshoe distribution also has fat (Cauchy-like) tails, which allow the HSMRF to behave like a spike-and-slab mixture model [41], giving the HSMRF a property known as local adaptivity. The horseshoe distribution needs an auxiliary variables σ_i and is represented as a scale mixture of normal distributions

$$\begin{aligned}\sigma_i &\sim \text{halfCauchy}(0, 1), \\ \lambda_{i+1}^* \mid \sigma_i &\sim \text{Normal}(\lambda_i^*, \sigma_i^2\gamma^2).\end{aligned}$$

This mixture representation helps explain the local adaptivity of the HSMRF: one or a few (relatively) large changes can be handled by large σ_i without increasing γ. We place a $\text{Normal}(\ln(\hat{\lambda}), \xi)$ prior distribution on λ_1^*, where $\hat{\lambda}$ is a rough estimate of net diversification rate. When there are extant lineages in the tree, $\hat{\lambda}$ is the maximum likelihood estimator for the net diversification rate, d, from Magallon and Sanderson (2001) [42]. When there are no extant lineages in the tree, we put a lower bound on the net diversification rate using the number of births in the tree (excluding the origin or root as appropriate), B_{obs}. The expected net number of births observed in a tree by time t is given by $\mathbb{E}(B_t) = 2e^{t \cdot d} - 2$ if starting at the time of the most recent common ancestor, and $\mathbb{E}(B_t) = e^{t \cdot d} - 1$ if starting with a single lineage. By the method of moments, we can obtain (for the case of starting with the MRCA) $\hat{d} = (\ln(B_{obs} + 2) - \ln(2))/t$, where t is the age of the tree. As not all lineages that are born will be sampled in our tree, the number of observed births will be an underestimate of the number of births and our rate will be underestimated, but it will suffice. In practice, when setting the prior for the first birth rate, we use $\xi = 1.17481$, producing, *a priori*, $\Pr(\hat{\lambda}/10 \leq \lambda_1 < 10\hat{\lambda}) = 0.95$. We use a halfCauchy(0, ζ) prior on γ, where ζ is the global shrinkage prior, and we discuss how to set it in a later section. A list of all parameters in the model and their prior distributions can be found in Table 1. The

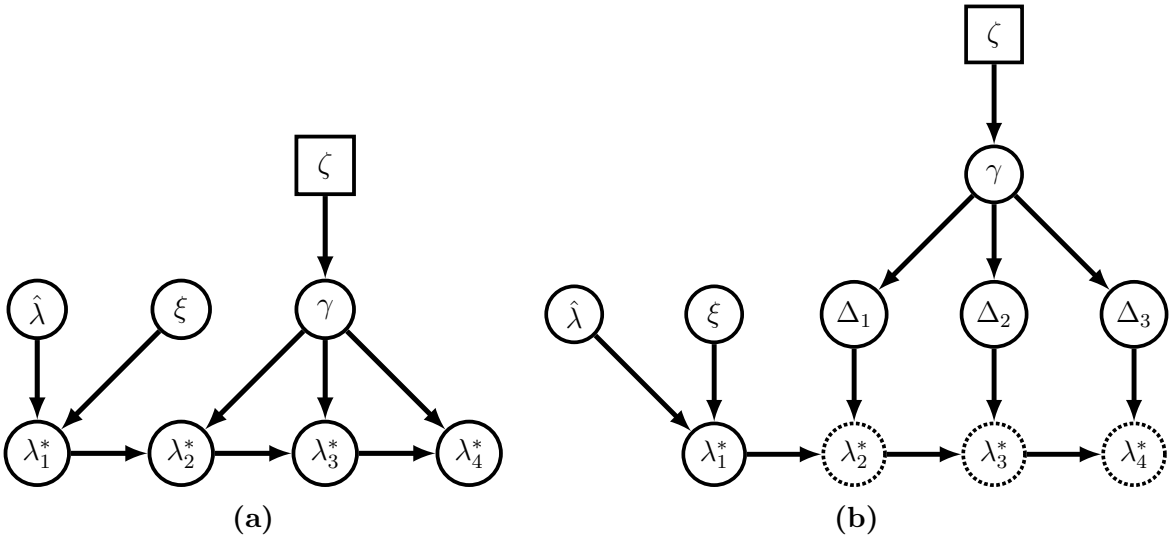


Figure 1. Simplified versions of our MRF-based models, shown as a grid of size 4. To highlight the structural similarities between the GMRF- and HSMRF-based models, we draw the directed acyclic graph (DAG) as if we had an analytical form of the horseshoe distribution (that is, we omit the local scale parameters of the HSMRF). In (a), we show the idealized general MRF model, while in (b), we show how we can reparameterize the model in terms of a vector $\boldsymbol{\Delta}$ of independent random variables. This reparameterization greatly improves the efficiency of MCMC sampling. When drawing the model as a DAG, squares represent constant values, closed circles stochastic values, and open circles deterministic transformations of other nodes.

full posterior distribution of our HSMRF-based model parameters is,

$$\Pr(T, t_o, \boldsymbol{\theta}, \boldsymbol{\lambda}^*, \mu, \gamma, \boldsymbol{\sigma} \mid \boldsymbol{D}) \propto \Pr(\boldsymbol{D} \mid \boldsymbol{\theta}, T)\ \Pr(\boldsymbol{\theta})\ \Pr(T \mid \boldsymbol{\lambda}^*, \mu, t_o, \rho)\ \Pr(\boldsymbol{\lambda}^* \mid \gamma, \boldsymbol{\sigma}) \times\ \Pr(\boldsymbol{\sigma})\ \Pr(\gamma)\ \Pr(\mu)\ \Pr(t_o).$$

We approximate the above posterior distribution using the following MCMC strategy. We use standard Metropolis-Hastings kernels available in `RevBayes` to update the tree T, time of the root t_o, substitution model parameters $\boldsymbol{\theta}$, and extinction rate μ, and the first log-speciation rate, λ_1^* (see Höhna *et al.* (2017) for a description of the standard `RevBayes` Metropolis-Hastings kernels [43]). Since vectors $\boldsymbol{\lambda}^*$ and $\boldsymbol{\sigma}$ can be high dimensional, we update the vectors in blocks. First, we reparameterize the model to work with the first order differences $\Delta_i = \lambda_{i+1}^* - \lambda_i^*$, $i = 1, \ldots, n-1$ instead of $\boldsymbol{\lambda}^*$ (see Figure 1). This allows us to sample the vector $\boldsymbol{\Delta}$, where all elements are *a priori* independent, instead of the vector $\boldsymbol{\lambda}$ where the adjacent values are highly correlated, greatly increasing the efficiency of the MCMC. Further, under the GMRF and the hierarchical representation of the HSMRF, all the $\boldsymbol{\Delta}$ are Normal random variables, enabling us to employ an elliptical slice sampler [44] for $\boldsymbol{\Delta} = (\Delta_1, \ldots, \Delta_{n-1})$. The (conditional) normality of the $\boldsymbol{\Delta}$ also allows us to employ a Gibbs sampler for γ and $\boldsymbol{\sigma}$, which allows us to adequately sample the tails of the posterior distribution. Without this elliptical slice sampler and Gibbs sampler combination, MCMC for these models fails to converge to the posterior distribution. We defer a more thorough discussion of our MCMC strategy to the supplemental methods.

Gaussian Markov random field prior. Our GMRF-based model can be seen as a special case of an HSMRF-based model where $\sigma_1 = \cdots = \sigma_n = 1$, meaning $\lambda_{i+1}^* \mid \lambda_i^*, \gamma \sim$

Normal(λ_i^*, γ^2). The lack of local scale parameters makes the GMRF-based model a non-locally-adaptive model. For the GMRF-based model, the posterior distribution is

$$\Pr(T, t_o, \boldsymbol{\theta}, \boldsymbol{\lambda}^*, \mu, \gamma, \mid \boldsymbol{D}) \propto \Pr(\boldsymbol{D} \mid \boldsymbol{\theta}, T)\ \Pr(\boldsymbol{\theta})\ \Pr(T \mid \boldsymbol{\lambda}^*, \mu, t_o, \rho)\ \Pr(\boldsymbol{\lambda}^* \mid \gamma) \times \Pr(\gamma)\ \Pr(\mu)\ \Pr(t_o).$$

The MCMC algorithm to approximate the above posterior distribution is the same as for the HSMRF-based model, except we do not need to update the vector $\boldsymbol{\sigma}$.

Setting the prior on the global scale parameter. In both HSMRF and GMRF-based models, the global scale parameter, γ, controls the smoothness of the overall field, with smaller values favoring less variability. Following Faulkner *et al.*, we take a hierarchical approach and place a prior distribution on the global scale parameter, such that $\gamma \sim$ halfCauchy$(0, \zeta)$ [29]. We choose ζ in terms of s_e, which is the number of "effective shifts" in the birth rate and we define an effective shift to be an event $\{\lambda_{i+1}/\lambda_i < 1/\epsilon$ or $\lambda_{i+1}/\lambda_i \geq \epsilon\}$. That is, an effective shift is the event where two adjacent birth rates are different by more than ϵ-fold. We set $\epsilon = 2$, reflecting that a 2-fold change in the birth rate is biologically meaningful and statistically detectable. Setting ζ is then accomplished implicitly by setting the prior expected number of effective shifts, $\mathbb{E}[s_e]$, which is more interpretable than ζ. In this setup, $\mathbb{E}[s_e]$ is the expectation of a binomial random variable with probability p that there is an effective shift between λ_{i+1} and λ_i. Since we can compute p given a particular value of ζ, and since there is no obvious closed form solution, we use numerical methods to solve for ζ. Code to calculate ζ from $\mathbb{E}[s_e]$ is available in the GitHub repository, see section "Code and data availability."

We find that in practice $\mathbb{E}[s_e] = \ln(2)$ produces a prior that is reasonably conservative yet flexible. This yields $\zeta_{HSMRF} \approx 0.0021$ for HSMRF-based models and $\zeta_{GMRF} \approx 0.0094$ for GMRF-based models. An alternative approach to specify ζ examines the implied prior distribution on λ_n/λ_1, *i.e.*, the prior distribution on the fold change across the entire process. *A priori*, for the HSMRF on a grid size $n = 100$, $\mathbb{E}[s_e] = \ln(2)$ leads to $\Pr(0.5 \leq \lambda_n/\lambda_1 < 2) \approx 0.76$ and $\Pr(0.1 \leq \lambda_n/\lambda_1 < 10) \approx 0.9$. While we do not use this approach to set ζ, it shows that our chosen value for ζ focuses the prior mass on reasonable regimes while leaving room for rather substantial amounts of change. For completion, in the supplementary materials we provide more context for these choices of prior, including an alternative choice of $\mathbb{E}[s_e]$ following Drummond and Suchard (2010), and examine two additional frameworks, bounding the marginal variance of the GMRF and HSMRF (explored by Sørbye and Rue (2014) and Faulkner *et al.* (2018)), and bounding the effective number of parameters in the model (explored by Piironen and Vehtari (2017)) [45, 46, 29, 47].

Table 1. All parameters in our models, their prior distributions, and their role in the model. In phylodynamic applications, there may be more information to set the death rate, μ, and the sampling rate, ϕ. The sampling fraction at present, Φ_0 and the probability of death upon sampling, r are taken to be known *a priori*. The age of the tree, t_{or} is fixed to the observed height if the tree is data, else it is a variable with the prior determined by the user. For models with 100 intervals, we set $\zeta = 0.0021$ for HSMRF-based models and $\zeta = 0.0094$ for GMRF-based models. The GMRF-based model lacks local scale parameters $\boldsymbol{\sigma}$. We adopt an empirical Bayes approach to setting the prior on the first log-birth-rate using, using a guess at the tree age and the number of tips to obtain $\hat{\lambda}_1^*$ and in practice set $\xi = 1.17481$.

Parameter	Prior	Role
μ	Exponential(10)	death rate
ϕ	Exponential(10)	serial sampling rate
Φ_0	Fixed	sampling fraction at present
r	Fixed	probability of death upon sampling
t_{or}	User choice	age of tree
ζ	Fixed(0.0021) or Fixed(0.0094)	global scale hyperparameter
γ	halfCauchy(0,ζ)	global scale of the MRF
σ_i	halfCauchy(0,1)	local scale of HSMRF
λ_1^*	Normal($\ln(\hat{\lambda}), \xi$)	log-scale birth rate at present
$\lambda_{i>2}^*$	Normal(λ_{i-1}^*,$\gamma^2\sigma_i^2$)	log-scale birth rates

Results

Simulation study. To understand statistical properties of both random field birth-death models, we perform a (nonexhaustive) simulation study. Some of the most debated questions in species diversification concern diversification-rate decreases [48, 49, 9, 50, 51, 52, 53], and the ability to detect effective epidemiological interventions hinges on the ability to accurately estimate decreases in the rate of infection, so we consider simulation scenarios where the birth-rate declines through time. We devise a series of piecewise-linear functions $\lambda(t)$ in which the birth rate decreases through time. For each model, we use the R package `TESS` [54] to simulate 100 trees conditioned on the tree age ($t_o = 100$), with complete species sampling ($\Phi_0 = 1$), and choosing values for $\lambda(t)$ and μ to give an expectation of 200 species/tips at the present. Given the underdeveloped infrastructure for simulating serially-sampled trees, we focus on trees where all samples are at the present day ($\phi = 0$), but see Barido-Sottani *et al.* (2019) for recent developments [55]. When analyzing these simulations, we take the tree and sampling fraction to be known. Treating the tree as data allows us to focus on the performance of the random field birth-death models without worrying about potential sources of bias during time-calibrated tree estimation [56]. Taking the tree as data also mirrors the predominant historical usage of models of rate variation, detecting variation in trees previously inferred [11, 2, 3, 15].

We assess model performance by looking at four summaries of the inferred birth-rate trajectories. We take as our estimate of $\lambda(t)$ the birth-rate trajectory defined by the median posterior of each birth rate λ_i. First, to quantify bias we use the Mean Absolute Deviation (MAD) of the estimated birth-rate trajectory, given by $(1/n)\sum_i^{n-1}|\hat{\lambda}_i - \lambda_i|$. Second, we look at the Mean Absolute Sequential Variation (MASV) of the estimated trajectory, the gross change inferred, given by $(1/(n-1))\sum_i^{n-1}|\hat{\lambda}_{i+1} - \hat{\lambda}_i|$. Where the simulated trajectory is

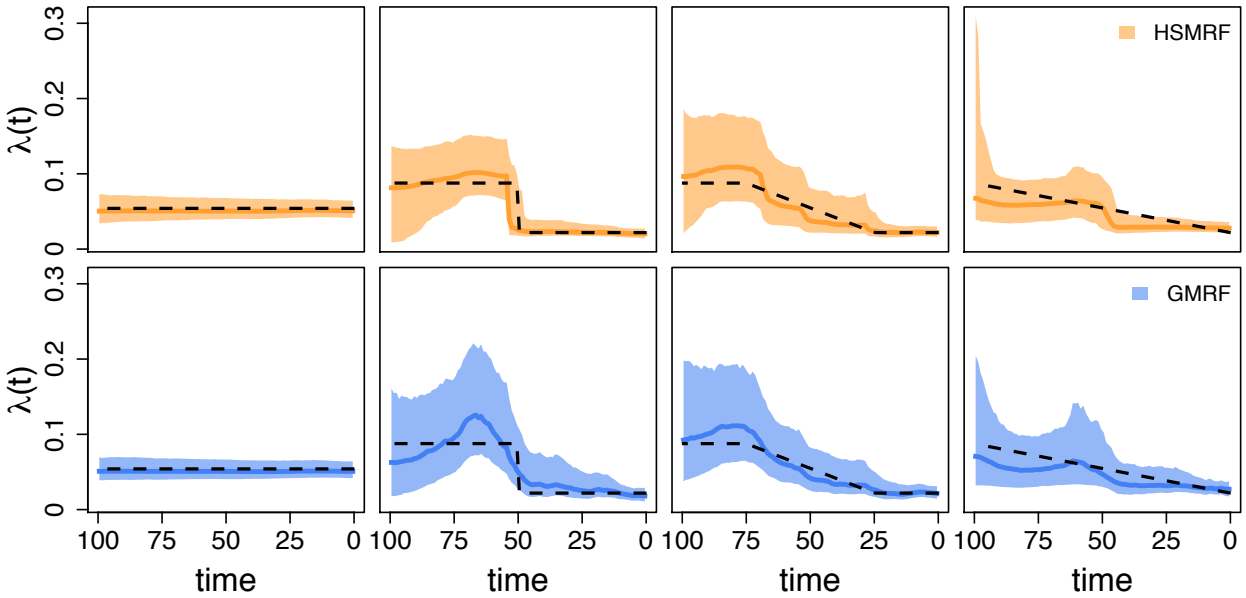


Figure 2. Inferred birth-rate trajectories from four individual simulations. The dashed line is the true simulating birth rate, the dark colored line is the posterior median trajectory (the median is taken separately for each grid cell), and the shaded region show the 90% Credible Interval (CI) for the rate. The leftmost column is from the constant-rate simulations, and the right three columns demonstrate the effect of changing the shift duration (the length of the tree over which the birth rate changes), from an instantaneous shift to a constant change model. When we focus instead on the location of the shift, all simulations are piecewise-constant as in the second column. In each column, we show the simulation with the most average performance measured in terms of the Mean Absolute Deviation of both the GMRF and HSMRF.

variable, it is more useful to consider the relative MASV (RMASV), MASV($\hat{\lambda}$)/MASV(λ). If RMASV > 1, the inferred trajectory is more variable than the true trajectory, and if RMASV < 1, it is less variable. Third, we look at the fold change (FC) of the estimated trajectory, $\hat{\lambda}_n/\hat{\lambda}_1$. This will show us if we capture the presence of an overall change in the birth rate, even if we fail to capture the specific pattern. Finally, we look at the average width (across all estimated birth rates, λ_i) of the 90% posterior credible interval as a measure of precision, $(1/n)\sum_1^n(\hat{\lambda}_i^{0.95} - \hat{\lambda}_i^{0.05})/\hat{\lambda}_i$. This measure, which we call relative precision (RP), is both more interpretable than the raw credible interval and more comparable across simulations.

Constant-rate simulations. Our first simulations are from a constant-rate diversification model, such that $\lambda(t) = \lambda$. This allows us to test the tendency towards what could be termed "false positives," the detection of spurious rate variation. Both the GMRF and HSMRF birth-death models can produce effectively constant-rate trajectories, though their flexibility is not without minor drawbacks. Ridge plots of performance measure histograms across all simulations are shown in Figure 3. The trajectories estimated by both models have low MAD, FC ≈ 1, and small RP, indicating generally good performance. Further, compared to fitting constant-rate models, the increase in MAD from inferring the variable-rate models is negligible and the decrease in precision is small (Supplementary Figure S1). There are two primary drawbacks to using these models to fit constant-rate trajectories. The models

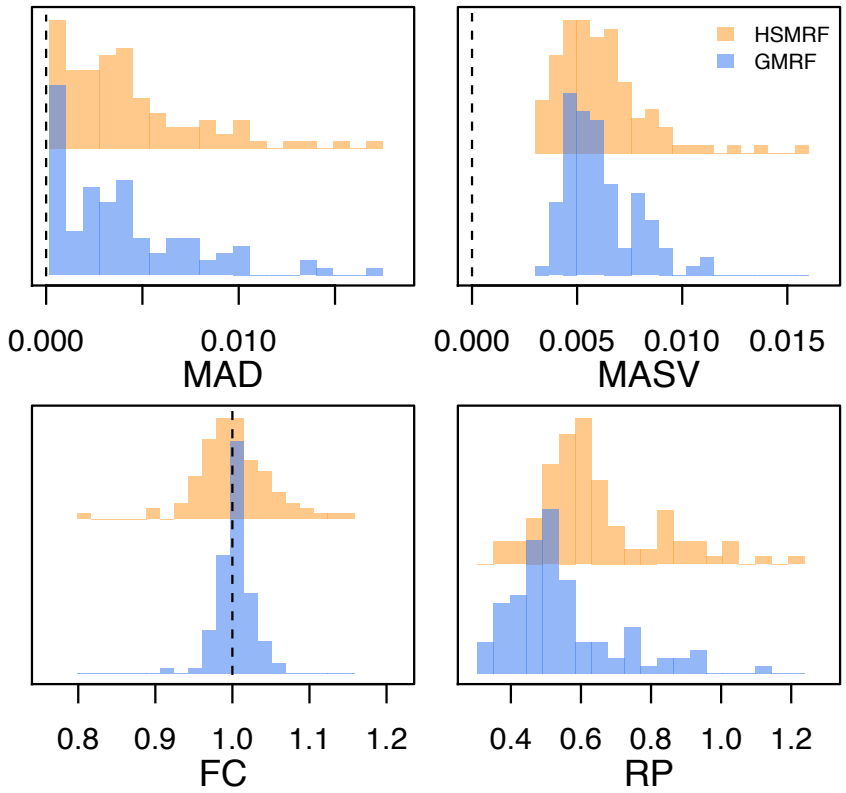
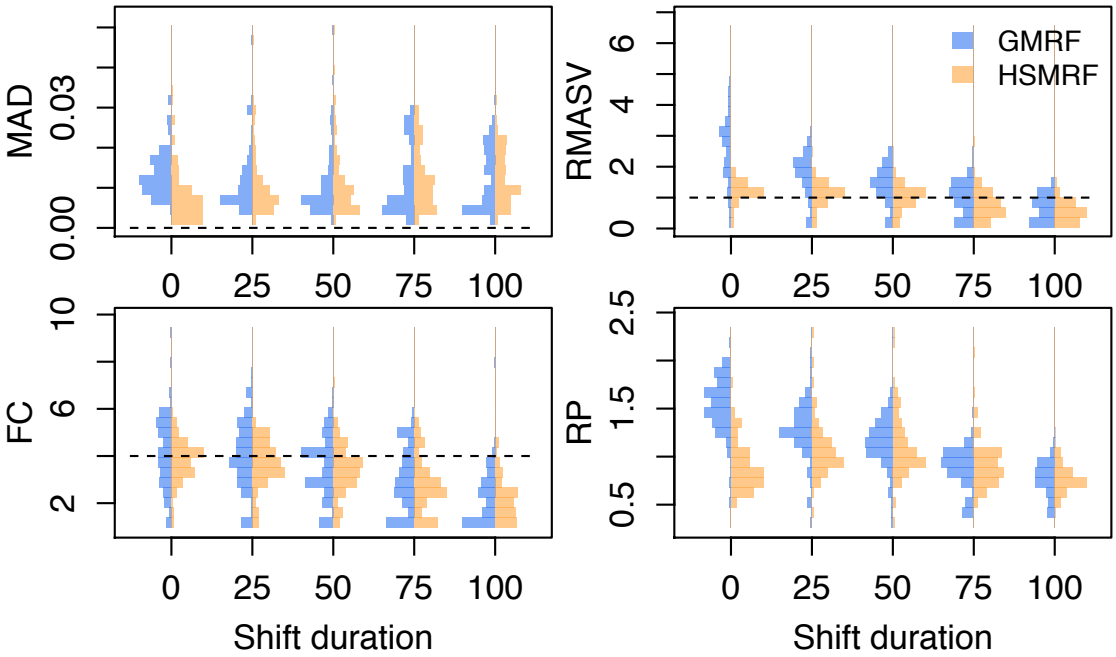


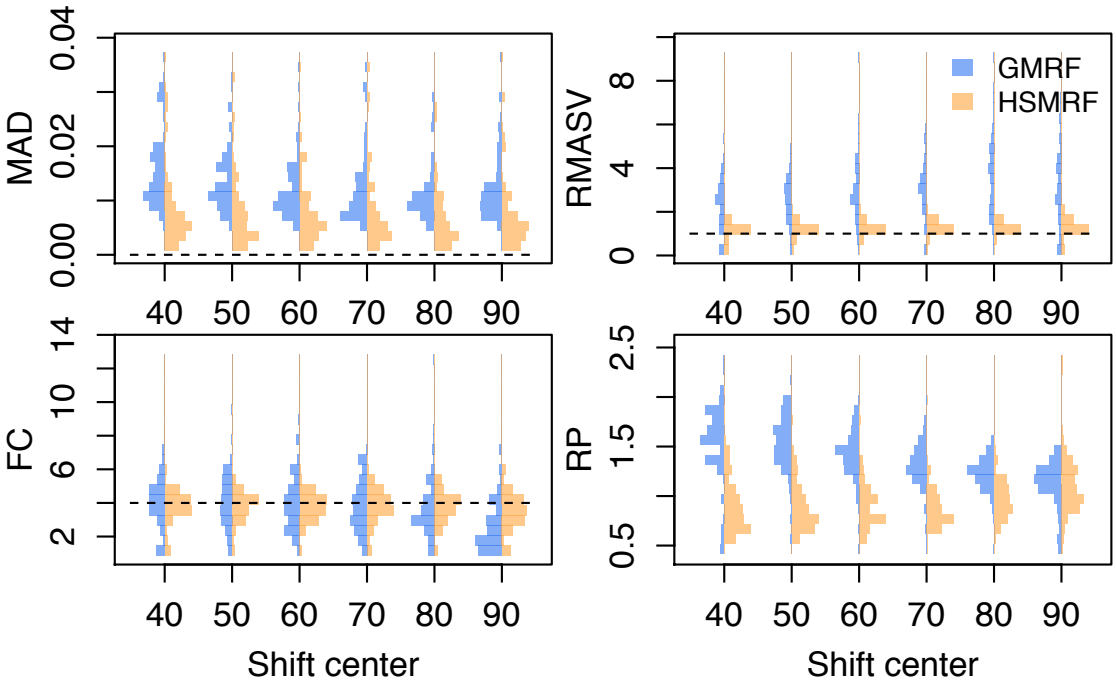
Figure 3. Performance of the models on simulated constant-rate datasets. MAD measures the error in the estimated trajectory. MASV measures the total amount of change relative in the trajectory, horizontal line at true value for reference. FC measures the fold change from present to past, dashed line at true value for reference. RP is a measure of precision, the average width of the 90% Credible Interval relative to the birth rate.

occasionally fit trajectories where the inferred change between the beginning and end of the process does not appear negligible. However, comparisons to the prior make it quite clear that both the GMRF and HSMRF are fitting effectively constant-rate trajectories. For both models roughly 99% of the prior MASV is greater than 0.01, while roughly 5% of the posterior MASV is greater than 0.01, further indicating that the models are producing effectively constant trajectories. The HSMRF and GMRF produce very similar average error and fold change, though the distributions of these metrics for the GMRF are more tightly focused around the target values (MAD of 0, FC of 1), and the GMRF has slightly tighter credible intervals. The GMRF generally estimates narrower credible intervals, while the HSMRF generally estimates trajectories with lower MASV.

Piecewise linear simulations. Our primary time-variable simulations examine the impact of the shift duration, *i.e.*, the amount of time over which the birth-rate changes. To examine this, we build a piecewise-linear birth-rate function, where the birth rate is λ_1 for $100 \geq t > t_1$, λ_2 for $t \leq t_2$, and a linear interpolation for $t_1 \geq t > t_2$. We center the shift at 50 ($(t_1 + t_2)/2 = 50$), and simulate shift durations $(t_2 - t_1)$ of 0%, 25%, 50%, 75%, and 100% of the age of the tree. All simulation parameters are recorded in Supplementary Table S1.



(a)



(b)

Figure 4. The effect on parameter inference of (a) changing the (four-fold) rate shift from instantaneous to the entire length of the trajectory and (b) changing the center of an instantaneous (four-fold) rate shift. MAD measures the error in the estimated trajectory. Relative MASV measures the total amount of change relative to the true MASV, horizontal line at 1 for reference. FC measures the fold change from present to past, dotted line at true value for reference. RP is a measure of precision, the average width of the 90% Credible Interval relative to the birth rate.

The HSMRF-based model performs better when the shift is fast (when $t_2 - t_1$ is small), and the GMRF-based model performs better when the shift is slow (when $t_2 - t_1$ is large, Figure 4a). For the HSMRF-based model, the MAD statistic is lower and both the MASV and FC statistics are closer to the truth when the true shift is shorter. In contrast, for the GMRF-based model, the MASV statistic gets closer to the truth, *i.e.*, the error decreases, and the RP statistic gets narrower as the shift duration increases. Both models though have difficulty with continuous, slow declines where they have a tendency to underestimate the total change. In some simulations, both models effectively fit constant-rate trajectories. The HSMRF-based model also has a tendency towards fitting steep shifts even in cases where the true shift is slow (Figure 2).

Piecewise constant simulation. We also examine the effect of varying the location of the instantaneous birth-rate shift. To do this, we build a piecewise-constant birth-rate function, where the birth rate is λ_1 for $100 \leq t < t_{shift}$, λ_2 for $t \leq t_{shift}$; we simulate $t_{shift} = 90, 80, ..., 40$ (see for example Figure 2 second panel). The location of the rate shift should influence the capacity for detection by altering the expected number of births in the pre-shift portion of the tree. As the shift moves from past to present, for the HSMRF-based model the MAD statistic decreases and the RP statistic gets smaller (Figure 4b). However, for the GMRF-based model, as the shift becomes more recent, the RMASV statistic becomes increasingly inflated, indicating trajectories that are too variable. This is due to the GMRF-based model estimating rather substantial variation in the more ancient portions of the tree. The HSMRF-based model outperforms the GMRF-based model in most statistics and for most shift locations.

Shift magnitude. The magnitude of the birth-rate shift should also impact the capacity for detection, so we simulate shifts of two magnitudes for all scenarios outlined above. For our low magnitude shift, we simulate a two-fold change, and for our larger shift, we simulate a four-fold change. Unsurprisingly, it is harder to detect smaller shifts. Results for different functional forms are qualitatively similar between shift magnitudes, so we present only the results for the four-fold shifts in Figure 4. In many cases with two-fold shifts, the inferred trajectory was effectively constant. Thus in general the MAD statistic is higher, the RMASV, FC, and RP statistics are lower. Supplementary Figures S2 and S3 give full simulation results for the two-fold case comparable to Figure 4.

Empirical analysis of Pygopodidae. Pygopodidae is a clade of approximately 46 legless geckos [6]. Recently, Brennan *et al.* (2017) used several birth-death models to investigate the history of diversification in this group, examining trends in speciation over time using a posterior sample of 100 phylogenies estimated via BEAST 1.8.3 [6, 57]. The majority of their analyses revealed a drastic speciation-rate decrease in the recent (2-5 million years) past, though there was some disagreement between methods over the significance and timing of the shift. Here we revisit the question of significance and timing of the birth-rate shift in full joint analyses of phylogeny and both our GMRF and HSMRF birth-death models. Details of the substitution and clock models are available in the supplemental materials, as are details of MCMC convergence diagnostics performed.

Our dataset includes 41 out of 46 representatives of Pygopodidae, which we used to set the species sampling fraction, $\Phi_0 = 0.89$. We employed calibrations on the same nodes as Brennan *et al.* (2017), resulting in a calibration for the root node and one each on the genera *Delma* and *Apprasia* [6]. Following Brennan *et al.* (2017), we place a Uniform(19.5, 29.0)

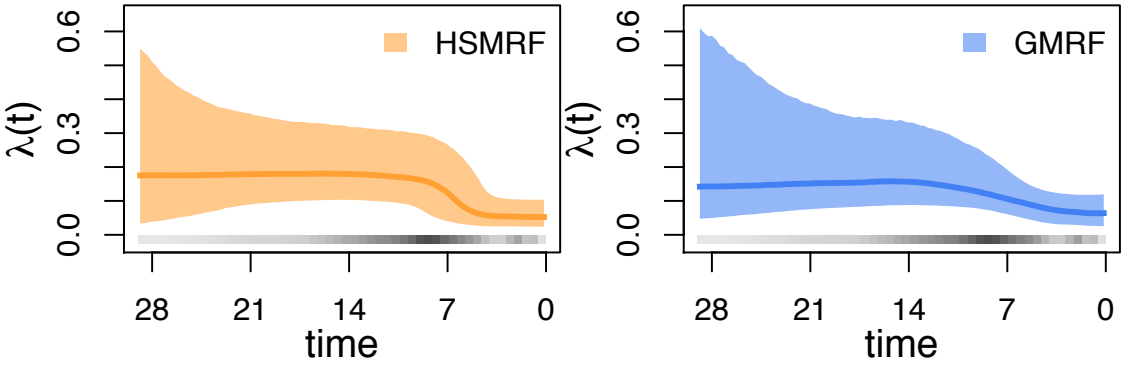


Figure 5. Analyses of the Pygopodidae dataset. Plotted are posterior median trajectories (dark lines) and 90% credible intervals (shaded regions). Time is in millions of years before the present day. In grey is a heatmap of the inferred divergence times.

prior on the root age [6]. To set up our grid, we thus choose to divide the interval $[0, 29]$ into 100 intervals/epochs of equal length.

GMRF and HMRF-based models produce a clear visual signature of a diversification-rate decrease (Figure 5), with a higher rate from the origin of the clade up until at least 12 ma, and a lower rate afterwards. The HSMRF-based model favors a steeper decrease ending approximately 6 ma, while the GMRF-based model favors a much slower decline that starts approximately 14 ma and lasts until approximately 2 ma. Over the range [14ma, 2ma], the HSMRF estimates a 3.43-fold decrease (90% Credible Interval (CI) [1.12, 8.49]), while the GMRF estimates a 2.41-fold decrease (90% CI [1.00, 7.58]). The HSMRF produces 90% credible intervals for the speciation rate that are generally narrower than the GMRF-based model's intervals. The behavior of both models is in line with the simulation results for fast to intermediate shifts, with the HSMRF inferring a faster shift of larger magnitude with tighter credible intervals than the GMRF-based model.

Given that the posterior distributions of adjacent birth rates are highly correlated, testing for a shift in a specific interval from λ_i to λ_{i+1} could suggest there is no shift even when there is clearly a shift present in the overall trajectory. However, we can avoid this issue by testing hypotheses over longer timespans. The Bayes Factor [58] in support of an s-fold decrease between t_{start} and t_{end} is given by,

$$\frac{\Pr(\lambda(t_{start})/\lambda(t_{end}) < s \mid \boldsymbol{D})}{\Pr(\lambda(t_{start})/\lambda(t_{end}) \geq s \mid \boldsymbol{D})} \Big/ \frac{\Pr(\lambda(t_{start})/\lambda(t_{end}) < s)}{\Pr(\lambda(t_{start})/\lambda(t_{end}) \geq s)}.$$

For an s-fold increase, the inequalities are reversed. If we are interested in the evidence of a shift over the range [2ma, 12ma], we can compare the speciation rates in the appropriate intervals for a given shift size s. For our grid, the 7th interval ends at 2.03ma, while the 43rd starts at 12.18ma, and we would test hypotheses regarding λ_7/λ_{43}. Then all we need to know are the posterior and prior probabilities of observing a shift of at least s (or less than s if testing a decrease). If we were instead interested in testing simply for the presence of a shift, then we choose $s = 1$. Under both our HSMRF-based and GMRF-based models, the prior probability $\Pr(\lambda_i/\lambda_j < 1 \mid HSMRF) = 0.5$ (for any $i \neq j$), making the denominator (the prior odds) 1 and only requiring us to compute the numerator (the posterior odds). For the HSMRF-based model, $\Pr(\lambda_7/\lambda_{43} < 1.0 \mid \boldsymbol{D}, HSMRF) = 0.98$, and the 2ln(BF) in favor of a birth-rate shift over this interval is 7.73 (using the nomenclature of Kass and Raftery

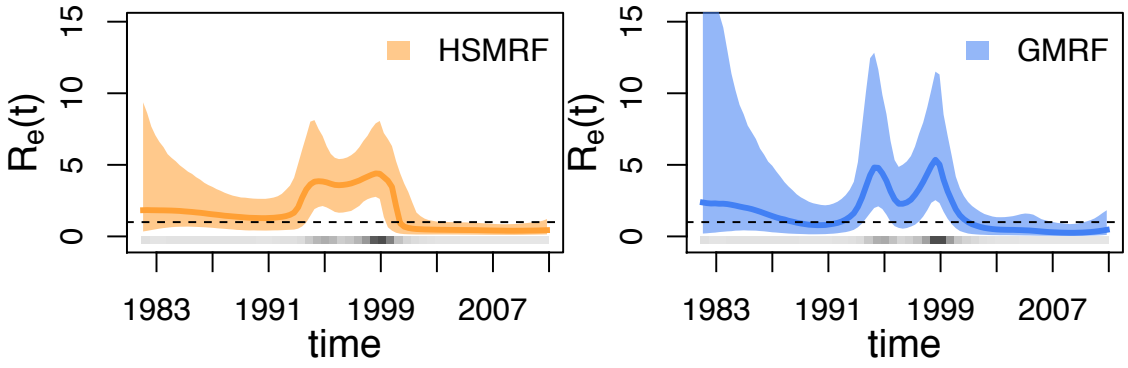


Figure 6. Analyses of the HIV dataset. Plotted are posterior median trajectories (dark lines) and 90% credible intervals (shaded regions). The upper CI for the GMRF-based analysis extends to ≈26, we have truncated the figure for a clearer view of the rest of the trajectory. Time is plotted as calendar time. A line at $R_e = 1$ is provided for convenience, as below this threshold the epidemic cannot be sustained. In grey is a heatmap of the inferred divergence times.

(1995), "strong" support [58]). For the GMRF-based model, equivalent calculations produce a 2ln(BF) in favor of a birth-rate shift of 5.53 ("positive" support). If we had instead been interested in testing for a shift of a particular magnitude, we could simulate under the prior to estimate the prior odds.

HIV Dynamics in Russia and Ukraine. In Eastern Europe and Asia, the use of injected drugs was a driving force in HIV epidemics for many years and continues to be an important factor in the spread of HIV [59]. Russia and Ukraine have a particularly high number of people who inject drugs, 2 million individuals combined, and a total of 1 million HIV infected individuals [60]. These factors, plus a limited effort to reduce the scope of the problem in the beginning of the epidemic, make Russia and Ukraine a good source of data for estimating how HIV spreads among those who inject drugs. Vasylyeva *et al.* (2016) used a number of approaches, including phylodynamic methods, to study the course of the epidemic from the 1980s through 2011 [60]. They estimated that half of all secondary infections take place during the first month post-infection. They further identified a massive increase in the size of the infected population during the 1990s, and estimated that during this period each newly infected individual transmitted to at least 5 others.

When using birth-death models for infectious disease phylodynamics, the primary parameter of interest is the effective reproductive number at time t, $R_e(t)$. This is defined as the average number of individuals who will be infected by a single infectious individual introduced into a population with the same numbers of susceptible and removed individuals as are present in the population of interest at time t [61]. In a constant-rate birth-death-sampling-treatment process, the average duration of an infection is the inverse of the total rate of becoming noninfectious, or $(\mu + r\phi)^{-1}$. The expected number of infections an individual will cause over a timespan t is given by $\lambda \cdot t$, approximately for small t. Thus, in the constant-rate case, the expected number of secondary infections caused by an individual is $R_e = \lambda/(\mu+r\phi)$. In the time-varying case, if an individual becomes infected at time t, we use the rates at that time to compute the expectation and obtain $R_e(t) = \lambda(t)/(\mu(t) + r(t)\phi(t))$.

To understand the dynamics of HIV in Russia and Ukraine in the time period of interest, we use the sequence alignment for the *env* region from Vasylyeva *et al.* (2016) [60]. We analyze

this dataset (457 sites for 92 sequences) under both the HSMRF-based and GMRF-based models, defining 2011 (the time of the most recent sample) to be the present day and dividing the range [0,29.1] into 100 evenly-sized intervals. We employ a Normal(29.1,5.0) root age prior, truncated to be older than the oldest sample age of 18. We fix $r = 1$, corresponding to the assumption that an individual, once sequenced and diagnosed, will not cause any further infections because they will be provided treatment and will have undetectable viral load. As there is information about the duration of infection in HIV, and thus the death rate, we replace our usual Exponential(10) prior with a Lognormal(-2.272,0.073) prior on the death rate (the rate of becoming noninfectious in the absence of sampling and treatment). This corresponds to an *a priori* 95% probability that an untreated individual will be infectious for between 8.4 and 11.2 years [60, 62]. We use an Exponential(10^{-5}) prior on the serial sampling rate. Details of the substitution and clock models are available in the supplemental materials, as are details of MCMC convergence diagnostics performed.

While the model we fit only has a time-varying birth rate, we plot the more informative $R_e(t)$ instead in Figure 6. Both the HSMRF-based and GMRF-based models show evidence for a spike in $R_e(t)$ in the early 1990s and a sharp decrease at the end of the 1990s. We quantify support for shifts in $\lambda(t)$ instead of $R_e(t)$, as we do not directly parameterize effective reproductive number. The 2ln(BF) in favor of an increase between 1992 and mid-1994 (of any magnitude) are 5.88 (positive support) for the HSMRF-based model and 7.57 (strong support) for the GMRF-based model. Similarly, the 2ln(BF) in favor of a decrease between 1999 and 2001 are 7.37 (strong support) for the HSMRF-based model and 9.53 (strong support) for the GRMF-based model. However, where the HSMRF-based model largely shows evidence for a consistently elevated rate in this period, the GMRF-based model shows a sharp dip mid-way through the decade, with the 90% CI including $R_e(t) = 1$. The HSMRF-based model estimates an average rate in this interval of 3.89, with rates that may be as low as 1.65 or as high as 8.07, and the GMRF-based model estimates an average rate of 3.55 with rates possibly as low as 0.54 or as high as 11.51.

The results of our HSMRF-based model analysis are largely consistent with those of Vasylyeva *et al.* (2016), who also observe an increased rate of infection from 1995 to 2000 [60]. Our GMRF-based analysis, with its large decrease in $R_e(t)$, does not align with either the prevalence data or any analysis performed by Vasylyeva *et al.* (2016) [60]. While both our HSMRF-based and GMRF-based models estimated $R_e(t) < 1$ throught the 2000s, there is no evidence from HIV prevalence that the epidemic is decreasing [63, 64]. Examining the posterior distribution on phylogenies provides some insight into this apparent conflict: there are few infections inferred to have happened post-2000, and thus there is no information suggesting that $R_e(t) > 1$ in this period. Previous coalescent analyses have favored a higher $R_e(t)$ persisting with no sign of a decrease, however such models can have difficulty inferring decreases in the absence of coalescent events [26]. This highlights the fact that while birth-death process and coalescent models are good at peering into the past, without birth (coalescent) events there is little to no information from which to infer birth (coalescent) rates and thus the posterior distribution is largely determined by the prior distribution. On the other hand, there is outside evidence that the epidemic has slowed since 2005 [65], so it is possible that our models are picking up on a real signal and simply exaggerating it.

Code and data availability. We have implemented all models and necessary samplers in `RevBayes` [31]. Analysis were performed with `RevBayes` v1.0.11

(https://github.com/revbayes/revbayes). Scripts used for our real data analyses and simulations are available at github.com/afmagee/hsmrfbdp.

Discussion and Conclusion

In this paper, we use a piecewise-constant birth-death model, combined with both GMRF and HSMRF prior distributions, to approximate arbitrary changes in the birth rate through time. We implemented these models in the statistical phylogenetic software platform `RevBayes`, allowing for both inference of birth-death process parameters using a phylogeny as data and for joint inference of BDP parameters, phylogeny, and nuisance parameters directly from molecular sequence data. We find that both GMRF and HMRF-based models are capable of inferring variable diversification rates and correctly rejecting variable models in favor of effectively constant models. We see that in general the HSMRF-based model has higher precision than its GMRF counterpart, with little to no loss of accuracy. Applied to a macroevolutionary dataset of the Australian gecko family Pygopodidae (where birth rates are interpretable as speciation rates), our models detect a speciation-rate decrease in the last 12 million years. Applied to an infectious disease phylodynamic dataset of sequences from HIV subtype A in Russia and Ukraine, our models detect a complex pattern of variation in the rate of infection.

Through simulations we find that different functional forms of birth-rate variation produce unique challenges in estimating these forms, even if they share the same magnitude of change. Slow changes are easy to miss, intermediate shifts are largely detectable, and fast shifts are generally hard for the GMRF-based model but easy for the HSMRF-based model to estimate. Fast shifts cause issues for the GMRF-based model because they require the global scale parameter γ to be large, which results in noisy and imprecise inference of slowly changing parts of the birth trajectory. At the same time, the GMRF-based model has a tendency to over-smooth the rapid changes. More recent changes are generally easier to detect than older changes, and very recent changes are often missed. Larger magnitude shifts are easier to detect than smaller magnitude shifts for both models, regardless of the functional form. In general, factors that make detecting shifts easier also exacerbate the poor behavior of the GMRF-based model. The HSMRF-based model often favors a trajectory with one or a few steeper shifts, even when the truth is a more gradual change. However, even if the duration of the shift is not accurately estimated, the HSMRF can recover the presence of rate variation even when the GMRF fails. Overall, we find that the performance of the HSMRF is quite good, and it is only clearly outperformed by the GMRF on a few types of birth rate trajectories. Therefore, we recommend using HSMRF as a Bayesian nonparametric prior for birth/death/sampling rate trajectories.

On real datasets with full joint inference, we see evidence of many of the same patterns observed in our simulation study. In both of our empirical analyses, there is evidence from both the HSMRF-based and GMRF-based models of large shifts, and the HSMRF-based model indicates periods of relatively constant rates outside of these jumps. As we see in the simulations with more rapid shifts (shift durations of 50 or less), the HSMRF-based model has slightly narrower credible intervals than the GMRF-based model in both analyses. In both analyses, the HSMRF-based model favors trajectories that are much closer to piecewise-constant than the GMRF-based model. In the HIV analysis, the GMRF-based model infers rather extreme variation in the birth rate where the HSMRF-based model infers very little, and based on the simulations it seems likely this is an artifact of the GMRF-based model's lack of local adaptivity rather than a feature that the HSMRF-based model misses. Based

on our simulations, while we cannot confidently say whether the HSMRF-based model more accurately estimates the duration of the observed birth-rate shifts in either case, we can be more confident in its estimates of the magnitude of change.

There are several avenues by which random field birth-death processes might be extended. It would be useful to devise models that can detect slower declines, situations where the models we have put forth here fail. One option for this would be to build second order Markov random field models, which can more easily collapse to linear models. These models have shown promise in coalescent modeling [29], but they have a higher risk of over-smoothing than first order models. Models incorporating time-varying rates of death and sampling are possible, though preliminary results suggest detecting time-varying death rates is very difficult without serial samples. Covariates may be added to time-varying birth-death models as has been done in the previous work related to our GMRF-based model [20]. Adding covariates to the HSMRF-based model may allow for better success in inferring time-varying death rates by providing additional information. Models that allow for the serial sampling rate to vary may have better success (with or without covariates), as there is more direct information about this rate. However, in cases where a number of samples have the same recorded age but there is not a sampling event (such as when some epidemiological sampling dates are available only to the year), may prove difficult. In such a case, the apparent variation in the sampling rate will likely overwhelm any signal of true variation in the sampling rate and may lead to erroneous estimates of the birth rate. Finally, for phylodynamic applications like HIV, it is clear that GMRF-based and HMRF-based birth-death models would benefit strongly from the inclusion of occurrence data, which has been incorporated into time-homogenous birth-death-sampling-treatment process by Gupta *et al.* (2019) [66].

In this work, we have developed and explored the performance of two flexible, time-varying birth-death process models. Using simulations, we show that both of these models have a very good ability to collapse to an effictively constant-rate model, and thus a low tendency towards false positives. Further, we show that the HSMRF-based model is good at discerning true signals of rate variation from spurious signals, and is capable of inferring very abrupt changes in the birth rate, enabling precise estimation of the timing of birth-rate shifts. On real data, we show that both models can infer complex patterns of birth-rate variation. Additionally, we present an intuitive scheme for setting the key hyperparameter for these models, the global shrinkage parameter, and provide an efficient and tuning-parameter free inference framework that enables inference for these high-dimensional models. Implementation in the software package `RevBayes` allows practitioners to employ these models while simultaneously inferring the phylogeny and all nuisance parameters (namely the substitution and clock models).

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