A class of identifiable birth-death models

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Abstract

In a striking result, Louca and Pennell (2020) recently proved that a large class of birth-death models are statistically unidentifiable from lineage-through-time (LTT) data. Specifically, they showed that any pair of sufficiently smooth birth and death rate functions is "congruent" to an infinite collection of other rate functions, all of which have the same likelihood for any LTT vector of any dimension. This fact has distressing implications for the thousands of studies which have utilized birth-death models to study evolution.

In this paper, we qualify their finding by proving that an alternative and widely used class of birth-death models is indeed identifiable. Specifically, we show that piecewise constant birth-death models can, in principle, be consistently estimated and distinguished from one another, given a sufficiently large extant time tree and some knowledge of the present day population. Subject to mild regularity conditions, we further show that any unidentifiable birth-death model class can be arbitrarily closely approximated by a class of identifiable models. The sampling requirements needed for our results to hold are explicit, and are expected to be satisfied in many contexts such as the phylodynamic analysis of a global pandemic.

1 Introduction

The generalized birth-death process (Kendall, 1948) is a classic model of population growth. Recently, it has also been used to study the processes of

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speciation and extinction (Nee et al., 1994; Morlon et al., 2010, 2011; Morlon, 2014), and also the evolution of pathogens (Stadler et al., 2013). Data-driven inquiry in these fields is inherently challenging, because the majority of species and pathogens that have ever lived have left no record of their existence. Thus, we can only make inferences about evolution on the basis of a somewhat biased sample of the species or lineages that happened to survive to the present day (Quental and Marshall, 2010; Morlon, 2014). Scientific interest in the birth-death process arises in part from the fact that it provides a principled way to account for this bias (Höhna et al., 2011; Cusimano et al., 2012).

Realizations of the birth-death process can be viewed from a phylogenetics perspective as rooted trees, where each leaf node represents a species that survived until the present, internal nodes are unobserved species, and edges represent lines of descent. The shape of the tree is governed by two non-negative functions which describe, at any given time t before the present, the per-capita rates of birth and death. As noted above, a distinguishing feature of this model is that lineages which died out before the present are not reflected in the resulting tree. Given birth and death rates, as well as a third parameter known as the sampling rate, we refer to the resulting distribution over random trees as a birth-death (henceforth, BD) model. (A precise definition is given in the next section.) The BD model implies a distribution over observed evolutionary data, and given such data, we can use statistical estimation to make inferences about the model parameters.

Phylogenetic BD models have been utilized in thousands of published studies (McPeek and Brown, 2007; Condamine et al., 2019; Henao Diaz et al., 2019), despite possessing known and somewhat troubling limitations. Stadler (2009) showed there exist different birth-death models that have the same likelihood in terms of observable data. In statistical terms, this implies that BD model is *unidentifiable* without further assumptions. The models considered by Stadler are highly parsimonious, consisting of constant birth and death rates that do not change over time. The problem is made even more challenging if the rates are time-varying (Gavryushkina et al., 2014).

Very recently, Louca and Pennell (2020, cited hereafter as LP) proved that the situation is in fact much worse than was previously realized: for *any* reasonably smooth birth and death rate functions, there are *infinitely* many other such functions that result in the same likelihood over phylogenetic trees. Although each of these functions represents a qualitatively different evolutionary scenario, LP's result shows that it is impossible to tell which

of them produced a given data set, even if the data were infinite. In light of the huge number of times that this model has appeared in the literature, this finding is highly worrisome.

Consistent estimation is impossible in an unidentifiable statistical model, so when faced with one, there are two ways forward: a) use a different model, or b) impose additional regularity conditions on the parameter space to restore identifiability. For the BD model, option a) may be warranted in some settings, but such a debate is beyond our scope. In this paper, we focus on option b). Our main result is to prove that there exists a class of BD models which are identifiable based on LTT data from an extant time tree. By identifiable, we mean that, within the space of rate functions we consider, each distinct BD model corresponds to one and only one likelihood function, and conversely. In fact, this space consists simply of piecewise constant functions, which are already widely used to fit BD models in practice.

Our results show that this class is identifiable once there are enough leaves in the extant tree, and we derive explicit lower bounds on the requisite number of samples. These bounds depend on a measure of parsimony of the underlying model class, in a sense which is made precise below. Roughly speaking, they require that identifiable classes of birth-death rate functions do not oscillate unnaturally. The same phenomenon has previously been noticed in population genetics (Myers et al., 2008; Bhaskar and Song, 2014), and our proofs are based in part on these earlier works.

2 Preliminaries

In this section we introduce the BD model and lay out some key definitions.

Throughout the paper, n is used to denote sample size. We assume $n \geq 2$ and suppress explicit dependence on it when there is no risk of confusion. Given n sampled taxa, an *extant timetree* is a bifurcating tree which traces out the ancestry of the sample. Therefore, the extant timetree has $n-1$ internal nodes which denote the times at which various taxa diverged from common ancestors. These are denoted $0 \leq \tau_{n-1} < \cdots < \tau_1$, where time runs backwards from the present. As in LP, we assume that all n samples are collected at time $t = 0$. There is also a root node referred to as the *origin* which occurs at height $\tau_o < \infty$, when the process is assumed to have started. Note that the height of the origin node is not resolvable from character data evolving along the tree since it is ancestral to the entire sample. Its value is

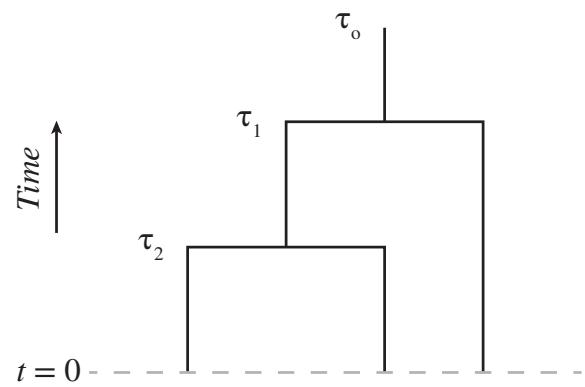

Figure 1: An extant timetree on $n = 3$ leaves.

therefore conditioned on using prior information. An example of an extant time tree with sample size $n = 3$ is shown in Figure 1.

Extant timetrees are assumed to be stochastically generated by a BD process (Morlon et al., 2010). This process has three parameters: two positive rate functions $\lambda : \mathbb{R}_{\geq 0} \to \mathbb{R}_{>0}$ and $\mu : \mathbb{R}_{\geq 0} \to \mathbb{R}_{>0}$, and an initial sampling fraction $\rho \in (0, 1]$. Here λ and μ represent the instantaneous rate per capita at which lineages are born and die going forwards in time, and ρ is the fraction of extant lineages that are sampled at the present time $t = 0$. In the sequel, we refer to different BD models by their corresponding parameter triples (λ, μ, ρ). Under the BD model with parameters (λ, μ, ρ), the density of an extant time tree is denoted $L^{(\lambda,\mu,\rho)}(\tau_1, \ldots, \tau_n)$. The precise form of $L^{(\lambda,\mu,\rho)}$ is not important for what follows, but can be found in e.g. Morlon et al. (2011, equation 1). Note that the topology of the time tree is uninformative in this model; the likelihood depends only on the merger times τ_i.

Abstracting away from the BD model, we now turn to the concept of identifiability. Let Θ be an arbitrary parameter space, and let L_θ denote a likelihood function parameterized by $\theta \in \Theta$. The *statistical model* $\mathcal{L}_\Theta = \{L_\theta : \theta \in \Theta\}$ is the image of Θ under L_θ; that is, the set of all possible likelihood functions that can be obtained from the parameter space Θ. (If Θ is a set of BD parameters, we use the notation

$$\mathcal{B}_\Theta = \left\{L^{(\lambda,\mu,\rho)} : (\lambda, \mu, \rho) \in \Theta\right\} \tag{1}$$

to emphasize that we are focusing specifically on the BD model.)

Definition 1 (Identifiability)**.** The statistical model $\mathcal{L}_\Theta = \{L_\theta : \theta \in \Theta\}$ is

identifiable if L_θ is injective; that is, for all $\theta_1, \theta_2 \in \Theta$, we have $L_{\theta_1} = L_{\theta_2} \implies \theta_1 = \theta_2$.

(In the BD model (1), the statement "$(\lambda_1, \mu_1, \rho_1) = (\lambda_2, \mu_2, \rho_2)$" is understood to mean that $\rho_1 = \rho_2$, and that the corresponding rate functions are equal almost everywhere.) If different parameters yield the same likelihood function, they cannot be distinguished using any amount of observable data. Consistent estimation is impossible. Identifiability is therefore the most minimal regularity condition one can place on a statistical model.

3 Results

In this section we summarize LP's results, prove that piecewise constant BD models are identifiable, and explore some additional corollaries and conjectures.

3.1 The result of Louca and Pennell

The key new quantity that underlies LP's result is the so-called *pulled (birth) rate function*, which is defined as

$$\lambda_p = \lambda(1 - E), \tag{2}$$

where $E(t)$ is the probability that a lineage alive at time t has no descendants sampled at time 0. The antiderivative of λ_p is denoted

$$\Lambda_p(\tau) = \int_0^\tau \lambda_p(u)\,\mathrm{d}u.$$

The function E satisfies the ordinary differential equation

$$\frac{\mathrm{d}E}{\mathrm{d}\tau} = -\mu + (\lambda + \mu) \cdot E + E^2\lambda, \tag{3}$$

with initial condition $E(0) = 1 - \rho$. The solution to (3) is (Morlon et al., 2011)

$$E(t) = 1 - \frac{e^{\int_0^t \lambda(u) - \mu(u)\,\mathrm{d}u}}{\rho^{-1} + \int_0^t \lambda(u) e^{\int_0^u \lambda(v) - \mu(v)\,\mathrm{d}v}\,\mathrm{d}u}. \tag{4}$$

Note that $E(t)$ is continuous, even if λ and μ are not.

The pulled rate function completely characterizes the likelihood of an extant timetree. Specifically, by equation (34) of LP,

$$L^{(\lambda_p)}(\tau_1, \ldots, \tau_n) \propto e^{-\Lambda_p(\tau_o)} \prod_{j=1}^{n} \lambda_p(\tau_j) e^{-\Lambda_p(\tau_j)}, \quad 0 \leq \tau_n \leq \cdots \leq \tau_1 < \tau_o. \quad (5)$$

By implication, any two BD parameter triples $(\lambda_1, \mu_1, \rho_1)$ and $(\lambda_2, \mu_2, \rho_2)$ which generate the same λ_p via (2) are indistinguishable. LP's contribution is to show that this phenomenon emerges in a surprisingly general class of models. Restated in our notation, their main result is:

Theorem (LP)**.** *Given an extant timetree on n taxa with origin τ_o, let $\mathcal{C}^1_+[0, \tau_o]$ denote the space of all functions which are strictly positive and continuously differentiable on $[0, \tau_o]$, and let*

$$\mathcal{U} = \left\{(\lambda, \mu, \rho) : \lambda, \mu \in \mathcal{C}^1_+, \rho \in (0, 1]\right\}$$

be the set of all BD parameterizations derived from this space. Then the BD model $\mathcal{B}_{\mathcal{U}}$ is unidentifiable.

Importantly, the theorem holds for any sample size n and also if ρ is fixed. LP's proof is constructive and provides, for any given BD model, a set of infinitely many "congruent" models which all have the same likelihood. As LP argue in their discussion, this result has disturbing implications for the reliability of statistical estimates obtained from BD models, which have been widely reported in phylogenetics, phylodynamics, paleogenetics, and related fields.

3.2 Piecewise constant models are identifiable

In this section we state and prove our main results.

Definition 2. Let

$$C^{\oplus K}_+[0, \tau_o] = \left\{ \sum_{k=1}^{K} a_k \mathbf{1}_{[t_{k-1}, t_k)}(t) : \mathbf{a} \in \mathbb{R}^K_{>0}, 0 = t_0 < t_1 < \cdots < t_K = \tau_o \right\} \quad (6)$$

be the set of all positive piecewise constant functions with K pieces defined on $[0, \tau_o]$. If $K = 1$ then we economize on notation and denote the space of constant rate models by $C_+ (= C^{\oplus 1}_+[0, \tau_o])$.

Note from the definition that $C_+^{\oplus K}[0, \tau_o]$ encompasses all possible piecewise constant functions with K breakpoints; the breakpoints are not considered fixed or known in advance, and can vary from one function to another.

Next, we define the class of BD parameterizations that forms the basis of our identifiability proof. In the definition and in what follows, we assume that the sampling fraction $\rho \in (0, 1]$ is a fixed, known parameter. This is necessary because if ρ is allowed to vary, then as noted in the introduction, Stadler (2009) has shown that even the *constant rates* BD model is unidentifiable.

Definition 3. Let

$$\mathcal{I}_{K,\rho} = \left\{(\lambda, \mu, \rho) : \lambda, \mu \in C_+^{\oplus K}[0, \tau_o]\right\}$$

be the space of all piecewise-constant BD parameterizations with rate functions in $C_+^{\oplus K}[0, \tau_o]$ and fixed sampling fraction $\rho \in (0, 1]$.

The following is our main result.

Theorem 4. *If $n > 16K - 5$, then the BD model $\mathcal{B}_{\mathcal{I}_{K,\rho}}$ is identifiable.*

The theorem is proved in Section 3.3. Unpacking the result, it asserts that *both* the positions of the breakpoints (the vector $\mathbf{t}$ in Definition 2) as well as the levels of each piece (the vector $\mathbf{a}$ in the definition) of both $\lambda(t)$ and $\mu(t)$ are estimable given sufficient data, and that these break points are not assumed to be shared between the two rate functions, or indeed between any two functions in the piecewise constant model space considered by the theorem. If, as is common in practice, we do assume that $\lambda(t)$ and $\mu(t)$ are defined on the same set of breakpoints (while still allowing this set to vary between different parameterizations in $\mathcal{I}_{K,\rho}$), then easy modifications to the proof show that $n > 8K - 3$ suffices for identifiability.

Note that the theorem only establishes a *sufficient* condition for identifiability. It does not imply that piecewise models are unidentifiable if n is below the stated bounds; in other words, we do not know if our bound is tight. In our view, the main message is that piecewise constant models are identifiable if $\mathcal{O}(K)$ tips are sampled. Further implications of the theorem are discussed in Section 4.

Several extensions and conjectures follow naturally from Theorem 4. Since it is possible to uniformly approximate a regular function class over a compact set using step functions, identifiable BD models are in some sense dense in the space of all BD models. A prototypical result is:

Theorem 5. *Let $\rho \in (0,1]$ be fixed, let*

$$\mathcal{F} = \left\{ f \in \mathcal{C}^1_+[0,\tau_o] : \|f'\|_\infty < B \right\}$$

be the set of positive, continuously differentiable functions with bounded first derivative over $[0,\tau_o]$, and let $\Theta_{\mathcal{F},\rho} = \{(\lambda,\mu,\rho) : \lambda,\mu \in \mathcal{F}\}$ denote the resulting BD parameter space. Then

1. $\mathcal{B}_{\Theta_{\mathcal{F},\rho}}$ is unidentifiable; and
2. There exists a set of functions $\mathcal{G}$ defined over $[0,\tau_o]$ such that for any $\epsilon > 0$,
   (a) $\sup_{f\in\mathcal{F}} \inf_{g\in\mathcal{G}} \|f-g\|_\infty < \epsilon$, and
   (b) $\mathcal{B}_{\Theta_{\mathcal{G},\rho}}$ is identifiable if $n > 16B\tau_o/\epsilon - 5$.

Proof. The first claim follows from LP, because their congruence classes include e.g. smooth perturbations of constant-rate BD parameterizations. For the second, if $f \in \mathcal{F}$ then

$$\begin{aligned}
&\left| \sum_{k=0}^{K-1} f(\tau_o k/K) \mathbf{1}_{[k/K,(k+1)/K)}(x/\tau_o) - f(x) \right| \\
&\quad \le \max_k \sup_{x/\tau_o \in [k/K,(k+1)/K)} |f(x) - f(\tau_o k/K)| \\
&\quad \le \max_k \sup_{x/\tau_o \in [k/K,(k+1)/K)} B|x - \tau_o k/K| \\
&\quad = B\tau_o/K.
\end{aligned}$$

Letting $K = B\tau_o/\epsilon$ yields the claim. □

An obvious caveat to this theorem is that the sample size needed to have (provable) identifiability grows rapidly as $\epsilon \to 0$.

Another possible extension concerns estimating birth-death models using polynomials. Since constant functions are polynomials of degree zero, it is natural to conjecture that identifiability holds for higher degrees as well.

Conjecture 6. *Let $P^{(\oplus K)}_{d,+}[0,\tau_o]$ be the set of non-negative, piecewise polynomials (splines) of order d with $K-1$ internal knots defined over $[0,\tau_o]$, and let $\Theta_{P^{(\oplus K)}_{d,+},\rho}[0,\tau_o]$ be the corresponding BD parameter space, again for fixed ρ. Then the BD model $\mathcal{B}_{\Theta_{P^{(\oplus K)}_{d,+},\rho}[0,\tau_o]}$ is identifiable if $n > 16K(1+d) - 5$.*

The conjecture would seem to imply that n grows with d, but this would be offset by having to use fewer pieces K to get a good approximation. We are unable to prove this conjecture because of substantial difficulties that arise when trying to extend our proof technique to non-constant functions. Specifically, we do not know how to bound the sign change complexity of spline-based BD models (see Lemma 14) except when $d = 0$.

3.3 Proof of Theorem 4

Our proof derives from a general technique developed by Bhaskar and Song (2014) for establishing identifiability of rate functions in coalescent-type models. We follow their method closely, reproducing their results where necessary for completeness of exposition.

To build the necessary connections between the BD and coalescent models, we first notice that $L^{(\lambda_p)}$ in (5) can be re-written as

$$L(\tau_1, \ldots, \tau_n) \propto \prod_{j=1}^{n} j\lambda_p(\tau_j) e^{-j[\Lambda_p(\tau_j) - \Lambda_p(\tau_{j+1})]} \tag{7}$$

where we defined $\tau_{n+1} \equiv 0$. This is a coalescent-type likelihood where the rate of merging (backwards in time) when there are j remaining lineages in the tree is $j - 1$ instead of the usual $\binom{j}{2}$. Hence, retrospectively, lineages are each killed at rate $\lambda_p(\tau)$, except for one which must survive past time τ_o.

Our first proposition, which may be useful elsewhere, extends a result from coalescent theory for the marginal density of τ_k in (7).

Proposition 7. *Let $L(\tau_1, \ldots, \tau_n)$ be defined by (7). Then for $1 \leq k \leq n$,*

$$\begin{aligned} \pi_k(\tau_k) &= \int_{\tau_1} \cdots \int_{\tau_{k-1}} \int_{\tau_{k+1}} \cdots \int_{\tau_n} L(\tau_1, \ldots, \tau_n) \, \mathrm{d}\tau_n \cdots \mathrm{d}\tau_{k+1} \mathrm{d}\tau_{k-1} \cdots \mathrm{d}\tau_1 \\ &= \sum_{j=k}^{n} A_{kj} q_j(\tau_k), \end{aligned} \tag{8}$$

where

$$q_j(\tau) = j\lambda_p(\tau) e^{-j\Lambda_p(\tau)}, \tag{9}$$

and the matrix $\mathbf{A} \in \mathbb{Q}^{n \times n}$ is upper-triangular and invertible, with entries

$$A_{kj} = \prod_{\ell=k, \ell \neq j}^{n} \frac{\ell}{\ell - j}, \quad 1 \leq k \leq j \leq n.$$

Proof. The results of Polanski et al. (2003) can be straightforwardly applied[1]: equation (7) is equation (2) of their paper, with $\binom{j}{2}$ replaced by j and $\int_{t_{j+1}}^{t_j} \mathrm{d}\sigma/N_e(\sigma)$ replaced by $\Lambda_p(\tau_j) - \Lambda_p(\tau_{j+1})$. The integral transform $\Upsilon\{\cdot\}$ (compare with equation (17) of Polanski et al.) becomes

$$\Upsilon\{\pi(\tau_k)\} = \prod_{j=k}^{n} \frac{j}{s+j} = \sum_{j=k}^{n} A_{kj} \frac{j}{s+j}.$$

Applying the inverse transform Υ^{-1} to the left and right hand sides of the previous display yields (8). Finally, since the diagonal entries of A are $A_{jj} = \binom{n}{n-j}$, we have $\det A \neq 0$ so that A is invertible. □

Our strategy for establishing identifiability is to construct a vector of invariants which, for a sufficiently large sample size, uniquely identifies the pulled rate function λ_p. To that end, given any pulled rate function λ_p and sample size n, we form an associated moment vector $\mathbf{c}^{(\lambda_p)} \in \mathbb{R}^n$, with entries

$$c_j^{(\lambda_p)} = \int_0^{\tau_o} \tau q_j^{(\lambda_p)}(\tau)\,\mathrm{d}\tau, \quad 1 \leq j \leq n. \tag{10}$$

Proposition 8. *Suppose that $L^{(\lambda_p^{(1)})}$ and $L^{(\lambda_p^{(2)})}$ are equal almost everywhere. Then $\mathbf{c}^{(\lambda_p^{(1)})} = \mathbf{c}^{(\lambda_p^{(2)})}$.*

Proof. Define the function vectors

$$\boldsymbol{\pi}^{(\lambda_p)} = (\pi_1^{(\lambda_p)}, \ldots, \pi_n^{(\lambda_p)})^\intercal$$
$$\mathbf{q}^{(\lambda_p)} = \left(q_1^{(\lambda_p)}, \ldots, q_n^{(\lambda_p)}\right)^\intercal,$$

whose individual entries are given by (8) and (9). By Proposition 7,

$$\mathbf{q}^{(\lambda_p)} = \mathbf{A}^{-1}\boldsymbol{\pi}^{(\lambda_p)}.$$

[1]Polanski et al. assume no restriction on the timing of coalescence events, but a simple limiting argument (let $N_e(\sigma) \to 0$ for all $\sigma > \tau_o$) shows that their result holds when the process is conditioned to have a most recent common ancestor before τ_o as well.

By assumption, $\boldsymbol{\pi}^{(\lambda_p^{(1)})} = \boldsymbol{\pi}^{(\lambda_p^{(2)})}$ almost everywhere. Hence,

$$\begin{aligned}
\mathbf{c}^{(\lambda_p^{(1)})} &= \int_0^\infty t\mathbf{q}^{(\lambda_p^{(1)})}(t)\,\mathrm{d}t \\
&= \mathbf{A}^{-1}\int_0^\infty t\boldsymbol{\pi}^{(\lambda_p^{(1)})}(t)\,\mathrm{d}t \\
&= \mathbf{A}^{-1}\int_0^\infty t\boldsymbol{\pi}^{(\lambda_p^{(2)})}(t)\,\mathrm{d}t \\
&= \mathbf{c}^{(\lambda_p^{(2)})}.
\end{aligned}$$

□

Contrapositively, if $\mathbf{c}^{(\lambda_p^{(1)})} \neq \mathbf{c}^{(\lambda_p^{(2)})}$, then $L^{(\lambda_p^{(1)})}$ and $L^{(\lambda_p^{(2)})}$ differ on a set of positive measure. The rest of the proof amounts to showing that if $\lambda_p^{(1)}$ and $\lambda_p^{(2)}$ are generated by piecewise constant BD models, and n is sufficiently large, then they have different moment vectors.

Next, define $\mathbf{d}^{(\lambda_p)}$ to have entries $d_j^{(\lambda_p)} = c_j^{(\lambda_p)}/j$; clearly $\mathbf{d}^{(\lambda_p^{(1)})} = \mathbf{d}^{(\lambda_p^{(2)})}$ if and only if $\mathbf{c}^{(\lambda_p^{(1)})} = \mathbf{c}^{(\lambda_p^{(2)})}$. By (9) and (10),

$$d_j^{(\lambda_p)} = \int_0^{\tau_o} \tau\lambda_p(\tau)e^{-j\Lambda_p(\tau)}\,\mathrm{d}\tau = \int_0^{\Lambda_p(\tau_o)} \Lambda_p^{-1}(u)e^{-ju}\,\mathrm{d}u, \tag{11}$$

where the second equality follows from a change of variables $\Lambda_p(\tau) \to u$.

The next theorem is restated for completeness.

Theorem (Generalized rule of signs, Bhaskar and Song, 2014; Jameson, 2006)**.** *Let $f : \mathcal{D} \to \mathbb{R}$ be a piecewise-continuous function defined on some domain $\mathcal{D} \subset \mathbb{R}$, which is not identically zero and has a finite number $\sigma(f)$ of sign changes. Then the function*

$$G(x) = \int_{\mathcal{D}} f(t)e^{-tx}\,\mathrm{d}t$$

has at most $\sigma(f)$ zeros in $\mathbb{R}$ (counted with multiplicity).

Informally, f is said to have a sign change any time it crosses zero, including by jump discontinuities. For a precise statement, refer to Definition 3 of Bhaskar and Song.

Given any pulled rate function λ_p, we define

$$I^{(\lambda_p)} : \mathbb{R} \to \mathbb{R}_{\geq 0}$$
$$I^{(\lambda_p)}(x) = \begin{cases} \Lambda_p^{-1}(x), & x \in [0, \Lambda_p(\tau_o)) \\ 0, & \text{otherwise} \end{cases}$$

to be the inverse function of the cumulative integral of λ_p, and extend its definition to the reals by defining it to be zero outside of the appropriate domain.

Proposition 9. *Suppose that $\lambda_p^{(1)}$ and $\lambda_p^{(2)}$ are two pulled rate functions for which $\mathbf{c}^{(\lambda_p^{(1)})} = \mathbf{c}^{(\lambda_p^{(2)})} \in \mathbb{R}^n$. Then either $\lambda_p^{(1)} = \lambda_p^{(2)}$, or $I^{(\lambda_p^{(1)})} - I^{(\lambda_p^{(2)})}$ has at least n sign changes.*

Proof. Suppose that $\lambda_p^{(1)} \neq \lambda_p^{(2)}$, and let $M = \max(\Lambda_p^{(1)}(\tau_o), \Lambda_p^{(2)}(\tau_o))$. Then $I^{(\lambda_p^{(1)})} - I^{(\lambda_p^{(2)})}$ is not identically zero, and by equation (11),

$$G(z) := \int_0^M \left[I^{(\lambda_p^{(1)})}(x) - I^{(\lambda_p^{(2)})}(x) \right] e^{-zx} \, \mathrm{d}x$$

has zeros at $z = 1, \ldots, n$. By the generalized rule of signs, this implies that $I^{(\lambda_p^{(1)})} - I^{(\lambda_p^{(2)})}$ has at least n sign changes on $[0, M)$. □

Based on the preceding result, we define the following complexity measure on BD model spaces. This is an adaptation of the Definition 4 in Bhaskar and Song to our setting. In the definition, the notation $\lambda_p^{(\theta)}$ is used to denote the pulled rate function corresponding to a particular BD parameterization $\theta = (\lambda, \mu, \rho)$.

Definition 10 (Pulled sign change complexity)**.** Let Θ be a set of BD models. The *pulled sign change complexity* $\mathscr{S}_p(\Theta)$ is defined as

$$\mathscr{S}_p(\Theta) = \sup \left\{ \sigma \left(I^{(\lambda_p^{(\theta_1)})}(x) - I^{(\lambda_p^{(\theta_2)})}(x - a) \right) : \lambda_p^{(\theta_1)}, \lambda_p^{(\theta_2)} \in \Theta, a \in \mathbb{R} \right\},$$

where $\sigma(g)$ denotes the number of sign changes of g.

Using Proposition 9 and the preceding definition, we immediately have the following sample size criterion for the identifiability of BD models.

Theorem 11. *Suppose that $\mathscr{S}_p(\Theta) \leq S$, and that the mapping $\theta \mapsto \lambda_p^\theta$ is injective over Θ. Then $\mathcal{B}_\Theta$ is identifiable if $n > S$.*

Theorem 11 is a general result that holds for any class of BD models. However, we can only apply it to spaces where the injectivity condition holds and where we know how to bound the pulled sign change complexity. Next, we establish these properties when $\Theta = \mathcal{I}_{K,\rho}$.

For any pulled rate function λ_p, define

$$\tilde{\lambda}_p(x) = \lambda_p(\Lambda_p^{-1}(x)).$$

By supplemental equation (9) of LP,

$$\frac{\mathrm{d}\lambda_p}{\mathrm{d}t} = \lambda_p \left(\frac{1}{\lambda} \frac{\mathrm{d}\lambda}{\mathrm{d}t} - \mu + \lambda E \right).$$

Hence,

$$\frac{\mathrm{d}\tilde{\lambda}_p}{\mathrm{d}x} = \frac{\mathrm{d}\lambda}{\mathrm{d}t}(\Lambda_p^{-1}(x)) \times \frac{\mathrm{d}\Lambda_p^{-1}}{\mathrm{d}x}(x) = \frac{1}{\lambda} \frac{\mathrm{d}\lambda}{\mathrm{d}t} - \mu + \lambda E \Big|_{t=\Lambda_p^{-1}(x)}, \tag{12}$$

where in the second equality we used

$$\frac{\mathrm{d}\Lambda_p^{-1}}{\mathrm{d}x} = \frac{1}{\lambda_p(\Lambda_p^{-1}(x))} = [\tilde{\lambda}_p(x)]^{-1}. \tag{13}$$

Now by (2),

$$\lambda E|_{t=\Lambda_p^{-1}(x)} = -\tilde{\lambda}_p(x) + \lambda(\Lambda_p^{-1}(x)), \tag{14}$$

If λ and μ are constant, then $\mathrm{d}\lambda/\mathrm{d}t = 0$, and we obtain from (12) and (14) the first-order ordinary differential equation

$$\begin{aligned} \frac{\mathrm{d}\tilde{\lambda}_p}{\mathrm{d}x} &= \lambda - \mu - \tilde{\lambda}_p \\ \tilde{\lambda}_p(0) &= \rho\lambda. \end{aligned} \tag{15}$$

The solution to this differential equation is

$$\tilde{\lambda}_p(x) = (\lambda - \mu)(1 - e^{-x}) + \rho\lambda e^{-x}, \quad x \in [0, \Lambda_p(\tau_o)). \tag{16}$$

More generally, if λ and μ are constant over some interval $[t, t')$, then

$$\tilde{\lambda}_p(x) = (\lambda - \mu)(1 - e^{-(x - \Lambda_p(t))}) + \lambda_p(t) e^{-(x - \Lambda_p(t))}, \quad x \in [\Lambda_p(t), \Lambda_p(t')). \tag{17}$$

Proposition 12. *Let θ_1, θ_2 be two different models in $\mathcal{I}_{K,\rho}$ with pulled rate functions $\lambda_p^{(1)}$ and $\lambda_p^{(2)}$. Then $\lambda_p^{(1)} \neq \lambda_p^{(2)}$.*

Proof. Let $(\lambda_1, \mu_1) \neq (\lambda_2, \mu_2)$ be two different models in $\mathcal{I}_{K,\rho}$. Then there is a non-empty interval $[t, t') \subset [0, \tau_o]$ such that

1. $(\lambda_1(s), \mu_1(s)) = (\lambda_2(s), \mu_2(s))$ for all $0 < s < t$; and
2. $\lambda_1, \mu_1, \lambda_2, \mu_2$ are all constant over $[t, t')$ and $(\lambda_1(s), \mu_1(s)) \neq (\lambda_2(s), \mu_2(s))$ for all $t \leq s < t'$.

(Note that we could have $t = 0$, in which case condition 1 becomes vacuous.) To show $\lambda_p^{(1)} \neq \lambda_p^{(2)}$, it is sufficient to show that $\tilde{\lambda}_p^{(1)} \neq \tilde{\lambda}_p^{(2)}$. By (17), for all x greater than $\Lambda_p^{(1)}(t) = \Lambda_p^{(2)}(t)$ but less than $\min(\Lambda_p^{(1)}(t'), \Lambda_p^{(2)}(t'))$, we have

$$\tilde{\lambda}_p^{(2)}(x) - \tilde{\lambda}_p^{(1)}(x) = c_1 e^{-(x - \Lambda_p^{(1)}(t))} + c_2,$$

where

$$\begin{aligned} c_1 &= \lambda_p^{(1)}(t) - \lambda_p^{(2)}(t) - \lambda_2 + \mu_2 + \lambda_1 - \mu_1 \\ c_2 &= \lambda_2 - \mu_2 - \lambda_1 + \mu_1. \end{aligned}$$

Suppose $c_2 = 0$. Let $\varepsilon = E^{(1)}(t) = E^{(2)}(t) \in (0, 1)$, where the equality follows from condition 1 and the facts that a) $E(0) = \rho$ across all models, and b) $E(t)$ is continuous (cf. equation 4). Then $c_1 = \lambda_p^{(1)}(t) - \lambda_p^{(2)}(t) = [\lambda_1(t) - \lambda_2(t)](1 - \varepsilon)$. If $c_1 = 0$ then this would contradict condition 2. □

Remark. The preceding result makes crucial use of the fact that all models in $\mathcal{I}_{K,\rho}$ are constrained to have the same sampling fraction ρ. Without this assumption, the proposition would not even hold for $K = 1$ (Stadler, 2009).

Next, we bound $\mathscr{S}_p(\mathcal{I}_{K,\rho})$. First, let

$$\mathcal{S}_K = \bigcup_{\rho \in (0,1]} \mathcal{I}_{K,\rho}$$

be the space of all K-piecewise constant BD models with unconstrained sampling proportions. As remarked above, this space is not identifiable, since in particular Proposition 12 does not hold for it. Nevertheless, it follows directly from Definition 10 that $\mathscr{S}_p(\mathcal{I}_{K,\rho}) \leq \mathscr{S}_p(\mathcal{S}_K)$, so bounding the pulled sign change complexity of $\mathcal{S}_K$ is all that is required for our purposes.

We first show that $\mathscr{S}_p(\mathcal{S}_K)$ can be bounded in terms of the simpler quantity $\mathscr{S}_p(\mathcal{S}_1)$.

Lemma 13. *The pulled sign change complexity of $\mathcal{S}_K$ is bounded by the pulled sign change complexity of $\mathcal{S}_1$ as*

$$\mathscr{S}_p(\mathcal{S}_K) \leq (4K-2) + (4K-1)\mathscr{S}_p(\mathcal{S}_1).$$

Proof. If $\lambda_1, \mu_1, \lambda_2, \mu_2 \in C_+^{\oplus K}$, then for $i = 1, 2$ we can place λ_i, μ_i onto a common set of $2K$ pieces, with break points

$$0 = t_0^{(i)} < t_1^{(i)} < \cdots < t_{2K}^{(i)} = \tau_o.$$

Assume without loss of generality that $\Lambda_p^{(1)}(\tau_o) \leq \Lambda_p^{(2)}(\tau_o)$. Let

$$\mathcal{X} = \left\{ \Lambda_p^{(i)}(t_k^{(i)}) : 1 \leq i \leq 2, 0 \leq k \leq 2K \right\},$$

and sort the points in $\mathcal{X}$ to form a partition

$$0 = x_0 < \cdots < x_{4K} = \Lambda_p^{(2)}(\tau_o)$$

of $[0, \Lambda_p^{(2)}(\tau_o))$.

As there are no zeros of $I^{(1)}(x) - I^{(2)}(x)$ for $\Lambda_p^{(1)}(\tau_o) \leq x < \Lambda_p^{(2)}(\tau_o)$, we conservatively assume that $x_i \leq \Lambda_p^{(1)}(\tau_o)$ for all $0 \leq i < 4K$. For each i and j, there exists an integer $0 \leq k(i,j) < 2K$ such that

$$(x_j, x_{j+1}) \subset \left(\Lambda_p^{(i)}(t_{k(i,j)}^{(i)}), \Lambda_p^{(i)}(t_{k(i,j)+1}^{(i)}) \right), \quad i = 1, 2.$$

Therefore, there exists a BD parameterization $(\lambda_{ij}, \mu_{ij}, \rho_{ij}) \in \mathcal{S}_1$ such that

$$\lambda_p^{(\lambda_{ij}, \mu_{ij})}(s - t_{k(i,j)}^{(i)}) = \lambda_p^{(i)}(s), \quad s \in (t_{k(i,j)}^{(i)}, t_{k(i,j)+1}^{(i)});$$

concretely, the initial sampling fraction is

$$\rho_{ij} = 1 - E^{(i)}(t_{k(i,j)}^{(i)}).$$

Thus,

$$\Lambda_p^{(i)}(\tau) = \Lambda_p^{(i)}(t_{k(i,j)}^{(i)}) + \int_{t_{k(i,j)}^{(i)}}^{\tau} \lambda_p^{(\lambda_{ij}, \mu_{ij})}(s - t_{k(i,j)}^{(i)}) \mathrm{d}s, \quad t_{k(i,j)}^{(i)} \leq \tau < t_{k(i,j)+1}^{(i)}.$$

The above equality implies

$$I^{(i)}(x) = t_{k(i,j)}^{(i)} + I^{(\lambda_{ij}, \mu_{ij})}(x - \Lambda_p^{(i)}(t_{k(i,j)}^{(i)})), \quad x_j \leq x < x_{j+1}.$$

Hence, within (x_j, x_{j+1}), the number of sign changes of $I^{(1)}(x) - I^{(2)}(x)$ is at most the number of sign changes of

$$I^{(\lambda_{1j},\mu_{1j})}(x - \Lambda_p^{(1)}(t_{k(1,j)}^{(1)})) - I^{(\lambda_{2j},\mu_{2j})}(x - \Lambda_p^{(2)}(t_{k(2,j)}^{(2)})),$$

which is bounded above by $\mathscr{S}_p(\mathcal{S}_1)$. A sign change is also possible at each of the $4K-2$ jump points x_j. Hence, the number of sign changes is at most $(4K-2) + (4K-1)\mathscr{S}_p(\mathcal{S}_1)$. □

We conclude the proof by bounding $\mathscr{S}(\mathcal{S}_1)$.

Lemma 14. *Let $(\lambda_1, \mu_1, \rho_1) \neq (\lambda_2, \mu_2, \rho_2)$ be two sets of constant rate functions, with corresponding pulled rate functions $\lambda_p^{(1)}$ and $\lambda_p^{(2)}$, and let*

$$g(x) = I^{(\lambda_p^{(1)})}(x) - I^{(\lambda_p^{(2)})}(x - a),$$

where $\rho_1, \rho_2 \in (0, 1]$ are arbitrary sampling fractions and a is an arbitrary real number. Then $\sigma(g) \leq 3$.

Proof. Without loss of generality, assume that $\Lambda_p^{(1)}(\tau_o) \leq \Lambda_p^{(2)}(\tau_o)$. By Rolle's theorem and (13), the number of sign changes of g on $[0, \Lambda_p^{(1)}(\tau_o)]$ is at most one plus the number of zeros of

$$h(x) := \frac{\mathrm{d}g(x)}{\mathrm{d}x} = \frac{1}{\tilde{\lambda}_p^{(1)}(x)} - \frac{1}{\tilde{\lambda}_p^{(2)}(x-a)} = \frac{\tilde{\lambda}_p^{(2)}(x-a) - \tilde{\lambda}_p^{(1)}(x)}{\tilde{\lambda}_p^{(1)}(x)\tilde{\lambda}_p^{(2)}(x-a)}.$$

By (16), the numerator is of the form $c_1 e^{-x} + c_2$ for some c_1, c_2 that depend on λ_i, μ_i, ρ_i, and a. Since this function is always monotone, h has at most one zero on $[0, \Lambda_p^{(1)}(\tau_o))$, so g has at most two zeros there.

If $\Lambda_p^{(1)}(\tau_o) < \Lambda_p^{(2)}(\tau_o)$, then g could have a jump discontinuity at $\Lambda_p^{(1)}(\tau_o)$, leading to an additional sign change. Finally, $I^{(\lambda_p^{(1)})} = 0$ and $I^{(\lambda_p^{(2)})} > 0$ on the remaining piece $x \in [\Lambda_p^{(1)}(\tau_o), \Lambda_p^{(2)}(\tau_o)]$, so $g < 0$ and has no zeros. □

By the preceding lemma, $\mathscr{S}_p(\mathcal{S}_K) \leq 3$, so that by Lemma 13,

$$\mathscr{S}_p(\mathcal{S}_\mathcal{K}) \leq 16K - 5.$$

Finally, the claim follows from Theorem 11.

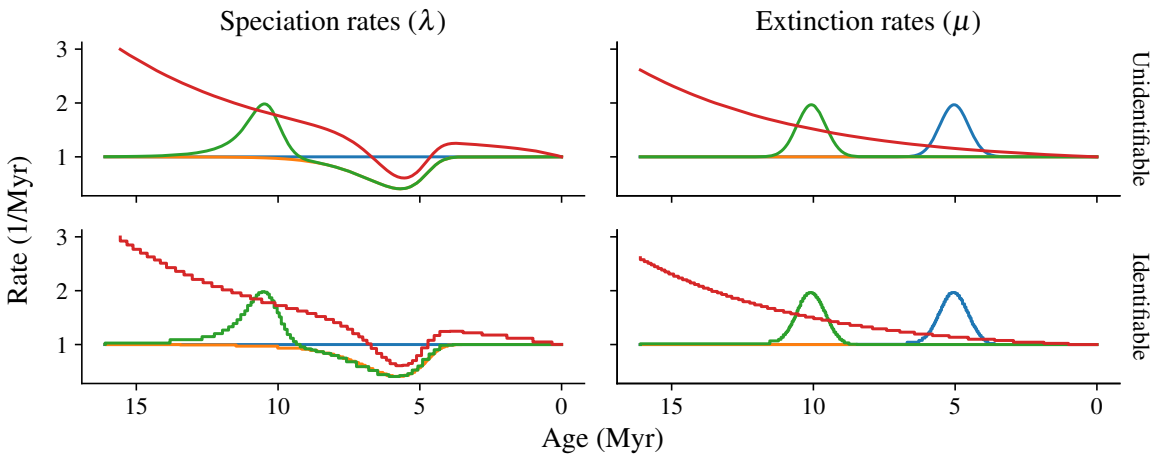

Figure 2: Unidentifiable vs. identifiable BD models. The top row contains four indistinguishable models exhibited in LP Figure 1. In the bottom row, we approximated these models using piecewise constant functions using $K = 50$ pieces. The models in the bottom row are identifiable given sufficiently many samples. All models are assumed to have the same ρ.

4 Discussion

In this paper, we proved that piecewise-constant BD models with K pieces are identifiable from extant timetrees with a sufficient number of tips. We also showed that, under mild assumptions, unidentifiable BD models of the type considered by LP can be approximated to within arbitrary accuracy by identifiable BD models. Finally, we conjecture, but are unable to prove, that spline-based BD models are similarly identifiable.

In the short time since their publication, LP's findings have generated considerable discussion (e.g., Morlon et al., 2020; Helmstetter et al., 2021; Parry, 2021), with some authors concluding that they "will be dispiriting to evolutionary scientists" seeking to understand the factors affecting speciation and extinction (Pagel, 2020). Our results may serve to lift those spirits, while also illustrating the subtleties that arise when reasoning about a limiting concept like identifiability. For example, consider the BD models shown in Figure 2. The top row is reproduced from Figure 1 of LP and shows four color-coded BD models which all have the same pulled birth rate, and hence same likelihood function. On the bottom, we approximated these functions

over the domain $[0, 16]$ using piecewise constant functions. By Theorem 4, these models can, in principle, be distinguished given a sufficiently large time-tree. Is the underlying natural process that is modeled in Figure 2 inferable from data? The answer seemingly depends on whether the researcher believes that the piecewise functions shown on the bottom panel can faithfully model this process. Empirically, we note that it would be nearly impossible to differentiate (using, say, a simple hypothesis test) between one of the $\mathcal{C}_+^1$ models in the figure and its corresponding $C_+^{\oplus 50}$ approximation on the basis a realistically achievable amount of data.

Still, practitioners should be careful not to overinterpret affirmative identifiability results as conclusive evidence that high quality estimates can be obtained on real problems. As we noted above, identifiability is a minimal regularity criterion that makes no guarantees about the ability to accurately infer model parameters using a finite amount of data. Even in identifiable models, it is often that case that potentially significant amounts of regularization and/or prior information have to be incorporated to obtain sensible results (Stadler et al., 2013; Kim et al., 2015; Bhaskar et al., 2015; Morlon et al., 2020; DeWitt et al., 2021). Having established identifiability, the next step would be to understand the finite-sample accuracy and rate of convergence of piecewise constant estimators in BD models. This is a challenging theoretical problem that will require new ideas and techniques. Fortunately, since several popular software packages (e.g., Bouckaert et al., 2019) already implement the piecewise constant BD model, there are already many simulation studies in the literature to help guide the way.

The reader may wonder whether our result is somehow a byproduct of the fact that we consider piecewise constant—hence discontinuous—rate functions, whereas in LP they are assumed to be continuously differentiable. In our opinion, this is not the main driver of our result; indeed we believe that (cf. Conjecture 6) identifiable parameter spaces consisting of smooth functions also exist. This conjecture, if it were true, would not contradict LP's result, because the construction they use to generate their congruence classes (specifically, the operator $S[S_o, f]$ defined by supplementary equation 75) is not closed over simple function spaces like fixed-degree polynomials. In other words, even f is e.g. a spline, $S[S_o, f]$ is in general not. Thus, while there infinitely large congruence classes of alternative BD parameterizations that are indistinguishable, the conjecture asserts that the intersection between these classes and a sufficiently simple function space consists of at most a single element. LP provide an heuristic argument supporting this conjecture

in Section S.3 of their supplement.

Another criticism related to our use of piecewise constant models is that they require a potentially large number samples to become (provably) identifiable. In some settings (e.g., phylodynamic analysis of a global pandemic) these bounds would be achievable, while in others they would plainly exceed the amount of available data. Using a more efficient representation, for example splines, would lead to BD models with lower sampling requirements, but which currently lack identifiability guarantees.

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