

EXACT PHYLODYNAMICS VIA STRUCTURED MARKOV GENEALOGY PROCESSES

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ABSTRACT. We derive an algorithm for the exact computation of the likelihood of an observed transmission tree.

1. Introduction.

Problem of phylodynamics. Factorization of problem into two subproblems.

Relation to previous work. Existing methods (Volz et al., 2009; Stadler, 2010). Large-population, small sample-size approximations.

For structured but deterministic models, approach of Volz (2012); Rasmussen et al. (2014), based on approximation as birth-death processes: approximation no longer needed.

Extension of previous results (King et al., 2022). Broader class of state-spaces. Accommodating discrete structure.

Classes of Markov processes. Utility and flexibility of Markov assumptions.

Population process induces Markov history and genealogy processes. Using these, we derive equations for the likelihood of a genealogy conditional on the history. We then integrate out the history to obtain nonlinear filtering equations, the solution of which yields the likelihood. These readily lend themselves to a family of sequential Monte Carlo algorithms for computing the likelihood. We demonstrate with several examples.

In the following, we show a Markov population process of the kind that is a staple in epidemiology induces a Markov process on the space of genealogies. We then show how one can compute the likelihood of a given genealogy.

2. Mathematical preliminaries.

2.1. Notation. Throughout the paper, we will adopt the convention that a bold-face symbol (e.g., \mathbf{X}), denotes a random element. We will be concerned with a variety of stochastic processes, in both discrete and continuous time. In both cases, we will use a subscript to indicate the time parameter: e.g., \mathbf{X}_t or \mathbf{G}_k , where t takes values in the non-negative reals \mathbb{R}_+ and k in the non-negative integers \mathbb{Z}_+ . In the case of continuous-time processes, we will assume that sample paths are càdlàg i.e., , right-continuous with left limits. We will frequently need to refer to the left-limit of such a process. Accordingly, if \mathbf{Z}_t is a càdlàg random process, we define

$$\tilde{\mathbf{Z}}_t := \begin{cases} \lim_{s \uparrow t} \mathbf{Z}_s, & t > 0, \\ \mathbf{Z}_0, & t = 0. \end{cases}$$

Note that $\tilde{\mathbf{Z}}_t$ is thus left-continuous with right limits.

If \mathbf{Z}_t , $t \in \mathbb{R}_+$ is a pure jump process, knowledge of its sample path is equivalent to knowledge of the number, \mathbf{K}_t , of jumps it has taken as of time t , the jump times $\hat{\mathbf{T}}_k$, and the embedded chain $\hat{\mathbf{Z}}_k := \mathbf{Z}_{\hat{\mathbf{T}}_k}$, $k = 0, \dots, \mathbf{K}_t$. In particular, if we adopt the convention that $\hat{\mathbf{T}}_0 = 0$ and $\hat{\mathbf{T}}_{\mathbf{K}_t+1} = t$, then $\mathbf{Z}_t = \hat{\mathbf{Z}}_k$ for $t \in [\hat{\mathbf{T}}_k, \hat{\mathbf{T}}_{k+1})$, $k = 0, \dots, \mathbf{K}_t$.

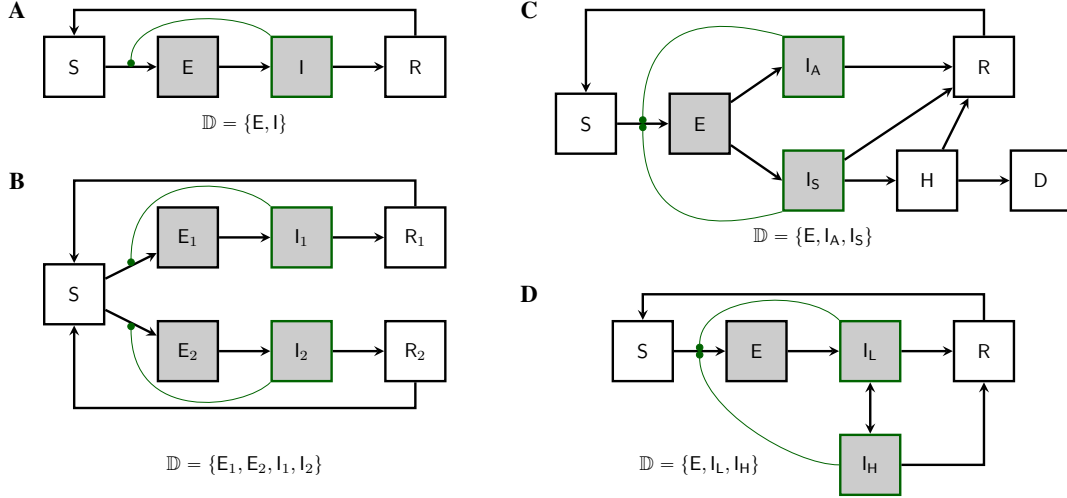


FIGURE 1. Examples of discretely-structured population models. Demes are shaded. Compartments containing infectious hosts are outlined in green. Curved green lines connect transmission rates with the compartments whose occupancies control their modulation; each such connection gives rise to a nonlinearity in the model. **(A)** An SEIRS model. Susceptible individuals (S), once infected, enter a transient incubation phase (E) before they become infectious (I). Upon recovery (R), individuals experience immunity from reinfection. If this immunity wanes, they re-enter the susceptible compartment. Pathogen lineages are to be found in hosts within the E and I compartments only. Accordingly, there are two demes ($\mathbb{D} = \{E, I\}$). If there is exactly one lineage per host, then the occupancy, $n(\mathbf{X}_t) = (n_E(\mathbf{X}_t), n_I(\mathbf{X}_t))$, is the integer 2-vector giving the numbers of hosts in the respective compartments. **(B)** In this four-deme model, two distinct pathogen strains compete for susceptibles. **(C)** A three-deme model for SARS-CoV-2 infection. After an incubation period, individuals may develop asymptomatic infection (I_A). If they do not recover, symptomatically infected individuals (I_S) can progress to hospitalization (H) and death (D). **(D)** A three-deme model with heterogeneity in transmission behavior. Contagious individuals move randomly between low-transmission (I_L) and high-transmission (I_H) behaviors.

2.2. Population process. Motivating examples: compartmental models in ID epidemiology, phylogenetics and systematics. Wide variety of models are of interest (Fig. 1). Linear chain trick. Migration, superspreading, competition between strains.

We will assume that our population process is a time-inhomogeneous Markov jump process, $\mathbf{X}_t, t \in \mathbb{R}_+$, taking values in some space \mathbb{X} . In earlier work (King et al., 2022), we limited ourselves to the case $\mathbb{X} = \mathbb{Z}^d$, but here we assume only that \mathbb{X} is a complete metric space with a countable dense subset, i.e., a Polish space. The population process is completely specified by its initial-state density, p_0 , and its transition rates α . In particular, we suppose that

$$\text{Prob}[\mathbf{X}_0 \in \mathcal{E}] = \int_{\mathcal{E}} p_0(x) dx \quad (1)$$

for all measurable sets $\mathcal{E} \subseteq \mathbb{X}$. For any $t \in \mathbb{R}_+$, $x, x' \in \mathbb{X}$, we think of the quantity $\alpha(t, x, x')$ as the instantaneous hazard of a jump from x to x' . More precisely, the transition rates have the following properties:

$$\alpha(t, x, x') \geq 0, \quad \int_{\mathbb{X}} \alpha(t, x, x') dx' < \infty,$$

for all $t \in \mathbb{R}_+$ and $x, x' \in \mathbb{X}$. [We could mention that we use the continuity of α with respect to t in some of the following, but that this condition can be relaxed.] Henceforth, we understand that integrals are taken over all of \mathbb{X} unless otherwise specified. Let \mathbf{K}_t be the number of jumps that \mathbf{X} has taken by time t . We assume that \mathbf{K}_t is a

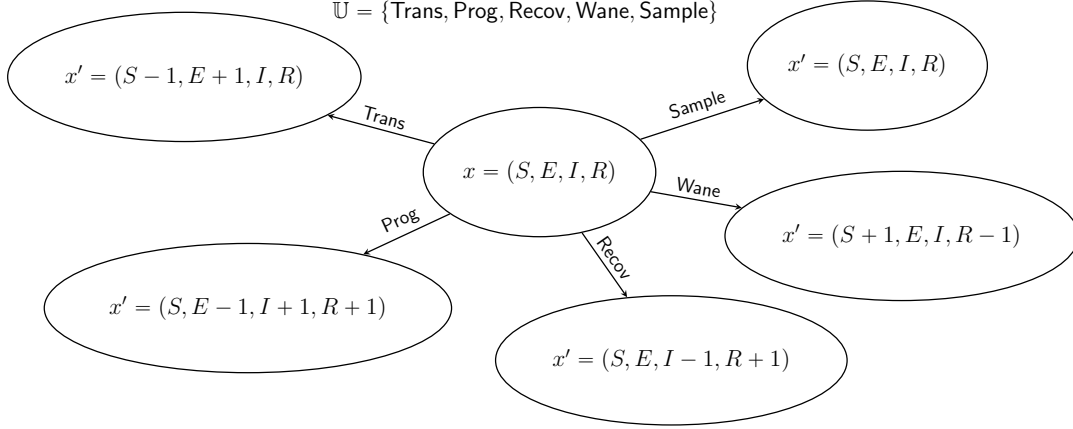


FIGURE 2. Markov state transition diagram for the SEIRS model depicted in Fig. 1A. The state, x , is characterized by four numbers, S , E , I , and R . From a given state x , there are five possible kinds of jumps $x \mapsto x'$. Accordingly, the set, \mathbb{U} , of jump marks has five elements. Each of these is of a different type: Trans (transmission) is of birth type, Prog (progression) is of migration type, Recov (recovery) is of death type, Sample (sampling) is of sample type, and Wane (loss or waning of immunity) is of neutral type. See §3.1 for a description of these jump types. Note that, in this formulation, when a sampling event occurs, the state does not change.

simple counting process so that

$$\begin{aligned} \text{Prob}[\mathbf{K}_{t+\Delta} = n+1 \mid \mathbf{K}_t = n] &= \Delta \int \alpha(t, x, x') dx' + o(\Delta), \\ \text{Prob}[\mathbf{K}_{t+\Delta} > n+1 \mid \mathbf{K}_t = n] &= o(\Delta), \\ \text{Prob}[\mathbf{X}_{t+\Delta} \in \mathcal{E} \mid \mathbf{X}_t = x, \mathbf{K}_{t+\Delta} - \mathbf{K}_t = 1] &= \frac{\int_{\mathcal{E}} \alpha(t, x, x') dx'}{\int \alpha(t, x, x') dx'}. \end{aligned}$$

We will further assume that \mathbf{X}_t is non-explosive, so that $\text{Prob}[\mathbf{K}_t < \infty] = 1$ for all t .

2.2.1. Kolmogorov forward equation. The above may be compactly summarized by stating that if $v(t, x)$ satisfies the Kolmogorov forward equation (KFE),

$$\frac{\partial v}{\partial t}(t, x) = \int v(t, x') \alpha(t, x', x) dx' - \int v(t, x) \alpha(t, x, x') dx', \quad (2)$$

and if, moreover, $v(0, x) = p_0(x)$, then $\int_{\mathcal{E}} v(t, x) dx = \text{Prob}[\mathbf{X}_t \in \mathcal{E}]$ for every measurable $\mathcal{E} \subseteq \mathbb{X}$. Eq. 2 is sometimes called the *master equation* for \mathbf{X}_t .

Another perspective on the Markov processes is to be had from its Markov state transition diagram (Fig. 2).

2.2.2. Structured populations, demes, and deme occupancy. In an *unstructured* Markov population process, every lineage is exactly like every other. King et al. (2022) showed how every such process induces an unstructured Markov genealogy process. Here, our aim is to expand the theory considerably by allowing our population of lineages to have discrete structure. In particular, we suppose that there are a countable set of subpopulations that may differ in their vital rates, but within each of which, individual lineages are statistically identical. We call these subpopulations *demes*, and use the symbol \mathbb{D} to denote an index set for them. We define the *deme occupancy* function $n : \mathbb{D} \times \mathbb{X} \rightarrow \mathbb{Z}_+$ so that for $i \in \mathbb{D}$, $x \in \mathbb{X}$, $n_i(x)$ is the number of lineages in deme i when the population is in state x .

2.3. Jump marks. In the following, it will be useful to divide the jumps of the population process \mathbf{X}_t into distinct categories. For this purpose, we let \mathbb{U} be a countable set of jump marks such that

$$\alpha(t, x, x') = \sum_u \alpha_u(t, x, x').$$

Fig. 2 shows an example with five distinct marks. Here and in the following, sums over u are taken over the whole of \mathbb{U} unless otherwise indicated.

Let us define the *jump mark* process, \mathbf{U}_t , to be the mark of the latest jump as of time t . As usual, we take the sample paths of \mathbf{U}_t to be càdlàg. Observe that, though \mathbf{X}_t and $(\mathbf{X}_t, \mathbf{U}_t)$ are Markov processes, \mathbf{U}_t is not.

2.4. Examples.

2.4.1. SIRS model. King et al. (2022) worked out formulas for the exact likelihood of a genealogy induced by an SIRS model. The theory developed in this paper applies, but since there is only one deme in this model, this is a simple case. Its state vector is $x = (S, I, R)$ and its KFE is

$$\begin{aligned} \frac{\partial v}{\partial t}(t, S, I, R) = & \frac{\beta(t) I (S + 1)}{N} v(t, S + 1, I - 1, R) - \frac{\beta(t) I S}{N} v(t, S, I, R) \\ & + \gamma (I + 1) v(t, S, I + 1, R - 1) - \gamma I v(t, S, I, R) \\ & + \omega (R + 1) v(t, S - 1, I, R + 1) - \omega R v(t, S, I, R). \end{aligned}$$

Note that we have here allowed for the possibility that the transmission rate, β , depends on time.

2.4.2. SEIRS model. A simple, yet interesting, model with more than one deme is the SEIRS model (Fig. 1A). The state space is \mathbb{R}_+^4 , with the state $x = (S, E, I, R)$ defined by the numbers of hosts in each of the four compartments. It has two demes ($\mathbb{D} = \{E, I\}$) and the KFE

$$\begin{aligned} \frac{\partial v}{\partial t}(t, S, E, I, R) = & \frac{\beta(t) I (S + 1)}{N} v(t, S + 1, E - 1, I, R) - \frac{\beta(t) I S}{N} v(t, S, E, I, R) \\ & + \sigma (E + 1) v(t, S, E + 1, I - 1, R) - \sigma E v(t, S, E, I, R) \\ & + \gamma (I + 1) v(t, S, E, I + 1, R - 1) - \gamma I v(t, S, E, I, R) \\ & + \omega (R + 1) v(t, S - 1, E, I, R + 1) - \omega R v(t, S, E, I, R), \end{aligned}$$

where $N = S + E + I + R$ is the total population size. The deme occupancy function in this case is $n(x) = (E, I)$. Note that the terms associated with sampling cancel each other in the KFE, since, in this model, sampling has no effect on the state.

2.4.3. Two-strain competition model. A simple model for the competition of two strains for susceptible hosts is depicted in Fig. 1B. In this model, the state vector consists of seven numbers: $x = (S, E_1, E_2, I_1, I_2, R_1, R_2)$. There are four demes ($\mathbb{D} = \{E_1, E_2, I_1, I_2\}$) and the occupancy function is $n(x) = (E_1, E_2, I_1, I_2)$. This model has KFE

$$\begin{aligned} \frac{\partial v}{\partial t} = & \frac{\beta_1(t) I_1 (S + 1)}{N} v(t, S + 1, E_1 - 1, E_2, I_1, I_2, R_1, R_2) - \frac{\beta_1(t) I_1 S}{N} v(t, S, E_1, E_2, I_1, I_2, R_1, R_2) \\ & + \frac{\beta_2(t) I_2 (S + 1)}{N} v(t, S + 1, E_1, E_2 - 1, I_1, I_2, R_1, R_2) - \frac{\beta_2(t) I_2 S}{N} v(t, S, E_1, E_2, I_1, I_2, R_1, R_2) \\ & + \sigma_1 (E_1 + 1) v(t, S, E_1 + 1, E_2, I_1 - 1, I_2, R_1, R_2) - \sigma_1 E_1 v(t, S, E_1, E_2, I_1, I_2, R_1, R_2) \\ & + \sigma_2 (E_2 + 1) v(t, S, E_1, E_2 + 1, I_1, I_2 - 1, R_1, R_2) - \sigma_2 E_2 v(t, S, E_1, E_2, I_1, I_2, R_1, R_2) \\ & + \gamma_1 (I_1 + 1) v(t, S, E_1, E_2, I_1 + 1, I_2, R_1 - 1, R_2) - \gamma_1 I_1 v(t, S, E_1, E_2, I_1, I_2, R_1, R_2) \\ & + \gamma_2 (I_2 + 1) v(t, S, E_1, E_2, I_1, I_2 + 1, R_1, R_2 - 1) - \gamma_2 I_2 v(t, S, E_1, E_2, I_1, I_2, R_1, R_2) \\ & + \omega_1 (R_1 + 1) v(t, S - 1, E_1, E_2, I_1, I_2, R_1 + 1, R_2) - \omega_1 R_1 v(t, S, E_1, E_2, I_1, I_2, R_1, R_2) \\ & + \omega_2 (R_2 + 1) v(t, S - 1, E_1, E_2, I_1, I_2, R_1, R_2 + 1) - \omega_2 R_2 v(t, S, E_1, E_2, I_1, I_2, R_1, R_2) \end{aligned}$$

2.4.4. Superspreading model. Fig. 1D depicts a model of superspreading. There are three demes ($\mathbb{D} = \{E, I_L, I_H\}$). The state vector is $x = (S, E, I_L, I_H, R)$ and the KFE is

$$\begin{aligned} \frac{\partial v}{\partial t} = & \frac{\beta(t)(I_L + \theta I_H)(S + 1)}{N} v(t, S + 1, E - 1, I_L, I_H, R) - \frac{\beta(t)(I_L + \theta I_H)S}{N} v(t, S, E, I_L, I_H, R) \\ & \sigma(E + 1) v(t, S, E + 1, I_L - 1, I_H, R) - \sigma E v(t, S, E, I_L, I_H, R) \\ & \varepsilon_{LH}(I_L + 1) v(t, S, E, I_L + 1, I_H - 1, R) - \varepsilon_{LH} I_L v(t, S, E, I_L, I_H, R) \\ & \varepsilon_{HL}(I_H + 1) v(t, S, E, I_L - 1, I_H + 1, R) - \varepsilon_{HL} I_H v(t, S, E, I_L, I_H, R) \\ & \gamma(I_L + 1) v(t, S, E, I_L + 1, I_H, R - 1) - \gamma I_L v(t, S, E, I_L, I_H, R) \\ & \gamma(I_H + 1) v(t, S, E, I_L, I_H + 1, R - 1) - \gamma I_H v(t, S, E, I_L, I_H, R) \\ & \omega(R + 1) v(t, S - 1, E, I_L, I_H, R + 1) - \omega R v(t, S, E, I_L, I_H, R). \end{aligned}$$

2.4.5. Linear birth-death model.

$$\frac{\partial v}{\partial t} = \lambda(N - 1) v(t, N - 1) - \lambda N v(t, N) + \mu(N + 1) v(t, N + 1) - \mu N v(t, N)$$

2.4.6. Moran model and the Kingman coalescent.

2.5. History. [Maybe it would be better to speak instead of \mathbf{H}_t being the random σ -algebra generated by the sequences $(\hat{\mathbf{T}}_k, \hat{\mathbf{X}}_k, \hat{\mathbf{U}}_k)_{k=1}^{K_t}$. The only thing we do with \mathbf{H} is condition on it. One (perhaps minor) problem with this is that we cannot then speak about the measure on histories.]

Consider the Markov process $(\mathbf{X}_t, \mathbf{U}_t)$. We define its *history process*, \mathbf{H}_t , to be the restriction of the random function $s \mapsto (\mathbf{X}_s, \mathbf{U}_s)$ to the interval $[0, t]$. Note that \mathbf{H}_t is itself trivially a Markov process, since it contains its own history.

Alternatively, one can think of \mathbf{H}_t as consisting of the sequence $\left((\hat{\mathbf{T}}_k, \hat{\mathbf{X}}_k, \hat{\mathbf{U}}_k) \right)_{k=0}^{K_t}$. In particular, conditional on \mathbf{H}_t , both \mathbf{X}_t and \mathbf{U}_t are deterministic as are \mathbf{K}_t and the embedded chains, $\hat{\mathbf{X}}_k, \hat{\mathbf{U}}_k$, and the point process of event times $\hat{\mathbf{T}}_k$. The probability measure, $\pi^{\mathbf{H}}$, for \mathbf{H}_t can be expressed in terms of these:

$$\begin{aligned} \pi^{\mathbf{H}}(d\mathbf{H}_t) = & p_0(\hat{\mathbf{X}}_0) d\hat{\mathbf{X}}_0 \prod_{k=1}^{K_t} \alpha_{\hat{\mathbf{U}}_k}(\hat{\mathbf{T}}_k, \hat{\mathbf{X}}_{k-1}, \hat{\mathbf{X}}_k) d\hat{\mathbf{X}}_k d\hat{\mathbf{T}}_k \\ & \times \exp \left(- \sum_{k=0}^{K_t} \int_{\hat{\mathbf{T}}_k}^{\hat{\mathbf{T}}_{k+1}} \sum_u \int \alpha_u(t', \hat{\mathbf{X}}_k, x') dx' dt' \right), \end{aligned}$$

where again, by convention, $\hat{\mathbf{T}}_0 = 0$ and $\hat{\mathbf{T}}_{K_t+1} = t$.

If \mathbf{H} is such a history, we define $t(\mathbf{H})$ to be the right endpoint of its domain and use the notation $\hat{\mathbf{H}} = \{ \hat{\mathbf{T}}_1, \dots, \hat{\mathbf{T}}_{K_t} \} \subset [0, t(\mathbf{H})]$ to denote the set of its jump times.

2.6. Genealogies. A *genealogy*, \mathbf{G} , encapsulates the relationships of shared ancestry among a set of lineages that are extant at some time $t(\mathbf{G}) \in \mathbb{R}_+$, and perhaps a set of samples collected at earlier times (Fig. 3A). A genealogy has a tree- or forest-like structure, with four distinct kinds of nodes: (i) *tip nodes*, which represent labeled living lineages; (ii) *internal nodes*, which represent events at which lineages diverged and/or moved from one deme to another; (iii) *sample nodes*, which represent labeled samples; and (iv) *root nodes*, at the base of each tree. Each node a is associated with a specific time, $t(a)$. In particular, if a is a tip node in \mathbf{G} , then $t(a) = t(\mathbf{G})$; if a is a sample node, then $t(a)$ is the time at which the sample was taken. Moreover, if node a is ancestral to node a' , then $t(a) \leq t(a')$ and $t(a') - t(a)$ is the distance between a and a' along the genealogy. Without loss of generality we assume that $t(a) = 0$ for all root nodes a . We let $\hat{\mathbf{G}}$ denote the set of all internal and sample node-times of the genealogy \mathbf{G} ; we refer to these as *genealogical event times*.

Importantly, a genealogy informs us not only about the shared ancestry of any pair of lineages, but also about where in the set of demes any given lineage was at all times. Accordingly, we can visualize a genealogy as a tree, the nodes and edges of which are painted with a distinct color for each deme (Fig. 3A). Note that a genealogy

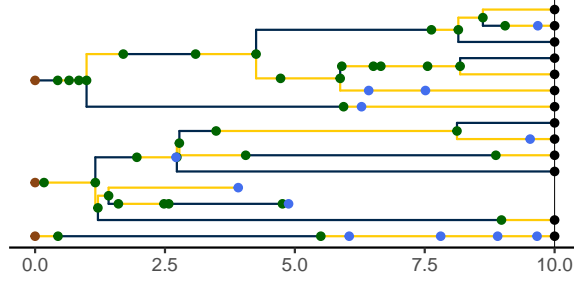


FIGURE 3. $t(G) = 10$. Two demes, $\mathbb{D} = \{\text{blue, yellow}\}$. Tip nodes, denoting extant lineages, are shown in black; sample nodes are shown in blue; internal nodes are indicated using green dots. Note that internal nodes occur both at branch-points and inline. Wherever a lineage moves from one deme (color) to another, an internal node occurs, but not conversely.

will in general have *branch-point nodes*, i.e., internal nodes with more than one descendant, but may also have internal nodes with only one descendant. These occur whenever the color changes along a branch, but can also occur without a color-change. We refer to such nodes as *inline nodes*.

Formally, we define a genealogy, G , to be an ordered pair (y, z) . The z element specifies the genealogy's tree structure, as follows. Let L be a countable set of labels and let Z be the set of all partitions of subsets of L . Partition *fineness* defines a partial order on Z . Specifically, for $\zeta, \zeta' \in Z$, we say $\zeta \preceq \zeta'$ if and only if for every $b' \in \zeta'$ there is $b \in \zeta$ such that $b \supseteq b'$. If $t(G) = T$, the tree structure of G is defined by a càdlàg map $z : [0, T] \rightarrow Z$ that is monotone in the sense that $t_1 \leq t_2$ implies $z_{t_1} \preceq z_{t_2}$. An element $b \in z_t$ is a set of labels; it represents the branch of the tree that bears the corresponding lineages. We use the notation \dot{z} to denote the set of all event-times in the tree z . Note that \dot{z} includes the times of all tip, sample, and branch-point nodes, but excludes inline and root nodes. Therefore, $\dot{z} \subseteq \dot{G}$.

The y element of G specifies the coloring of branches and locations of tip, sample, and internal nodes (including inline nodes). In particular, if a is the label of any tip or sample node and $t \in [0, T]$, we define $d_t(a)$ to be the deme in which the lineage of a was found at time t and think of this as the color of the corresponding branch at that time. We will also need to count the number of nodes along each lineage: let $m_t(a)$ be the number of internal or sample nodes encountered as one descends along lineage a from time $t = t(a)$ to $t = 0$. Observe that $m_t(a)$ is a simple counting process, with $m_0(a) = 0$ for all a . Formally, we define the coloring component y as follows. Let $\mathbb{Y} = \mathbb{D} \times \mathbb{Z}_+$ and write $v \in \mathbb{Y}$ component-wise as $v = (v^d, v^m)$. For any $\zeta \in Z$, an element $\eta \in \mathbb{Y}^\zeta$ is a map from the partition ζ into \mathbb{Y} . Now, suppose we are given a tree $z : [0, T] \rightarrow Z$ and a càdlàg map $y : [0, T] \rightarrow \prod_{t \in [0, T]} \mathbb{Y}^{z_t}$. Let \dot{y} denote the set of discontinuities of y . We say that y is *compatible* with z if it is a valid coloring of the tree z . Formally, compatibility requires the following: (i) $\dot{y} \supseteq \dot{z}$; (ii) for every $t \in [0, T]$, $y_t \in \mathbb{Y}^{z_t}$; (iii) if $0 \leq t_1 \leq t_2 \leq T$, $b_1 \in z_{t_1}$, $b_2 \in z_{t_2}$, and $b_1 \supseteq b_2$, then $y_{t_1}^m \leq y_{t_2}^m$; (iv) $y_{t_1}^m = y_{t_2}^m$ implies $y_{t_1}^d = y_{t_2}^d$. Let $Y(z)$ denote the set of such maps compatible with z and $Y_t(z) := \{y_t \mid y \in Y(z)\}$. [These conditions are necessary but not sufficient.] [The coproduct is a fiber bundle over the z and $Y(z)$ is a section of this bundle.]

The two càdlàg functions y and z specify a genealogy completely and uniquely. When the genealogy is not clear from context, we write G^y and G^z to refer to the respective components of genealogy G .

2.7. Binomial ratio. For $n, r, \ell, s \in \mathbb{Z}_+^{\mathbb{D}}$, define the *binomial ratio*

$$\binom{n \quad \ell}{r \quad s} := \begin{cases} \frac{\prod_{i \in \mathbb{D}} \binom{n_i - \ell_i}{r_i - s_i}}{\prod_{i \in \mathbb{D}} \binom{n_i}{r_i}}, & \text{if } \forall i \ n_i \geq \{\ell_i, r_i\} \geq s_i \geq 0, \\ 0, & \text{otherwise.} \end{cases}$$

Observe that $\binom{n}{r} \binom{\ell}{s} \in [0, 1]$. Moreover, in consequence of the Chu-Vandermonde identity, we have

$$\sum_{s \in \mathbb{Z}_+^D} \binom{n}{r} \binom{\ell}{s} \binom{\ell}{s} = 1,$$

whenever $n_i \geq \{\ell_i, r_i\} \geq 0$ for all i .

3. The induced genealogy process.

3.1. Event types. We will show how a given population process naturally induces a process in the space of genealogies. Specifically, we will describe how, at each jump in the population process, a corresponding change occurs in the genealogy, according to whether lineages branch, die, move between demes, or are sampled. For this purpose, there are five distinct *pure types* of events:

- (a) *Birth-type events* result in the branching of one or more new lineages, each from some existing lineages. Examples of birth-type events include transmission events, speciations, and actual births. Importantly, we assume that all new lineages arising from a birth event share the same parent and that at most one birth event occurs at a time, almost surely.
- (b) *Death-type events* result in the extinction of one or more lineages. Examples include recovery from infection, death of a host, and species extinctions. We allow for the possibility that multiple lineages die simultaneously.
- (c) *Migration-type events* result in the movement of a lineage from one deme to another. Spatial movements, changes in host age or behavior, and progression of an infection can all be represented as migration-type events. We permit multiple lineages to move simultaneously.
- (d) *Sample-type events* result in the collection of a sample from a lineage but do not in themselves affect the inventory process. We allow for the possibility that multiple samples are collected simultaneously, though we require that, in this case, each extant lineage is sampled at most once.
- (e) *Neutral-type events* result in no change to any of the lineages.

Fig. 2 depicts an example with jumps of all five pure types. It is not necessary that an event be of a pure type; *compound events* partake of more than one type. For example, a sample/death-type event, in which a lineage is simultaneously sampled and removed, has been proposed (Leventhal et al., 2014), as have birth/death events in which one lineage reproduces at the same moment that another dies (e.g., the Moran (1958) process). The theory presented here places few restrictions on the complexity of the events that can occur by combining events of the various pure types.

3.2. Genealogy process. We now show how a given population process induces a stochastic process, \mathbf{G}_t , on the space of genealogies. In the case of unstructured population processes (i.e., those having a single deme), King et al. (2022) gave a related construction that is equivalent to the one presented here.

At each jump in the population process, a change is made to the genealogy, according to the mark, u , of the jump (Fig. 4). In particular:

- (a) If u is of birth-type (Fig. 4A), it results in the creation of one new internal node, call it b . A tip node, a , of the appropriate deme is chosen with uniform probability from among those present and b is inserted so that its ancestor is that of a , while a takes b as its ancestor. One new tip node, of the appropriate deme, is created for each of the children, all of which take b as their immediate ancestor.
- (b) If u is of death-type (Fig. 4B), one or more tip nodes of the appropriate demes are selected with uniform probability from among those present. These are deleted. Next, branch nodes without children are recursively removed. Sample nodes are never removed.
- (c) At a migration-type event (Fig. 4C), the appropriate number of migrating lineages are selected at random with uniform probability, from among those present in the appropriate demes. For each selected lineage, one new branch node is inserted between the selected tip node and its ancestor. The color of the descendant branch changes accordingly.

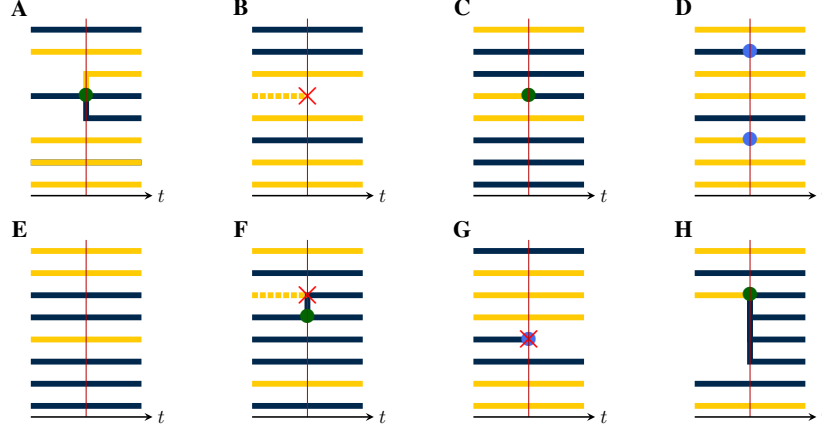


FIGURE 4. Jump types differ by their effects on the genealogy. This can be seen by examining the local structure of the genealogy in a neighborhood of a jump event. **(A)** A birth-type jump results in the branching of one or more child lineages from the parent. There can be only one parent, though the demes of the child lineages may differ from that of their parent. Here, a parent of the blue deme sires one child lineage in each of the blue and yellow demes. The production of an event is an integer vector, with one entry for each deme. The production of this event is therefore $r = (r_{\text{blue}}, r_{\text{yellow}}) = (2, 1)$. The deme occupancy at this event is $n = (n_{\text{blue}}, n_{\text{yellow}}) = (3, 5)$. **(B)** A death-type event causes the extinction of a lineage. Since internal node without children are recursively removed, the affected branch disappears. The production of this event is $r = (0, 0)$ and the deme occupancy is $n = (3, 4)$. **(C)** A migration-type event results in the movement of one or more lineages from one deme to another. Here, one lineage moves from the yellow to the blue deme. The production of this event is $r = (1, 0)$, i.e., the production is 1 for the blue deme and 0 for the yellow. The deme occupancy is $n = (6, 2)$. **(D)** In a sample-type event, one or more sample nodes (blue circles) are inserted. Here, there are two samples, one in each of the blue and yellow demes. Accordingly, $r = (1, 1)$ and $n = (2, 6)$. **(E)** A neutral-type event has no effect on the genealogy and zero production in all demes: $r = (0, 0)$, $n = (5, 3)$. **(F)** The theory presented here allows for compound events. As an example, here a birth/death-type event occurs, wherein one yellow lineage is extinguished and a blue lineage simultaneously sires a blue child. For this event, we have $r = (2, 0)$ and $n = (6, 2)$. **(G)** Here, a compound sample/death-type event with $r = (0, 0)$ and $n = (2, 5)$ occurs. A blue lineage is sampled and simultaneously extinguished. Note that recursive removal does not occur, since sample nodes are never removed. **(H)** A compound birth/migration-type event with $r = (4, 0)$ and $n = (6, 2)$.

- (d) At a sample-type event (Fig. 4D), the appropriate number of sampled lineages are selected at random from among the tip nodes, with uniform probability according to deme. One new sample node is introduced for each selected lineage: each is inserted between a selected tip nodes and its ancestor.
- (e) At a neutral-type event (Fig. 4E), no change is made to the genealogy.
- (f) Finally, events of compound type (e.g., Fig. 4F–H) are accommodated by combining the foregoing rules.

In each of these events, the new node or nodes that are introduced have node-times equal to the time of the jump.

3.2.1. Emergent lineages and production. The lineages which descend from an inserted node are said to *emerge* from the event. Thus, after a birth-type event, the emerging lineages include all the new offspring as well as the parent. Likewise, at pure migration- or sample-type events, each migrating or sampled lineage emerges from the event. At pure death-type events, no lineages emerge. In general, at an event of mark u , there are r_i^u emergent lineages in deme i . We require that r_i^u be a constant, for each u and i . Since, in applications, one is free to expand the set of jump-marks \mathbb{U} as needed, this is not an important restriction on the models that the theory can

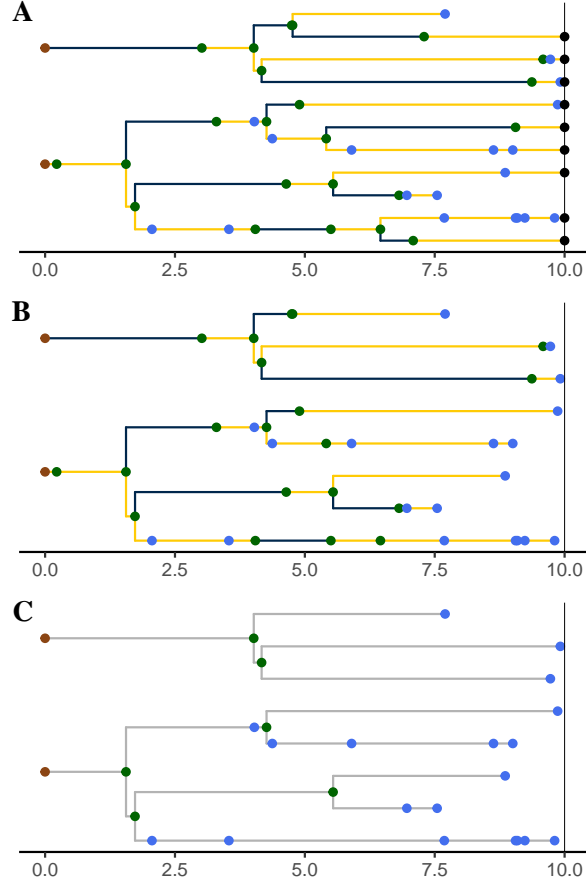


FIGURE 5. Unpruned, pruned, and obscured genealogies from a single realization of the genealogy process induced by the SEIRS model depicted in Figs. 1 and 2. (A) A realization of the unpruned genealogy process \mathbf{G}_t is shown at $t = 10$. Tip nodes, corresponding to lineages alive at time $t = 10$ are indicated with black points. Blue points represent samples; green points, internal nodes. Branches are colored according to the deme in which the corresponding lineage resided at that point in time: blue denotes E and yellow, I. (B) The genealogy is *pruned* by deleting all tip nodes and then recursively pruning away childless internal nodes. Sample nodes are never removed. (C) A genealogy is *obscured* by effacing all deme information from lineage histories: the colors are erased, as are all inline nodes. See the text (§§2.6, 3.3.1, and 3.3.4) for more detail.

accommodate. Thus there is a function $r : \mathbb{U} \times \mathbb{D} \rightarrow \mathbb{Z}_+$, such that r_i^u lineages of deme i emerge from each event of mark u . We say $r^u = (r_i^u)_{i \in \mathbb{D}}$ is the *production* of an event of mark u . Note that the lineages that die as a result of an event do not count in the production but that a parent lineage that survives the event does count.

3.2.2. Conditional independence and exchangeability. Application of these rules at each jump of \mathbf{X}_t constructs a chain of genealogies $\hat{\mathbf{G}}_k$. In particular, at each jump-time $\hat{\mathbf{T}}_k$, the genealogy $\hat{\mathbf{G}}_{k-1}$ is modified according to the jump-mark $\hat{\mathbf{U}}_k$ to yield $\hat{\mathbf{G}}_k$. We view $\hat{\mathbf{G}}_k$ as the embedded chain of the continuous-time genealogy process \mathbf{G}_t . It is very important to note that, conditional on $\hat{\mathbf{U}}_k$, the number of parents and number of offspring in each deme is determined and the random choice of which lineages die, migrate, are sampled, or sire offspring is independent of the choices at any other times and independent of $(\hat{\mathbf{T}}_k, \hat{\mathbf{X}}_k)$ for all k . Moreover, by construction, any lineage within a deme is as likely as any other lineage in that deme to be selected as a parent or for death, sampling, or migration. We refer to this property as the *exchangeability* of lineages within a deme.

3.3. Pruned and obscured genealogies. The process just described yields a genealogy that relates all extant members of the population, and all samples. Moreover, it details each lineage's complete history of movement through the various demes. The data we ultimately wish to analyze will be based only on samples, however. Nor, in general, will the histories of deme occupancy be observable. A generative model must account for this loss of information. We therefore now describe how genealogies are *pruned* to yield sample-only genealogies and then *obscured* via the erasure of color from their branches.

3.3.1. Pruned genealogy. Given a genealogy G , one obtains the *pruned genealogy*, $P = \text{prune}(G)$ by first dropping every tip node and then recursively dropping every childless internal node (Fig. 5A–B). In a pruned genealogy only internal and sample nodes remain, and sample nodes are found at all of the leaves and possibly some of the interior nodes of the genealogy. Observe that a pruned genealogy is a colored genealogy: it retains information about where among the demes each of its lineages was through time (Fig. 5B). Note also that a pruned genealogy P is characterized by functions P^y and P^z just as an un-pruned genealogy is. Finally, observe that, since it contains within itself all of its past history, the pruned genealogy process $\mathbf{P}_t = \text{prune}(\mathbf{G}_t)$ is Markov, even though the unpruned genealogy process, \mathbf{G}_t , is not.

3.3.2. Lineage count and saturation. In the following, we will find that we need to count the deme-specific numbers of lineages present in a given pruned genealogy at a given time. Accordingly, suppose $P = (y, z)$ is a pruned genealogy with $\mathfrak{t}(P) = T$ and suppose $t \in [0, T]$. Let ℓ_i denote the number of lineages in deme i at time t and $\ell = (\ell_i)_{i \in \mathbb{D}} \in \mathbb{Z}_+^{\mathbb{D}}$. Clearly, ℓ depends only on the values, (y_t, z_t) , of y and z at time t . Therefore, we can define ℓ as a function such that, whenever $P = (y, z)$ is a pruned genealogy, $\ell(y_t, z_t)$ is the vector of deme-specific lineage counts at time t . We refer to ℓ as the *lineage-count function* (cf. Fig. 6).

We will also have occasion to refer to the deme-specific number of lineages emerging from a given event. In particular, given a node time t in a pruned genealogy $P = (y, z)$, the number s_i of lineages of deme i emerging from all nodes with time t is well defined and we can write $s = (s_i)_{i \in \mathbb{D}}$. Like the lineage-count function, s depends only on the local structure of P . However, s depends not only on (y_t, z_t) , but also on $(\tilde{y}_t, \tilde{z}_t)$. Thus, we can define the *saturation function* such that, whenever $P = (y, z)$ is a pruned genealogy, $s(\tilde{y}_t, y_t, \tilde{z}_t, z_t)$ is the integer vector of deme-specific numbers of emerging lineages at time t . Fig. 6 illustrates.

3.3.3. Compatibility. Suppose P is a pruned genealogy, with $\mathfrak{t}(P) = T$ and $t \in \mathring{P}$. The local structure of P at t is, in general, compatible with only a subset of the possible jumps \mathbb{U} . For example, if the event in P at t is a branch node or a sample node, then it is compatible only with birth-type or sample-type jumps, respectively. Similarly, if the node in P at time t is one at which a lineage moves from deme i to deme i' , then u must be either of $i \rightarrow i'$ migration type or of a birth type with parent in i and $r_i^u > 0$. To accommodate all possibilities, let us introduce the indicator function Q such that $Q = 1$ if the local genealogy structure—which is captured by the values of y and z just before and after t —is compatible with an event of type u and $Q = 0$ otherwise. That is, $Q_u(\eta, \eta', \zeta, \zeta') = 1$ if and only if there is a feasible genealogy, $G = (y, z)$, and history, H , and a $t \in [0, T]$ such that, given $\mathbf{G}_T = G$ and $\mathbf{H}_T = H$, $U_t = u$, $\tilde{y}_t = \eta$, $y_t = \eta'$, $\tilde{z}_t = \zeta$, and $z_t = \zeta'$. We refer to Q as the *compatibility indicator*.

3.3.4. Obscured genealogy. The *obscured genealogy* is obtained by discarding all information about demes and events not visible from the topology of the tree alone. In particular, if $P = (y, z)$ is a pruned genealogy, we write $\text{obs}(P) = P^z = z$ to denote the obscured genealogy.

4. Results.

4.1. Likelihood for pruned genealogies. Our first result will be an expression for the likelihood of a given pruned genealogy given the history of the population process.

Theorem 1. Suppose $P^* = (y^*, z^*)$ is a given pruned genealogy with $\mathfrak{t}(P^*) = T$. Define

$$\phi_u(x, y, y', z, z') := \begin{pmatrix} n(x) & \ell(y', z') \\ r^u & s(y, y', z, z') \end{pmatrix} Q_u(y, y', z, z'), \quad (3)$$

where n is the deme occupancy (§2.2.2), ℓ and s are the lineage-count and saturation functions, respectively (§3.3.2), Q is the compatibility indicator (§3.3.3), and the binomial ratio is as defined in §2.7. Then

$$\text{Prob}[\mathbf{P}_T = P^* \mid \mathbf{H}_T = H] = \mathbb{1}\{\mathring{H} \supseteq \mathring{P}^*\} \prod_{t \in \mathring{H}} \phi_{U_t}(X_t, \tilde{y}_t^*, y_t^*, \tilde{z}_t^*, z_t^*).$$

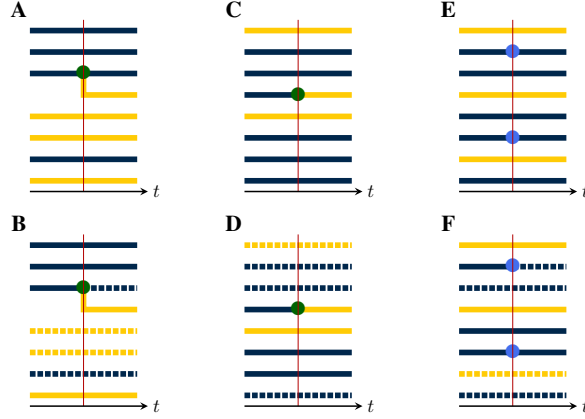


FIGURE 6. **Lineage count and saturation.** Each panel shows the neighborhood of a single event in the unpruned genealogy (top row) and the corresponding pruned genealogy (bottom row). **(A)** A birth-type event with production $r = (r_{\text{blue}}, r_{\text{yellow}}) = (1, 1)$ occurs. **(B)** Pruning results in the removal of the dashed lineages. The lineage count at this event-time is $\ell = (\ell_{\text{blue}}, \ell_{\text{yellow}}) = (2, 2)$. The saturation is $s = (0, 1)$ since only a single, yellow lineage emerges from the event. **(C)** A migration-type event with production $r = (0, 1)$ occurs. **(D)** After pruning, $\ell = (2, 2)$ and $s = (0, 1)$. **(E)** A sample-type event occurs in which two blue lineages are sampled (production $r = (2, 0)$). **(F)** After pruning, $\ell = (2, 2)$ and $s = (1, 0)$. Observe that in panels B and D, the local structures of the pruned genealogies are identical, though they arise from events of different type.

Proof. If $\hat{H} \not\subseteq \hat{P}^*$, then H and P^* are incompatible and $\text{Prob}[\mathbf{P}_T = P^* \mid \mathbf{H}_T = H] = 0$. Similarly, if any event of H is incompatible with the local structure of P^* in the sense of §3.3.3, then $\text{Prob}[\mathbf{P}_T = P^* \mid \mathbf{H}_T = H] = 0$. Let us therefore suppose that neither of these conditions hold. Conditional on $\mathbf{H}_T = H$, at each time $t \in \hat{H}$, a jump of mark U_t occurred, with a production of $r^{U_t} = (r_i)_{i \in \mathbb{D}}$, resulting in a deme-occupancy of $n(X_t) = (n_i)_{i \in \mathbb{D}}$. In P^* , at time t , there are $\ell_i = \ell_i(y_t^*, z_t^*)$ lineages in deme i , of which $s_i = s_i(\tilde{y}_t^*, y_t^*, \tilde{z}_t^*, z_t^*)$ are emergent. By assumption, at each genealogical event, lineages within a deme are exchangeable: each has an identical probability of being involved. This exchangeability implies that each lineage present in a deme at time t was equally likely to have been one of the emergent lineages. In particular, at time t , the probability that s_i of the ℓ_i deme- i lineages were among the r_i of n_i lineages emergent in the inventory process is the same as the probability that, upon drawing ℓ_i balls without replacement from an urn containing r_i red balls and $n_i - r_i$ black balls, exactly s_i of the drawn balls are red, namely

$$\frac{\binom{n_i - \ell_i}{r_i - s_i} \binom{\ell_i}{s_i}}{\binom{n_i}{r_i}}.$$

Because our lineages are labelled, each of the $\binom{\ell_i}{s_i}$ equally probable sets of s_i lineages is distinct; just one of these is the one present in P^* . Moreover, since, again conditional on $\mathbf{H}_T = H$, the identities of the lineages involved in a genealogical event are random and independent of the identities selected at all other events, we have established that

$$\text{Prob}[\mathbf{P}_T = P^* \mid \mathbf{H}_T = H] = \prod_{t \in \hat{H}} \binom{n(X_t)}{r^{U_t}} \frac{\ell(y_t^*, z_t^*)}{s(\tilde{y}_t^*, y_t^*, \tilde{z}_t^*, z_t^*)}.$$

Returning to the possibility that H is incompatible with P^* , since $\text{Prob}[\mathbf{P}_T = P^*] = 0$ if either any $Q_u = 0$ or $\hat{P}^* \not\subseteq \hat{H}$, we obtain the result. \square

Next, we show how the likelihood of a pruned genealogies, unconditional on the history, can be computed. For this, we use the filter equation technology developed in Appendix A. In particular, the following theorem follows immediately from Lemma A2.

Theorem 2. *Suppose that $P^* = (y^*, z^*)$ is a pruned genealogy with $\mathfrak{t}(P^*) = T > 0$. Suppose that $w = w(t, x)$ satisfies the initial condition $w(0, x) = p_0(x)$ and the filter equation*

$$\begin{aligned} \frac{\partial w}{\partial t}(t, x) &= \sum_u \int w(t, x') \alpha_u(t, x', x) \phi_u(x, \tilde{y}_t^*, y_t^*, \tilde{z}_t^*, z_t^*) dx' - \sum_u \int w(t, x) \alpha_u(t, x, x') dx', \quad t \notin \mathring{P}^*, \\ w(t, x) &= \sum_u \int \tilde{w}(t, x') \alpha_u(t, x', x) \phi_u(x, \tilde{y}_t^*, y_t^*, \tilde{z}_t^*, z_t^*) dx', \quad t \in \mathring{P}^*, \end{aligned} \quad (4)$$

where ϕ is defined in Eq. 3. Then the likelihood of P^* is

$$\mathcal{L}(P^*) = \int w(T, x) dx.$$

4.2. Likelihood for obscured genealogies. Our next result concerns the likelihood of a given obscured genealogy conditional on the history.

Theorem 3. *Suppose z^* is a given obscured genealogy with $\mathfrak{t}(z^*) = T$. Let q and π be probability kernels, such that for all $u \in \mathbb{U}$, $t \in \mathbb{R}_+$, $x, x' \in \mathbb{X}$, $y, y' \in Y_t(z^*)$,*

$$q(x, y) \geq 0, \quad \sum_{y \in Y_0(z^*)} q(x, y) = 1, \quad \pi_u(t, x, x', y, y') \geq 0, \quad \sum_{y' \in Y_t(z^*)} \pi_u(t, x, x', y, y') = 1.$$

Suppose moreover that $\pi_u(t, x, x', y, y') > 0$ whenever $\alpha_u(t, x, x') Q_u(y, y', \tilde{z}_t^, z_t^*) > 0$ and that $q(x, y) > 0$ whenever $\text{Prob}[P_0^y = y \mid \mathbf{X}_0 = x] > 0$. Then there is a stochastic jump process \mathbf{y}_t with sample paths in $Y(z^*)$ such that $(\mathbf{X}_t, \mathbf{U}_t, \mathbf{y}_t)$ is Markov and*

$$\text{Prob}[\mathbf{P}_T^z = z^* \mid \mathbf{H}_T = H] = \mathbb{1}\{\mathring{H} \supseteq \mathring{z}^*\} \mathbb{E} \left[\frac{1}{q(X_0, \mathbf{y}_0)} \prod_{t \in \mathring{H}} \frac{\phi_{U_t}(X_t, \tilde{\mathbf{y}}_t, \mathbf{y}_t, \tilde{z}_t^*, z_t^*)}{\pi_{U_t}(t, \tilde{X}_t, X_t, \tilde{\mathbf{y}}_t, \mathbf{y}_t)} \right],$$

where ϕ is defined in Eq. 3 and the expectation is taken over the sample paths of \mathbf{y}_t .

Proof. First, observe that, since obs is a deterministic operator,

$$\text{Prob}[\mathbf{z}_T = z^* \mid \mathbf{H}_T = H] = \mathbb{E}[\mathbb{1}\{\mathbf{P}_T^z = z^*\} \mid \mathbf{H}_T = H]. \quad (5)$$

Our strategy will be to evaluate Eq. 5 using importance sampling: we will propose pruned genealogies compatible with z_t^* as sample paths from a stochastic process driven by \mathbf{X}_t and evaluate the expectation in Eq. 5 by summing over these paths. Conditional on $\mathbf{H}_T = H$, the initial distribution q and probability kernel π generate a Markov chain, $\hat{\mathbf{y}}_k$ such that

$$\text{Prob}[\hat{\mathbf{y}}_0 \mid \mathbf{H}_T = H] = q(X_0, \hat{\mathbf{y}}_0), \quad \text{Prob}[\hat{\mathbf{y}}_k \mid \hat{\mathbf{y}}_{k-1}, \mathbf{H}_T = H] = \pi_{\hat{U}_k}(\hat{T}_k, \hat{X}_{k-1}, \hat{X}_k, \hat{\mathbf{y}}_{k-1}, \hat{\mathbf{y}}_k).$$

The required process \mathbf{y}_t is the unique càdlàg process with event times \hat{T}_k and $\hat{\mathbf{y}}_k$ as its embedded chain. This construction of \mathbf{y}_t obviously guarantees that $\mathring{H} \supseteq \mathring{y} \supseteq \mathring{z}^*$ and that $(\mathbf{X}_t, \mathbf{U}_t, \mathbf{y}_t)$ is Markov.

Now, for $y \in Y(z^*)$, let us define $C(y) = (y, z^*)$. Then, by construction, $\text{obs}(C(y)) = z^*$ and, conversely, for every pruned genealogy P satisfying $P^z = z^*$, $C(P^y) = P$. Moreover, the conditions on the kernels q and π guarantee that, if $\text{Prob}[\mathbf{P}_T = P \mid \mathbf{H}_T = H] > 0$ and $P^z = z^*$, then $\text{Prob}[\mathbf{y} = P^y] > 0$. We therefore have that

$$\text{Prob}[\mathbf{z}_T = z^* \mid \mathbf{H}_T = H] = \mathbb{E} \left[\frac{\text{Prob}[\mathbf{P}_T = C(\mathbf{y}) \mid \mathbf{H}_T = H]}{\pi(\mathbf{y} \mid H)} \right],$$

the expectation being taken with respect to the random process \mathbf{y} . Here, by definition,

$$\pi(\mathbf{y} \mid H) = q(X_0, \mathbf{y}_0) \prod_{t \in \mathring{H}} \pi_{U_t}(t, \tilde{X}_t, X_t, \tilde{\mathbf{y}}_t, \mathbf{y}_t).$$

The result then follows from Theorem 1. □

The final result shows how to compute the likelihood of an obscured genealogy. It is an immediate consequence of Theorem 3 and Lemma A2.

Theorem 4. *Let z^* be a given obscured genealogy and $T = \mathfrak{t}(z^*)$. Then there are probability kernels q and π as in Theorem 3 such that if*

$$\beta_u(t, x, x', y, y') = \alpha_u(t, x, x') \pi_u(t, x, x', y, y'), \quad \psi_u(t, x, x', y, y') = \frac{\phi_u(x', y, y', \tilde{z}_t^*, z_t^*)}{\pi_u(t, x, x', y, y')},$$

and if $w = w(t, x, y)$ satisfies the initial condition $w(0, x, y) = p_0(x) q(x, y)$ and the filter equation

$$\frac{\partial w}{\partial t} = \sum_{uy'} \int w(t, x', y') \beta_u(t, x', x, y', y) \psi_u(t, x', x, y', y) dx' - \sum_{uy'} \int w(t, x, y) \beta_u(t, x, x', y, y') dx', \quad t \in \mathbb{Z}^*,$$

$$w(t, x, y) = \sum_{uy'} \int \tilde{w}(t, x', y') \beta_u(t, x', x, y', y) \psi_u(t, x', x, y', y) dx', \quad t \in \mathbb{Z}^*,$$

then the likelihood of z^* is

$$\mathcal{L}(z^*) = \sum_y \int w(T, x, y) dx.$$

5. Examples.

5.1. SEIRS. Jumps: $\mathbb{U} = \{\text{Inf}, \text{Prog}, \text{Recov}, \text{Wane}, \text{Birth}, \text{Death}_S, \text{Death}_E, \text{Death}_I, \text{Death}_R, \text{Sample}\}$.

Demes: $\mathbb{D} = \{E, I\}$.

Jump rates:

- $\alpha_{\text{Inf}}(t, x, x') = \beta(t) \frac{x^S x^I}{N(t)} \mathbb{1}\{x' = x + (-1, 1, 0, 0)\}$
- $\alpha_{\text{Prog}}(x, x') = \rho x^E \mathbb{1}\{x' = x + (0, -1, 1, 0)\}$
- $\alpha_{\text{Recov}}(x, x') = \gamma x^I \mathbb{1}\{x' = x + (0, 0, -1, 1)\}$
- $\alpha_{\text{Wane}}(x, x') = \nu x^R \mathbb{1}\{x' = x + (1, 0, 0, -1)\}$
- $\alpha_{\text{Sample}}(t, x, x') = \psi x^I \mathbb{1}\{x' = x\}$
- $\alpha_{\text{Birth}}(t, x, x') = B(t) \mathbb{1}\{x' = x + (1, 0, 0, 0)\}$
- $\alpha_{\text{Death}_k}(x, x') = \mu x^k \mathbb{1}\{x'^j = x^j - \delta_{jk}\}, k \in \{S, E, I, R\}$

6. Discussion.

Generalization of coalescent and birth-death process approaches. Both Moran model and birth-death processes are special cases.

Allows models with demographic stochasticity. Incorporating environmental stochasticity is likely possible: extension to stochastic processes with a diffusion component.

Freedom to choose models with many demes. Freedom to choose model of sampling.

Price of flexibility is variability in the Monte Carlo estimation. Freedom to choose importance sampling distribution. Allowable to borrow information from the future.

Filter equation formalism suggests approximations based on discretization of time.

References.

- King, A. A., Lin, Q., & Ionides, E. L. (2022) Markov genealogy processes. *Theor. Popul. Biol.* **143**:77–91.
<https://doi.org/10.1016/j.tpb.2021.11.003>
- Leventhal, G. E., Günthard, H. F., Bonhoeffer, S., & Stadler, T. (2014) Using an epidemiological model for phylogenetic inference reveals density dependence in HIV transmission. *Mol. Biol. Evol.* **31**:6–17.
<https://doi.org/10.1093/molbev/mst172>
- Moran, P. A. P. (1958) Random processes in genetics. *Math. Proc. Cambridge Philos. Soc.* **54**:60–71.
<https://doi.org/10.1017/s0305004100033193>

Rasmussen, D. A., Volz, E. M., & Koelle, K. (2014) Phylodynamic inference for structured epidemiological models. *PLoS Comput. Biol.* **10**:e1003570.

<https://doi.org/10.1371/journal.pcbi.1003570>

Stadler, T. (2010) Sampling-through-time in birth-death trees. *J. Theor. Biol.* **267**:396–404.

<https://doi.org/10.1016/j.jtbi.2010.09.010>

Volz, E. M. (2012) Complex population dynamics and the coalescent under neutrality. *Genetics* **190**:187–201.

<https://doi.org/10.1534/genetics.111.134627>

Volz, E. M., Kosakovsky Pond, S. L., Ward, M. J., Leigh Brown, A. J., & Frost, S. D. W. (2009) Phylodynamics of infectious disease epidemics. *Genetics* **183**:1421–1430.

<https://doi.org/10.1534/genetics.109.106021>

Appendix A. Filter equations.

Explicit expressions for the quantities that arise in this paper are not always readily available. Here, we develop tools for manipulating complex expressions that are otherwise cumbersome.

Definition. Suppose \mathbf{X}_t is a continuous-time Markov process with Kolmogorov forward equation (KFE)

$$\frac{\partial u}{\partial t}(t, x) = \int u(t, x') \beta(t, x', x) dx' - \int u(t, x) \beta(t, x, x') dx'. \quad (\text{A1})$$

Suppose that $B(t, x, x') \geq 0$ and $\lambda(t, x)$ are given, real-valued, measurable functions. We say that the equation

$$\frac{\partial w}{\partial t}(t, x) = \int w(t, x') \beta(t, x', x) B(t, x', x) dx' - \int w(t, x) \beta(t, x, x') dx' - \lambda(t, x) w(t, x). \quad (\text{A2})$$

is the *filter equation* with *driver* \mathbf{X}_t (or *generated by* β), *boost* B , and *decay* λ .

Remark 1. Trivially, a Kolmogorov forward equation is itself a filter equation with boost 1 and decay 0.

The following results show how filter equations allow one to integrate over random histories.

Lemma A1. Suppose that $B : \mathbb{R}_+ \times \mathbb{X}^2 \rightarrow \mathbb{R}_+$ is measurable. If \mathbf{V}_t is an \mathbb{R}_+ -valued random process satisfying

$$\mathbb{E}[\mathbf{V}_t \mid \mathbf{H}_t = H] = \prod_{e \in \tilde{H}t} B(e, \tilde{X}_e, X_e),$$

then $\mathbb{E}[\mathbf{V}_t \mid \mathbf{X}_t = x]$ is a measure-valued deterministic process on \mathbb{X} with density $w(t, x)$ that satisfies the filter equation

$$\frac{\partial w}{\partial t} = \int w(t, x') \alpha(t, x', x) B(t, x', x) dx' - \int w(t, x) \alpha(t, x, x') dx'. \quad (\text{A3})$$

Moreover, $\mathbb{E}[\mathbf{V}_t] = \int w(t, x) dx$.

Proof. The expectation can be broken into three terms, according to whether H_t has zero, one, or more than one event in $(t - \Delta, t]$. Accordingly, as $\Delta \downarrow 0$,

$$\begin{aligned} w(t, x) &= \left(1 - \Delta \int \alpha(t - \Delta, x, x') dx'\right) w(t - \Delta, x) \\ &\quad + \Delta \int \alpha(t - \Delta, x', x) B(t - \Delta, x', x) w(t - \Delta, x') dx' + o(\Delta). \end{aligned}$$

In the limit, we obtain Eq. A2. The last statement follows by definition. \square

Lemma A2. Suppose $\mathcal{M} \subset \mathbb{R}_+$ is finite and let $\mathcal{M}_t := \mathcal{M} \cap [0, t]$. Suppose that $B : \mathbb{R}_+ \times \mathbb{X}^2 \rightarrow \mathbb{R}_+$ is measurable and \mathbf{V}_t is an \mathbb{R}_+ -valued process satisfying

$$\mathbb{E}[\mathbf{V}_t \mid \mathbf{H}_t = H_t] = \mathbb{1}_{\{\tilde{H}t \supseteq \mathcal{M}_t\}} \prod_{e \in \tilde{H}t} B(e, \tilde{X}_e, X_e).$$

Then $\mathbb{E}[\mathbf{V}_t \mid \mathbf{X}_t = x]$ is a measure-valued process on $\mathbb{R}_+^{|\mathcal{M}_t|} \times \mathbb{X}$ with density $w(t, x)$ that satisfies

$$\begin{aligned} \frac{\partial w}{\partial t}(t, x) &= \int w(t, x') \alpha(t, x', x) B(t, x', x) dx' - \int w(t, x) \alpha(t, x, x') dx', & t \notin \mathcal{M}, \\ w(t, x) &= \int \tilde{w}(t, x') \alpha(t, x', x) B(t, x', x) dx', & t \in \mathcal{M}. \end{aligned} \quad (\text{A4})$$

Moreover, $\mathbb{E}[\mathbf{V}_t] = \int w(t, x) dx$.

Lemma A3. Showing how Eq. A4 can be stated as a singular filter equation.

$$\begin{aligned} \frac{\partial w}{\partial t}(t, x) &= \int w(t, x') \beta(t, x', x) B(t, x', x) dx' - \int w(t, x) \beta(t, x, x') dx' \\ &+ \sum_e \int w(t, x') \delta(t, e) \pi(t, x', x) C(t, x', x) dx' - \sum_e \int w(t, x) \delta(t, e) \pi(t, x, x') dx' \\ &- \lambda(t, x) w(t, x). \end{aligned} \quad (\text{A5})$$

Filter equations afford a convenient means of computing expectations and likelihoods for pure jump processes. This is facilitated by the following Lemma, the statement of which uses a one-sided Dirac delta function. Specifically, let $\delta(v, v')$ be the right-sided Dirac delta function satisfying $\delta(v, v') = 0$ for $v \neq v'$ and

$$\int_a^b f(v) \delta(v, v') dv = f(v') \mathbb{1}\{v' \in [a, b)\},$$

whenever f is càdlàg and $-\infty \leq a < b \leq \infty$.

Lemma A4. The filter equation (A2) is satisfied by $w(t, x) = \int_0^\infty v u(t, x, v) dv$, where $u(t, x, v)$ satisfies the KFE

$$\begin{aligned} \frac{\partial u}{\partial t} &= \int_0^\infty \int u(t, x', v') \beta(t, x', x) \delta(v, B(t, x', x) v') dx' dv' \\ &- \int_0^\infty \int u(t, x, v) \beta(t, x, x') \delta(v', B(t, x, x') v) dx' dv' + \frac{\partial}{\partial v} [\lambda(t, x) v u(t, x, v)]. \end{aligned} \quad (\text{A6})$$

Proof.

$$\begin{aligned} \frac{\partial w}{\partial t} &= \int_0^\infty v \frac{\partial u}{\partial t}(t, x, v) dv \\ &= \int_0^\infty \int \int_0^\infty v u(t, x', v') \beta(t, x', x) \delta(v, B(t, x', x) v') dv dx' dv' \\ &\quad - \int_0^\infty \int \int_0^\infty v u(t, x, v) \beta(t, x, x') \delta(v', B(t, x, x') v) dv dx' dv' \\ &\quad + \int_0^\infty v \frac{\partial}{\partial v} [\lambda(t, x) v u(t, x, v)] dv. \end{aligned}$$

Here, the non-explosivity assumption guarantees that we can differentiate under the integral sign and exchange the order of integration. Moreover, it ensures that $u \rightarrow 0$ as $v \rightarrow \infty$. Hence, by evaluating the first integral with respect to v , the second with respect to v' , and the third by parts, we obtain

$$\begin{aligned} \frac{\partial w}{\partial t} &= \int v' u(t, x', v') \beta(t, x', x) B(t, x', x) dv' dx' - \int v u(t, x, v) \beta(t, x, x') dv dx' \\ &\quad - \lambda(t, x) \int v u(t, x, v) dv, \end{aligned}$$

which is simplified to obtain Eq. A2. \square

Eq. A6 is recognizable as the KFE of a certain process $(\mathbf{X}_t, \mathbf{V}_t)$. In particular, \mathbf{X}_t is the driver with KFE (A1). The \mathbf{V}_t is directed by \mathbf{X}_t in the sense that \mathbf{V} has jumps wherever \mathbf{X} does: when \mathbf{X} jumps at time t from x to x' , \mathbf{V} jumps by the multiplicative factor $B(t, x, x') \geq 0$. Between jumps, \mathbf{V}_t decays deterministically and exponentially

at rate $\lambda(t, x)$. If we view \mathbf{V}_t as a weight, then Lemma A4 tells us how the \mathbf{V}_t -weighted average of \mathbf{X}_t evolves in time: this average is simply $\int w(t, x) dx$.

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