STATS 700-002 Class 4. Sampling through time in birth-death trees

Edward Ionides and Aaron King

September 18, 2025

Stadler (2010)

Stadler, T. (2010). Sampling-through-time in birth-death trees. Journal of Theoretical Biology, 267(3), 396-404. https://doi.org/10.1016/j.jtbi.2010.09.010.

Here, we start developing models for heterochronous genealogical trees (not all leaves are at the same time).

Birth-death trees vs the coalescent

Stadler, T. (2009). On incomplete sampling under birth–death models and connections to the sampling-based coalescent. *Journal of Theoretical Biology*, 261(1), 58-66. https://doi.org/10.1016/j.jtbi.2009.07.018

Deals with homochronous sampling (i.e., all samples at the end time, T)

Birth-death trees vs the coalescent

Stadler, T. (2009). On incomplete sampling under birth–death models and connections to the sampling-based coalescent. *Journal of Theoretical Biology*, 261(1), 58-66. https://doi.org/10.1016/j.jtbi.2009.07.018

- lackbox Deals with homochronous sampling (i.e., all samples at the end time, T)
- ▶ Similar to Kingman's coalescent, but not identical

Birth-death trees vs the coalescent

Stadler, T. (2009). On incomplete sampling under birth–death models and connections to the sampling-based coalescent. *Journal of Theoretical Biology*, 261(1), 58-66.

https://doi.org/10.1016/j.jtbi.2009.07.018

- lackbox Deals with homochronous sampling (i.e., all samples at the end time, T)
- Similar to Kingman's coalescent, but not identical
- What are the advantages and disadvantages?

Definitions

Notice the deletion of ancestors of unsampled lineages. We will call this *pruning*.

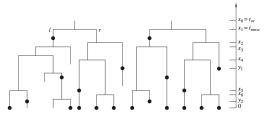


Fig. 1. An example of an oriented tree with root edge induced by the birth-death process displaying all sampled and non-sampled individuals is shown on the left. The left descendant of a bifurcation is l, the right descendant is r. Note that we only ladel one pair of descendants with l and r for easier readability. The right tree is the corresponding sampled tree with n=5 extant individuals, m=2 extinct individuals without sampled descendants, and k=3 extinct individuals with sampled descendants in the sampled tree, the bifurcation times are at x= $(x_1, \dots, x_{n-m}, 1)$ and the sampling times of extinct individuals without sampled descendants are at y= (y_1, y_2) . The time of origin is t_n = t_n 0 and the time of the most recent common ancestor of the extant species is t_{max} = t_n 1.

Lemma 2.3

How do you prove the first identity?

$$\sum_{N=n}^{\infty} \binom{N}{n} a^N = \frac{a^n}{(1-a)^{n+1}},$$

Lemma 2.3

How do you prove the first identity?

$$\sum_{N=n}^{\infty} \binom{N}{n} a^N = \frac{a^n}{(1-a)^{n+1}},$$

You can always ask Al

Master equations

$$\begin{split} \dot{p}_0(t) &= \mu - (\lambda + \mu + \psi) p_0(t) + \lambda p_0(t)^2, & p_0(0) = 1 - \rho, \\ \dot{p}_1(t) &= -(\lambda + \mu + \psi) p_1(t) + 2\lambda p_0(t) p_1(t), & p_1(0) = \rho. \end{split}$$

▶ What are these, and where do they come from?

An informal derivation

let $A_0(t)$, $A_1(t)$ be the events corresponding to $p_0(t)$, $p_1(t)$.

$$\begin{split} P[A_0(t+h)] &= E\Big[P\big[A_0(t+h)\,\big|\, \text{outcomes in } [t,t+h]\big]\Big] = \\ &\quad (1-[\lambda+\mu+\phi]h)P[A_0(t)] \\ &\quad + \lambda h(P[A_0])^2 \\ &\quad + \mu h \\ &\quad + o(h^2) \end{split} \tag{2}$$

Now substract $P[A_0(t)]$ from both sides, divide by h, and take a limit.

Note: we've passed a limit through expectation without justification.

Theorem 3.1.

How did Stadler guess this solution?

References I