STATS 700-002 Class 8.
Multi-type branching process models for phylodynamics

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Outline

Vaughan, T. G., & Stadler, T. (2025). Bayesian Phylodynamic Inference of Multitype Population Trajectories Using Genomic Data. *Molecular Biology and Evolution*, 42(6), msaf130. https://doi.org/10.1093/molbev/msaf130.

1. Extends Kühnert et al. (2016) to allow estimation of total population and ancestral types.
2. Uses a particle filter with a measurement model based on a combinatorial coalescence probability at each event. Compare with

   Rasmussen & Stadler (2019)

   Rasmussen, Volz & Koelle (2014)

   King, Lin & Ionides (2022)

   King, Lin & Ionides (2025)

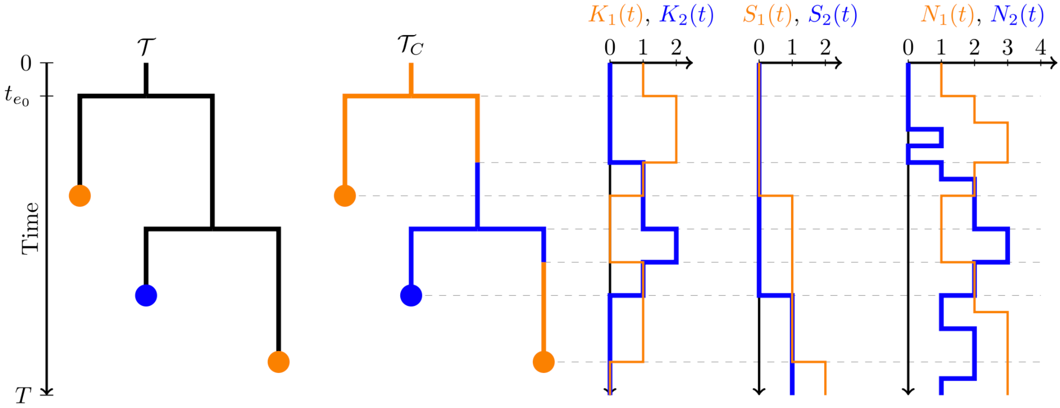
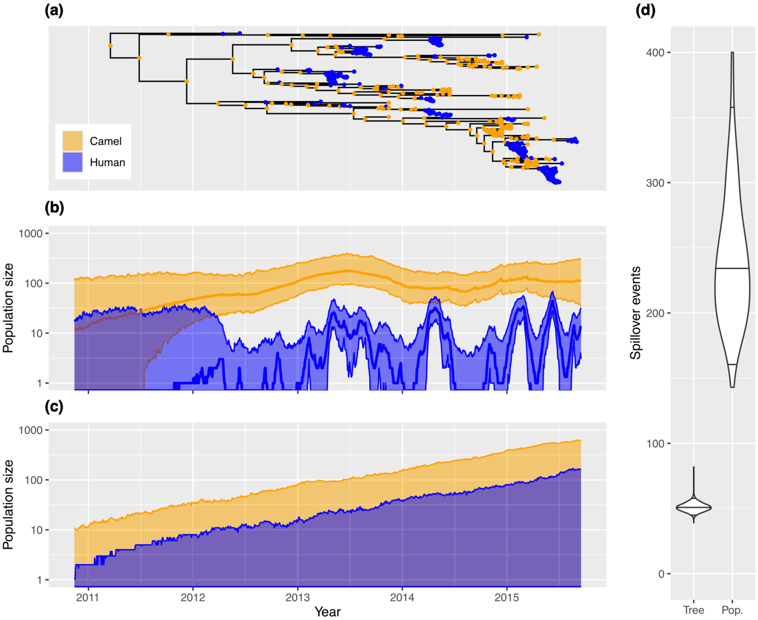
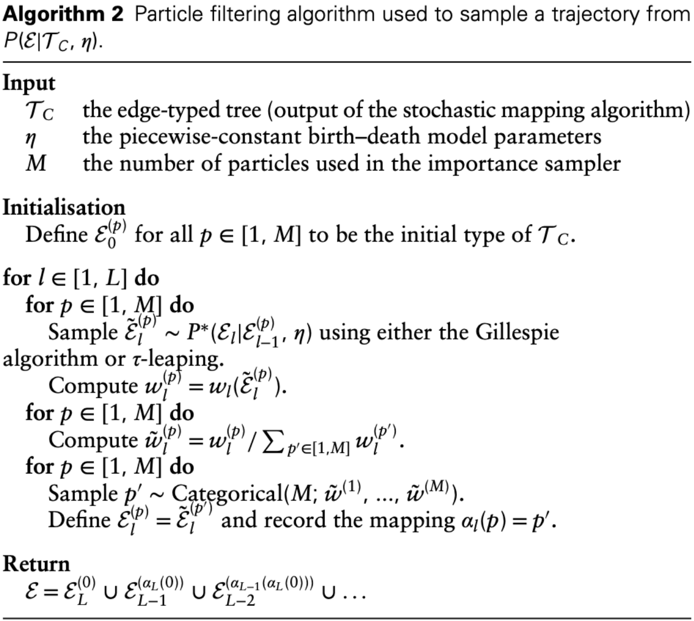


Fig. 1. Relationship between the tip-typed tree $\mathcal{T}$, the edge-typed tree $\mathcal{T}_C$, the multitype lineage-through-time function $\vec{K}(t)$, the cumulative sample count function $\vec{S}(t)$, and the multitype population size function $\vec{N}(t)$, for a single realization of a multitype birth–death-sampling model starting at time 0 and ending at time T. The time of the root of the tree is t_{e_0}.


(a)
Camel
Human
(b)
1000
100
10
1
Population size
(c)
1000
100
10
1
Population size
2011
2012
2013
2014
2015
Year
(d)
400
300
200
100
0
Spillover events
Tree
Pop.

(Fig. 4)



Algorithm 2 Particle filtering algorithm used to sample a trajectory from $P(\mathcal{E}|\mathcal{T}_C, \eta)$.

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Input
  $\mathcal{T}_C$   the edge-typed tree (output of the stochastic mapping algorithm)
  $\eta$     the piecewise-constant birth–death model parameters
  $M$     the number of particles used in the importance sampler

Initialisation
  Define $\mathcal{E}_0^{(p)}$ for all $p \in [1, M]$ to be the initial type of $\mathcal{T}_C$.

for $l \in [1, L]$ do
  for $p \in [1, M]$ do
    Sample $\tilde{\mathcal{E}}_l^{(p)} \sim P^*(\mathcal{E}_l|\mathcal{E}_{l-1}^{(p)}, \eta)$ using either the Gillespie algorithm or $\tau$-leaping.
    Compute $w_l^{(p)} = w_l(\tilde{\mathcal{E}}_l^{(p)})$.
  for $p \in [1, M]$ do
    Compute $\tilde{w}_l^{(p)} = w_l^{(p)} / \sum_{p' \in [1,M]} w_l^{(p')}$.
  for $p \in [1, M]$ do
    Sample $p' \sim \mathrm{Categorical}(M; \tilde{w}^{(1)}, ..., \tilde{w}^{(M)})$.
    Define $\mathcal{E}_l^{(p)} = \tilde{\mathcal{E}}_l^{(p')}$ and record the mapping $\alpha_l(p) = p'$.

Return
  $\mathcal{E} = \mathcal{E}_L^{(0)} \cup \mathcal{E}_{L-1}^{(\alpha_L(0))} \cup \mathcal{E}_{L-2}^{(\alpha_{L-1}(\alpha_L(0)))} \cup \dots$
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Review of the particle filter

- One perspective is https://kingaa.github.io/sbied/pfilter/slides.pdf
- This is lesson 3 of a short course on *Simulation-based Inference for Epidemiological Dynamics* at https://kingaa.github.io/sbied/

  Lessons 1 and 2 have overlap with material we've covered so far, from the point of view of time series data rather than phylogenies.

References

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