

# Asymptotic genealogies of sequential Monte Carlo algorithms

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4 December 2020

# Outline

1. Sequential Monte Carlo
2. Resampling and degeneracy
3. SMC genealogies
4. Examples

# Sequential Monte Carlo

Approximate a sequence of distributions by simulating a population of particles evolving in time

# Sequential Monte Carlo

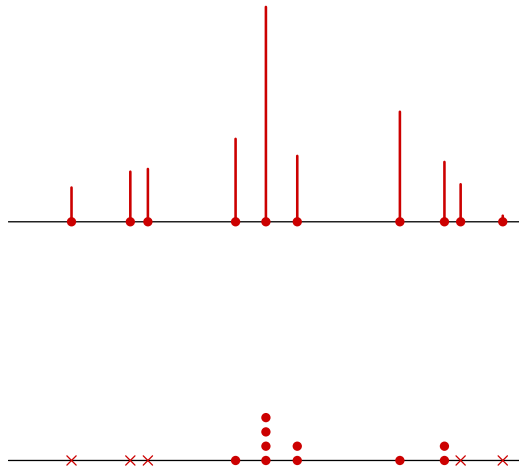
Approximate a sequence of distributions by simulating a population of particles evolving in time

Iterate these steps:

1. **Mutate** particles via Markov transition density  $q_t$
2. **Weight** particles by potential function  $g_t$
3. **Resample** particles in proportion to their weights

# Resampling

Stochastically map continuous weights  $(w_t^{(1)}, \dots, w_t^{(N)})$  to discrete offspring counts  $(\nu_t^{(1)}, \dots, \nu_t^{(N)})$

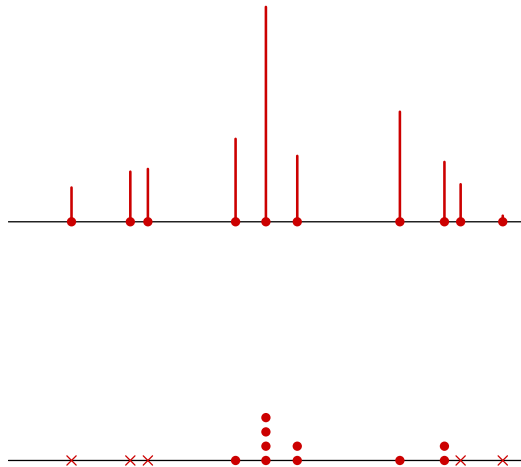


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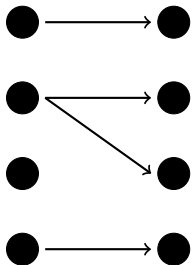
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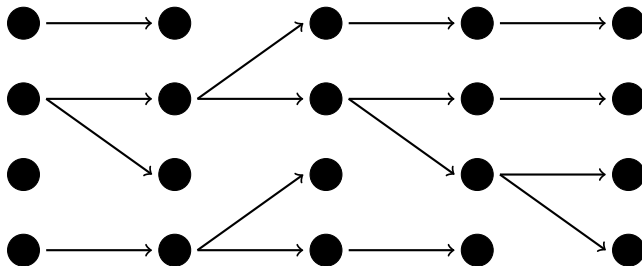
- ▶ Number of particles constant  
 $\sum_{i=1}^N \nu_t^{(i)} = N$
- ▶ Equal weights after resampling  
 $w_{t+}^{(i)} = 1/N$
- ▶ Unbiased  
 $\mathbb{E}[\nu_t^{(i)} | w_t^{(1:N)}] = N w_t^{(i)}$



## Resampling induces a genealogy

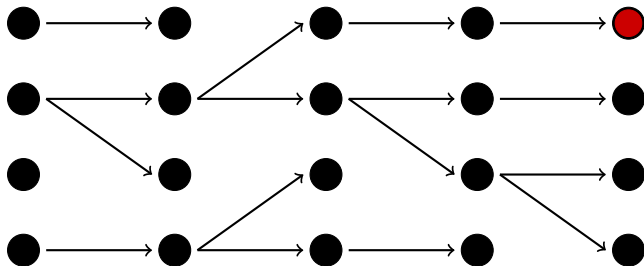


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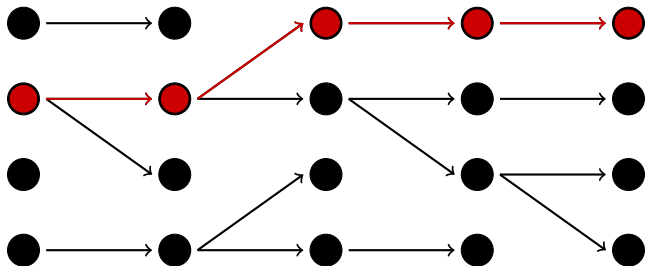




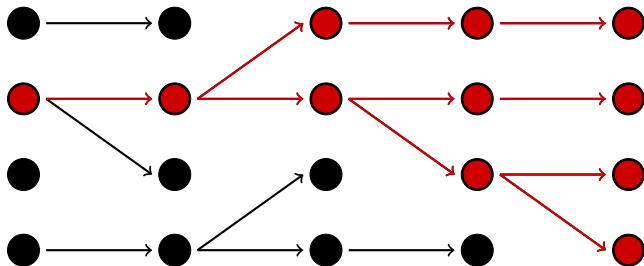
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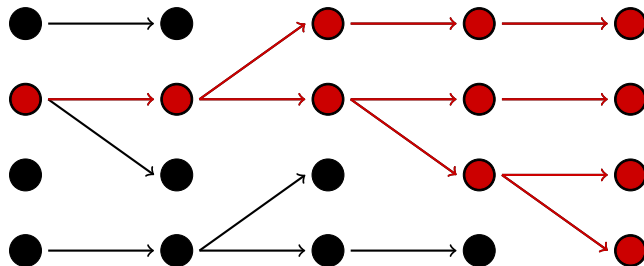
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**Ancestral degeneracy:** for  $t \ll T$ , few distinct samples are available

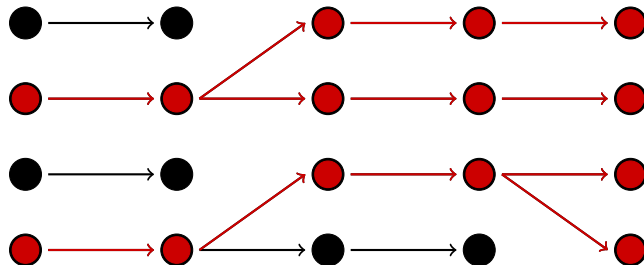
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**Adaptive resampling:** only resample when effective sample size falls below some threshold.



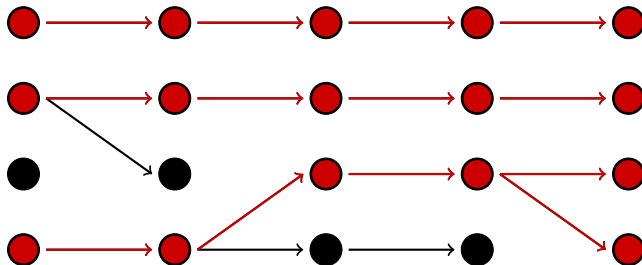
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**Low-variance resampling:** resample in a way that reduces the extra randomness added by the resampling step.





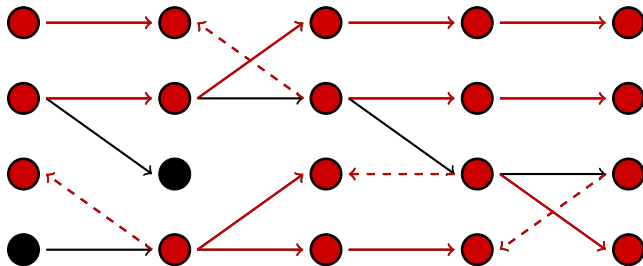
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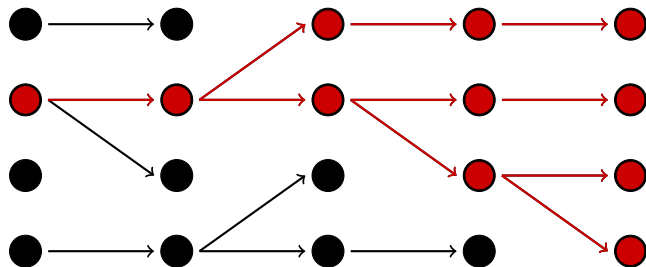
**Backward simulation:** use a backward pass to sample new ancestors for the terminal particles.



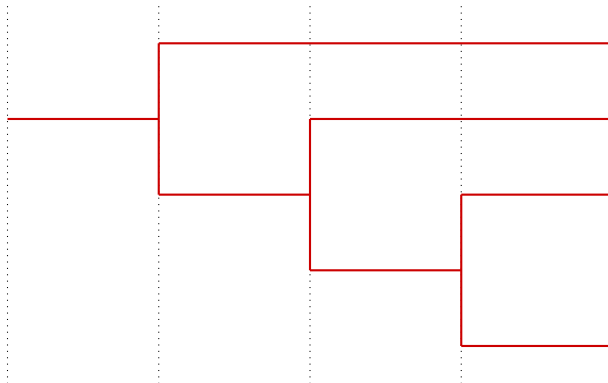
# Analysing genealogies

- ▶ How many particles should I use to maintain  $k$  distinct trajectories across time horizon  $T$ ?
- ▶ How big a lag can I use in fixed-lag smoothing?
- ▶ How reliable is my smoothing estimator?
- ▶ How do resampling schemes compare?

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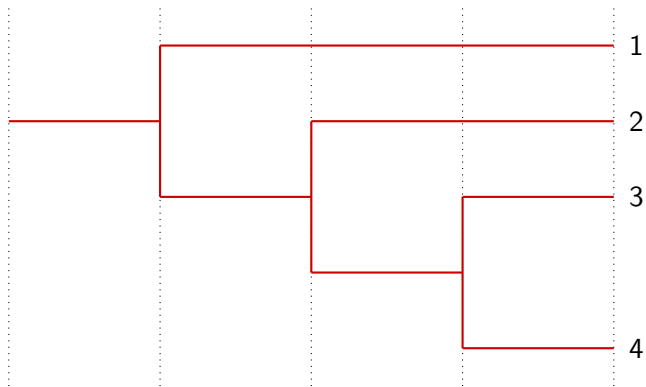
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- ▶ Describe genealogy by stochastic process  $(G_t^{(n,N)})_{t \in \mathbb{N}_0}$  on space of partitions of  $\{1, \dots, n\}$
- ▶ Elements  $i, j$  are in the same block of the partition  $G_t^{(n,N)}$  iff particles  $i$  and  $j$  share a common ancestor at time  $t$



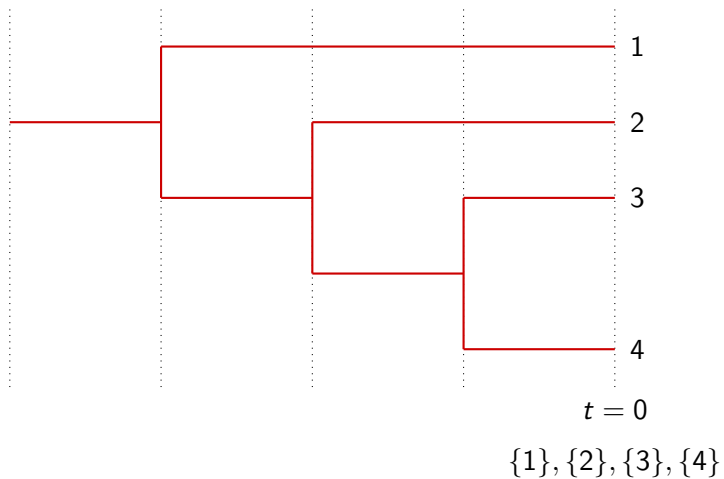
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- ▶ Initially  $G_0^{(n,N)} = \{\{1\}, \dots, \{n\}\}$
- ▶ The only possible non-identity transitions are those that merge blocks
- ▶ The trivial partition  $\{\{1, \dots, n\}\}$  is an absorbing state

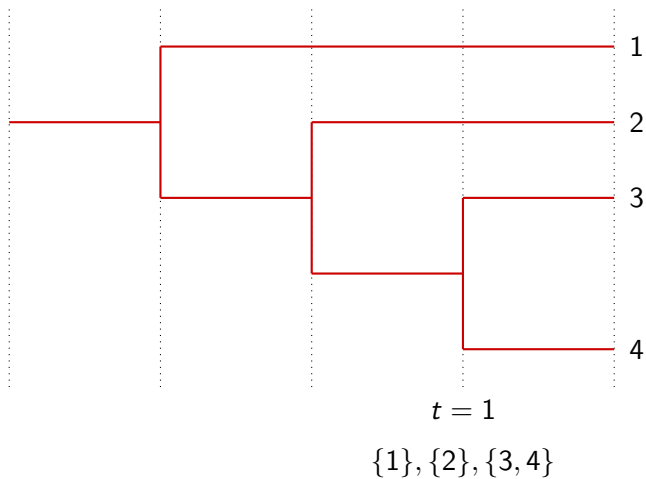
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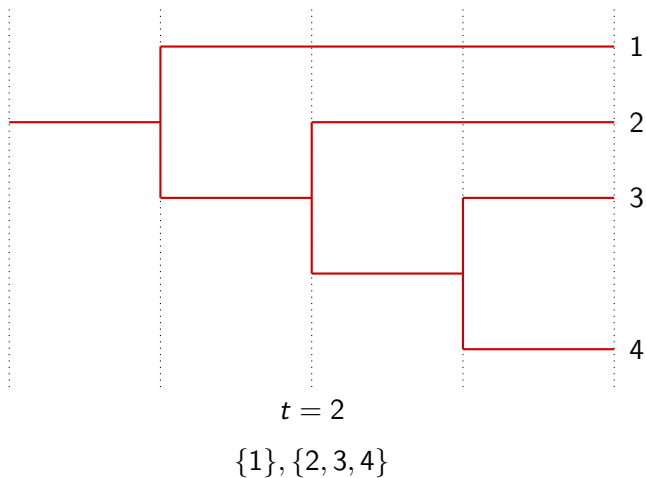
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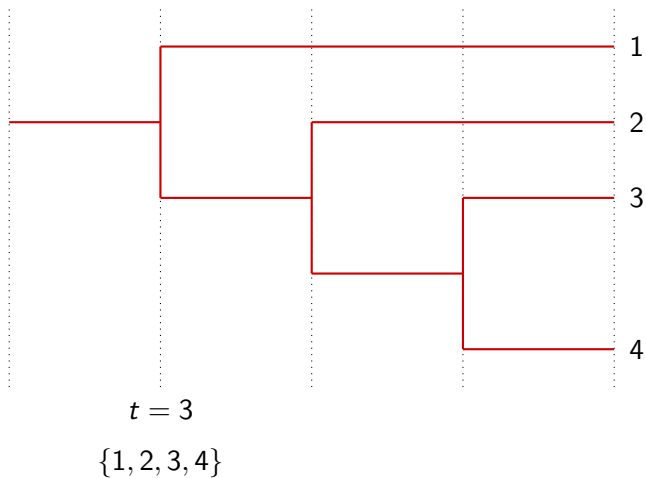
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# Kingman's $n$ -coalescent<sup>1</sup>

- ▶ Continuous-time Markov chain on the space of partitions of  $\{1, \dots, n\}$
- ▶ Single pair mergers only
- ▶ Each pair merges independently at rate 1 (total merge rate  $\binom{k}{2}$  while there are  $k$  distinct lineages)

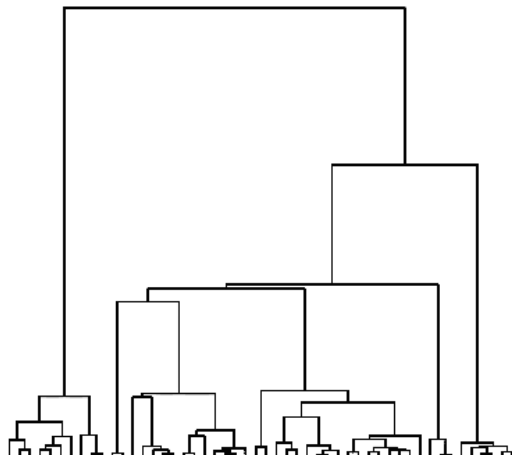


image: Wikimedia Commons

<sup>1</sup>J F C Kingman, *Stochastic Processes & their Applications*, 1982.

Pair merger probability conditional on  $(\nu_t^{(1)}, \dots, \nu_t^{(N)})$ :

$$c_N(t) = \frac{1}{(N)_2} \sum_{i=1}^N (\nu_t^{(i)})_2$$



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Rescale time by inverse:

$$\tau_N(t) := \inf \left\{ s \geq 1 : \sum_{r=1}^s c_N(r) \geq t \right\}$$

# Main theorem

Conditions:

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- ▶ There exists a sequence  $(b_N)$  such that  $\lim_{N \rightarrow \infty} b_N = 0$  and

$$\frac{1}{(N)_3} \sum_{i=1}^N \mathbb{E}_t[(\nu_t^{(i)})_3] \leq b_N \frac{1}{(N)_2} \sum_{i=1}^N \mathbb{E}_t[(\nu_t^{(i)})_2]$$

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Then the finite-dimensional distributions of the time-rescaled genealogies  $(G_{\tau_N(t)}^{(n,N)})_{t \geq 0}$  converge to Kingman's  $n$ -coalescent as  $N \rightarrow \infty$ .

# Examples

- ▶ Multinomial resampling
- ▶ Stochastic rounding
- ▶ Conditional SMC with multinomial resampling

# Multinomial resampling

Resample from a Categorical distribution, so offspring counts are Multinomial:

$$(\nu_t^{(1)}, \dots, \nu_t^{(N)}) \sim \text{Multinomial} \left( N, (w_t^{(1)}, \dots, w_t^{(N)}) \right)$$

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for constants  $0 < \varepsilon \leq 1 \leq a < \infty$ , and probability distribution  $h(\cdot)$ .

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# Stochastic rounding

$\mathbf{Y} : \mathbb{R}_+^N \rightarrow \mathbb{N}^N$  is a *stochastic rounding* of  $\mathbf{X}$  if for  $i = 1, \dots, N$

$$Y_i \mid X_i = \begin{cases} \lfloor X_i \rfloor & \text{with probability } 1 - X_i + \lfloor X_i \rfloor \\ \lfloor X_i \rfloor + 1 & \text{with probability } X_i - \lfloor X_i \rfloor \end{cases}$$

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- ▶ **Examples:** systematic, residual-stratified, branching system<sup>3</sup>, SSP<sup>4</sup> resampling

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A particle Gibbs<sup>5</sup> scenario...

- ▶ Want to target  $p(\theta, x_{0:T} \mid y_{0:T})$

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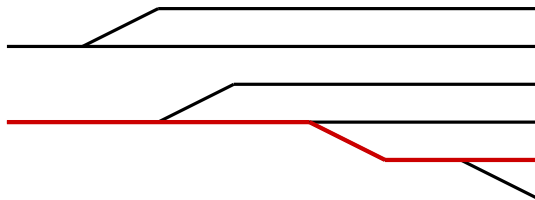
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- ▶ Resampling must deterministically propagate this “immortal lineage”

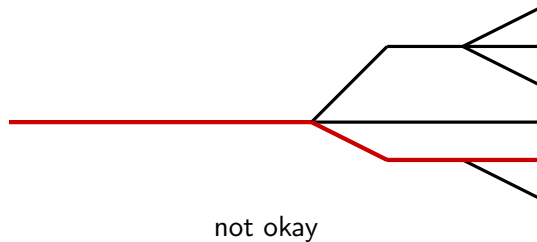
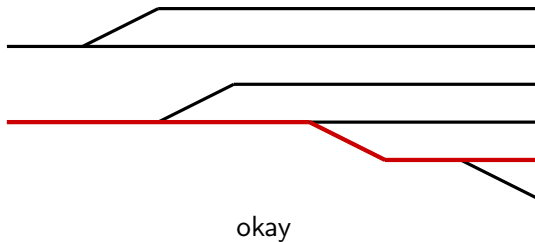
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## Quantities of interest

- Time to MRCA: first time when there is only one distinct lineage

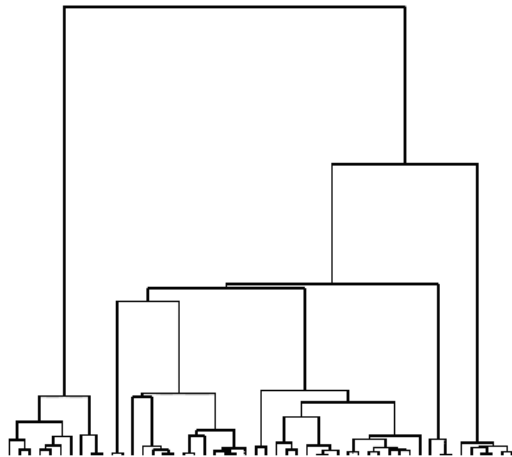


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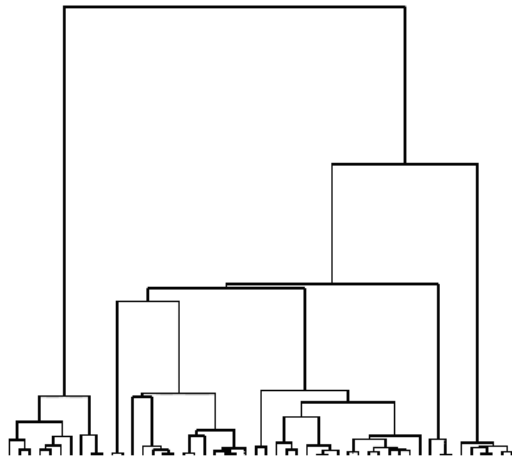


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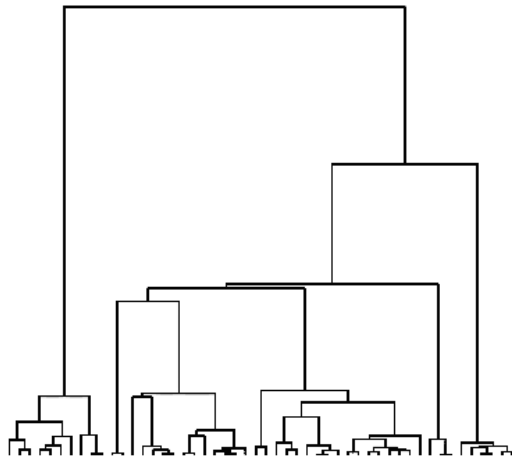


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- ▶ **Adaptive resampling**: should slow down the time-scale on which the coalescent is recovered (it may have some other effect)
- ▶ **Low-variance resampling**: stochastic rounding schemes have minimal variance
- ▶ **Backward simulation**: the backward-in-time process is not a pure coalescent, and is not induced by resampling



## In conclusion...

- ▶ Genealogies can help us to analyse performance of SMC algorithms which suffer ancestral degeneracy
- ▶ We have simple conditions under which these genealogies converge to Kingman's  $n$ -coalescent
- ▶ These conditions are verified for some important classes of SMC algorithms

# Open questions

- ▶ Weak convergence
- ▶ Other resampling schemes (stratified, residual-multinomial, ...)
- ▶ Effect of adaptive resampling
- ▶ Estimating the time scale  $\tau_N$  a priori (since it depends on observed offspring counts)
- ▶ Finite- $N$  behaviour

Thank you!

pre-print at [arXiv:2007.00096](https://arxiv.org/abs/2007.00096)