Kingman limit for non-neutral populations with applications to sequential Monte Carlo

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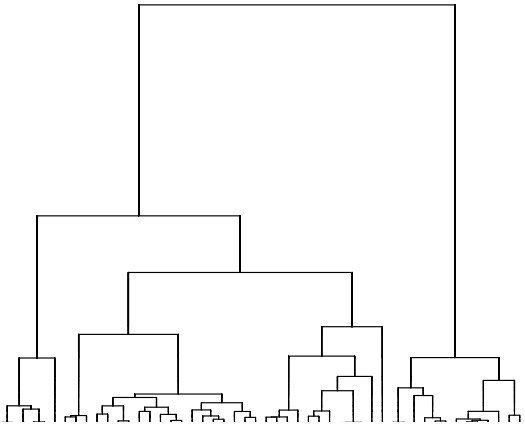
22 July 2021

Outline

1. Kingman's n-coalescent & population models
2. A history of convergence to the coalescent
3. Application to sequential Monte Carlo

Kingman's n-coalescent[1]

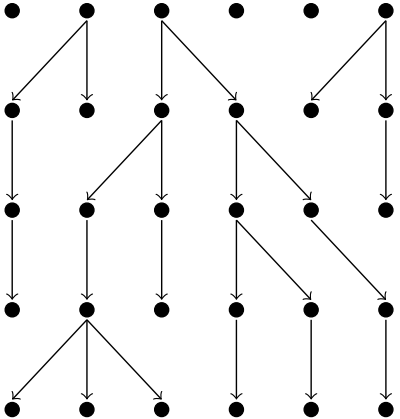
- Continuous-time Markov chain on the space of partitions of $\{1, \ldots, n\}$
- Single pair mergers only
- Each pair merges independently at rate 1 (total merge rate $\binom{k}{2}$ while there are k distinct lineages)
- Exchangeable



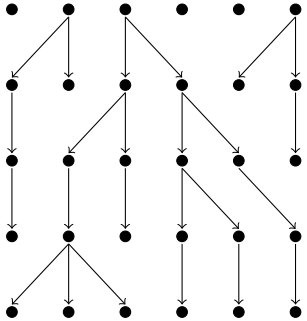
[1] JFC Kingman, *Stochastic Processes & their Applications*, 1982.

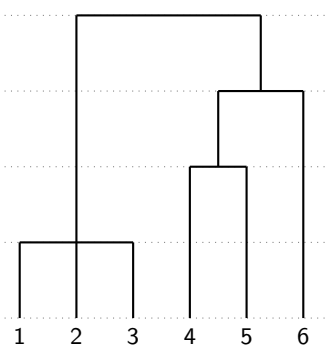
Question

Under what conditions does a population have genealogies that are asymptotically distributed as n-coalescents?



Encoding genealogies





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$G_0 = \{\{1\},\{2\},\{3\},\{4\},\{5\},\{6\}\}$

Common assumptions on population

- discrete generations
- population size $N(t)$ at generation t; define $N := N(0)$
- offspring counts $(\nu_1(t), \ldots, \nu_N(t))$ at generation t
- define the coalescence rate $c_N(t) := \frac{1}{(N)_2} \sum_{i=1}^{N} (\nu_i(t))_2$

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- define the coalescence rate $c_N(t) := \frac{1}{(N)_2} \sum_{i=1}^{N} (\nu_i(t))_2$
- consider a random sample of n individuals from the terminal generation
- scale time to obtain a non-trivial limiting process
- take $N \to \infty$

Kingman's sufficient conditions[2]

Population model:

- fixed population size $N(t) \equiv N$
- offspring counts $(\nu_1(t), \ldots, \nu_N(t))$ i.i.d. over t
- $(\nu_1, \ldots, \nu_N)$ exchangeable

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Time scale: $N\sigma^{-2}$

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- $\lim_{N\to\infty} \mathrm{Var}[\nu_1] = \sigma^2 \in (0, \infty)$
- $\mathbb{E}[\nu_1^k] \leq M_k$ for each $k \in \mathbb{N}$

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Then the finite-dimensional distributions of the rescaled sample genealogies converge to those of the n-coalescent as $N \to \infty$.

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Möhle's necessary & sufficient conditions[3]

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Time scale:

$$\frac{1}{\mathbb{E}[c_N]} = \frac{N-1}{\mathrm{Var}[\nu_1]}$$

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Möhle's necessary & sufficient conditions[3]

Conditions:

$$\lim_{N\to\infty} \frac{\mathbb{E}[(\nu_1)_3]}{N\mathbb{E}[(\nu_1)_2]} = 0$$

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Möhle's necessary & sufficient conditions[3]

Conditions:

$$\lim_{N\to\infty} \frac{\mathbb{E}[(\nu_1)_3]}{N\mathbb{E}[(\nu_1)_2]} = 0$$

if and only if the FDDs of the rescaled sample genealogies converge to those of the n-coalescent as $N \to \infty$.

[3] M Möhle, *Advances in Applied Probability*, 2000.

Möhle's sufficient conditions for weak convergence[4]

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- population size $N(t)$ any deterministic function of t; $N := N(0)$
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Time scale: some function $\tau_N(t)$ such that for all t

- $\lim_{N\to\infty} \sum_{r=1}^{\tau_N(t)} \mathbb{E}[c_N(r)] = t$
- $\lim_{N\to\infty} \sum_{r=1}^{\tau_N(t)} \mathbb{E}[c_N(r)]^2 = 0$

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Möhle's sufficient conditions for weak convergence[4]

Conditions: for all $t > 0, k \geq 0$

$$\limsup \frac{1}{N(t-1)^3 c_N(t)} \sum_{i=1}^{N(t)} \mathbb{E}[(\nu_i(t))_2 (\nu_i(t))^k] = 0$$

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Then the rescaled sample genealogies converge weakly to the n-coalescent as $N \to \infty$.

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A non-neutral population model

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genotypes	$X_{1:N}(t+1)$	$X_{1:N}(t)$	$X_{1:N}(t-1)$
fitnesses	$w_{1:N}(t+1)$	$w_{1:N}(t)$	$w_{1:N}(t-1)$
offspring counts	$\nu_{1:N}(t+1)$	$\nu_{1:N}(t)$	$\nu_{1:N}(t-1)$

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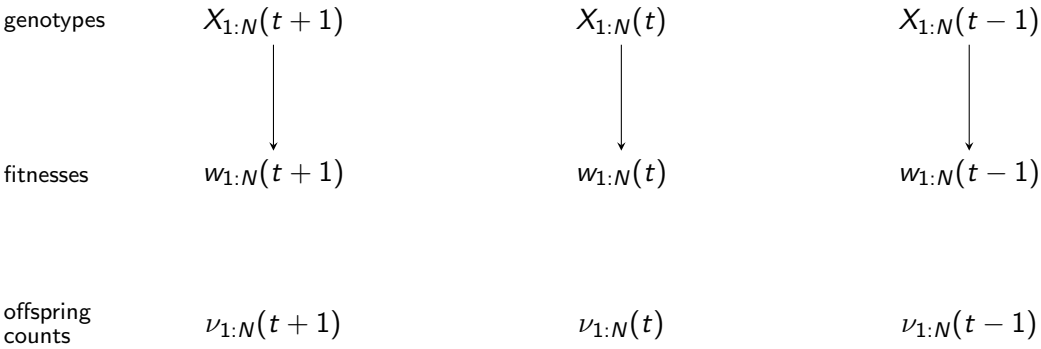

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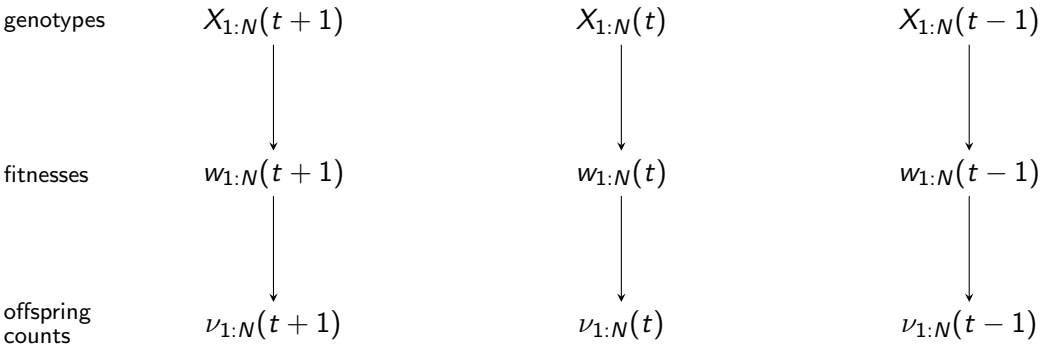

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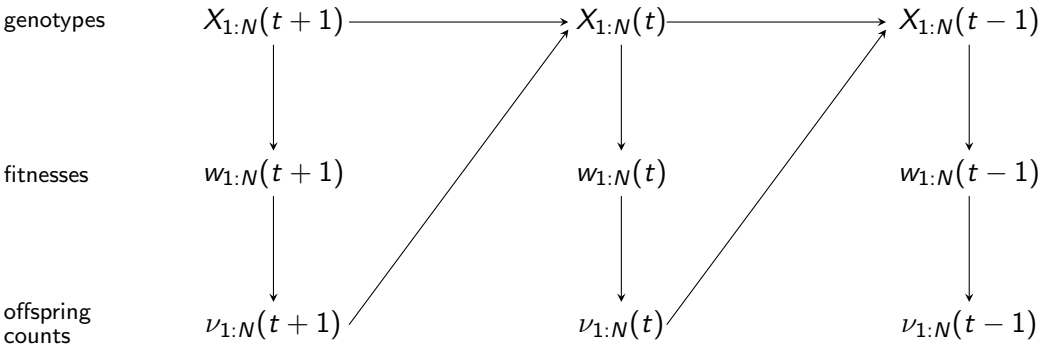

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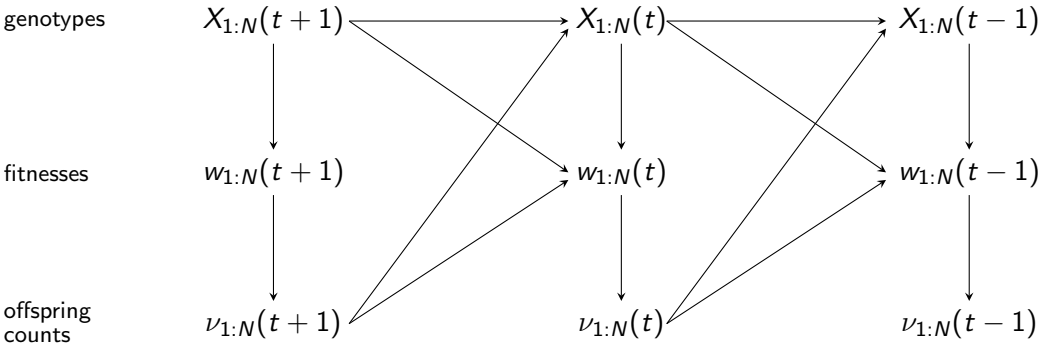

Sufficient conditions for weak convergence[5]

Population model:

- fixed population size $N(t) \equiv N$
- offspring counts $(\nu_1(t), \ldots, \nu_N(t))$ conditionally dependent over t as in previous slide
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[5] S Brown, PA Jenkins, AM Johansen, J Koskela, *Electronic Journal of Probability*, 2021.

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Time scale:

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

and assume that $\mathbb{P}[\tau_N(t) = \infty] = 0$ for all finite t

[5] S Brown, PA Jenkins, AM Johansen, J Koskela, *Electronic Journal of Probability*, 2021.

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Conditions: there exists a deterministic sequence $b_N \to 0$ such that for all N, t

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

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Sequential Monte Carlo

Aim: simulate a particle system that approximates a given sequence of probability distributions.

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Initialise N particles by sampling their genotypes $X_{1:N}$ from some distribution $\mu(\cdot)$

Then iterate these steps:

1. **(mutation)** update the genotypes via Markov kernel M_t
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- μ, (M_t) and (g_t) are chosen such that the particle system approximates the desired distributions
- The selection step induces a genealogy, which affects performance of the algorithm

Sequential Monte Carlo genealogies

- Most of the popular sequential Monte Carlo algorithms have asymptotically Kingman genealogies (under standard assumptions)[6]
- Behaviour of the time scale differs depending on the particular algorithm, and is an indicator of performance
- Explicitly characterising the time scale would allow better tuning and comparisons between algorithms

[6] S Brown, PA Jenkins, AM Johansen, J Koskela, *Electronic Journal of Probability*, 2021.

In conclusion...

- Many neutral population models are known to have asymptotically Kingman genealogies
- We add to these a large class of non-neutral models, having a particular conditional independence structure rather than independent generations
- For these models, weak convergence to the n-coalescent is proved under simple sufficient conditions
- This result is applied to several popular sequential Monte Carlo algorithms
- Next step: explicitly describe the time scale function in these cases

References

1,2 JFC Kingman (1982) *On the genealogy of large populations*, Stochastic Processes and their Applications.

3 M Möhle (2000) *Total variation distances and rates of convergence for ancestral coalescent processes in exchangeable population models*, Advances in Applied Probability.

4a M Möhle (1998) *Robustness results for the coalescent*, Journal of Applied Probability.

4b M Möhle (1999) *Weak convergence to the coalescent in neutral population models*, Journal of Applied Probability.

5,6 S Brown, PA Jenkins, AM Johansen, J Koskela (2021) *Simple conditions for convergence of sequential Monte Carlo genealogies with applications*, Electronic Journal of Probability.