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

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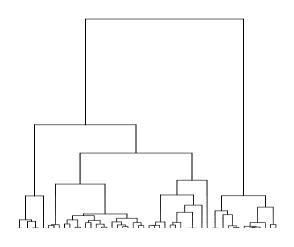
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Outline

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

Kingman's *n*-coalescent¹

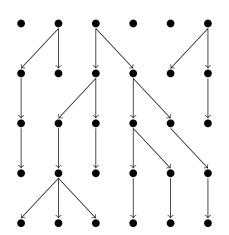
- ► Continuous-time Markov chain on the space of partitions of $\{1, \ldots, n\}$
- ► Single pair mergers only
- ► Each pair merges independently at rate 1 (total merge rate $\binom{k}{2}$ while there are k distinct lineages)
- Exchangeable



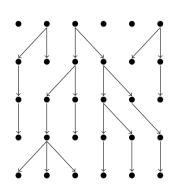
¹JFC Kingman, Stochastic Processes & their Applications, 1982.

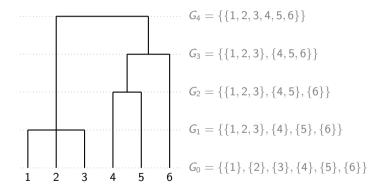
Question

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



Encoding genealogies





Common assumptions on population

- ▶ discrete generations
- **>** population size N(t) at generation t; define N := N(0)
- lacktriangle offspring counts $(
 u_1(t), \dots,
 u_N(t))$ at generation t
- lacktriangle 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
- ightharpoonup take $N o \infty$

Kingman's sufficient conditions²

Population model:

- ▶ fixed population size $N(t) \equiv N$
- \blacktriangleright offspring counts $(\nu_1(t), \dots, \nu_N(t))$ i.i.d. over t
- \blacktriangleright (ν_1,\ldots,ν_N) exchangeable

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

Conditions:

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

Then the FDDs of the rescaled sample genealogies converge to those of the *n*-coalescent as $N \to \infty$.

²JFC Kingman, Stochastic Processes & their Applications, 1982.

Möhle's necessary & sufficient conditions³

Population model:

- ▶ fixed population size $N(t) \equiv N$
- ▶ offspring counts $(\nu_1(t), \dots, \nu_N(t))$ i.i.d. over t
- \blacktriangleright (ν_1,\ldots,ν_N) exchangeable

Time scale:

$$rac{1}{\mathbb{E}[c_{\mathcal{N}}]} = rac{\mathcal{N}-1}{\mathsf{Var}[
u_1]}$$

³M Möhle, Advances in Applied Probability, 2000.

Möhle's necessary & sufficient conditions³

Conditions:

$$\lim_{N o\infty}rac{\mathbb{E}[(
u_1)_3]}{N\mathbb{E}[(
u_1)_2]}=0$$

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

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³M Möhle, Advances in Applied Probability, 2000.

Möhle's sufficient conditions for weak convergence⁴

Population model:

- **>** population size N(t) any deterministic function of t; N := N(0)
- ightharpoonup offspring counts $(\nu_1(t), \dots, \nu_N(t))$ independent over t
- ▶ random assignment condition: given $(\nu_1(t), \dots, \nu_N(t))$, assignment of offspring to parents is uniform over all valid assignments

Time scale: some function $\tau_N(t)$ such that for all t

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

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⁴M Möhle, Journal of Applied Probability, 1998, 1999.

Möhle's sufficient conditions for weak convergence⁴

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

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

and

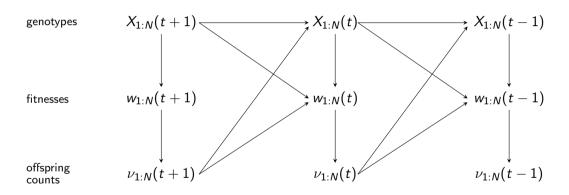
$$\limsup rac{1}{N(t-1)^4 c_N(t)} \sum_{i=1}^{N(t)} \sum_{j=1}^{N(t)} \mathbb{E}[(
u_i(t))_2 (
u_j(t))^2] = 0.$$

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

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⁴M Möhle, Journal of Applied Probability, 1998, 1999.

A non-neutral population model



Sufficient conditions for weak convergence⁵

Population model:

- ▶ fixed population size $N(t) \equiv N$
- \blacktriangleright offspring counts $(\nu_1(t), \dots, \nu_N(t))$ conditionally dependent over t as in previous slide
- random assignment condition

Time scale:

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

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

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

Sufficient conditions for weak convergence⁵

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

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

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

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

Sequential Monte Carlo

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

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
- 2. (fitness) calculate fitness scores by applying function g_t to the genotypes
- 3. (selection) resample particles according to their fitnesses
- \blacktriangleright 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 genealogies⁶
- ► 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

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⁶S 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

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- ▶ This result is applied to several popular sequential Monte Carlo algorithms
- ▶ The next step is to describe explicitly the time scale function in these cases

References

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 - 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.
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- 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.