

Asymptotic genealogies of non-neutral populations

Suzie Brown

University of Warwick, U.K.

with Paul Jenkins, Adam Johansen & Jere Koskela

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Interacting particle system

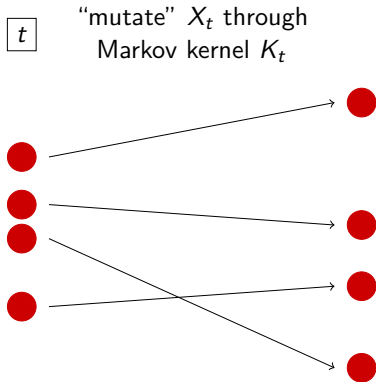
- ▶ Constant population size N
- ▶ “Genotype” $X_t^{(i)} \in \mathcal{X} \subseteq \mathbb{R}^d$
- ▶ Initial genotypes $X_0 \sim \mu$

Interacting particle system

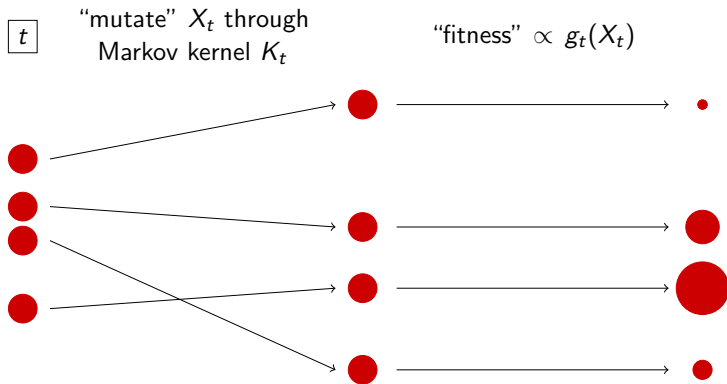
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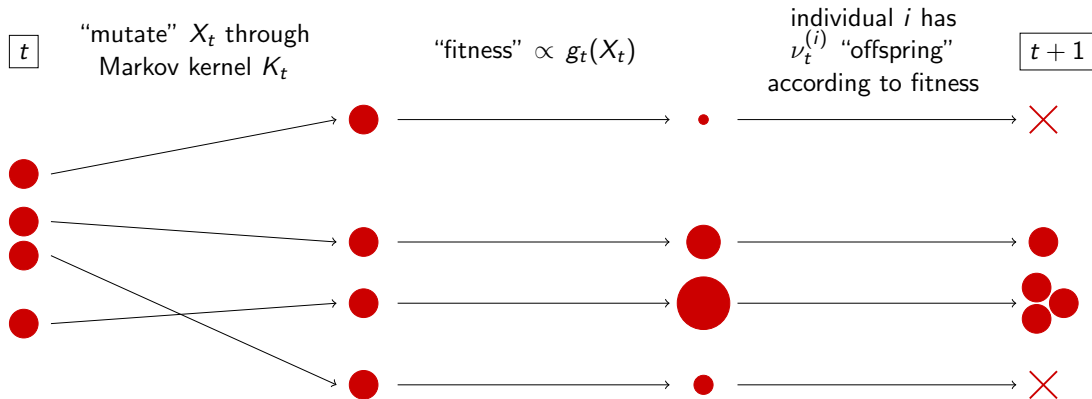
Interacting particle system



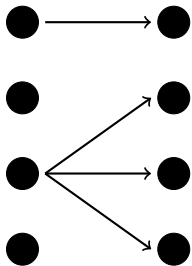
Interacting particle system



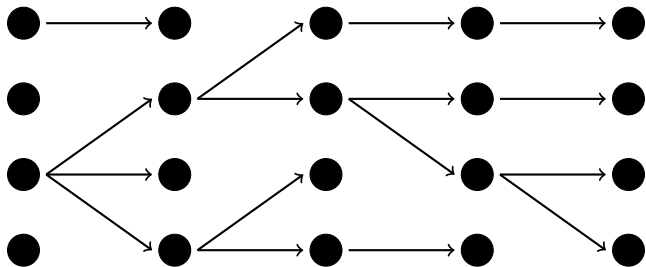
Interacting particle system



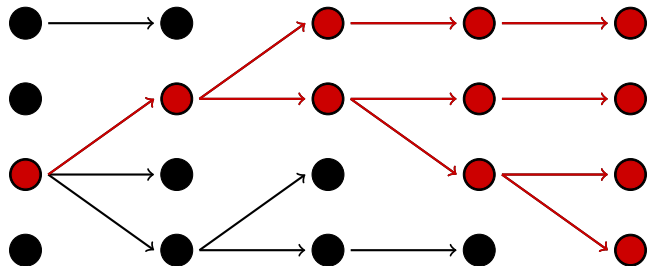
Genealogies



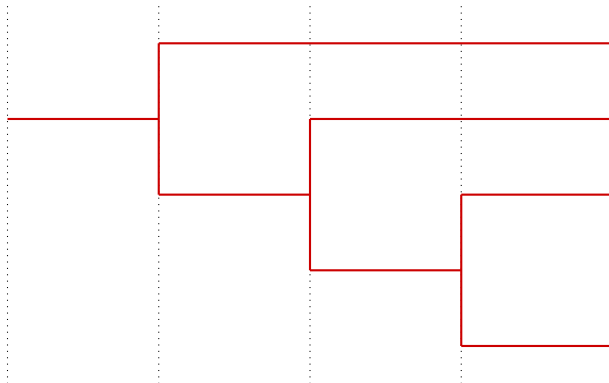
Genealogies



Genealogies

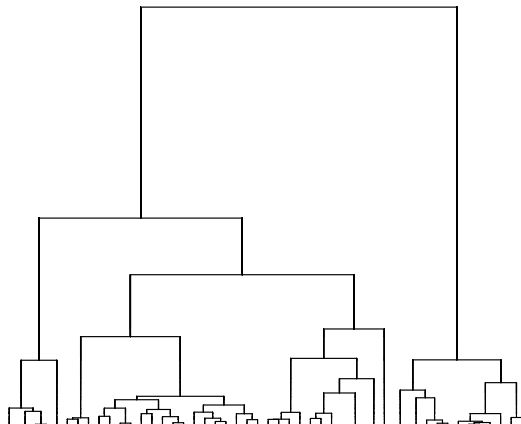


Genealogies



Kingman's n -coalescent

- ▶ 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)



Scenario

- ▶ Population size N
- ▶ Discrete generations
- ▶ Sample $n \leq N$ individuals from the terminal generation
- ▶ Rescale time appropriately
- ▶ Let $N \rightarrow \infty$

Sufficient conditions, neutral case

Theorem (Kingman 1982)

- ▶ *Individuals are exchangeable*
- ▶ *Offspring counts $\nu^{(1:N)}$ are i.i.d. across generations*
- ▶ $\text{Var}[\nu^{(1)}] = \sigma_N^2 \rightarrow \sigma^2 \in (0, \infty)$
- ▶ $\sup_N \mathbb{E}[(\nu^{(1)})^k] < \infty$ for all $k \geq 3$

Then the rescaled genealogy of n individuals converges weakly to the n -coalescent as $N \rightarrow \infty$.

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- ▶ **Wright-Fisher model:** $\nu^{(1:N)} \sim \text{Multinomial}(N, (\frac{1}{N}, \dots, \frac{1}{N}))$
- ▶ **Moran model:** $\nu^{(1:N)}$ uniform over permutations of $(2, 0, 1, \dots, 1)$

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- ▶ **Moran model:** $\nu^{(1:N)}$ uniform over permutations of $(2, 0, 1, \dots, 1)$
- ▶ Since $\sum \nu^{(i)} = N$ and individuals are exchangeable, $\mathbb{E}[\nu^{(i)}] = 1$.
- ▶ Case $\sigma^2 = 0$ would mean no coalescences in the limit

Necessary and sufficient conditions, neutral case

Theorem (Möhle Sagitov 2001, 2003)

- ▶ *Individuals are exchangeable*
- ▶ *Offspring counts $\nu^{(1:N)}$ are i.i.d. across generations*
- ▶ *$c_N > 0$ for all $N < \infty$*
- ▶ *$c_N \rightarrow 0$*
- ▶ *$d_N/c_N \rightarrow 0$*

If and only if the rescaled genealogy of n individuals converges weakly to the n -coalescent as $N \rightarrow \infty$.

$$d_N := \frac{N\mathbb{E}[(\nu^{(1)})_3]}{(N)_3}, \quad c_N := \frac{N\mathbb{E}[(\nu^{(1)})_2]}{(N)_2}$$

Necessary and sufficient conditions, neutral case

- ▶ The condition $c_N > 0$ plays the same role as Kingman's condition $\sigma^2 > 0$
- ▶ $c_N = \frac{\text{Var}[\nu^{(1)}]}{N-1}$, so $c_N \rightarrow 0$ is weaker than Kingman's condition $\text{Var}[\nu^{(1)}] \rightarrow \sigma^2$
- ▶ Only requires control up to 3rd moment, cf. Kingman requires *all* moments finite

Sufficient conditions, non-neutral case

Theorem (B Koskela Jenkins Johansen 2021)

- ▶ Given $\nu_t^{(1:N)}$, assignment of offspring to parents is uniform over all valid assignments
- ▶ Time scale is almost surely finite
- ▶ \exists deterministic sequence $b_N \rightarrow 0$ such that $\forall N, t$

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

Then the rescaled genealogy of n individuals converges weakly to the n -coalescent as $N \rightarrow \infty$.

Open questions

- ▶ Are the conditions necessary and sufficient in the non-neutral case?
- ▶ What does the random time scale look like?
- ▶ Rate of convergence?
- ▶ Can the conditions be verified for some interesting population genetic models?

References

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3. M Möhle, S Sagitov (2001) *A classification of coalescent processes for haploid exchangeable population models*. The Annals of Probability 29(4):1547–1562.
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5. S Brown, PA Jenkins, AM Johansen, J Koskela (2021) *Simple conditions for convergence of sequential Monte Carlo genealogies with applications*. Electronic Journal of Probability 26:1–22.