Evolution in a spatial continuum

Drift, draft and structure

Alison Etheridge

University of Oxford

Joint work with Nick Barton (Edinburgh) and Tom Kurtz (Wisconsin)

Kingman's Coalescent

Kingman (1982)

Neutral (haploid) population of constant size N

Wright-Fisher model: new generation determined by multinomial sampling with equal weights

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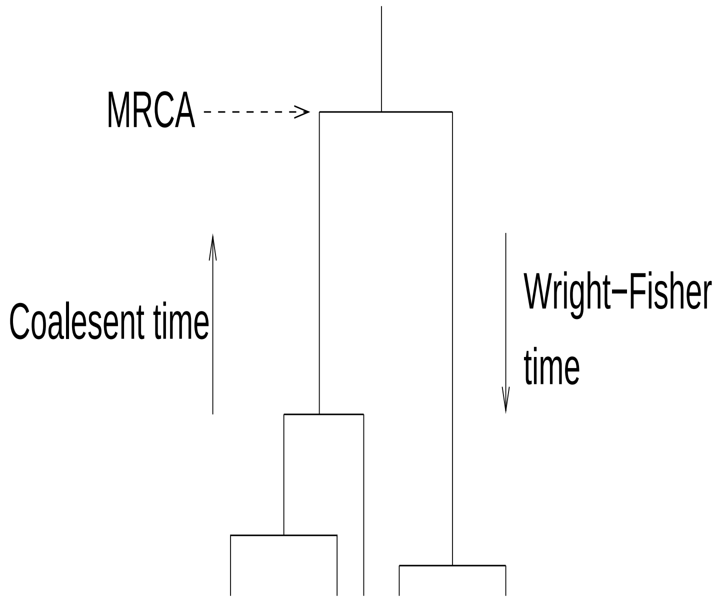

Coalescence rate $\binom{k}{2}$

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- Two types a and A.
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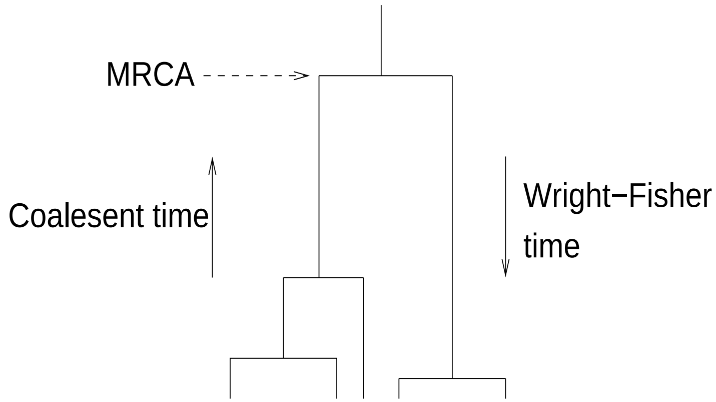

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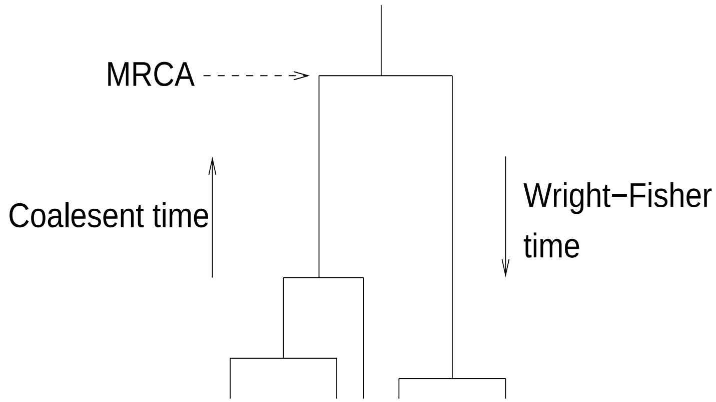

Coalescence rate $\frac{1}{N}\binom{k}{2}$

Basic observation

Genetic diversity is orders of magnitude lower than expected from census numbers and genetic drift.

Something else is going on. . .

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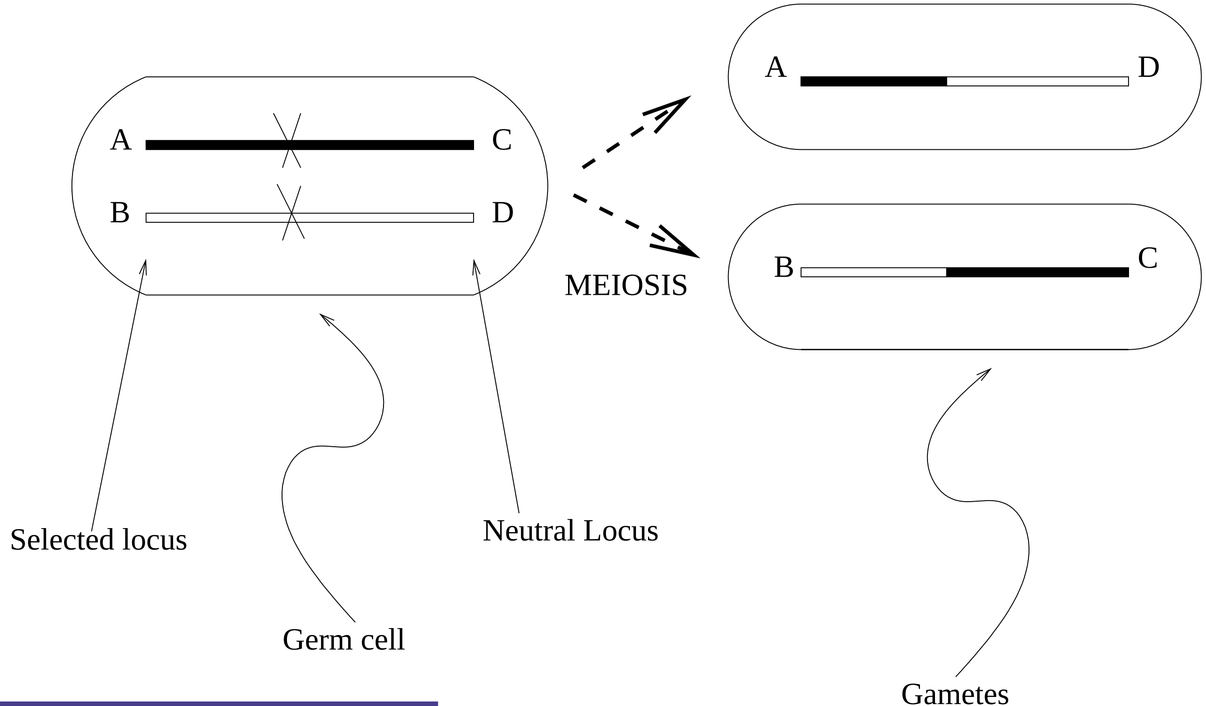

. . . genetic draft

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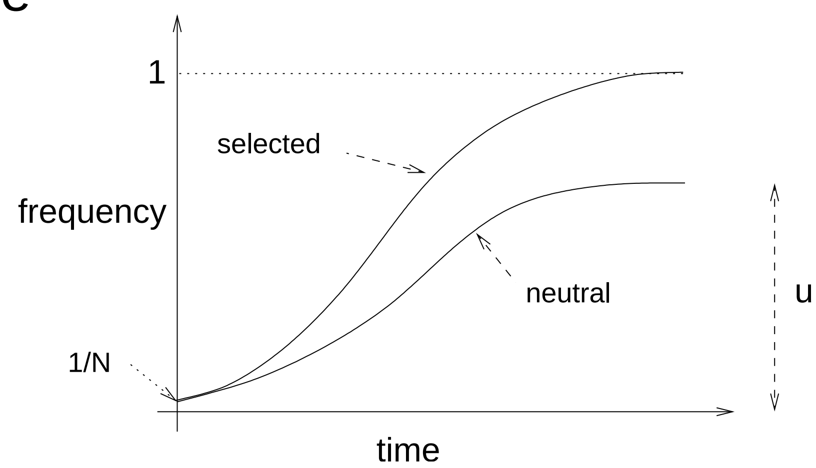
The frequency of the neutral allele linked to the new mutation will be boosted



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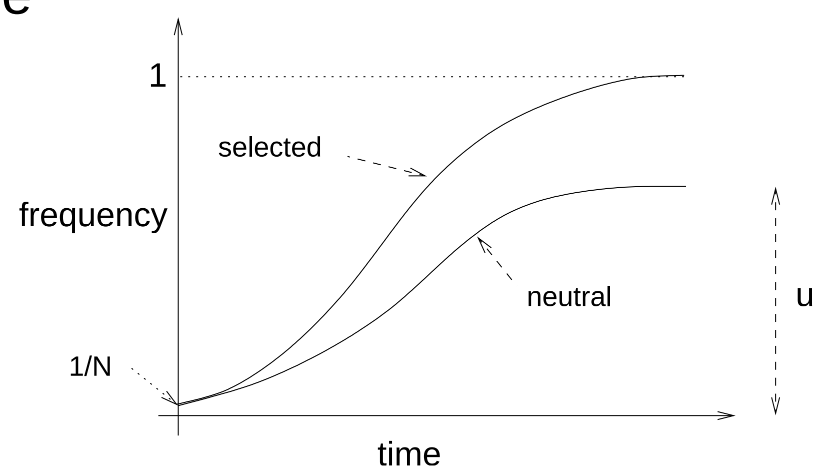

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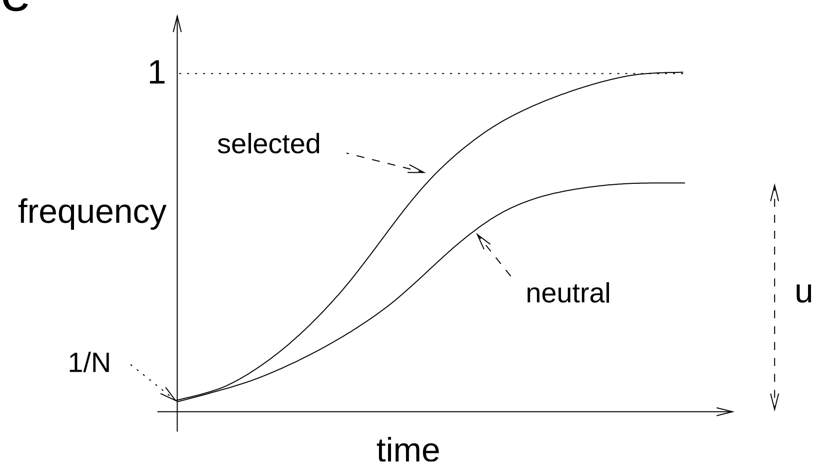

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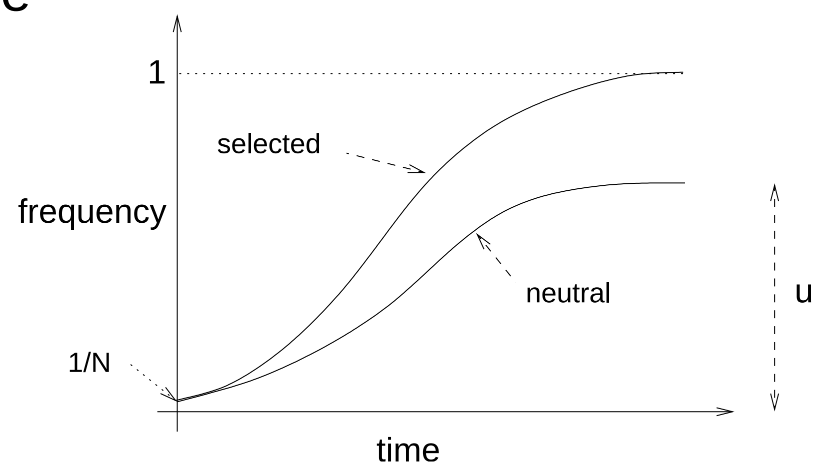

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$\mathbb{E}[(\Delta p)^3] = O(1) \implies$ *multiple* coalescences

Λ-coalescents

Pitman (1999), Sagitov (1999)

If there are currently p ancestral lineages, each transition involving j of them merging happens at rate

$$\beta_{p,j} = \int_0^1 u^{j-2}(1-u)^{p-j}\Lambda(du)$$

- Λ a finite measure on $[0,1]$
- Kingman's coalescent, $\Lambda = \delta_0$

Forwards in time

Bertoin & Le Gall (2003)

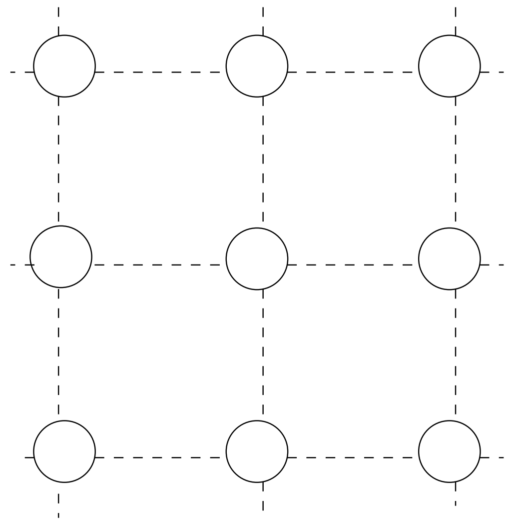
The Λ-coalescent describes the genealogy of a sample from a population evolving according to a Λ-Fleming-Viot process.

- Poisson point process intensity $dt \otimes u^{-2}\Lambda(du)$
- individual sampled at random from population
- proportion u of population replaced by offspring of chosen individual

Spatial structure

Kimura's stepping stone model

$$dp_i = \sum_j m_{ij}(p_j - p_i)dt + \sqrt{\frac{1}{N_e} p_i(1-p_i)}dW_i$$



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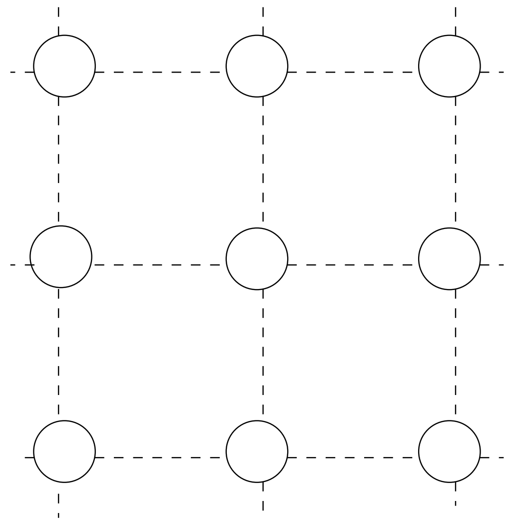

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Genealogy described by system of coalescing random walks

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- In two dimensions the equation has *no* solution
- Diffusive rescaling leads to the heat equation
- But anyway local populations are *finite*

Another basic observation

Real populations experience large scale fluctuations in which the movement and reproductive success of many individuals are correlated

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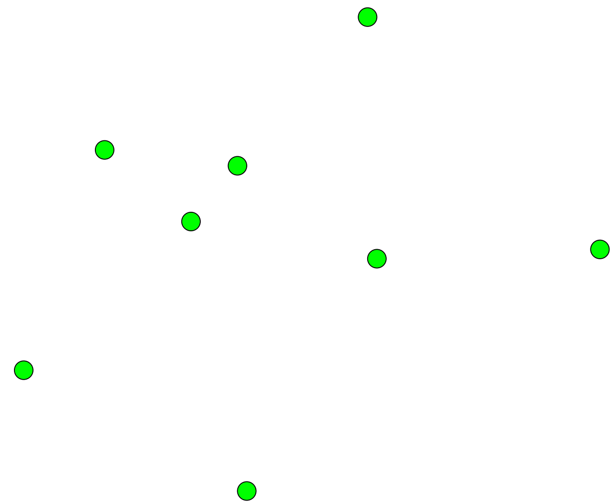

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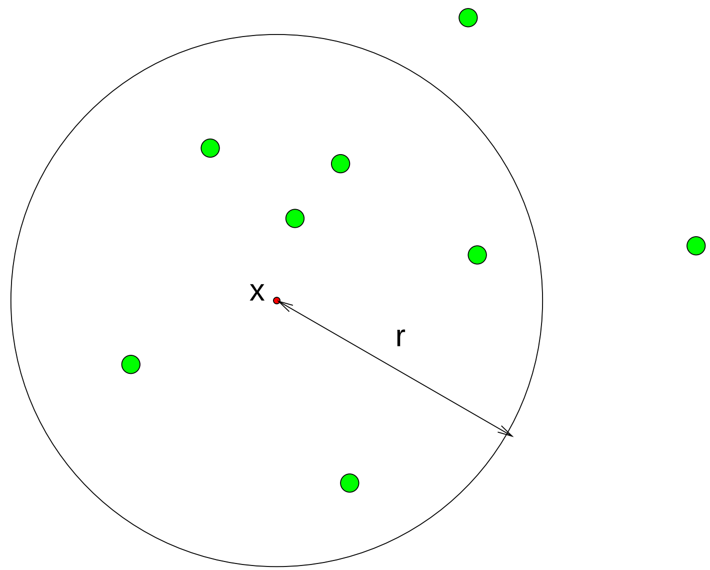

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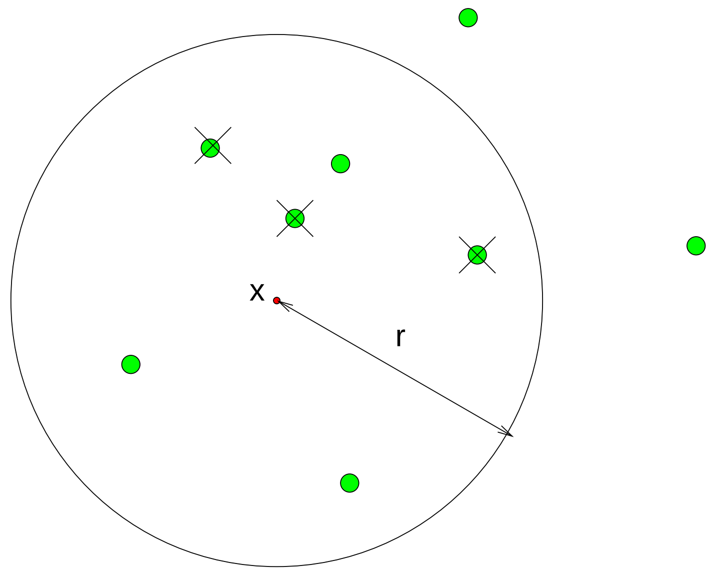

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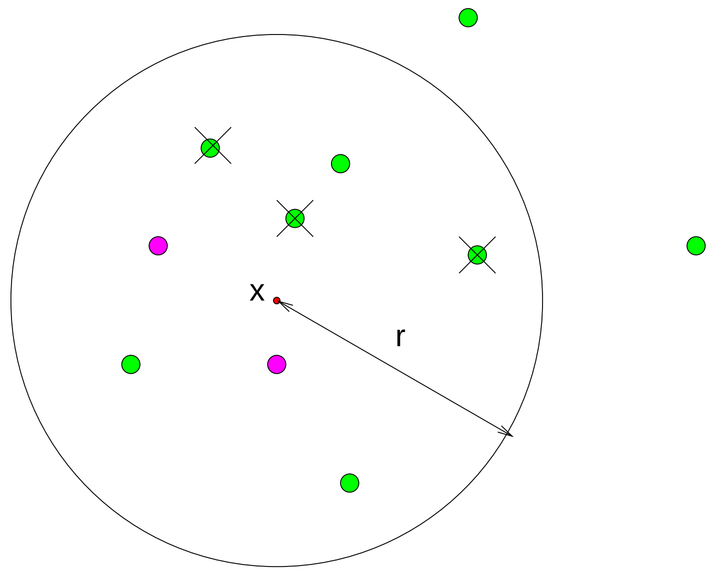

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- Rescale space and time to investigate large scale effects

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For all $y \in B_r(x)$,

$$\rho(t,y,\cdot) = (1-u)\rho(t-,y,\cdot) + u\delta_k.$$

Conditions (1)

$\rho(t, x, \cdot)$ experiences jump of size $u \in A \subseteq [0, 1]$ at rate

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A *single* ancestral lineage evolves in series of jumps with intensity

$$dt \otimes \int_{(|x|/2,\infty)} \int_{[0,1]} \frac{L_r(x)}{\pi r^2} u\, \nu_r(du)\mu(dr)dx$$

on $\mathbb{R}_+ \times \mathbb{R}^2$ where $L_r(x) = |B_r(0) \cap B_r(x)|$.

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Two lineages currently at separation $y \in \mathbb{R}^2$ coalesce at instantaneous rate

$$\int_{(|y|/2,\infty)} L_r(y) \left(\int_{[0,1]} u^2 \nu_r(du) \right) \mu(dr).$$

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