

SOME MATHEMATICAL MODELS
FROM POPULATION GENETICS
IV: HETEROGENEOUS LANDSCAPES

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What the world looks like



How we model it



How we model it



Justification: “homogenisation
over the timescales of evolution”

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What are we missing?



A model based on 'interacting branching processes'

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- ▶ A juvenile is born

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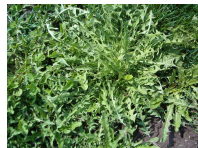
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- ▶ Dispersal distribution $q(x, dy)$ (Gaussian)



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- ▶ A juvenile is born per capita rate $\gamma(x, \eta(x))$
- ▶ Dispersal distribution $q(x, dy)$ (Gaussian)
- ▶ Establishment



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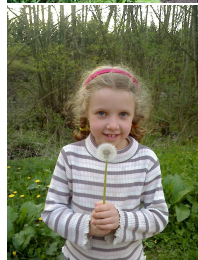
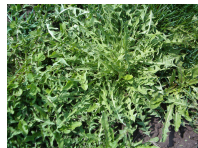
- ▶ A juvenile is born per capita rate $\gamma(x, \eta(x))$
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- ▶ Establishment probability $r(y, \eta(y))$



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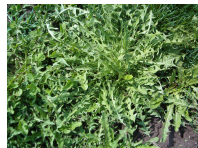
- ▶ A juvenile is born per capita rate $\gamma(x, \eta(x))$
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- ▶ Death of mature individuals



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Assume maturity reached instantly
We only track mature individuals



A cautionary tale

Simulations by Gilia Patterson, using SLiM

- ▶ death: $\mu = 0.3$ per generation
- ▶ establishment: $r = 0.7$
- ▶ dispersal: Gaussian with SD σ
- ▶ local density: in circles radius $\epsilon = 1$
- ▶ reproduction with $K = 2$, $\lambda = 3$,

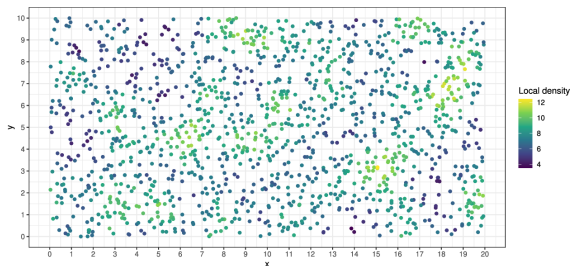
$$\gamma = \frac{\lambda}{1 + (\text{local density})/K}$$

- ▶ non-spatial equilibrium density:

$$K \left(\frac{\lambda}{1-r} - 1 \right)$$

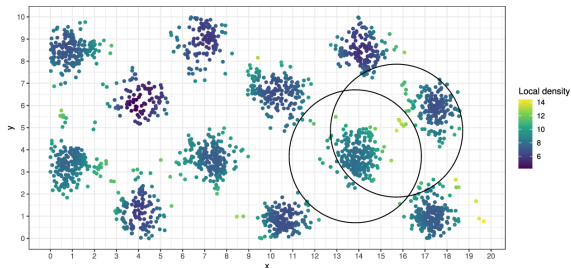
Large dispersal distance

- ▶ dispersal distance $\sigma = 3$
- ▶ interaction distance $\epsilon = 1$
- ▶ mean number offspring $\propto (1 + (\text{density})/K)^{-1}$



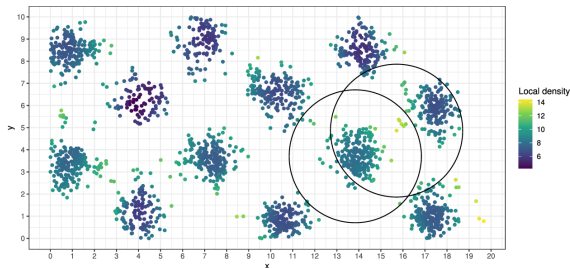
Small dispersal distance

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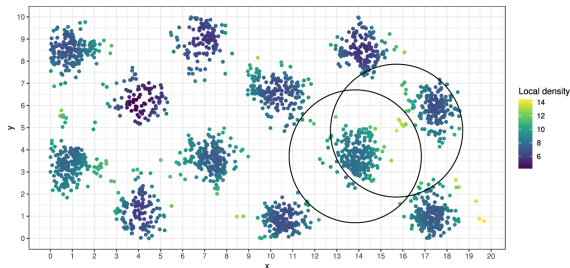
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True even in corresponding deterministic model

Characterising the model

Birth-death process with dynamics:

- ▶ A juvenile is born **per capita rate** $\gamma(x, \eta(x))$
- ▶ Dispersal **distribution** $q(x, dy)$ (Gaussian)
- ▶ (Instantaneous) establishment **probability** $r(y, \eta(y))$
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Think of population as a point measure, with atoms of mass $1/N$.

Write

$$\langle f, \eta \rangle = \frac{1}{N} \sum f(X_i) = \int f(x) \eta(dx)$$

Unpacking the notation:

$$\gamma(x, \eta(x)) = \gamma(x, \rho_\gamma * \eta(x)); \quad \rho_\gamma * \eta(x) = \int \rho_\gamma(x - y) \eta(dy)$$

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ρ_r need not be the same as ρ_γ

Birth-death process with dynamics:

- ▶ A juvenile is born per capita rate $\theta\gamma(x, \eta(x))$
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Assume:

Typically $\mathcal{B} = \Delta$

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(Roughly, r sufficiently smooth, and net per capita growth rate $\propto 1/\theta$)

Look for 'local characteristics'

- ▶ Individual at x gives birth to single mature offspring at z rate $\theta\gamma(x, \eta)r(z, \eta)q_\theta(x, dz)$ increment $\langle f, \eta \rangle = \frac{1}{N}f(z)$
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$$\begin{aligned}\mathcal{P}^N \langle f, \eta \rangle &= \lim_{\delta t \downarrow 0} \frac{1}{\delta t} \mathbb{E} \left[\langle f, \eta_{\delta t} \rangle - \langle f, \eta \rangle \mid \eta_0 = \eta \right] \\ &= \theta \int \int f(z) r(z, \eta) q_\theta(x, dz) \gamma(x, \eta) \eta(dx) - \theta \int f(x) \mu_\theta(x, \eta) \eta(dx).\end{aligned}$$

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$$\xrightarrow{\theta \rightarrow \infty} \int \gamma(x, \eta) \mathcal{B}(f(\cdot) r(\cdot, \eta))(x) \eta(dx) + \int f(x) F(x, \eta) \eta(dx)$$

Quadratic variation

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$$\xrightarrow{\theta \rightarrow \infty} \alpha \langle 2r(x, \eta) \gamma(x, \eta) f^2(x), \eta(dx) \rangle \quad \alpha := \lim \frac{\theta}{N}$$

Martingale characterisation of limit

$$\langle f(x), \eta_t(dx) \rangle - \langle f(x), \eta_0(dx) \rangle \\ - \int_0^t \langle \gamma(x, \eta_s) \mathcal{B}(f(\cdot)r(\cdot, \eta_s))(x) + F(x, \eta_s) f(x), \eta_s(dx) \rangle ds$$

is a martingale, $M_f(\cdot)$, with

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 $\partial_t \eta = r \mathcal{B}^*(\gamma \eta) + F \eta$
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e.g. $\gamma \equiv 1, r \equiv 1, F = 1 - p_\epsilon * \eta$, diffusion limit of Bolker-Pacala model: spatial branching process; reproductive success decreases in crowded regions.

What is needed to make this rigorous?

$\mathcal{D}([0, \infty), S)$ càdlàg paths in S

Theorem (S, d) complete and separable. $\{X^N\}_{N \geq 1}$ family of processes with sample paths in $\mathcal{D}([0, \infty), S)$. Suppose

- ▶ For every $\varepsilon > 0$, and $T > 0$, \exists compact $\Gamma_{\varepsilon, T}$ s.t.

$$\inf_N \mathbb{P} \left[X_t^N \in \Gamma_{\varepsilon, T} \quad \text{for } 0 \leq t \leq T \right] \geq 1 - \varepsilon$$

- ▶ For Θ a dense subset of the set of bounded continuous functions in topology of uniform convergence on compacts, for each $f \in \Theta$, $\{f(X^N)\}_{N \geq 1}$ is relatively compact as family of processes in $\mathcal{D}([0, \infty), \mathbb{R})$.

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If limit point unique have convergence.

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(We have already done the work in identifying the limit points)

Conditions on our parameters?

$$\begin{aligned} & \langle f(x), \eta_t^N(dx) \rangle - \langle f(x), \eta_0^N(dx) \rangle \\ & - \int_0^t \langle \gamma(x, \eta_s) \left(\theta \int (f(z)r(z, \eta_s) - f(x)r(x, \eta_s)) q_\theta(x, dz) \right) \right. \\ & \left. + F(x, \eta_s) f(x), \eta_s(dx) \right\rangle ds \end{aligned}$$

is a martingale, $M_f^N(\cdot)$, with

$$\begin{aligned} \langle M_f^N \rangle_t &= \frac{\theta}{N} \int_0^t \langle \gamma(x, \eta_s) \int f^2(y)r(y, \eta_s) q_\theta(x, dy) \\ & \quad + f^2(x) \left(r(x, \eta_s) \gamma(x, \eta_s) - \frac{1}{\theta} F(x, \eta_s) \right), \eta_s(x) \rangle ds \end{aligned}$$

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- ▶ γ bounded above
- ▶ F bounded above *but not necessarily below*,
c.f. Bolker-Pacala example

Compact containment of $\{\eta_t^N\}_{N \geq 1}$

$$\begin{aligned}\langle 1, \eta_t^N(dx) \rangle &= \langle 1, \eta_0^N(dx) \rangle \\ &+ \int_0^t \langle \gamma(x, \eta_s) \left(\theta \int (r(z, \eta_s) - r(x, \eta_s)) q_\theta(x, dz) \right) \\ &\quad + F(x, \eta_s), \eta_s(dx) \rangle ds + M_1^N(t) \\ &\leq \langle 1, \eta_0^N \rangle + C \int_0^t \langle 1, \eta_s^N \rangle ds + M_1^N(t)\end{aligned}$$

Grönwall's inequality \implies for all $t \in [0, T]$,

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For compact containment we'd like to bound $\mathbb{E}[\sup_{0 \leq t \leq T} \langle 1, \eta_t^N \rangle]$.

Taking suprema above, need to control $\sup_{0 \leq t \leq T} M_1^N(t)$

A useful trick

$$\begin{aligned} \langle M_1^N \rangle_t = & \frac{\theta}{N} \int_0^t \left\langle \gamma(x, \eta_s) \int r(y, \eta_s) q_\theta(x, dy) \right. \\ & \left. + \left(r(x, \eta_s) \gamma(x, \eta_s) - \frac{1}{\theta} F(x, \eta_s) \right), \eta_s(x) \right\rangle ds \end{aligned}$$

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Problem: F not bounded below

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Problem: F not bounded below

Solution: Rearrange equation for $\langle 1, \eta_t^N \rangle$

$$\begin{aligned}- \int_0^t \langle F(x, \eta_s), \eta_s(dx) \rangle ds &= \langle 1, \eta_0^N(dx) \rangle - \langle 1, \eta_t^N(dx) \rangle \\ + \int_0^t \langle \gamma(x, \eta_s) \left(\theta \int (r(z, \eta_s) - r(x, \eta_s)) q_\theta(x, dz) \right), \eta_s(dx) \rangle ds &+ M_1^N(t) \\ &\leq \langle 1, \eta_0^N \rangle + C \int_0^t \langle 1, \eta_s^N \rangle ds + M_1^N(t)\end{aligned}$$

Compact containment of $\{\eta_t^N\}_{N \geq 1}$

Combining boundedness of $\mathbb{E}[\langle 1, \eta_t^N \rangle]$ and the calculation above,
 $\mathbb{E}[\langle M_1^N \rangle_T] < C'_T$

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Still need to show that for suitable test functions, the sequence of *real-valued* processes $\{f(\eta^N)\}_{N \geq 1}$ is relatively compact

The Aldous-Rebolledo criterion

For each $T > 0$, for each fixed $0 \leq t \leq T$, the sequence $\{\langle f, \eta_t^N \rangle\}_{N \geq 1}$ is tight, and for any sequence of stopping times τ_N bounded by T , and each $\nu > 0$, there exist $\delta > 0$, $N_0 > 0$ s.t.

$$\sup_{N > N_0} \sup_{t \in [0, \delta]} \mathbb{P} \left\{ \left| \int_{\tau}^{\tau+t} \int_{\mathbb{R}^d} \{ \gamma(x, \eta_s^N) B_f(x, \eta_s^N) + f(x) F(x, \eta_s^N) \} \eta_s^N(dx) ds \right| > \nu \right\} < \nu,$$

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Follow easily from our calculations above

- ▶ When limit points deterministic, can scale again to get classical pde
- ▶ Can also go direct to deterministic pde in some circumstances

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- ▶ Information about population history recovered from patterns of genetic variation. By using a lookdown construction, we can retain information about genealogies as we pass to our scaling limit.

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Consider a single ancestral lineage

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For the purpose of this talk, work in classical PDE limit

Reaction diffusion equations and range expansion ($d = 1$)

$$\frac{\partial u}{\partial t} = \frac{\partial^2 u}{\partial x^2} + u(1 - u)$$

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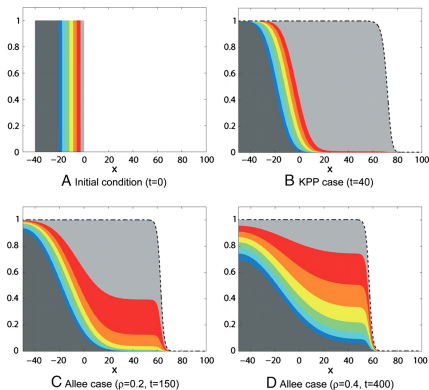
Fisher (1937)

Kolmogorov, Petrovskii, Piskunov
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$$\frac{\partial u_k}{\partial t} = \frac{\partial^2 u_k}{\partial x^2} + u_k(1 - u)$$

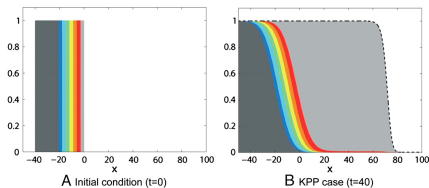
$$u = \sum_k u_k$$



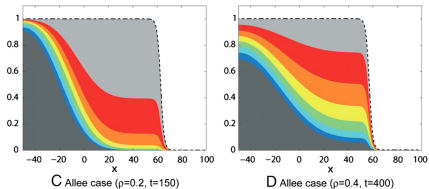
Individuals in front descended from individuals in front at previous time

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$$\frac{\partial u_k}{\partial t} = \frac{\partial^2 u_k}{\partial x^2} + u_k(1 - u) (u - \rho), \quad \rho \in (0, 1/2) \quad u = \sum_k u_k$$



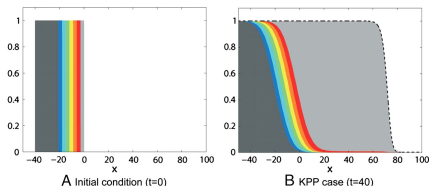
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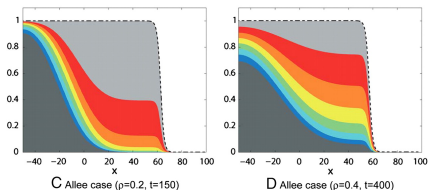
Individuals in front can be descended from individuals in bulk.

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Individuals in front descended from individuals in front at previous time



Individuals in front can be descended from individuals in bulk.

When add noise, \rightsquigarrow different genealogies
(c.f. E-Penington 2022)

A less classical example $\gamma \propto$ pop density, logistic control

$$\frac{\partial u}{\partial t} = \frac{\partial^2}{\partial x^2}(u^2) + u(1 - u),$$

'Effective' density dependent dispersal

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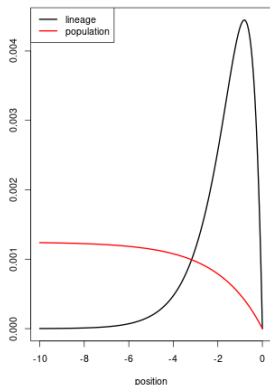
$$\frac{\partial u}{\partial t} = \frac{\partial^2}{\partial x^2}(u^2) + u(1 - u), \quad u(t, x) = \left(1 - \exp\left(\frac{1}{2}(x - t)\right)\right)_+$$

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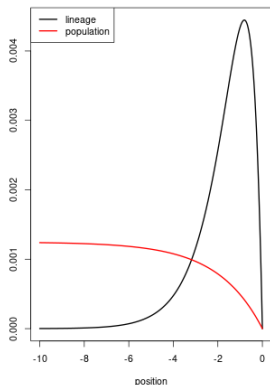


Ancestral lineage has stationary distribution $\pi(x) \propto e^x (1 - e^{x/2})$ for $x < 0$..., in contrast to the Fisher-KPP equation

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↪ When add noise can expect genealogy to be quite different from that under Fisher-KPP,

~ Allee effect

Closing remarks

- ▶ In spite of complexity, some mathematical tractability;
- ▶ A trace of the two-step reproduction mechanism persists over large temporal and spatial scales;
- ▶ Readily simulated in SLiM;
- ▶ Readily extended (but the paper is already over 100 pages long);

Take-home messages from these lectures

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- ▶ Space matters
- ▶ Local interactions matter, even over large scales

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THANK YOU FOR YOUR ATTENTION