Scaling limits in adaptive dynamics

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universität**bonn** iam   FSE PROBABILISTIC STRUCTURES IN EVOLUTION DFG SPP 1590   ImmunoSensation the immune sensory system Bonn cluster of excellence

Plan

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1. Modelling adaptive dynamics
2. Scaling limits and time scales
3. Three limits in one step

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- Generator acting on a suitable core of functions $f : \mathcal{M}_p(\mathcal{X}) \to \mathbb{R}$ by

$$
\begin{aligned}
Lf(\nu) \;=\; & \int_{\mathcal{X}} [f(\nu + \delta_x) - f(\nu)] b(x)(1 - m(x)) \nu(dx) \\
+ & \int_{\mathcal{X}} [f(\nu - \delta_x) - f(\nu)] \left[d(x) + \int_{\mathcal{X}} c(x, y) \nu(dy) \right] \nu(dx) \\
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- $M(x, dy)$: probability distribution of the type of a mutant child of an individual of type x.

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$\Rightarrow$ Law of large numbers, deterministic (integro-differential) equations
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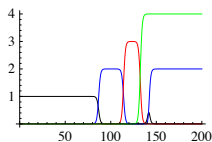**Case 1:** $K \uparrow \infty$, $u, \sigma > 0$, fixed; $T < \infty$ fixed
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Case 2: $K \uparrow \infty$, $\sigma > 0$, fixed, $u \downarrow 0$, $T \sim \ln(1/u)$: (B, Wang, 2012)
$\Rightarrow$ deterministic jump process (trait substitution sequence)

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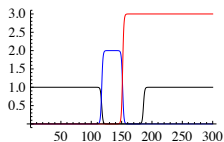**Case 1:** $K \uparrow \infty$, $u, \sigma > 0$, fixed; $T < \infty$ fixed
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- Evolutionary branching at critical points of invasion fitness (Polymorphic evolution sequence (PES))

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$$\frac{dx_t}{dt} = \int h\left[h\, m(x_t)\, \bar{z}(x_t)\, \partial_1 f(x_t, x_t)\right]_+ M(x_t, dh),$$

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$\bar{z}(x) = \frac{b(x)-d(x)}{c(x,x)}$: equilibrium of a monomorphic population of trait x

$f(x,y) = b(y) - d(y) - \bar{z}(x)c(x,y)$: invasion fitness of trait y from x.

All limits in one step.....

Theorem ((Baar, B, Champagnat, '15))

Assume that all functions are smooth that for some $\alpha > 0$,

$$K^{-\frac{1}{2}+\alpha} \ll \sigma_K \ll 1 \qquad \text{and}$$

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Let $\nu_0^K \sim \overline{z}(x)\delta_x$, $x \in \mathcal{X}$. Then, for all $T > 0$,

$$\left(\nu_{t/(K u_K \sigma_K^2)}^K\right)_{0 \le t \le T} \to \left(\overline{z}(x_t)\delta_{x_t}\right)_{0 \le t \le T}$$

in probability, as $K \to \infty$, where $(x_t)_{0 \le t \le T}$ solves the CEAD.

Steps in the proof

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Basic strategy similar to the one in Champagnat et al: First show that a momomorphic initial population with trait x is replaced by a monomorphic population with trait $x + h$, if $f(x, x + h) > 0$ and h is in the support of $M(x, \cdot)$. Happens in three phases:

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- The resident population dies out.

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Almost all of this brakes down, if $\sigma = \sigma_K \downarrow 0$.........

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- Phase 2 takes time of order $\sigma_K^{-1} \ln K$: cannot use LLN!

In pictures
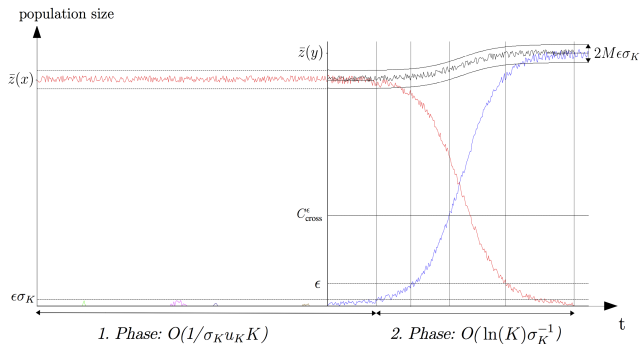
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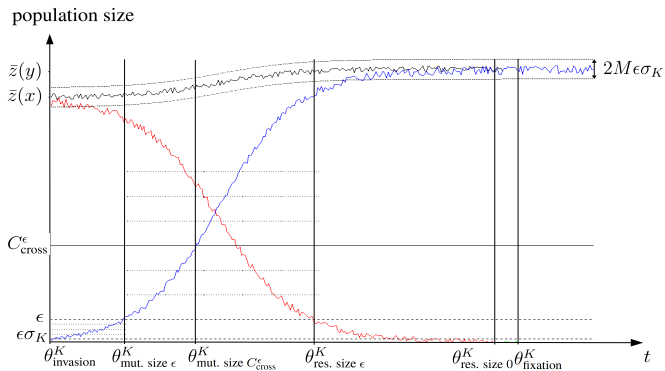
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- $1/(Ku_K\sigma_K^2)$ is the number of mutations (σ_K^{-2}) necessary to move the population by order 1 times the mean time $(1/Ku_K)$ between two mutations.

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- A rigorous stochastic Euler scheme to replace the LLN in Phase 2.

The deterministic system

For $\sigma = 0$, the deterministic Lotka-Volterra system with traits x and $x + h$ has an invariant manifold of fixed points connecting the monomorphic resident and monomorphic mutant populations.
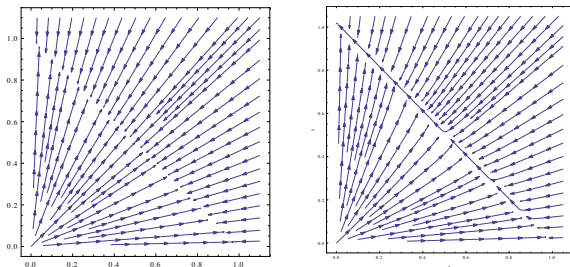
When $\sigma_K > 0$, this turns into an integral curve along which drift is $O(\sigma_K)$. Show that the stochastic system moves along this curve with speed $O(\sigma_K)$.

Stochastic Euler scheme

Control the motion in small increments, similar to Euler schemes. Use that **total mass** changes only with speed σ_K^2!
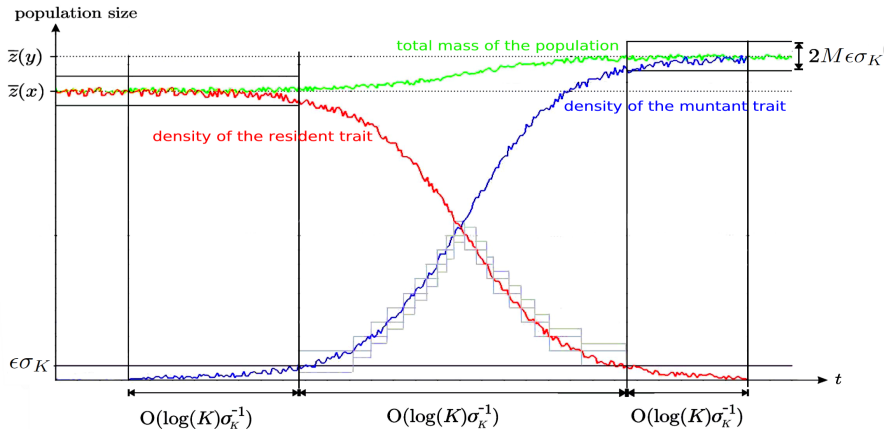
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Thus, speed of change of x_t is

$$u_K K \bar{z}(x_t)m(x_t) \ \ \sigma_K h \ \ \sigma_K h[\partial_1 f(x_t, x_t)]_+$$

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Finally, LLN leads to CEAD.

Thank you for your attention!