Asexual mode

Sexual mode

Maladaptation

Equilibria in quantitative genetics models

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Phenotypic distribution

selection vs. diversity

Darwin's On the origin of species, personal copy of A.R. Wallace (Cambridge Library).

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Darwin's *original drawing* (Cambridge Library).

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Quantitative genetics models

An individual is indexed by its phenotypical trait $x \in \mathbb{R}$ The phenotypical distribution is denoted by f(t,x)

$$\partial_t f(t, x) =$$
birth - death
(+ migration / aging...)

- birth: various modes of reproduction; mutation/ recombination → phenotypic diversity
- death: both trait-dependent and density dependent

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Selection only: concentration effect Example: pure clonal reproduction (no diversity at birth)

$$\begin{cases} \partial_t f(t,x) = b(x,\rho(t))f(t,x) - m(x,\rho(t))f(t,x), \\ \rho(t) = \int f(t,x) \, dx \end{cases}$$

Under certain assumptions on b, m:

- ρ converges to a constant $\overline{\rho}$ (self-regulation)
- f converges to a Dirac mass at \overline{x} such that

$$b(\overline{x},\overline{\rho}) = m(\overline{x},\overline{\rho})$$

(all the population is concentrated around a common trait) An important assumption is the *monotonicity* of b - m with respect to ρ : competition decreases fertility and increases mortality.

Perthame: Transport equations in biology (2007); Barles-Mirrahimi-Perthame (2009); Lorz-Mirrahimi-Perthame (2011)

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Various modes of reproduction (2 options so far) Two modes of reproduction are considered here: (' parental trait)

• Asexual: clonal + mutations

 $x' \longrightarrow x = x' + \sigma Y$, Y random number (any distribution)

• Sexual: mating + recombination (Fisher's infinitesimal model):

$$(x'_1, x'_2) \longrightarrow x = \frac{x'_1 + x'_2}{2} + \sigma Y$$
, Y normally distributed

Asymptotic analysis in the case of small deviation σ :

$$\varepsilon = \frac{\sigma}{\textit{selection unit}} \ll 1$$

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Integro-differential equations

Asexual reproduction

$$\varepsilon \partial_t f_{\varepsilon}(t,x) + m(x,\rho_{\varepsilon}(t)) f_{\varepsilon}(t,x) = \frac{1}{\varepsilon^d} \int_{\mathbb{R}} K\left(\frac{x-x'}{\varepsilon}\right) b(x',\rho_{\varepsilon}(t)) f_{\varepsilon}(t,x') \, dx' \, .$$

Sexual reproduction (Fisher's infinitesimal model)

$$\varepsilon^{2} \partial_{t} f_{\varepsilon}(t, x) + (m(x) + \rho_{\varepsilon}(t)) f_{\varepsilon}(t, x) = \frac{1}{(\varepsilon \sqrt{\pi})^{d}} \iint_{\mathbb{R}^{2}} \exp\left(-\frac{1}{\varepsilon^{2}} \left(x - \frac{x_{1} + x_{2}}{2}\right)^{2}\right) f_{\varepsilon}(t, x_{1}) \frac{f_{\varepsilon}(t, x_{2})}{\int_{\mathbb{R}} f_{\varepsilon}(t, y) \, dy} \, dx_{1} dx_{2} \, .$$



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Objectives:

- Comparison between various modes of reproduction.
- Quantification of (*mal*-)adaptation of a population to a changing environment

Tools:

Asymptotic analysis as $\varepsilon \to 0$



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Asexual mode of reproduction: singular limit

Main observation: the density f^{ε} is expected to converge to a singular measure as $\varepsilon \to 0$, but

$$u_{\varepsilon}(t,x) = -\varepsilon \log f_{\varepsilon}(t,x)$$

converges to a non-singular object (as for a Gaussian with variance $\mathcal{O}(\varepsilon)$).

Rk. This fits in the framework of Large Deviations theory.

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Hamilton-Jacobi equation

$$\varepsilon \partial_t f_{\varepsilon}(t,x) + m(x,\rho_{\varepsilon}(t)) f_{\varepsilon}(t,x) = \frac{1}{\varepsilon^d} \int_{\mathbb{R}} \mathcal{K}\left(\frac{x-x'}{\varepsilon}\right) b(x',\rho_{\varepsilon}(t)) f_{\varepsilon}(t,x') \, dx' \, .$$

On the left hand side:

$$\frac{\varepsilon \partial_t f_{\varepsilon}(t,x) + m(x,\rho_{\varepsilon}(t)) f_{\varepsilon}(t,x)}{f_{\varepsilon}(t,x)} = -\partial_t u_{\varepsilon}(t,x) + m(x,\rho_{\varepsilon}(t))$$

On the right hand side:

$$\frac{1}{\varepsilon^d}\int_{\mathbb{R}} K\left(\frac{x-x'}{\varepsilon}\right) b(x',\rho_{\varepsilon}(t)) \frac{f_{\varepsilon}(t,x')}{f_{\varepsilon}(t,x)} \, dx' \to \mathbf{?}$$

Diekmann-Jabin-Mischler-Perthame (2005); Barles-Perthame (2008); Barles-Mirrahimi-Perthame (2009)

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Convergence result

Theorem (Barles-Mirrahimi-Perthame)

Under suitable assumptions on (b, m), $\rho_{\varepsilon}(t)$ is locally uniformly BV, and, after extraction of a subsequence, u_{ε} converges locally uniformly towards u solution of the following constrained Hamilton-Jacobi problem in the viscosity sense:

$$\begin{cases} \partial_t u(t,x) + H(\rho(t), x, \nabla_x u(t,x)) = 0, \quad t > 0, \ x \in \mathbb{R}^d\\ (\forall t > 0) \quad \min_{x \in \mathbb{R}^d} u(t,x) = 0,\\ u(0,x) = g(x). \end{cases}$$

• The Hamiltonian is given by:

$$H(\rho, x, p) = b(x, \rho) \int e^{pz} K(z) \, dz - m(x, \rho)$$

There is no equation for ρ!, but see the constraint min u = 0.

Uniqueness of the limit problem?

Lack of uniqueness prevents from passing to the full limit $\varepsilon \rightarrow 0$.

Uniqueness results were available under stringent assumptions:

- Competition on reproduction or mortality (but not both) & multiplicative form (Barles-Perthame 2008)
- Particular regime of mutations: H(ρ, x, p) = |p|² + R(ρ, x) & convexity of the initial data & concavity with respect to x (Mirrahimi-Roquejoffre 2016)

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Theorem (C-Lam (2018))

Assume that H is C^2 , convex with respect to p and monotonic with respect to ρ . Under some technical assumptions on the Lagrangian, there is a unique ρ in the class of BV functions such that the constrained Hamilton-Jacobi admits a viscosity solution. **Method:** By convexity, reformulation as a variational solution:

$$\begin{cases} u(t,x) = \inf_{\substack{\{\gamma \in AC(0,t) \\ \gamma(t)=x\}}} \left\{ \int_0^t L(\rho(s),\gamma(s),\dot{\gamma}(s)) \, ds + g(\gamma(0)) \right\}, \\ (\forall t > 0) \quad \min_{x \in \mathbb{R}^d} u(t,x) = 0, \\ (\forall t > 0) \quad \inf_{\gamma \in AC(0,t)} \left\{ \int_0^t L(\rho(s),\gamma(s),\dot{\gamma}(s)) \, ds + g(\gamma(0)) \right\} = 0 \end{cases}$$

Then, compare ρ_1 and ρ_2 .

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Sexual mode of reproduction: similar singular limit

So far, we restrict to equilibrium solutions in dimension d = 1:

$$(m(x) + \rho_{\varepsilon}) F_{\varepsilon}(x) = \frac{1}{(\varepsilon \sqrt{\pi})^{d}} \iint_{\mathbb{R}^{2}} \exp\left(-\frac{1}{\varepsilon^{2}} \left(x - \frac{x_{1} + x_{2}}{2}\right)^{2}\right) F_{\varepsilon}(x_{1}) \frac{F_{\varepsilon}(x_{2})}{\int_{\mathbb{R}} F_{\varepsilon}(y) \, dy} \, dx_{1} dx_{2} \, .$$

Main observation: the density F^{ε} is expected to converge to a singular measure as $\varepsilon \to 0$, but

$$U_{\varepsilon}(x) = -\varepsilon^2 \log F_{\varepsilon}(x)$$

converges to a non-singular object.

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Main differences with the asexual problem

- Non-linear operator, but one-homogeneous (amenable to exponential change of unknown)
- No maximum principle (no theory of viscosity solutions)
- Reproduction is the dominant part of the problem: The operator

$$\mathcal{B}_{\varepsilon^2}(F) = \iint G_{\frac{\varepsilon^2}{2}}\left(x - \frac{x_1 + x_2}{2}\right) F(x_1) \frac{F(x_2)}{\int F(y) \, dy} \, dx_1 dx_2$$

admits a family of fixed points: $\lambda G_{\varepsilon^2}(x - x_0)$. These are equilibria without selection.

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Formal computations

Expand
$$U_{\varepsilon}(x) = \frac{(x-x_0)^2}{2} + \varepsilon^2 V_{\varepsilon}(x).$$

Suppose that $\rho_{\varepsilon} \rightarrow \rho_0$, and $V_{\varepsilon} \rightarrow V_0$ then formally we get:

$$\log(m(x) + \rho_0) = V_0(x) - 2V_0\left(\frac{x + x_0}{2}\right) + V_0(x_0).$$

The values of x_0 and ρ_0 follow directly from solvability conditions:

$$m'(x_0) = 0$$
,
 $ho_0 + m(x_0) = 1$.

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What are the most likely parental traits?



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Gaussian at the leading order + correction



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Rigorous construction: perturbative result

Assume that m is smooth, uniformly convex with minimum at the origin, with polynomial growth at most.

Theorem (C-Garnier-Patout (2018))

There exists a compact subset K of C^3 with uniformly decaying third derivatives, and $\varepsilon_0 > 0$ such that for all $\varepsilon < \varepsilon_0$ there exists a unique $(\rho_{\varepsilon}, V_{\varepsilon}) \in \mathbb{R} \times K$. Moreover, $\rho_{\varepsilon} \rightarrow 1 - m(0)$, and $V_{\varepsilon} \rightarrow V_0$:

$$V_0(x) = \left(\frac{\partial_x^3 m(0)}{2\partial_x^2 m(0)}\right) x + \sum_{k=0}^{\infty} 2^k \log\left(1 - m(0) + m\left(2^{-k}x\right)\right)$$

Method: Decompose $V_{\varepsilon}(x) = \gamma_{\varepsilon}x + W_{\varepsilon}(x)$: the linear part should be dealt with separately.

Derive contraction estimates on the third derivative $W_{\varepsilon}^{(3)}$. The number γ_{ε} is derived using a solvability condition within the fixed point operator.

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Alternative scaling

Raoul (2018) analyzed a different scaling:

$$\partial_t f_{\varepsilon}(t,x) + (m(x) + \rho_{\varepsilon}(t)) f_{\varepsilon}(t,x) = \frac{1}{\varepsilon} \left(\mathcal{B}_1(f_{\varepsilon}(t,\cdot)) - f_{\varepsilon}(t,\cdot) \right) \,.$$

with an additional space variable. He uses strongly contraction in the quadratic Wasserstein distance.

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Application: mal-adaptation to a changing environment

Assume that selection acts on mortality only (for simplicity), but it gradually changes in time:

$$m(x-ct) + \rho(t)$$

where m is a uniform convex function.



Review paper by Kopp and Matuszewski (2013)

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Aim: Compute the equilibrium distribution F as $\sigma \ll$ selection unit which is stationary in the moving frame:

$$z = x - ct$$
, $\partial_t \to \partial_t - c\partial_z$



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Asexual reproduction

$$-\varepsilon c \partial_z F(z) + (\rho + m(z)) F(z) = \frac{1}{\varepsilon} \int_{\mathbb{R}} K\left(\frac{z - z'}{\varepsilon}\right) F(z') \, dz' \, .$$

Sexual reproduction (Fisher's infinitesimal model)

$$-\varepsilon^{2}c\partial_{z}F(z) + (\rho + m(z))F(z) = \frac{1}{\varepsilon\sqrt{\pi}}\iint_{\mathbb{R}^{2}}\exp\left(-\frac{1}{\varepsilon^{2}}\left(z - \frac{z_{1} + z_{2}}{2}\right)^{2}\right)F(z_{1})\frac{F(z_{2})}{\int_{\mathbb{R}}F(y)\,dy}\,dz_{1}dz_{2}\,.$$

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Asexual case (formal results)

The stationary Hamilton-Jacobi equation is:

$$c\partial_z U_0(z) + \rho_0 + m(z) = 1 + H(\partial_z U_0(z)) .$$

The Hamiltonian function H depends only on the effects of mutations:

$$H(p) = \int K(y) e^{py} \, dy - 1 \, ,$$

H comes with the Lagrangian function (convex conjugate):

$$L(v) = \max_{p} \left(p \cdot v - H(p) \right)$$

Fathi, Lecture notes on weak KAM theory (2010); Barles and Roquejoffre (2006)

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Explicit formula

The number ρ_0 is obtained explicitly:

$$p_0 = 1 - m(0) - L(c)$$
.

L(c) comes as an additional cost due to mutations (lag load).



As a by-product, we obtain the value of the lag z_0 :

 $\rho_0 + m(z_0) = 1 \quad \Longleftrightarrow \quad m(z_0) - m(0) = L(c)$

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Sexual case (formal results)

$$U(z) = \frac{(z-z_0)^2}{2} + \varepsilon^2 V(z) + \dots$$

where V is solution of a difference equation:

$$\log\left(c(z-z_0)+\rho_0+m(z)\right) = U_1(z)-2U_1\left(\frac{z+z_0}{2}\right)+U_1(z_0).$$

Again, the values of z_0 and ρ_0 follow directly from solvability conditions:

$$m'(z_0) = -c ,$$

 $ho_0 + m(z_0) = 1 .$

Joint work with Bouin, Bourgeron, Cotto, Garnier, Lepoutre, Ronce.

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The loads and the lags



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Evolution of aging



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Age-dependent selection

Suppose selection acts at a given age (or after some age threshold)

Hamilton (1966); Charlesworth (1994, 2001).



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MALADAPTATION AS A SOURCE OF SENESCENCE IN HABITATS VARIABLE IN SPACE AND TIME

Olivier Cotto¹ and Ophélie Ronce^{1,2}

In this study, we use a quantitative genetics model of structured populations to investigate the evolution of senescence in a variable environment. Adaptation to local environments depends on phenotypic traits whose optimal values vary with age and

a changing environment can have a different impact on different age classes.

results highlight the need to study age-specific adaptation, as a changing environment can have a different impact on different age classes.

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A quantitative genetics model of aging populations

(adapted from Cotto and Ronce 2014 to a continous setting)

$$\begin{cases} \partial_t f(t, a, z) + \partial_a f(t, a, z) + (\mu(a, m(z)) + \rho(t)) f(t, a, z) = 0\\ f(t, 0, z) = \int_{\mathbb{R}} K(z - z') \left(\int_0^\infty \beta(a) f(t, a, z') \, da \right) \, dz' \, . \end{cases}$$

Ex. $\mu(a, m) = \mu(a) + m\delta_{a=a*}, \ m(z) = \alpha |z|^2.$

Rk. Here, asexual reproduction, but similar framework in the case of sexual reproduction.

Goal: Investigate the mutation/selection balance as a function of the age class a*.

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A quantitative genetics model of aging populations

(adapted from Cotto and Ronce 2014 to a continous setting)

$$\begin{cases} \partial_t f(t, a, z) + \partial_a f(t, a, z) + (\mu(a, m(z - ct)) + \rho(t)) f(t, a, z) = 0\\ f(t, 0, z) = \int_{\mathbb{R}} K(z - z') \left(\int_0^\infty \beta(a) f(t, a, z') \, da \right) \, dz' \, . \end{cases}$$

Ex. $\mu(\mathbf{a}, \mathbf{m}) = \mu(\mathbf{a}) + \mathbf{m}\delta_{\mathbf{a}=\mathbf{a}*}, \ \mathbf{m}(z) = \alpha |z|^2.$

Rk. Here, asexual reproduction, but similar framework in the case of sexual reproduction.

Goal: Investigate the mutation/selection balance as a function of the age class *a** in a changing environment.

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Maladaptation under age structure (I)

$$\begin{cases} -\varepsilon c \partial_z F(a,z) + \partial_a F(a,z) + (\mu(a,m(z)) + \rho) F(a,z) = 0\\ F(0,z) = \int_{\mathbb{R}} K_{\varepsilon}(z-z') \left(\int_0^{\infty} \beta(a) F(a,z') \, da \right) \, dz' \, . \end{cases}$$

Dynamics of an isolated trait (without mutations) are encoded in the spectral problem:

$$\begin{cases} r(m)G(a,m) + \partial_a G(a,m) + \mu(a,m)G(a,m) = 0\\ G(0,m) = \int_0^\infty \beta(a)G(a,m) \, da, \end{cases}$$

where the eigenvalue r(m) is given by:

$$\int_0^\infty \beta(a) \exp\left(-r(m)a - \int_0^a \mu(a',m) \, da'\right) \, da = 1 \, .$$

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Shape of the eigenvalue r(m(z)) (effective fitness)

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Maladaptation under age structure (II)

The logarithmic density

$$U^{arepsilon}(a,z) = -arepsilon \log\left(rac{F^{arepsilon}(a,z)}{G(a,m(z))}
ight)\,.$$

converges towards a viscosity solution of the Hamilton-Jacobi equation

$$\rho_0 + c\partial_z U(z) = R(m(z), \partial_z U(z)).$$

where the hamiltonian R(m, p) is defined by

$$\int_0^\infty \beta(a) \exp\left(-aR(m,p) - \int_0^a \mu(a',m) \, da'\right) \, da = \frac{1}{\widehat{\mathcal{K}}(p)}$$

For a rigorous derivation, see recent work with Gabriel and Mateos González in the context of anomalous diffusion, and also Nordmann, Perthame and Taing.

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(Severe) maladaptation

In the age-free model, the lag z_0 increases gradually with c.

It can be more singular in the age-structured model. It can even diverge for some critical speed c * *:

$$\lim_{c\to c**} z_0(c) = \infty$$

It means that the population in the age classes $a > a^*$ goes extinct if c * * < c < c * (the critical speed for population extinction)

More precisely, we find,

$$z_0 = \left(-\frac{1}{\alpha}\log\left(1 - \frac{L(c)e^{-L(c)a^*}}{\beta e^{-\beta a^*}}\right)\right)^{1/2}$$

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Numerical vs. analytical results (asexual mode)



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Severe maladaptation

Similar analysis in the case of sexual reproduction.

In this case, the lag is given by the simple formula:

$$\frac{d}{dz}r(m(z))=c$$



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Numerical vs. analytical results (sexual mode)



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Thank your attention!