

Random modeling of adaptive dynamics for diploid populations

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Darwinian or Adaptive Evolution

The population has the propensity to generate as well to select individual diversity.

Three main ingredients :

- ▶ Heredity.
- ▶ Mutation.
- ▶ Selection.

Adaptive Dynamics (Hofbauer-Sigmund 1990, Marrow-Law-Cannings 1992, Metz-Geritz-Meszéna et al. 1992, 1996, Dieckmann-Law 1996)

- ▶ Focus on the interplay between ecology and evolution.
- ▶ Emphasis on the **ecological interactions** :
density-dependent selection model.
- ▶ BUT
 - ▶ Asexual (clonal) reproduction
 - ▶ No genetics in the reproduction

Three biological assumptions :

- ▶ (1) large populations
- ▶ (2) rare mutations
- ▶ (3) small mutation steps

and long (evolutive) time scale.

- ▶ Our approach (Metz et al., Champagnat 06) : (1) + (2) then (3).
- ▶ Individual-based model with stochastic tools mixed with dynamical system arguments.
(Bolker-Pacala 97, Kisdi 99, Dieckmann-Law 00, Fournier-M. 04, Ferrière-Champagnat-M. 06, Champagnat-M. 10)
- ▶ OUR AIM IN THIS PAPER : To generalize this approach to diploid populations : a link between ecology, genetics and evolution

The Microscopic Model

- ▶ Each individual i is characterized by two allelic traits (u_1^i, u_2^i) . (u^i real number or vector).
- ▶ The corresponding phenotypic trait is given by a symmetric function $\phi(u_1^i, u_2^i)$.
- ▶ K scales the size of the population : K large .
- ▶ u_K scales the probability of mutation : u_K small. (Only rare mutations affect the phenotype of the individual).
- ▶ Population of $N^K(t)$ individuals with weights $\frac{1}{K}$ and allelic traits $(u_1^1, u_2^1), \dots, (u_1^{N^K(t)}, u_2^{N^K(t)})$.

The size of the allelic trait vector evolves with time.

Transitions for an individual with trait (u_1, u_2) in the population

- ▶ **Fertility rate** $f(u_1, u_2)$. An individual i is chosen with probability

$$\frac{f(u_1^i, u_2^i)}{\sum_{j=1}^{N^K} f(u_1^j, u_2^j)}.$$

- ▶ With probability $1 - u_K \mu$, **sexual Mendelian reproduction** : 4 possibilities

$$(u_1, u_1^i), (u_1, u_2^i), (u_2, u_1^i), (u_2, u_2^i),$$

with probability 1/4.

- ▶ With probability $u_K \mu$: **mutation on an allele**. Let ε denote the scale of the mutation.

A mutant from the allelic trait u_1 is $u_1 + \varepsilon h$, with $|h| \leq 1$ chosen following a distribution $m(u_1, h)dh$. (Example : a Gaussian law centered on u_1 and conditioned to $[-1, 1]$).

Death rate :

$$D^0(u_1, u_2) + \frac{1}{K} \sum_{j=1}^{N^K} \alpha(u_1, u_2; u_1^j, u_2^j).$$

D^0 is the natural death and α describes the competition between individuals.

Biologically, all coefficients (except the mutation law) are depending on their allelic traits u_1 and u_2 by their phenotypic trait $\phi(u_1, u_2)$.

Example :

$$\phi(u_1, u_2) = \frac{u_1 + u_2}{2}.$$

\implies symmetry of all (rate) functions in (u_1, u_2) .

Assumptions :

- ▶ Initial size of order K (**large**).
- ▶ f , D^0 , α , and m smooth enough.
- ▶ f , D^0 and α are bounded.
- ▶ "Natural growth rate" of the population of type (u_1, u_2) :
 $f(u_1, u_2) - D^0(u_1, u_2) > 0$.
- ▶ Interaction rate :
 $\alpha(u_1, u_2; v_1, v_2) > 0, \quad \forall u_1, u_2, v_1, v_2 \in \mathcal{U}$.

Notation : If we consider two alleles A and a , we identify u_A and A , u_a and a :

$$f_{AA} = f(u_A, u_A); \quad D_{AA}^0 = D^0(u_A, u_A); \quad \alpha_{AA,AA} = \alpha(u_A, u_A; u_A, u_A),$$

and the same for Aa and aa .

Behavior of the population for large population and rare mutation. **Time scale of order 1**

Large K ; small mutation probability $u_K \simeq 0$.

Theorem (Fournier-M. 04) : For large K , the dynamics of the population is almost **deterministic**. The density $W_t(u, v)$ of the allelic pair (u, v) is solution of the equation

$$\begin{aligned} \partial_t W_t(u, v) = & -W_t(u, v)(D^0(u, v) + \int \alpha(uv; u'v') W_t(u', v') du' dv') \\ & + \frac{(\int f(u, u_1) W_t(u, u_1) du_1) (\int f(v, v_1) W_t(v, v_1) dv_1)}{\int f(u_1, u_2) W_t(u_1, u_2) du_1 du_2}. \end{aligned}$$

No mutation appears at this time scale ($u_K \simeq 0$).

Monomorphic homozygote case AA

If the initial population is composed of individuals with allelic trait (u_A, u_A) , it will stay monomorphic with trait (u_A, u_A) at this time scale.

The population process is a birth and death process with birth rate f_{AA} and death rate $D_{AA}^0 + \alpha_{AA,AA}N$, if N is the typical state.

For large K , the population size $N^K(t)$ is close to $n(t)$, solution of the logistic equation

$$\dot{n} = (f_{AA} - D_{AA}^0 - \alpha_{AA,AA}n)n.$$

A unique stable equilibrium

$$\bar{n}_{AA} = \frac{f_{AA} - D_{AA}^0}{\alpha_{AA,AA}}.$$

Three genotypes case AA , Aa and aa

- ▶ $t \mapsto (X_t^K, Y_t^K, Z_t^K)$: population process of individuals with genotype AA , Aa and aa .
- ▶ Birth and death process with three types and birth rates b_{AA} , b_{Aa} , b_{aa} and death rates d_{AA} , d_{Aa} , d_{aa} .
- ▶ If (x, y, z) is the typical state of the population process, the birth rates are given by :

$$b_{AA} = \frac{(f_{AA}x + f_{Aa}y/2)^2}{f_{AA}x + f_{Aa}y + f_{aa}z},$$
$$b_{Aa} = \frac{2(f_{AA}x + f_{Aa}y/2)(f_{aa}z + f_{Aa}y/2)}{f_{AA}x + f_{Aa}y + f_{aa}z},$$
$$b_{aa} = \frac{(f_{aa}z + f_{Aa}y/2)^2}{f_{AA}x + f_{Aa}y + f_{aa}z}.$$

Death rates given by

$$\begin{aligned}d_{AA} &= (D_{AA}^0 + \alpha_{AA,AA} X + \alpha_{AA,Aa} Y + \alpha_{AA,aa} Z) X \\d_{Aa} &= (D_{Aa}^0 + \alpha_{Aa,AA} X + \alpha_{Aa,Aa} Y + \alpha_{Aa,aa} Z) Y, \\d_{aa} &= (D_{aa}^0 + \alpha_{aa,AA} X + \alpha_{aa,Aa} Y + \alpha_{aa,aa} Z) Z.\end{aligned}$$

Theorem : For large K , the population dynamics is close to the solution $(\psi(t), t \in [0, T])$ of the dynamical system $DS(AA, Aa, aa)$:

$$\dot{\psi}(t) = \vec{X} \circ \psi(t) = \vec{X}(\psi_1(t), \psi_2(t), \psi_3(t)),$$

where \vec{X} is the vector field

$$\vec{X}(x, y, z) = \begin{pmatrix} b_{AA} - d_{AA} \\ b_{Aa} - d_{Aa} \\ b_{aa} - d_{aa} \end{pmatrix} (x, y, z).$$

Long time behavior of DS(AA,Aa,aa)

The vector field has a lot of fixed points, but two main points : $(\bar{n}_{AA}, 0, 0)$, $(0, 0, \bar{n}_{aa})$ with

$$\bar{n}_{AA} = \frac{f_{AA} - D_{AA}^0}{\alpha_{AA,AA}} , \bar{n}_{aa} = \frac{f_{aa} - D_{aa}^0}{\alpha_{aa,aa}} .$$

Theorem : The Jacobian matrix DX_{AA} is a triangular matrix with two negative eigenvalues and the third one is equal to the invasion fitness of mutant Aa in the resident population AA :

$$S_{Aa,AA} = f_{Aa} - D_{Aa}^0 - \alpha_{Aa,AA} \bar{n}_{AA} ,$$

and a similar property for DX_{aa} .

The non linear vector fields in dimension 3 may have complex long time behavior. To study \vec{X} , we will assume that mutants have small amplitudes (a is close to A).

Neutral case (all parameters are equal : $AA = aa$) :

Theorem : The vector field has a curve of fixed points.

Small mutations : $u_a = u_A + \varepsilon h$ with $|h| \leq 1$.

Fitness of a mutant Aa in the resident population AA :

$$S_{Aa,AA} \simeq \varepsilon \frac{dS_{Aa,AA}}{d\varepsilon}(0), \text{ for } \varepsilon \text{ sufficiently small.}$$

Theorem : For ε small enough, if $\frac{dS_{Aa,AA}}{d\varepsilon}(0) \neq 0$, only two equilibria which are the homozygote populations AA and aa .

if $\varepsilon \frac{dS_{Aa,AA}}{d\varepsilon}(0) > 0$, the fixed point AA is unstable and we have invasion (by aa) for the macroscopic dynamics.

If $\varepsilon \frac{dS_{Aa,AA}}{d\varepsilon}(0) < 0$, the fixed point AA is stable and the mutant disappears in the macroscopic dynamics.

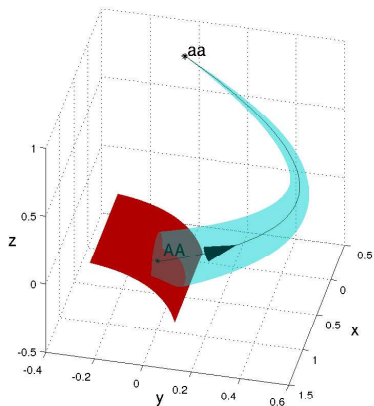
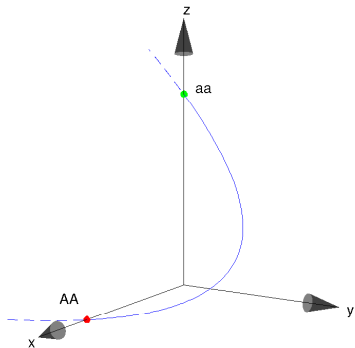
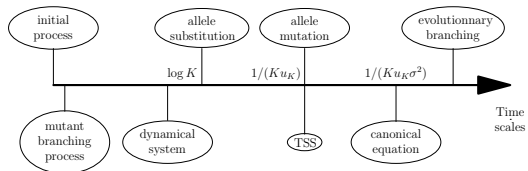


Figure: Left : neutral case - Right : small mutant case

The time scales



Mutation time scale : **of order** $\frac{t}{K u_K}$

Dynamics of the microscopic process :

Theorem : Monomorphic homozygote initial population with trait $A_0 A_0$. Assume that

$$\forall C > 0, \quad \ln K \ll \frac{1}{K u_K} \ll \exp(CK), \quad \text{for large } K. \quad (1)$$

Then, for ε small enough, the population process at time $\frac{t}{K u_K}$ is approximated by a jump process defined as follows :

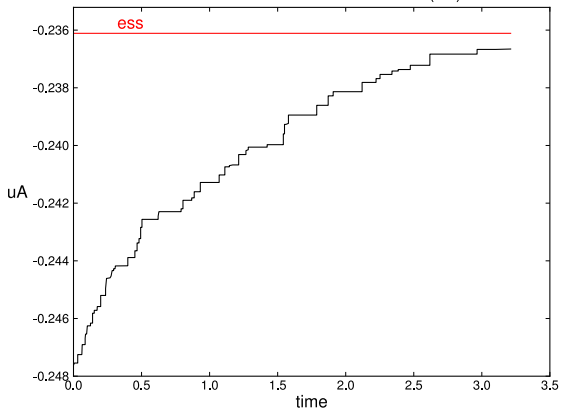
The initial process : individuals with traits (u_{A_0}, u_{A_0}) .

The process jumps from \bar{n}_{AA} individuals with trait (u_A, u_A) to \bar{n}_{aa} individuals with trait (u_a, u_a) , with $u_a = u_A + \varepsilon h$.

The jump happens after an exponential time with parameter $2\mu f_{AA} \bar{n}_{AA} \frac{[S_{Aa,AA}]_+}{f_{Aa}}$.

The amplitude of the jump is distributed following $m(u_A, h)dh$.

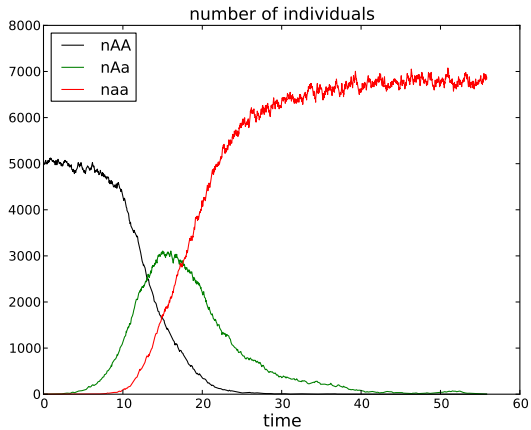
Evolution of the resident allelic trait (tss)



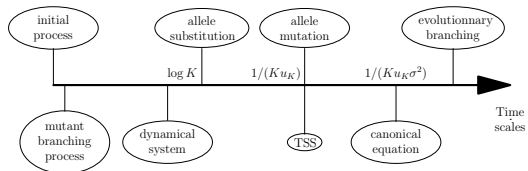
Generalization of the trait substitution sequence (TSS) .
Monomorphic asexual case : Metz et al. 1996 ; Champagnat
06.

Philosophy of the proof :

- ▶ The selection process has sufficient time between two mutations to eliminate disadvantaged types (**time scale separation**).
- ▶ **Assumption of large populations** : between mutations, the population is close to the **deterministic population dynamics**, so that one can **predict the outcome of competition** between the traits.
- ▶ Succession of phases of **mutant invasion**, and phases of **competition** between traits



The time scales



The Canonical Equation of Adaptive Dynamics

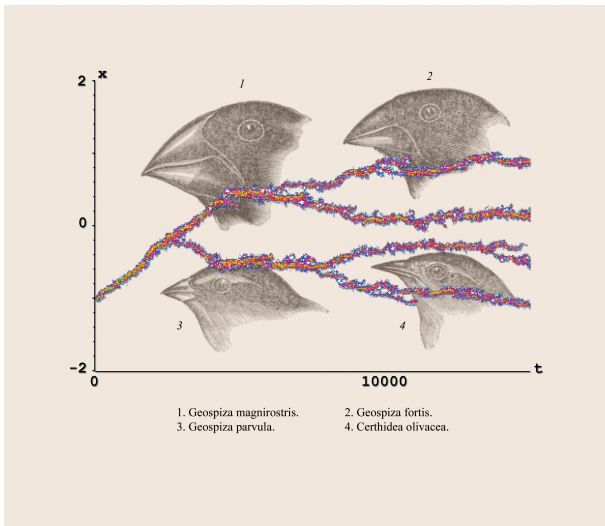
When ε small ?

- ▶ At its time scale, the TSS process disappears (no more jumps).
- ▶ We need to rescale the time : longer time $\frac{t}{Ku_K\varepsilon^2}$.
- ▶ **Theorem** : When ε is small, the dynamics of equilibria allelic traits is given by

$$\frac{du}{dt} = 2\mu \bar{n}_{uu} \partial_1 S(u, u; u, u) \int_{\mathbb{R}} h^2 m(u, h) dh.$$

Canonical equation of the adaptive dynamics.

Evolutionary singularities : points (u, u) such that $\partial_1 S(u, u; u, u) = 0$: possibility of evolutionary branching.



Evolutionary branching for $u \in \mathbb{R}$ such that $\partial_1 S(u, u; u, u) = 0$. Champagnat-M. 2010 (asexual case).

Before the first mutation, K large

- ▶ Monomorphic population with genotype AA : the size of the population for t large enough is close to \bar{n}_{AA} .
- ▶ If $\frac{1}{Ku_K} \ll e^{CK}$, the first mutation occurs before the exit time of a neighborhood of \bar{n}_{AA} with high probability. (Large deviations).
- ▶ Before this exit time, the rate of mutation from trait (u_A, u_A) is close to $2\mu u_K f_{AA} K \bar{n}_{AA}$.
- ▶ On the time scale $\frac{t}{Ku_K}$: $2\mu f_{AA} \bar{n}_{AA}$.

After the first mutation : competition phasis

- ▶ An allelic mutant trait appears at time t_0 .
- ▶ **between t_0 and t_1** : the number of mutant individuals with trait Aa is close to a **branching process** with birth rate f_{Aa} and death rate $D_{Aa}^0 + \alpha_{Aa,AA} \bar{n}_{AA}$.
- ▶ **Growth rate = fitness function** :

$$S_{Aa;AA} = f_{Aa} - D_{Aa}^0 - \alpha_{Aa,AA} \bar{n}_{AA}.$$

- ▶ Survival probability : $\frac{[S_{Aa,AA}]_+}{f_{Aa}}$.
- ▶ **After t_1** : close to $DS(AA, Aa, aa)$.

- ▶ Convergence of $DS(AA, Aa, aa)$ to the equilibrium \bar{n}_{aa} .
- ▶ The population density of genotype aa reaches the η -neighborhood of \bar{n}_{aa} at time t_2 .
- ▶ **After t_2** : the densities of genotypes AA and Aa are approximated by **sub-critical branching process**.
- ▶ **Time scale** : $\ln K$.
- ▶ If $\ln K \ll \frac{1}{Ku_K}$, the next mutation occurs after these three phases with high probability.
- ▶ We reiterate the procedure by Markovian arguments.