

Probability of fixation and adaptive dynamics in a nearly neutral finite logistic population

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Adaptive dynamics (AD)

Adaptive dynamics (Hofbauer and Sigmund 1990, Marrow et al. 1992, Metz et al. 1992):

- describe the evolution of a population by putting emphasis on the ecological interactions
- heredity (in a first approach) is simplified as much as possible: asexual (clonal) reproduction

The basic idea is to describe the evolution of the population as a succession of mutant invasions (Metz et al., 1996). Starting from an individual-based, stochastic model, this approach corresponds to the assumptions of

- large population
- rare mutations
- small mutation steps

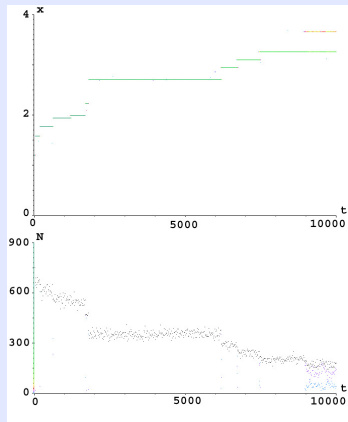
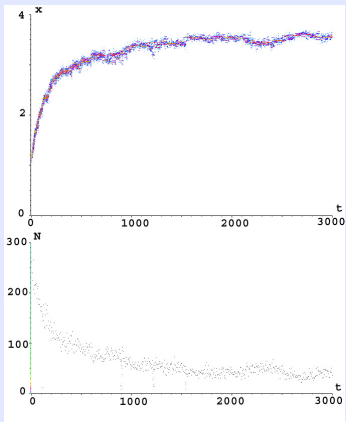
No fitness is given. It has to be deduced from the model.

AD: trait substitution sequence (TSS)

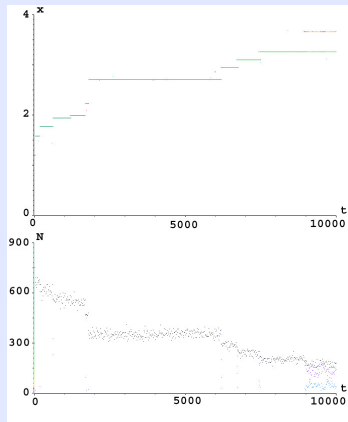
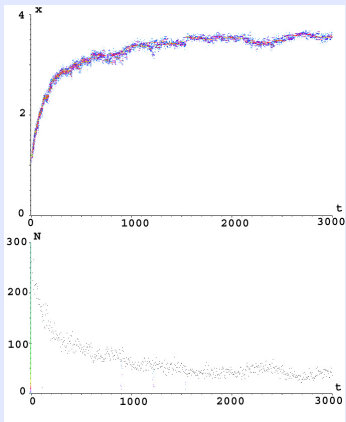
The trait substitution sequence (TSS, Metz et al., 1996, C, 2006) proceeds from two assumptions.

- **Assumption of rare mutations**
 - sufficient time is given to selection and genetic drift to eliminate unlucky types between two mutations
 - only one trait survives at a time on the mutation timescale
 - evolution proceeds through a sequence of mutant invasions and fixations: jump process over the trait space
- **Assumption of large population**
 - only advantageous mutants can invade and fixate
 - direction of evolution is deterministic (no genetic drift).

TSS: Two figures



TSS: Two figures



AD: canonical equation of adaptive dynamics

The canonical equation of adaptive dynamics (Dieckmann and Law, 1996) proceeds from an extra **assumption of small mutations** applied to the TSS.

- Deterministic ODE (without genetic drift)

$$\frac{dx}{dt} = \frac{1}{2} \sigma(x)^2 \mu(x) \bar{n}(x) \frac{\partial}{\partial y} f(x, x)$$

- σ^2 variance of the mutation steps
- μ probability of mutation at each birth event
- $\bar{n}(x)$ equilibrium size of a pure x -type population
- $f(x, y)$ growth rate of a mutant type y in an equilibrium x -type resident population (fitness)

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Our goal

- Use the same approach from microscopic models to macroscopic ones
- Keep the population **finite** and **stochastic** to include genetic drift
 - first in the TSS (limit of rare mutations alone)
 - next in the canonical equation of adaptive dynamics (limit of small mutations)

Monotype finite logistic branching process

Finite population $X_t \in \mathbb{N}$.

Each individual:

- gives birth to a new individual at rate b
- dies at rate $d + c(X_t - 1)$

c represents the competitive pressure exerted by **other** individuals on the focal individual.

- If $d > 0$, the process goes a.s. extinct in finite time
- If $d = 0$, the process is positive recurrent, with stationary Poisson distribution of parameter b/c conditioned on being nonzero.

2-types finite logistic branching process

Two finite populations $(X_t^1, X_t^2) \in \mathbb{N}^2$.

Each individual of type i :

- gives birth to a new individual at rate b_i
- dies at rate $d_i + c_{ii}(X_t^i - 1) + c_{ij}X_t^j, j \neq i$

The dynamics is characterized by:

$$B = \begin{pmatrix} b_1 \\ b_2 \end{pmatrix}, \quad C = \begin{pmatrix} c_{11} & c_{12} \\ c_{21} & c_{22} \end{pmatrix}, \quad D = \begin{pmatrix} d_1 \\ d_2 \end{pmatrix}$$

- The process is absorbed in $\mathbb{N} \times \{0\}$ and $\{0\} \times \mathbb{N}$.
- If $d_1 = d_2 = 0$, the process does not go extinct.

Microscopic model

A general multitype logistic model with mutation (Bolker and Pacala 1997, Dieckmann and Law 2000, Fournier and Méléard 2004,...)

- each individual is characterized by a phenotypic **trait** x (individual size, age at maturity,...) in a closed subset \mathcal{X} of \mathbb{R}^k
- a population of $N(t)$ individuals holding traits $x_1, \dots, x_{N(t)} \in \mathcal{X}$

is represented by $\nu_t = \sum_{i=1}^{N(t)} \delta_{x_i}$

Transitions

- Each individual with trait x gives birth at rate $\mathbf{b}(\mathbf{x})$ to a single individual of trait x
- Each individual of trait \mathbf{x} dies from competition from any other individual of trait \mathbf{y} at rate $\mathbf{c}(\mathbf{x}, \mathbf{y})$
 \rightsquigarrow an individual with trait x dies at rate

$$\sum_{i=1}^{N_t} c(x, x_i) - c(x, x) = \int_{\mathcal{X}} c(x, y)(\nu_t(dy) - \delta_x(dy))$$

- At each birth from an individual with type x
 - $\mu(x)$ mutation probability
 - $x + h$ mutant trait, where $h \sim m(x, dh)$

Assumptions

$$(A) \quad 0 < \underline{c} \leq c(\cdot, \cdot) \leq \bar{c} < +\infty$$
$$0 \leq b(\cdot) \leq \bar{b} < +\infty$$

Observe that such a population cannot go extinct, so that taking the limit of rare mutation will not lead to the extinction of the population before the first mutation.

Limit of rare mutations

- $\mu(x) \rightsquigarrow \gamma \mu(x)$, $\gamma \rightarrow 0$ (timescales separation)

Before the first mutation

- As already said, when $\mu \equiv 0$ and $\nu_0 = n\delta_x$, the population size converges in distribution to a r.v. $\xi(x)$ with

$$\mathbb{P}(\xi(x) = i) = \frac{e^{-\theta(x)} \theta(x)^i}{1 - e^{-\theta(x)} i!}, \quad i \geq 1.$$

where $\theta(x) := b(x)/c(x, x)$

- Let τ be the first mutation time

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Lemma

If $\nu_0 = n\delta_x$, $(\gamma\tau, \langle \nu_{\tau-}^\gamma, \mathbf{1} \rangle)$ converges in distribution to (T, N) where T and N are independent, $T \sim \text{Exp}(\beta(x))$ with

$$\beta(x) := \mu(x)b(x)\mathbb{E}(\xi(x)) = \mu(x)b(x)\theta(x)/(1 - e^{-\theta(x)})$$

and N is the size-biased distribution of $\xi(x)$

$$\mathbb{P}(N = k) = \frac{k\mathbb{P}(\xi(x) = k)}{\mathbb{E}(\xi(x))} = e^{-\theta(x)} \frac{\theta(x)^{i-1}}{(i-1)!}.$$

After the first mutation

Assume that $\mu \equiv 0$ and $\nu_0 = n\delta_x + m\delta_y$, where x is the resident trait and y the mutant one. Then $\nu_t = X_t\delta_x + Y_t\delta_y$, where $(X_t, Y_t)_t$ is a two-types logistic branching process.

Let $T = \inf\{t \geq 0 : X_t = 0 \text{ or } Y_t = 0\}$. Then $T < \infty$ a.s.

- The event $\{X_T = 0\}$ is called **fixation of the mutant y**
- We denote by $u_{n,m}(x, y)$ the **fixation probability**

Convergence of the support to the TSS

Let ρ_k be the first time after the k -th mutation time τ_k when the population gets monomorphic, and V_k the then surviving type.

Theorem

Assume $\nu_0 = n\delta_x$. The *support* process $(S_t^\gamma; t \geq 0)$ defined as

$$S_t^\gamma = \sum_{k=0}^{\infty} V_k \mathbf{1}_{\{\rho_k \leq t/\gamma < \rho_{k+1}\}}$$

converges in distribution as $\gamma \rightarrow 0$ on $\mathbb{D}(\mathbb{R}_+, \mathcal{X})$ to the Markov process $(Z_t; t \geq 0)$ whose jumping rates $q(x, dh)$ from x to $x + h$ are given by $q(x, dh) = \beta(x)\chi(x, x + h)M(x, dh)$, where

$$\chi(x, y) = \sum_{n \geq 1} e^{-\theta(x)} \frac{\theta(x)^{n-1}}{(n-1)!} u_{n,1}(x, y).$$

Interpretation

- Population is monomorphic at all times
- Evolution proceeds by jumps (TSS) that are possible in any direction of space

$$q(x, dh) = \beta(x)\chi(x, x+h)M(x, dh),$$

where

$$\beta(x) = \mu(x)b(x)\mathbb{E}(\xi(x))$$

is the **total production rate of mutants** (on the mutation timescale t/γ) in a stationary x -type population, and

$$\chi(x, y) = \sum_{n \geq 1} e^{-\theta(x)} \frac{\theta(x)^{n-1}}{(n-1)!} u_{n,1}(x, y).$$

is the **fixation probability** of a y -type mutant in a size-biased stationary x -type population (**invasion fitness**, Metz et al., 1992).

Limit of small jumps

Let us assume that $M(x, \cdot)$ has 0 expectation, i.e. $\int_{\mathbb{R}^k} hM(x, dh) = 0$.

We are going to apply a **limit of small jumps** to the TSS.

- Replace the mutation law $M(x, dh)$ with its image by $h \mapsto \epsilon h$ ($\epsilon > 0$)
- Rescale time as t/ϵ^2
- \rightsquigarrow rescaled process Z^ϵ

The canonical diffusion of adaptive dynamics

Let $\sigma(x)$ be the square root of the covariance matrix of $M(x, \cdot)$.

Theorem

As $\epsilon \rightarrow 0$, Z^ϵ converges in distribution on $\mathbb{D}(\mathbb{R}_+, \mathbb{R}^k)$ to the diffusion process solution to the SDE

$$dZ_t = \beta(Z_t)\sigma^2(Z_t)\nabla_2\chi(Z_t, Z_t)dt + \sqrt{\beta(Z_t)\chi(Z_t, Z_t)}\sigma(Z_t)dB_t$$

where B is a standard k -dimensional Brownian motion.

Discussion

- We obtain a **diffusion model of evolution** grounded on a microscopic population dynamics
- **Genetic drift** proportional to the square root of $\beta(x)$, the neutral fixation probability $\chi(x, x)$ and the covariance matrix of $M(x, \cdot)$.
- Directional selection similar to the one of the canonical ODE

$$\frac{dx}{dt} = \frac{1}{2} \sigma(x)^2 \mu(x) \bar{n}(x) \frac{\partial}{\partial y} f(x, x)$$

- the covariance matrix of $M(x, \cdot)$
 - the total mutant production rate $\beta(x)$
 - the gradient of the fixation probability $\chi(x, y)$ of a y -type mutant in a stationary x -type resident population.
- $y \mapsto \chi(x, y)$ defines a fitness landscape that depends on the current state of the population

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Parameters of the two-type logistic branching process

- the two-type logistic branching process is denoted $(X_t, Y_t; t \geq 0)$, with birth vector B , competition matrix C and death vector D

$$B = \begin{pmatrix} b(x) \\ b(y) \end{pmatrix}, \quad C = \begin{pmatrix} c(x, x) & c(x, y) \\ c(y, x) & c(y, y) \end{pmatrix}, \quad D = \begin{pmatrix} d(x) \\ d(y) \end{pmatrix}$$

- where \mathbf{x} refers to the **resident** type, and \mathbf{y} refers to the **mutant** type
- $\mathbf{n} = X_0$ is the initial number of residents
- $\mathbf{m} = Y_0$ is the initial number of mutants
- $\mathbf{p} = m/(n + m)$ denotes the initial frequency of mutants.

Neutrality

- the case where types are exchangeable is referred to as (selective) **neutrality**, that is

$$B = \begin{pmatrix} b \\ b \end{pmatrix}, \quad C = \begin{pmatrix} c & c \\ c & c \end{pmatrix}, \quad D = \begin{pmatrix} d \\ d \end{pmatrix}$$

- under neutrality, the fixation probability u equals the initial frequency p of the mutant

$$u_{n,m} = \frac{m}{n+m}$$

Five fundamental selection coefficients (1)

We will express **deviations from neutrality** as

$$B - \begin{pmatrix} b & \\ & b \end{pmatrix} = \begin{pmatrix} 0 & \\ & \lambda \end{pmatrix}, \quad D - \begin{pmatrix} d & \\ & d \end{pmatrix} = - \begin{pmatrix} 0 & \\ & \sigma \end{pmatrix},$$

$$C - \begin{pmatrix} c & c \\ c & c \end{pmatrix} = - \begin{pmatrix} 0 & 0 \\ \delta & \delta \end{pmatrix} + \begin{pmatrix} 0 & \alpha \\ 0 & \alpha \end{pmatrix} - \begin{pmatrix} 0 & \varepsilon \\ \varepsilon & 0 \end{pmatrix}.$$

The coefficients λ , δ , α , ε , σ are chosen to be **positive** when they confer an **advantage** to the mutant, and are called the five fundamental **selection coefficients**.

Five fundamental selection coefficients (2)

- 1 **fertility**, λ : positive λ means increased mutant birth rate
- 2 **defence** capacity, δ : positive δ means reduced competition sensitivity of mutant individuals w.r.t. the total population size
- 3 **aggressiveness**, α : positive α means raised competition pressure exerted from any mutant individual onto the rest of the population
- 4 **isolation**, ε : positive ε means lighter cross-competition between different morphs, that would lead, if harsher, to the exclusion of the less abundant one
- 5 **survival**, σ : positive σ means reduced mutant death rate.

Factorization of second-order terms

Theorem

The fixation probability u is differentiable w.r.t. $\mathbf{s} = (\lambda, \delta, \alpha, \varepsilon, \sigma)'$. In the neighbourhood of neutrality,

$$u = p + \mathbf{v}' \cdot \mathbf{s} + o(\mathbf{s}),$$

where the **selection gradient** $\mathbf{v} = (v^\lambda, v^\delta, v^\alpha, v^\varepsilon, v^\sigma)'$ can be expressed as

$$v_{n,m}^\iota = p(1-p) g_{n+m}^\iota \quad \iota \neq \varepsilon,$$

$$v_{n,m}^\varepsilon = p(1-p)(1-2p) g_{n+m}^\varepsilon$$

The g 's depend only on the resident's characteristics b, c, d , and on the total initial population size $n + m$. They are called **invasibility coefficients**, and they characterize the **robustness** of the resident.

Coefficients of the CDAD

- The invasibility coefficients g_k^ι can be explicitly computed
- $\chi(x, x) = \frac{e^{-\theta(x)} - 1 + \theta(x)}{\theta(x)^2}$
- $\nabla_2 \chi(x, x) = e^{-\theta(x)} (a_\lambda(x) \nabla b(x) - a_\delta(x) \nabla_1 c(x, x) + a_\alpha(x) \nabla_2 c(x, x))$
where, for $\iota = \lambda, \delta, \alpha$,

$$a_\iota(x) = \sum_{n=1}^{\infty} \frac{n g_{n+1}^\iota(x) \theta(x)^{n-1}}{(n+1)^2 (n-1)!}.$$

Example

Assume that

- $\mathcal{X} = \mathbb{R}$
- $c(x, y) = C((x - y)^2)$ and $C(0) = 1 \rightsquigarrow \frac{\partial c}{\partial x}(x, x) = \frac{\partial c}{\partial y}(x, x) = 0$
- $\sigma(x)$ is the standard deviation of $M(x, \cdot)$

The canonical diffusion of adaptive dynamics is given by

$$dZ_t = r(Z_t)dt + \sigma(Z_t)\mu(Z_t)^{1/2} \left(\frac{b(Z_t)}{1 - e^{-b(Z_t)}} - 1 \right)^{1/2} dB_t$$

where

$$r(x) = \frac{\mu(x)\sigma(x)^2}{2} \left(1 + \frac{4}{b(x)} + \frac{b(x) - 4}{1 - e^{-b(x)}} \right) b'(x).$$

Numerical computation of a^ι

Numerical computation of the coefficients $a_\iota(b, c)$ of the CDAD related to fertility ($\iota = \lambda$), aggressiveness ($\iota = \alpha$) and defense ($\iota = \delta$).

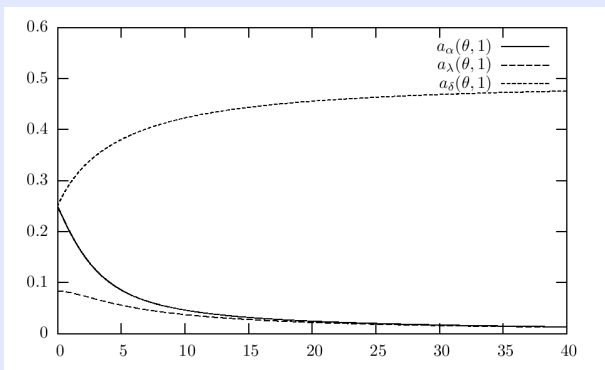


Figure: The functions $a_\lambda(\theta, 1)$, $a_\delta(\theta, 1)$ and $a_\alpha(\theta, 1)$ as functions of θ .

Numerical computation of a^l (2)

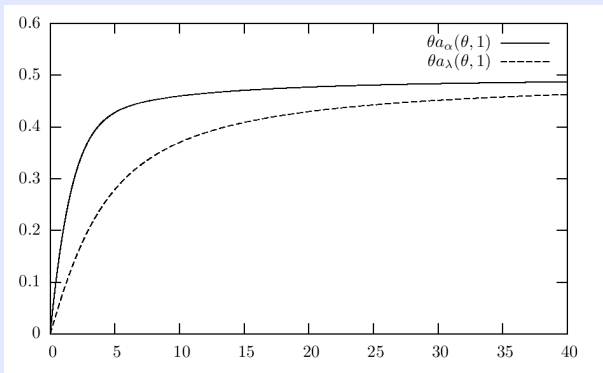


Figure: The functions $\theta \mapsto \theta a_\lambda(\theta, 1)$ and $\theta \mapsto \theta a_\alpha(\theta, 1)$.

Summary

We have

- included genetic drift in the adaptive models
 - diffusion process grounded on a microscopic ecological modeling of the population
- defined and computed a precise notion of fitness in finite populations
 - as usual in adaptive dynamics, the fitness landscape depends on the current state of the population
- characterized the robustness of a trait in a logistic population in terms of five fundamental components