Stochastic models and Evolution

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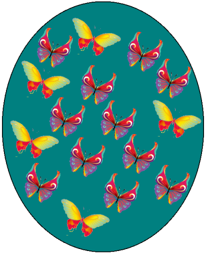
Haploid hermaphroditic sexual population

Conditions for the emergence of preferences

Ecological parameters

- b and d birth rate and intrinsic death rate
- c competitive pressure.
- $K \in \mathbb{Z}^+$: carrying capacity.



Traits

- A or a

→ joint work with Coron, Costa, Laroche, Smadi.

Haploid hermaphroditic sexual population

- Random meeting at rate B
- Mating with probability b/B
- Mendelian inheritance

Possible couples to generate a (first parent choosing and second parent chosen)

$$a \times a \ (1) \quad a \times A \ (1/2) \quad A \times a \ (1/2)$$

Birth rate

$$b_a(N) = b\left(N_a \frac{N_a + N_A/2}{N_a + N_A} + N_A \frac{0.N_A + N_a/2}{N_a + N_A}\right) = bN_a,$$

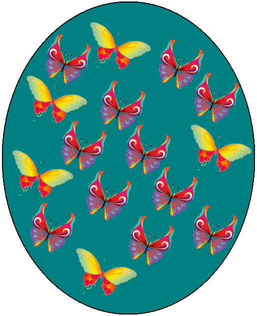
Death rate

$$d_a(N) = \left(d + \frac{c}{K}(N_A + N_a)\right)N_a.$$

Dimorphic population with random mating

When population size of order K, rescaled population process $(N_A/K, N_a/K)$ evolves as a competitive Lotka-Volterra equation (Ethier and Kurtz 1986):

$$\dot{z}_A = (b - d - c(z_A + z_a))z_A$$
$$\dot{z}_a = (b - d - c(z_A + z_a))z_a$$



Positive equilibrium if $b > d$

$$\begin{cases} z_A = p\dfrac{b-d}{c}, \\ z_a = (1-p)\dfrac{b-d}{c}, \end{cases}$$

for any $p \in [0, 1]$.

Mutation impacting the mate choice

- Random mating: allele p
- Mutation: allele P

- Advantage: higher birth rate with individuals of the same type (a/A): $b(1+\beta_1)$ ($\beta_1 \geq 0$)
- Cost: smaller birth rate with individuals of the other type (a/A): $b(1-\beta_2)$ ($0 \leq \beta_2 < 1$)

Assortative mating: preference for individuals of the same type

Possible couples to generate Ap (first parent choosing and second parent chosen)

$$
\begin{array}{ccc}
(1)\ Ap \times Ap & (1/2)\ Ap \times ap & (1/2)\ ap \times Ap \\
(1/2)\ Ap \times AP & (1/4)\ ap \times AP & (1/4)\ Ap \times aP \\
(1/2)\ AP \times Ap & (1/4)\ AP \times ap & (1/4)\ aP \times Ap
\end{array}
$$

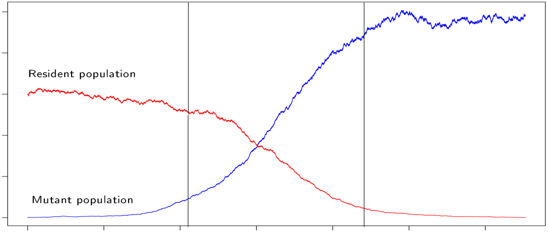
Assortative birth rate

$$
\begin{aligned}
b_{Ap}(N) =& \frac{b}{N_A + N_a}\Big[1 N_{Ap}N_{Ap} + \frac{1}{2}N_{Ap}N_{ap} + \frac{1}{2}N_{ap}N_{Ap} + \frac{1}{2}N_{Ap}N_{AP} \\
& \qquad\qquad + \frac{1}{4}N_{ap}N_{AP} + \frac{1}{4}N_{Ap}N_{aP}\Big] \\
& + \frac{(1+\beta_1)b}{N_A + N_a}\Big[\frac{1}{2}N_{AP}N_{Ap}\Big] + \frac{(1-\beta_2)b}{N_A + N_a}\Big[\frac{1}{4}N_{AP}N_{ap} + \frac{1}{4}N_{aP}N_{Ap}\Big].
\end{aligned}
$$

Questions

- Under which conditions the mutant P may invade?
- What is the invasion probability?
- What is the final state of the population?
- What is the invasion time scale?

How to study the invasion?



Three phases of study

Invasion with positive probability

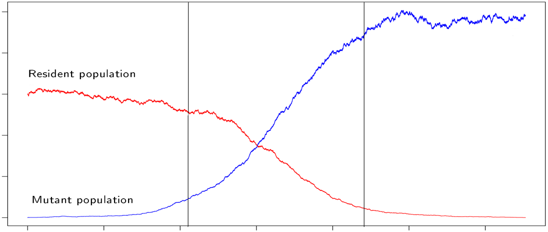
Invasion with positive probability if and only if

$$\beta_1 > \left(\frac{\beta_2}{2} + 1\right) \quad \text{or} \quad \frac{N_{ap}(0)}{N_p(0)} \frac{N_{Ap}(0)}{N_p(0)} < \frac{\beta_1(\beta_2 + 2)}{2(\beta_1 + \beta_2)(\beta_1 + 2)}.$$

Two conditions may foster the invasion

- ⇒ Advantage of the homogamous reproduction has to be large enough ($\beta_1 > 3/2$ is enough)
- ⇒ Small initial allelic diversity

How to study the invasion?



Three phases of study

Theorem

Assume that $N_A(0) > N_a(0)$, the initial mutant is of type α and

$$\beta_1 > \left(\frac{\beta_2}{2} + 1\right) \quad \text{or} \quad \frac{N_{ap}(0)}{N_p(0)} \frac{N_{Ap}(0)}{N_p(0)} < \frac{\beta_1(\beta_2 + 2)}{2(\beta_1 + \beta_2)(\beta_1 + 2)}.$$

Then with a probability $1 - q_\alpha$, fixation of AP in a time

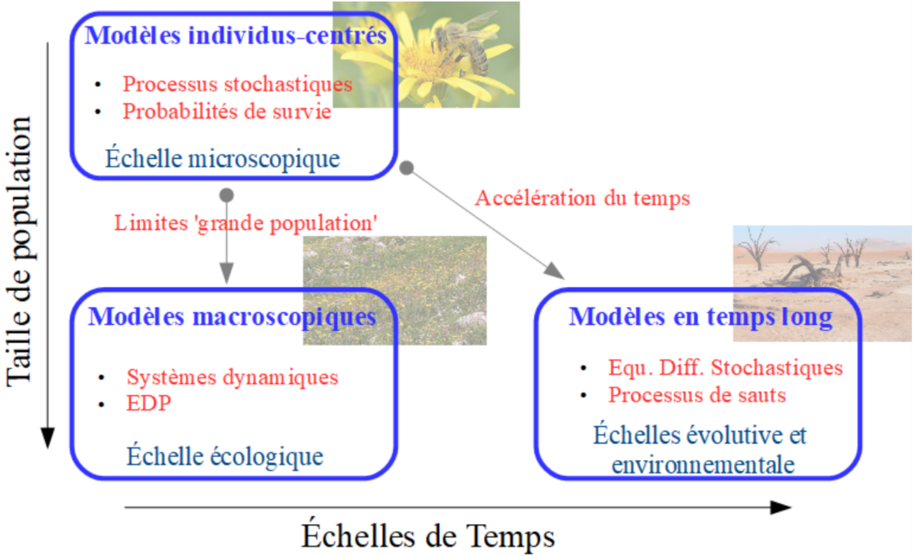
$$\left(\frac{1}{\lambda} + \frac{2}{b\beta_1}\right) \ln K.$$

Otherwise, extinction of the mutant population.

1. Evolutionary framework
   - Random mating
   - Mutation

2. Adaptive dynamics

Scaling



Modèles individus-centrés
Processus stochastiques
Probabilités de survie
Échelle microscopique
Limites 'grande population'
Accélération du temps
Modèles macroscopiques
Systèmes dynamiques
EDP
Échelle écologique
Modèles en temps long
Equ. Diff. Stochastiques
Processus de sauts
Échelles évolutive et environnementale
Taille de population
Échelles de Temps

Adaptive dynamics assumptions

At each birth, a mutation occurs with probability

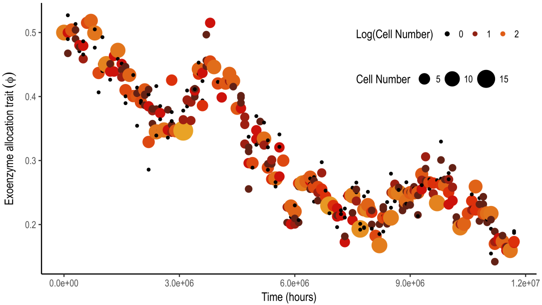
$$\boxed{\mu_K}.$$

Assumptions :

- **Large population**: $\boxed{K \to +\infty}$.
- **Rare mutations**: $\boxed{\mu_K \to 0}$.
- **Small effects**.
- **Ecological** and **evolutionary** scales are separated.

Metz et al. (1992, 1996), Champagnat (2006), Champagnat and Méléard (2011), Méléard and Tran (2009), Champagnat et al. (2011), Costa et al. (2015)

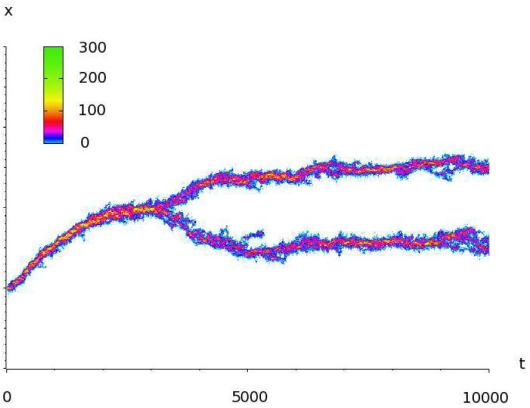
Simulations



Source: Abs-L-Ferrière, 2020

Substitution sequence.

Simulations



Source: Champagnat-Méléard, 2011

Diversification phenomenon: new species appearance.

Thank you for your attention