# Large deviations on the profile of mutation effects for a model of populations adapting to a changing environment



the population

<u>Aurelien Velleret</u>, E. Pardoux and M. Kopp (PhD advisors), D. Kim (host researcher) aurelien.velleret@nsup.org

### Introduction

In this elementary model for the adapatation of a population to changing environmental conditions, the main focus is to gain more insight in the contribution of the various mutation effects.

Averaged over a long time, by looking back at the ancestral line of a surviving population, a specific profile of mutation effects shall arise. So we want to investigate how this profile is constrained.

For instance : how exceptional is it for large

## Formalization of the stochastic process

Extinction happens at time  $\tau_{\partial}$  as soon as  $N_t$  reaches 0 (no more individuals in the population),

with 
$$N_t = n + \int_0^t (r(X_s) N_s - c_p (N_s)^2) ds + \sigma \int_0^t \sqrt{N_s} dB_s,$$

where B is a Brownian Motion and  $r(x) \xrightarrow[|x| \to \infty]{} -\infty$  (extreme values of  $X_t$  are not viable) General model for adaptation :

$$X_t = x - v t + \int_{[0,t] \times \mathbb{R}^d \times \mathbb{R}_+} w \mathbf{1}_{\{u \le f(N_s) \ g(X_{s-},w)\}} M(ds, dw, du),$$

mutations to have a larger contribution than expected.

# **Ecological aspects**

•  $(N_t)_{t>0}$  : size of the population •  $(X_t)_{t>0}$  : gap relative to the moving optimum we assume that the growth rate only depends on this adaptation coordinate  $X_t$ 

Environmental change :

• for simplicity, translation of the growth rate profile at constant speed v• compensated by the fixation of mutations in the population

# **Stability of the adaptation**



where M is a Poisson Point Process of intensity  $ds \nu(dw) du$ .

Another description of X when f is bounded  $(q \leq 1)$ : Let  $M = \{T_i\}_{i>1}$  be a Poisson Point Process with intensity  $||f||_{\infty}$ , ie inter-time are exponential r.v. with average  $1/||f||_{\infty}$ ;  $(W_i)_{i>1} \sim \nu(dw)$  be iid rv (effect of the mutations);  $(U_i)_{i>1} \sim \mathcal{U}([0,1])$  be iid rv (filtering of the proposal) :

$$X_t = x - v \ t + \sum_{T_i \le t} W_i \ \mathbf{1}_{\{U_i \le \frac{1}{\|f\|_{\infty}} f(N_{T_i}) \ g(X_{T_i}, W_i)\}}$$



Dynamics of adaptation inside the fitness landscape

med instantaneous

Population following the environmental change

# An expected profile of mutation effects

Convergence to a unique profile, independent of the initial condition  $\mu \in \mathcal{M}_1(\mathbb{R}^d \times \mathbb{R}^*_+)$ : Whatever the test function  $h: w \to \mathbb{R}$ , and  $\epsilon > 0$ :

$$\mathbb{P}_{\mu}\left[|\Delta_{t}(h)| > \epsilon \mid t < \tau_{\partial}\right] \xrightarrow[t \to \infty]{} 0$$
where  $\Delta_{t}(h) := \frac{1}{t} \sum_{T_{i} \leq t} \mathbf{1}_{\left\{U_{i} \leq \frac{1}{\|f\|_{\infty}} f(N_{T_{i}}) g(X_{T_{i}-}, W_{i})\right\}} h(W_{i})$ 

$$- \int_{\mathbb{R}^{d} \times \mathbb{R}^{*}} \alpha(dx, dn) \int_{\mathbb{R}^{d}} \nu(dw) \eta(x + w, n) f(n) g(x, n) h(w)$$

#### populations at time t $\mathcal{L}(X_t, N_t | t < \tau_\partial) \sim \alpha$

#### 1. Spontaneous adap-



# References

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Here, the law  $\alpha$  describes a typical surviving population at a large time T, while the correction  $\eta(x+w,n)$  precises how likely it is for the population after the fixation to still be surviving until time t.

# Large deviation results (to be done)

What we'd like to prove is that at least for some test functions h, we can measure these deviations :

 $\mathbb{P}_{\mu}\left[\Delta_t(h) \geq \epsilon \mid t < \tau_{\partial}\right] \sim C(h, \epsilon) \exp[-I(h, \epsilon) t].$ 

From the literature on Large Deviation theory, such an estimate of  $I(h, \epsilon)$  is related to the "quasistationarity" of  $(X_t, N_t)$  when the natural probability law  $\mathbb{P}_{\mu}$  is biased to favor larger values of h (see notably [2]).

It means that for each successful invasion, with effect w, in a given history, we give to the probability of it happening a bonus  $\exp[\zeta h(w)]$  and renormalize to get a probability law.  $\zeta > 0$  is then the critical value for which  $\Delta_t(h) \geq \epsilon$  is to be expected. Hopefully, the "quasi-stationarity" of the biased process shall rely on the same criteria as for the unbiased process (see [7], based on [5], [6], [1]).

# Unbiased profile

Mutations with predicted proportion with the

# **Biased** profile

Same profile when the probability gets a multi-

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blue crosses, realized with purple dots (one simulation, about 1500 jumps), with as a reference the profile  $\nu(dw)$  of occurring mutations.



**Figure 1:** Histogram of the observed mutations Case 1. gives the law of the surviving populations.

plicative penalty p = 0.7 for any mutation between 0 and 0.1.



Similar profile of biased mutations ! (but less numerous)





the phenotypic lag

along

Repartition