Demography, extinction and genetics

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Motivations

Joint works with:

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We aim at studying:

- Extinction of populations
 - Evolution of populations near extinction
 - Joint dynamics of demography and genetics
- Genetic composition of populations conditioned on survival

1 Model and rescaling

2 Demography and allele fixation

3 Path integrability

4 Rescaling and time changes

(5) Distance to the Wright-Fisher diffusion

Microscopic model

Features:

- Diploid individuals, 1 gene, L alleles
- Competition and sexual Mendelian reproduction
- Individual-based model

Model:

- Multi-type non-linear birth-and-death process
- Rescaling: Large population, frequent reproduction and death events

Jump rates

n = number of individuals $x_{ij} =$ proportion of genotype ij $\mathbf{x} = (n, (x_{ij})_{i \leq j}) =$ state of the population $x_i =$ proportion of allele i

$$\mu_{ij}(\mathbf{x}) = \left(d_{ij} + \sum_{1 \le k, l \le L} c_{ij,kl} n x_{kl}\right) n x_{ij},$$

$$\lambda_{ij}(\mathbf{x}) = b_{ij}n \times 2x_i x_j, \qquad \lambda_{ii}(\mathbf{x}) = b_{ii}n x_i^2.$$

Rescaling

Large population, frequent reproduction and death events

$$\mathbf{Z}_{t}^{K} = \left(\frac{N^{K}(t)X_{ij}^{K}(t)}{K}\right)_{i \leq j}$$
$$\mathbf{Z}_{0}^{K} \Longrightarrow \mathbf{Z}_{0}$$

$$b_{ij}^{K} = \gamma K + \beta_{ij},$$
$$d_{ij}^{K} = \gamma K + \delta_{ij},$$
$$c_{ij,kl}^{K} = \frac{\alpha_{ij,kl}}{K},$$

Slow-fast convergence

Fast convergence to Hardy-Weinberg structure (Ethier & Nagylaki (1980))

$$\sup_{t \le u \le t+s} \mathbb{E}((\epsilon_{ij}^K(u))^2) \xrightarrow[K \to \infty]{} 0$$

Slow convergence to a diffusion process:

$$((n^{K}(t), x_{2}^{K}(t), \dots, x_{L}^{K}(t)))_{t \leq T} \underset{K \to \infty}{\Longrightarrow} ((n(t), x_{2}(t), \dots, x_{L}(t)))_{t \leq T}$$

Limiting diffusion process

 $f(N(t), X_2(t), ..., X_L(t)) = M_t + \int_0^t \mathcal{L}f(N(s), X_2(s), ..., X_L(s))ds$

$$\begin{aligned} \mathcal{L}f(n, x_2, ..., x_L) &= n \left(\rho - \alpha n + \sum_{i=2}^L s_i x_i \right) \frac{\partial f}{\partial n}(n, x_2, ..., x_L) \\ &+ \gamma n \frac{\partial^2 f}{\partial n^2}(n, x_2, ..., x_L) \\ &+ \sum_{i=2}^L x_i \left(s_i - \sum_{j=1}^L x_j s_j \right) \frac{\partial f}{\partial x_i}(n, x_2, ..., x_L) \\ &+ \sum_{i=2}^L \gamma \, \frac{x_i(1 - x_i)}{2n} \frac{\partial^2 f}{\partial x_i^2}(n, x_2, ..., x_L) \\ &- \sum_{i \neq j \in [\![2,N]\!]} \gamma \, \frac{x_i x_j}{2n} \frac{\partial^2 f}{\partial x_i \partial x_j}(n, x_2, ..., x_L). \end{aligned}$$

Questions

- Behaviour of genetics at extinction
- Impact of adding demography

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Wright-Fisher with demography

Theorem

(i) The population gets extinct almost surely in finite time.

(*ii*) One of the allele will get fixed a.s. before extinction.

(iii) The population experiences successive allele extinctions.

Extinction and fixation

$$\begin{cases} dN_t &= \sigma(N_t) \, dB_t + N_t (\rho - \alpha N_t) dt, \quad \alpha > 0 \\ dX_t &= \sqrt{\frac{X_t (1 - X_t)}{f(N_t)}} \, dW_t \end{cases} \qquad t < T_{0+}^N, \quad (1)$$

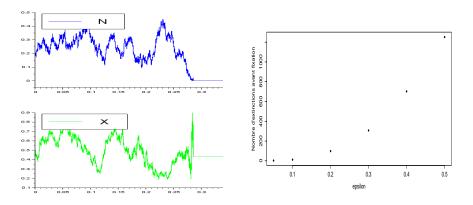
Theorem

Fixation occurs before extinction with probability one if and only if

$$\int_{0+} \frac{y}{\sigma^2(y)f(y)} \, dy = +\infty. \tag{2}$$

Extinction before fixation

$$dN_{t} = \sqrt{N_{t}^{(1-\varepsilon)}} dB_{t}^{1} + N_{t}(-1 - 0.1N_{t})dt$$
(3)
$$dX_{t} = \sqrt{\frac{X_{t}(1-X_{t})}{N_{t}}} dB_{t}^{2}$$
(4)



Ideas of the proof

Theorem

- (i) The population gets extinct almost surely in finite time. Well-known (Ikeda-Watanabe, Chapter VI.3).
- (ii) One of the allele will get fixed a.s. before extinction. Girsanov+Time change+Path integrability argument.
- (iii) The population experiences successive allele extinctions.Girsanov+Rescaling+Time change+Path integrability argument.

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Path integrability criterion

Theorem

- $(Z_t, 0 \le t \le T_0)$ regular diffusion process on $[0, +\infty)$
- Scale function s, speed measure m.

•
$$\mathbb{P}_{z}(T_{0} < +\infty) = 1 \text{ for all } z \in [0, +\infty)$$

• $f: (0, +\infty) \to \mathbb{R}_+$ locally bounded measurable function.

$$\int_{0^+} s(y) f(y) m(dy) < +\infty \iff \int_{0}^{T_0} f(Z_s) ds < +\infty \quad \mathbb{P}_z - a.s.$$
$$\int_{0^+} s(y) f(y) m(dy) = +\infty \iff \int_{0}^{T_0} f(Z_s) ds = +\infty \quad \mathbb{P}_z - a.s.$$

Path integrability criterion: proof

 Engelbert & Tittel (2002), Khoshnevisan, Salminen & Yor (2006) Mijatovic & Urusov (2012)

•
$$\mathbb{P}(\int_0^{T_0} f(Z_s) ds < \infty) \in \{0, 1\}$$

• If
$$\int_0^\infty s(y) f(y) m(dy) = +\infty$$
 then $\mathbb{P}_z\left(\int_0^{T_0} f(Z_s) ds = +\infty\right) \ge \frac{1}{20}$.

•
$$\mathbb{E}_{z}\left[\left(\int_{0}^{T_{0}}f(Z_{s})\,ds\right)^{n}\right]\leq n!\,\left(\int_{0}^{\infty}s(y)\,f(y)\,m(dy)\right)^{n}$$

Path integrability, Feller diffusion

Lemma

Let N be solution of

$$dN_t = \sqrt{\gamma N_t} \, dB_t + N_t (\rho - \xi N_t) dt.$$

Let $T_0^N = \inf\{t \ge 0, N_t = 0\}$. For any $x \in \mathbb{R}_+$,

$$\mathbb{P}_x\Big(\int_0^{T_0^N} \frac{1}{N_s} \, ds = +\infty\Big) = 1.$$

Path integrability, Wright-Fisher diffusion

Lemma

Let Y be solution of

$$dY_t = \sqrt{Y_t(1 - Y_t)} \, dB_t, \qquad Y_0 \in [0, 1).$$

Let $T_1 = \inf\{t \ge 0, Y_t = 1\}$. For any $y \in (0, 1)$,

$$\mathbb{P}_y\Big(\int_0^{T_1} \frac{1}{1-Y_s} \, ds = +\infty\Big) = 1.$$

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Wright-Fisher diffusion behaviour

Proposition

Let $(X^1, ..., X^{L-1})$ be an L-type Wright-Fisher neutral diffusion process.

- One of the L alleles is fixed a.s. in finite time. By induction on L.
- The population experiences successive allele extinctions. By induction on L: Time change+Path integrability

Proof: Time change+Path integrability

•
$$\int_0^{T_1^{X^L}} \frac{1}{1 - X_s^L} \, ds = +\infty$$

- Define τ on $[0, +\infty)$ such that $\int_0^{\tau(t)} \frac{1}{1-X^L(s)} ds = t$ for all $t \ge 0$.
- Let

$$(Y_t^1, Y_t^2, ..., Y_t^{L-2})_{t \ge 0} = \left(\frac{X^1}{1 - X^L}(\tau(t)), ..., \frac{X^{L-2}}{1 - X^L}(\tau(t))\right)_{t \ge 0}$$

Lemma

 $(Y_t^1, Y_t^2, ..., Y_t^{L-2})_{t \ge 0}$ is a L - 1-type Wright-Fisher diffusion process.

- Successive allele extinctions at time $S_1^Y < \ldots < S_{L-2}^Y < +\infty$
- Successive allele extinctions for $(X^1, X^2, ..., X^L)$ at times $\tau(S_1^Y) < ... < \tau(S_{L-2}^Y) < \tau(+\infty) = T_1^{X^L}$ if $T_1^{X^L} < \infty$

Demographic Wright-Fisher diffusion

 $\bullet~L\mbox{-dimensional}$ Girsanov transformation->neutral case

•
$$\int_0^{T_0^N} \frac{\gamma}{2N_s} ds = +\infty$$
 a.s.

•
$$\int_0^{\tau(t)} \frac{\gamma}{2N_s} ds = t$$
 for all $t \in \mathbb{R}_+$

• $\hat{X}_t = X_{\tau(t)}$ follows a neutral classical Wright-Fisher diffusion process.

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Effective population size

- 2 neutral alleles
- (X, N) demographic Wright-Fisher diffusion with parameters ρ , α .
- X^{WF} classical Wright-Fisher diffusion with parameter N_e
- Calibration: we impose

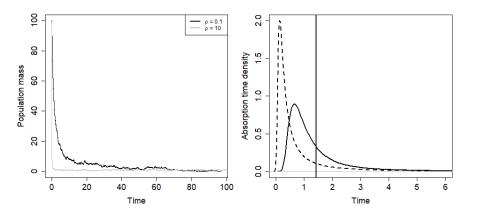
$$\mathbb{E}(T^X_{\{0,1\}}) = \mathbb{E}(T^{X^{WF}}_{\{0,1\}}),$$

which gives

$$N_e = \mathbb{E}\left(\frac{T_{\{0,1\}}^X}{\int_0^{T_{\{0,1\}}^X} \frac{1}{N_t} dt}\right).$$

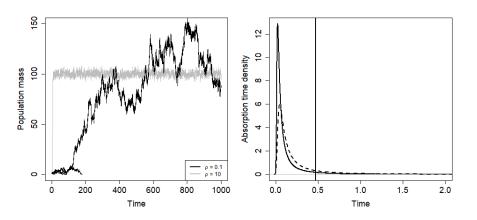
Law of absorption time

Decreasing population size



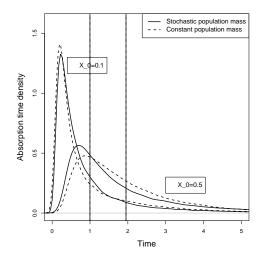
Law of absorption time

Increasing populations size



Law of absorption time

"Constant" population size



Distance to the Wright-Fisher diffusion

Perspectives

• Continuum of alleles: demographic Fleming-Viot process

• Quasi-stationary behaviour

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