Muller's Ratchet

In Populations Doomed to Extinction

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Turning Discovery Into Health

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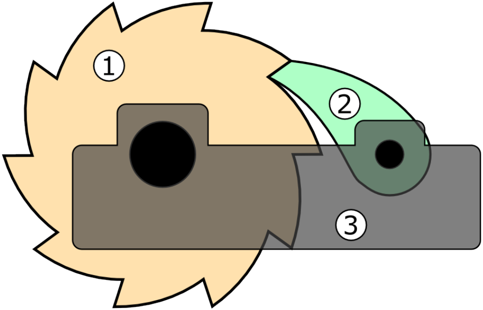

1.- Rueda

2.- Gatillo

3.- Soporte

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Fixed population size models, for example J. Haigh (1978), Gordo & Charlesworth (2000)

Branching process models, for example: Fontanari, Colato, Howard (2003), S. Pénisson, P. D. Sniegowski, A. Colato and P. J. Gerrish (2013)

Fixed population size: mutation rate u, Poisson mutations, selection coefficient s, population size N, Wright–Fisher with mutations, relative fitness, k mutations – fitness $(1-s)^k$.

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Haigh: Size of least-loaded class at equilibrium is $Ne^{-u/s}$, ratchet clicks at times linear in N (sort of).

Simple branching process model: binary splitting, at most one new mutation per offspring, type k of individual = number of mutations accumulated, $k \in \{0, 1, 2, ...\}$.

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Mutation probability u

Reproduction scheme:

$$k \to \begin{cases} k \\ k \end{cases} \quad \text{with probability } p(1-s)^k(1-u)^2$$

$$k \to \begin{cases} k \\ k+1 \end{cases} \quad \text{with probability } 2p(1-s)^k u(1-u)$$

$$k \to \begin{cases} k+1 \\ k+1 \end{cases} \quad \text{with probability } p(1-s)^k u^2$$

$$k \to \emptyset \quad \text{with probability } 1-p(1-s)^k$$

Mean reproduction matrix M with entries

$$\begin{cases} m_{k,k} & = & 2p(1-s)^k(1-u) \\ m_{k,k+1} & = & 2p(1-s)^k u \end{cases}$$

where $m_{i,j}$ is the expected number of offspring of type j generated by an individual of type i. All other entries of M are 0.

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Subcritical process: $2p(1-u) < 1$

Objective: Start with n_0 individuals. Describe consecutive clicks of the ratchet and the corresponding sizes of the new fittest class $t_0, n_1, t_1, n_2, \ldots$

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Specifically: Expected extinction time of 0-class, t_0, and expected size of 1-class at this time, n_1, particularly as $n_0 \to \infty$.

Extinction: Think single-type. Pgf φ, start from random number N_0 of individuals. Expected extinction time:

$$t_0 = E[T_0] = \sum_{k \geq 0} P(T_0 > k) = \sum_{k \geq 0} P(Z_k > 0)$$

$$= P(Z_0 > 0) + \sum_{k \geq 1} P(Z_k > 0)$$

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First-order Taylor:

$$t_0 \approx P(Z_0 > 0) + \sum_{k \geq 1} \left(1 - \left(\varphi^{(k)}(0)\right)^{n_0}\right) \tag{1}$$

Mean reproduction matrix for nth generation M^n has entries

$$m_{k,k+j}^{(n)} = a^{n-j} b^j (1-s)^{nk+\frac{j(j-1)}{2}} \prod_{i=1}^{j} \frac{(1-s)^{n+1-i}-1}{(1-s)^i-1}$$

where $a = m(0,0) = 2p(1-u)$ and $b = m(0,1) = 2pu$.

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$$m_{0,1}^{(n)} = (2p(1-u))^n \frac{u}{1-u} \frac{1-(1-s)^n}{s}$$

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Can use (1) and (2) repeatedly to find $t_0, n_1, t_1, n_2, \ldots$ What happens as $n_0 \to \infty$? Need asymptotics of t_0 ($t_0 \sim C \log n_0$ not good enough).

Jagers, Klebaner, Sagitov (2007):

$$t_0 = \frac{\log n_0 + c(n_0)}{-\log(2p(1-u))}$$

where $c(n_0) \to c$ as $n_0 \to \infty$.

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$$n_1 \to K \frac{u}{(1-u)s}$$

Hence

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\begin{aligned}
&n_0 \to \infty \\
&t_0 \to \infty \\
&n_1 \to \text{ constant} \\
&t_1 - t_0, n_2, t_2 - t_1, \ldots \text{ are ''small''}
\end{aligned}
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Total extinction time dominated by extinction of mutation-free class.

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Total extinction time dominated by extinction of mutation-free class.

Extinction of mutation-free class faster than fixed-population models: $t_0 \sim C \log n_0$ vs. $t_0 \sim C\, n_0$ (sort of).

A curiousity:

For small u, $1 - u \approx 1$ and

$$n_1 \to K \frac{u}{(1-u)s} \approx K \frac{u}{s}$$

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Don't know.