Some mathematical models from population genetics

5: Muller's ratchet and the rate of adaptation

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joint work with Peter Pfaffelhuber (Vienna), Anton Wakolbinger (Frankfurt) Charles Cuthbertson (Oxford), Feng Yu (Bristol)

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How many generations will it take for an asexually reproducing population to lose its best class?

Haigh's model

Wright-Fisher model:

Individuals in (t + 1)st generation select parent at random from generation t.

Probability individual which has accumulated k mutations is selected as parent proportional to *relative fitness* $(1 - s)^k$.

Number of mutations carried by offspring then k + J, where $J \sim \text{Poiss}(\lambda)$ (independent).

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$$\mathbb{P}[H=k] \propto (1-s)^k x_k(t),$$

 $J \sim \text{Poiss}(\lambda)$ independent of H. K_1, K_2, \ldots, K_N independent copies of H + J. Random type frequencies in next generation are

$$X_k(t+1) = \frac{1}{N} \#\{i : K_i = k\}.$$

Infinite populations

As $N \to \infty$, LLN \Rightarrow

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Suppose $\mathbf{x}(t) \sim \text{Poiss}(\alpha)$.

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Then $H \sim \operatorname{Poiss}(\alpha(1-s))$, $J \sim \operatorname{Poiss}(\lambda)$, so

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 $H + J \sim \operatorname{Poiss}(\alpha(1-s) + \lambda).$

Poisson weights \mapsto Poisson weights.

For every initial condition with $x_0 > 0$, the solution to the deterministic dynamics converges as $t \to \infty$ to the stationary point

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 $\pi := \operatorname{Poiss}(\lambda/s).$

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Condition on $\mathbf{Y}(t) = \mathbf{y}(t)$. Size of new best class,

 $y_0(t+1) \sim \text{Binom}(N, p_0(t))$, with $p_0(t)$ probability of sampling parent from best class *and* not acquiring any additional mutations:

$$p_0(t) = \frac{y_0(t)}{W(t)}e^{-\lambda}, \quad W(t) = \sum_{i=0}^{\infty} y_i(t)(1-s)^i$$

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Evolution of best class determined by W(t), the mean fitness in the

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population.

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- Phase one: deterministic dynamical system dominates, decaying exponentially fast towards its equilibrium
- Phase two: the 'bulk' of the population changes only slowly. Mean fitness assumed constant and then No. of individuals in best class approximated by Galton-Watson branching process with Poisson offspring distribution.

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k = 0, 1, 2, ... where $X_{-1} = 0$ and $(W_{jk})_{j>k}$ array of independent Brownian motions, $W_{kj} := -W_{jk}$. As before $Y_k = X_{k*+k}$,

$$dY_0 = s(M_1(\mathbf{Y}) - \lambda)Y_0(t)dt + \sqrt{\frac{1}{N}Y_0(1 - Y_0)}dW_0, \quad M_1(\mathbf{Y}) = \sum_j jY_j.$$

Infinite population limit

$$dx_k = (s(M_1(\mathbf{x}) - k) - \lambda)x_k + \lambda x_{k-1}) dt, \quad k = 0, 1, 2, \dots$$

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Transform into system of equations for cumulants:

$$\log\sum_{k=0}^{\infty} x_k e^{-\xi k} = \sum_{k=1}^{\infty} \kappa_k \frac{(-\xi)^k}{k!}$$

Assume $x_0 > 0$ and set $\kappa_0 = -\log x_0$. Then

$$\dot{\kappa}_k = -s\kappa_{k+1} + \lambda, \qquad k = 0, 1, 2, \dots$$

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System can be solved. In particular,

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$$\kappa_1(t) = \sum_{k=0}^{\infty} k x_k(t) = -\frac{\partial}{\partial \xi} \log \sum_{k=0}^{\infty} x_k(0) e^{-\xi k} \bigg|_{\xi=st} + \frac{\lambda}{s} (1 - e^{-st}).$$

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Notice the exponential decay towards the equilibrium vaue of λ/s . The time

$$\tau = \frac{\log(\lambda/s)}{s}$$

corresponds exactly to the end of Haigh's phase one.

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Approximations

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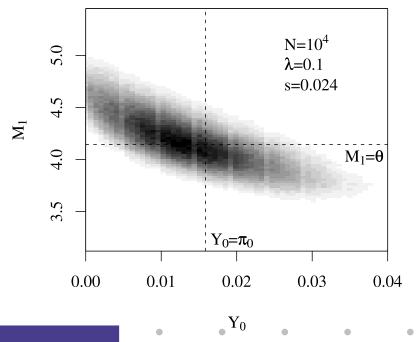
$$dY_0 = s(M_1(\mathbf{Y}) - \lambda)Y_0(t)dt + \sqrt{\frac{1}{N}Y_0(1 - Y_0)}dW_0.$$

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Cannot solve for $M_1(\mathbf{Y})$. Instead seek a *good approximation* of M_1 given Y_0 . Simulations suggest a good fit to a linear relationship between Y_0 and M_1 .



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Extending Haigh's approach

Haigh assumes at click times π_0 distributed evenly over other classes. Suppose now that this holds in between click times too: given Y_0 approximate state of system by *the PPA* (Poisson Profile Approximation)

$$\Pi(Y_0) = \left(Y_0, \frac{1 - Y_0}{1 - \pi_0}(\pi_1, \pi_2, \ldots)\right).$$

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Estimate M_1 not from PPA but from *relaxed* PPA obtained by evolving PPA according to the deterministic dynamical system for time $A\tau := A \log(\lambda/s)/s$. This gives

$$M_1 = \theta + \frac{\eta}{e^{\eta} - 1} \left(1 - \frac{Y_0}{\pi_0} \right), \quad \eta = (\lambda/s)^{1-A}.$$

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Three one dimensional diffusions

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Substituting in the one-dimensional diffusion approximation for Y_0 gives:

$$\begin{split} A \text{ small}, & dY_0 = \lambda (\pi_0 - Y_0) Y_0 dt + \sqrt{\frac{1}{N} Y_0} dW, \\ A = 1, & dY_0 = 0.58 s \Big(1 - \frac{Y_0}{\pi_0} \Big) Y_0 dt + \sqrt{\frac{1}{N} Y_0} dW, \\ A \text{ large}, & dY_0 = s \Big(1 - \frac{Y_0}{\pi_0} \Big) Y_0 dt + \sqrt{\frac{1}{N} Y_0} dW, \end{split}$$

A rescaling

$$Z(t) = \frac{1}{\pi_0} Y_0(N\pi_0 t).$$

Set

$$\gamma = \frac{N\lambda}{Ns\log(N\lambda)}.$$

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A small \equiv fast clicking:

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In order for $0.58 \frac{1}{\gamma \log(N\lambda)} (N\lambda)^{1-\gamma}$ to be > 5,

γ	0.3	0.4	0.5	0.55	0.6	0.7	0.8	0.9
$N\lambda \ge$	20	10^{2}	$9\cdot 10^2$	$4 \cdot 10^3$	$2 \cdot 10^4$	$4 \cdot 10^6$	$2 \cdot 10^{11}$	$8\cdot 10^{26}$

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Rule of thumb

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For biologically realistic parameters, transition from no clicks to moderate clicks (on evolutionary timescale) around $\gamma = 0.5$.

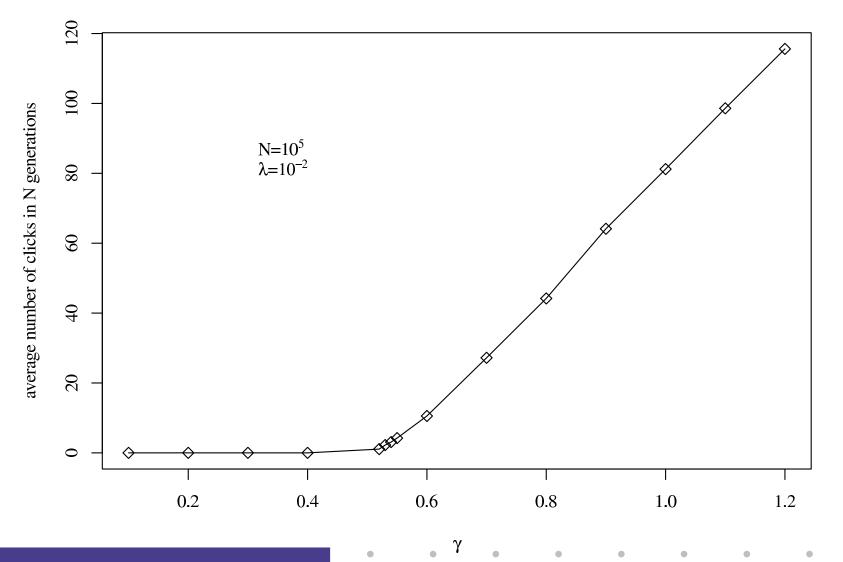
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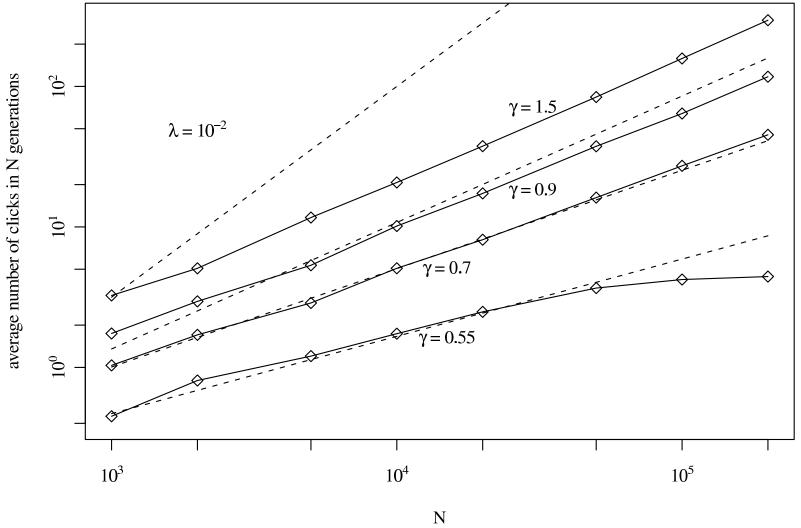
The rate of the ratchet is of the order $N^{\gamma-1}\lambda^{\gamma}$ for $\gamma \in (1/2, 1)$, whereas it is exponentially slow in $(N\lambda)^{1-\gamma}$ for $\gamma < 1/2$.

Simulations

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Is there a limit to the rate of adaptation?

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- *Mutation:* For each individual *i* a mutation event occurs at rate μ.
 With probability 1 q, X_i changes to X_i 1 and with probability q, X_i changes to X_i + 1.
- Selection: For each pair of individuals (i, j), at rate $\frac{\sigma}{N}(X_i X_j)^+$, individual *i* replaces individual *j*.
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Technical modification: suppress mutations which would make the 'width' of the population $> L \equiv N^{1/4}$.

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$$= [\bar{\mu}_k(P) + \sigma(k-m(P)) P_k] dt + dM_k^P$$

$$\bar{\mu}_k(P) \approx \mu \left(q P_{k-1} - P_k + (1-q) P_{k+1} \right)$$

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 M^P is a martingale with

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$$\left[M_{k}^{P}\right](t) \leq \frac{2\mu}{N}t + \frac{1}{N}\int_{0}^{t}\sum_{l\in\mathbb{Z}}(2+\sigma(k-l)^{+}+\sigma(l-k)^{+})P_{k}(s)P_{l}(s)\ ds$$

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Moments

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Mean fitness $m(P) = \sum_k k P_k$ satisfies

$$dm(P) = (\bar{\mu}(P) + \sigma c_2(P)) dt + dM^{P,m}$$
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Ignoring mutation terms, centred moments $c_k = \sum_k (k - m(p))^n P_k$ satisfy

 $dc_{2} \approx \sigma c_{3} \qquad dt + small noise terms$ $dc_{3} \approx \sigma(c_{4} - 3c_{2}c_{2}) \qquad dt + small noise terms$ $dc_{4} \approx \sigma(c_{5} - 4c_{3}c_{2}) \qquad dt + small noise terms$ $dc_{5} \approx \sigma(c_{6} - 5c_{4}c_{2}) \qquad dt + small noise terms$

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Stationary distribution approximately Gaussian.

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If there is a single individual at m(P) + K at time t = 0, how long until there is an individual at m(P) + K + 1?

Ignoring beneficial mutations occurring to individuals at m(P) + K - 1, until the front advances

$$Z(t) \approx e^{(\sigma K - (1-q)\mu)t}$$

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But wave speed is

$$\approx \mu(2q-1) + \sigma c_2(P) \approx \mu(2q-1) + \sigma b^2 \approx \mu(2q-1) + \frac{\sigma K^2}{2\log N}.$$

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Consistency condition:

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So *K* between $\log N$ and any fractional power of $\log N \Rightarrow$ rate of adaptation, of order between $\log N$ and any fractional power of $\log N$.

Rigorous result

Theorem.

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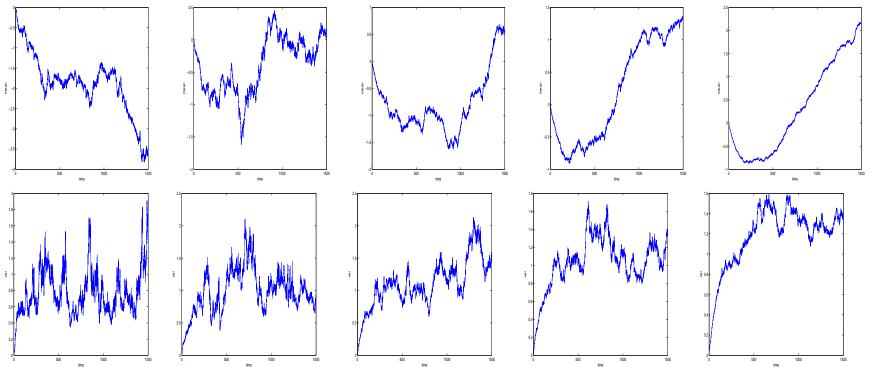
If q > 0, then for any $\beta > 0$, there exists a positive constant $c_{\mu,\sigma,q}$ such that

$$\mathbb{E}^{\pi}[m(1)] \ge \mathbb{E}^{\pi}[c_2] \ge c_{\mu,\sigma,q} \log^{1-\beta} N$$

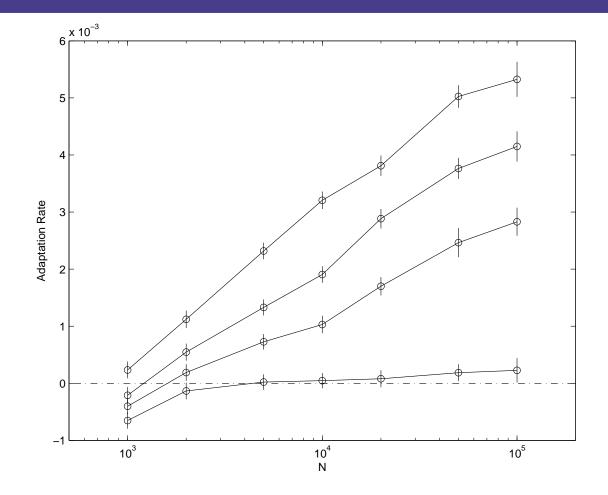
if N is sufficiently large.

Simulations

With $\mu = 0.01$, q = 0.01, $\sigma = 0.01$, N = 1000, 2000, 5000, 10000, 30000. First row: mean; second row: variance.



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Adaptation rate against population size.

From top to bottom, q = 4%, 2%, 1%, 0.2%, $\mu = 0.01$, $\sigma = 0.01$.