An individual-based model for the Lenski experiment, and the deceleration of the relative fitness

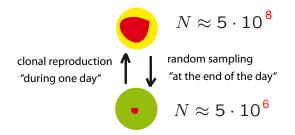
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Joint work with Noemi Kurt, Anton Wakolbinger and Linglong Yuan

14-06-2016



The Lenski experiment (one day cycle)



Relative fitness

Measuring adaptation

- A population of size A₀ of the unevolved strain and a population of size B₀ of the evolved strain perform a direct competition.
- ► The respective population sizes at the end of the day are denoted by A₁ and B₁.
- ► The (empirical) relative fitness F(B|A) of strain B with respect to strain A is

$$F(B|A) = \frac{\log(B_1/B_0)}{\log(A_1/A_0)}.$$

Lenski, Travisano, PNAS, 1994

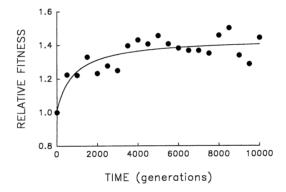
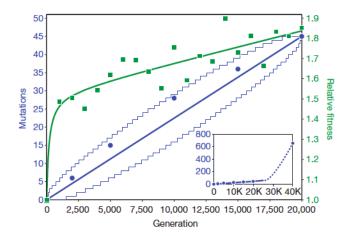


FIG. 4. Trajectory for mean fitness relative to the ancestor in one population of *E. coli* during 10,000 generations of experimental evolution. Each point is the mean of three assays. Curve is the best fit of a hyperbolic model.

Barrick, Yu, Yoon, Jeong, Oh, Schneider, Lenski, Kim, Nature 2009

$$\omega(t) = 1 + \frac{at}{t+b}$$



Wiser, Ribeck, Lenski, Science express 13-11-12

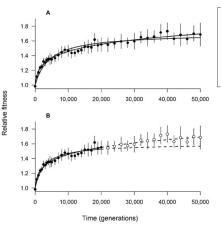


Fig. 2. Comparison of hyperbolic and power-law models. (A) Hyperbolic (red) and power-law (blue) models fit to the set of mean fitness values (black symbols) from all 12 populations. (B) Fit of hyperbolic (solid red) and power-law (solid blue) models to data from first 20,000 generations only (filled symbols), with model predictions (dashed lines) and later data (open symbols). Error bars are 95% confidence limits based on the replicate populations.

$w(t) = (1 + ct)^{1/2g}$

Questions

- Which curve describes better the trajectory of the relative fitness?
- Why is the relative fitness decelerating?

Possible explanations

- Clonal interference
- Epistasis
- The design of the experiment

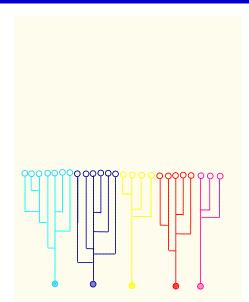
The daily cycle model¹

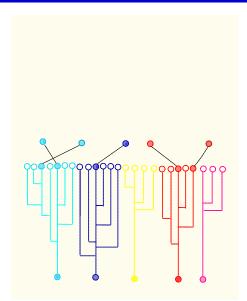
Information about the experiment

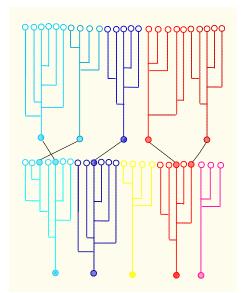
- At the beginning of each day there are *N* individuals.
- Within each day individuals split at constant rate.
- The reproduction process will stop when the glucose has been consumed. (This happens when there are around 100N individuals).
- ► N individuals out of the ~ 100N are uniformly sampled without replacement, to be starting individuals at the next day.

¹An individual-based model for the Lenski experiment, and the deceleration of the relative fitness. Adrian Gonzalez Casanova, Noemi Kurt, Anton Wakolbinger and Linglong Yuan. (2015) arXiv 1505.0175









Inside a day

Let $Y_{i,j}(t)$ be a pure birth process with rate $r \in \mathbb{R}^+$, for every $i \in \mathbb{N}$ and $j \in \{1, 2, ..., N\}$. (Yule Processes with parameter r). The total population size at time t of day i is

$$\sum_{j=1}^{N} Y_{i,j}(t)$$

Stopping rule

Each day, the reproduction stops at time σ , where

$$\sigma = \inf\{t : E[\sum_{j=1}^{N} Y_{i,j}(t)] = \gamma N\}.$$

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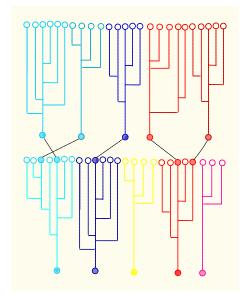
$$\sigma = \frac{\ln(\gamma)}{r}.$$

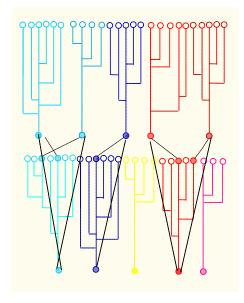
The total population size at the end of the day is

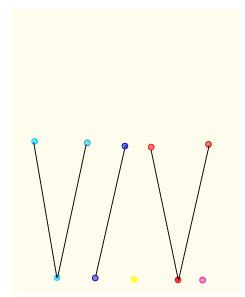
$$\sum_{j=1}^{N} Y_{i,j}(\sigma) \sim \gamma N.$$

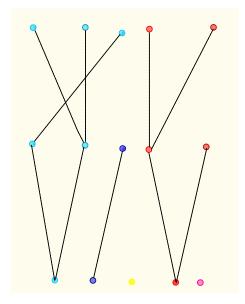
Sampling rule

To go from one day to the next, we sample uniformly at random N individuals (out of $\sim \gamma N$), and we say that each sampled individual is a root of a Yule tree in the next day.









Convergence to Kingman's coalescent

Let $(B_i^{(N,n)})_{i \in \mathbb{N}}$ be the ancestral process of a sample of *n* individuals, when the population at the beginning of each day is *N*.

Theorem

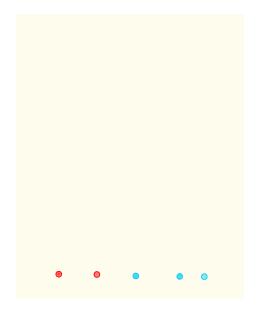
For all $n \in \mathbb{N}$, the sequence of ancestral processes $(B_{\lfloor Nt/2(1-\frac{1}{\gamma}) \rfloor}^{(N,n)})_{t\geq 0}$ converges weakly on the space of càdlàg paths as $N \to \infty$ to Kingman's *n*-coalescent.

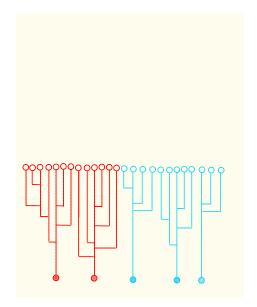
Introducing selective advantage

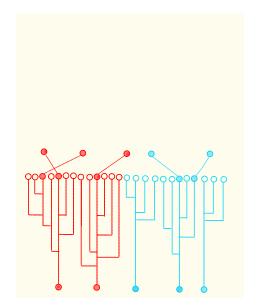
- Assume that some individuals reproduce at rate $r + \rho_N$ (mutants), while other reproduce at rate r (basis population).
- ► Stopping rule: the reproduction stops when the expectation of the total population is γN.
- Let $M_i(t)$ be the number of mutants at time t of day i.
- We are interested in the process

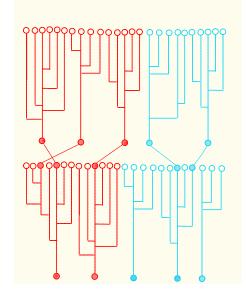
 $\{K_i\}_{i\in\mathbb{N}}:=\{M_i(0)\}_{i\in\mathbb{N}},$

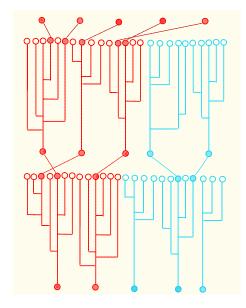
which is constructed recursively using uniform sampling.











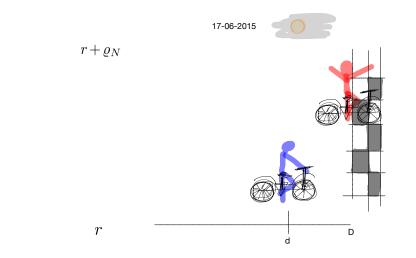
Selective advantage

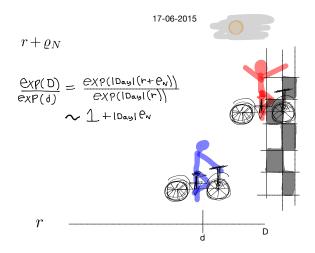
Basic population reproduces at rate r. Mutants reproduce at rate $r + \rho_N$.

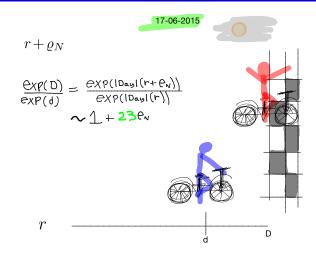
$$\mathbb{E}[K_1|K_0=1]=1+\varrho_N\frac{\log\gamma}{r}+o(\varrho_N).$$

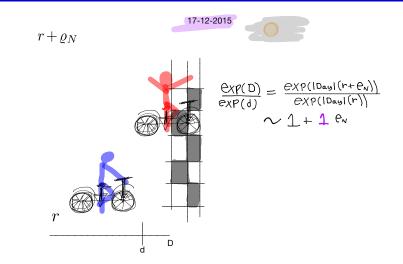


Day

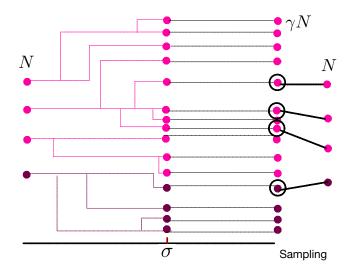








The effective competition time, and its dependence on r



Let
$$\pi_N := \mathbb{P}(\exists i \in \mathbb{N} : K_i = N \,|\, K_0 = 1)$$
, and $au^N := au_{ ext{fix}}^N \wedge au_{ ext{ext}}^N$.

Theorem (Probability and speed of fixation)

Under the assumptions of our model, as $N \to \infty$,

$$\pi_{\textit{N}} \sim \frac{\gamma}{\gamma - 1} \frac{\varrho_{\textit{N}} \log \gamma}{r}$$

Moreover, for any $\delta > 0$ there exists $N_{\delta} \in \mathbb{N}$ such that for all $N \ge N_{\delta}$

$$\mathbb{P}(\tau^{N} > \varrho_{N}^{-1-3\delta}) \leq (7/8)^{\varrho_{N}^{-\delta}}.$$

The weak mutation - moderate selection model (Assumption A)

- i) Beneficial mutations add ρ_N to the reproduction rate of the individual that suffers the mutation.
- ii) In each generation, with probability μ_N there occurs a beneficial mutation. The mutation affects only one (uniformly chosen) individual, and every offspring of this individual also carries the mutation.

iii) There exists 0 < b < 1/2, and a > 3b, such that $\mu_N \sim N^{-a}$ and $\rho_N \sim N^{-b}$ as $N \to \infty$.

$$\mu_N << \varrho_N$$

We define the fitness of the population at the beginning of day i with respect to that at the beginning of day 0 as

$$F_i := \frac{\log \frac{1}{N} \sum_{j=1}^{N} e^{R_{i,j}t}}{\log e^{r_0 t}}$$

where $R_{i,j}$, j = 1, ..., N are the reproduction rates of the individuals present at the beginning of day i, and t is a given time for which the two populations are allowed to grow together.

If the whole population reproduces at the same rate (R_i) , then

$$F_i = \frac{R_i}{r_0}$$

where $r_0 := R_0$.

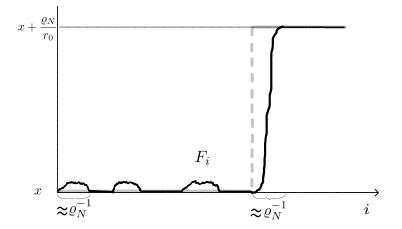


Figure: The number of attempts to go to fixation, when the reproduction rate of the basic population is x, is distributed Geometric with parameter $\pi_N \sim \varrho_N \frac{C(\gamma)}{x}$.

Theorem (Convergence of the relative fitness process)

Assume $R_{0,j} = r_0$ for j = 1, ..., N, and let $(F_i)_{i \in \mathbb{N}_0}$ be the process of relative fitness. Then under Assumption A, the sequence of processes $(F_{\lfloor (\varrho_N^2 \mu_N)^{-1} t \rfloor})_{t \ge 0}$ converges in distribution as $N \to \infty$ locally uniformly to the deterministic function

$$F(t) = \sqrt{1+rac{\gamma\log\gamma}{\gamma-1}rac{2t}{r_0^2}}, \ t\geq 0\,.$$

Table: Our model compared with Wiser et al.

	Our model	Wiser et al
Clonal interference	No	Yes
Epistasis	No	Yes
Design of the experiment	Yes	No
	$f(t) = (1 + \frac{2C(\gamma)t}{r_0^2})^{1/2}$	$w(t) = (1+ct)^{1/2g}$

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If we include Epistasis in our model, by assuming that the selective advantage provided by a single mutation to an individual that reproduce at rate x is $\varrho_N^{(x)} = x^q \varrho_N$, for some q > -1, then

$$h(t) = \left(1 + \frac{2(1+q)C(\gamma)}{r_0^2}t\right)^{\frac{1}{2(1+q)}}$$

▶ How to measure the fitness? (See Chevin, Biology Letters, 2011.)

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- Indirect evidence.
- Are there further consequences of the days getting shorter? (See Wahl, Dai Zhu, Genetics 2015)

Bibliography

A. González Casanova, N. Kurt, A. Wakolbinger and L. Yuan, An individual-based model for the Lenski experiment, and the deceleration of the relative fitness,

to appear in Stoch. Processes Appl.

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Thank you

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N = 4 σ_k $\sigma_{|\epsilon N|}$ $\mu_N^{-1}\varrho_N^{-1}$ $\mu_N^{-1}\varrho_N^{-2}$ $\frac{1}{-} - N^{-lpha}$ γ $\alpha \in (0, 1/2)$ Day i + 1

$$(A_{\lfloor Nt \rfloor}^N) \Rightarrow (|K_t|),$$

$$(X_{\lfloor Nt \rfloor}^N) \Rightarrow (X_t),$$

where (X_t) is the solution to the SDE

$$dX_t = \sqrt{X_t(1-X_t)} dB_t, X_0 = x \in [0,1]$$

$$\frac{N}{\gamma N}$$