13

Evolution and Extinction

13.1 History

13.1.1 How many bacterial generations have passed since life started on Earth? Assume near optimal growth, with 1 hour doubling time.

Set origin of life to be $3\,800\,000\,000$ years ago and 1 year = 365 times 24 hours. Notice that the 1 hour generation time is unrealistic, in free oceans the generation time 10 days = 240 hours, and it is in fact much longer an ocean floors.

13.1.2 Assume that there is on average one base pair mutation per bacterium per generation. Assume that there has always been about $5 \cdot 10^{30}$ bacteria on Earth. Give an estimate of how many of all the possible bacterial mutants have been tested?

13.1.3 With 5 000 000 million base pairs in the genome, what fraction of all mutants have been tested until now?

Answer The number of hours since the dawn of life is assumed to be 3 800 000 000 years ago is $t = 3.8 \cdot 10^9 \cdot 365 \cdot 24 = 3 \cdot 10^{13}$ hours.

The number of selection events is $n_s = 5 \cdot 10^{30} \cdot t = 1.7 \cdot 10^{49}$.

A bacterial genome consists of 5 000 000 base pairs, allowing $n_c = 4^{5000000}$ different genomes. The fraction of tested combinations is accordingly $n_s/n_c \sim 10^{-3\,000\,000}$, i.e. infinitely small.



Figure 13.1 Climbing in fitness at fixed landscape. The inherited fitness is f. At each time step, a new $f \in [0, 1]$ is explored. If the new f is larger than the previous one, the new f is adopted, otherwise there is no change. The left-hand plot shows how f increases with historic time, whereas the right-hand plot shows a histogram of activity per time unit since the start of evolution. The figure illustrates that evolution effectively stops, a statement that will be independent of which fixed distribution f is selected from.

13.2 Fitness landscapes

13.2.1 Draw random numbers from a continuous distribution, and remember the largest you have had until now. Simulate the times at which this largest number increases. Show that the times for such changes get subsequently larger as time passes. What is the distribution of these times? The numbers may be fitness values, and each new number a mutation attempt (only a fitter species will "outrun" the current species).

Answer Consider the number a = 1 - f, and start a simulation with a = 1. for each *a* value, the rate of finding a new smaller *a* value by drawing numbers from [0, 1] is $\propto a$. Thus the next time such a new smaller number will be found is $t = t - \ln(\operatorname{ran}_1)/a$, at which point $a = a \cdot \operatorname{ran}_2$ where ran_1 and ran_2 are two random numbers selected uniformly between 0 and 1. The results are shown in Fig. 13.1.



Figure 13.2 Barrier passing in a double well potential, modelled by Langevin dynamics. The left- and right-hand sides of the plots refer to exactly the same parameters, just simulated with a 100 times larger time step in the right-hand panel. As expected, the simulation results are consistent with each other.

13.2.2 Study numerically the space-time trajectory of a particle in a double well potential $V(x) = -2 \cdot x^2 + x^4$ using first-order Langevin dynamics and a noise term that sustains bistable behavior. Discuss the results in terms of evolution in the fitness landscape F = -V.

Answer: The Langevin dynamics dx/dt = -dV/dx plus noise reads:

$$dx = 4 \cdot (x - x^3) \cdot dt + \sigma \cdot (2 \cdot r - 1)\sqrt{dt}$$
(13.1)

where $r \in [0, 1]$ is a uniformly selected random number. The simulation with $\sigma = 2$ is shown in Fig. 13.2. One can observe characteristic intermittent dynamics, with long stasis times in each potential minimum, interrupted by sudden changes across the barrier at x = 0. The motion mimics the punctuated equilibrium where fitness peaks at x = +1, x = -1 are separated by less optimal genomes at $x \sim 0$ that separate the fitness peaks.

13.3 Punctuated equilibrium and co-evolution

13.3.1 Simulate the BS model for 100 species placed along a line in a variant of the model where only one of the neighbors is updated at each step. Plot the



Figure 13.3 Simulation of Bak–Sneppen model with the variation that only one (random one) of the neighbors is updated at each time-step. The self-organized threshold is ~ 0.74 .



Figure 13.4 Simulation of coherent noise model, with N = 1000 species exposed to random events of characteristic size 0.1 (in units of max strength 1).

selected B_{\min} as a function of time, as well as the maximum of all previous $B_{\min}s$. How do the minima of B change as time progresses toward a steady state (look at the envelope defined as the maximum over all B_{\min} at earlier times)?

Answer At each time step, select minimal B as well as either the right or the left neighbor of this. Update both of these sites to new random B values between 0 and 1. The resulting evolution of the system over 5000 time steps is shown in Fig. 13.3.

13.3.2 Consider externally driven version of an evolution based on stability of species [761]: Implement a system of N = 1000 species. Assign a random number B in [0, 1] to each species. At each timestep select an external noise x from a narrow distribution $p(x) \propto \exp(-x/\sigma)$, $\sigma = 0.1$. At each time step replace all B < x with new random numbers $\in [0; 1]$ and, in addition, select one random species and set its B to a new random number $\in [0; 1]$. Simulate this model.

Answer: The results of the simulation are shown in Fig. 13.4.