



Genealogical Dynamics in Noisy N-Branching Random Walks: How Stronger Selection Can Sustain Genetic Diversity

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DESCRIPTION

The Genealogical structure of populations evolving under repeated reproduction and selection provides an important way to understand how diversity is created, preserved and eventually lost. In an N-branching random walk, individuals reproduce while their positions change through random movement and a selection rule limits the population to a fixed number of survivors. When environmental noise is introduced, the resulting population history becomes more complicated because reproduction, random displacement and selective filtering interact continuously. An especially interesting possibility emerges when selection becomes stronger: instead of simply reducing diversity, it can sometimes maintain or even promote genetic differences by preventing one lineage from dominating for long periods. An N-branching random walk can be viewed as a population of N particles distributed across a spatial or fitness landscape. During each generation, every particle produces descendants, while the descendants experience random movement. Selection then retains a specified number of individuals according to their positions or associated fitness values. If individuals with larger positions have a greater probability of surviving, the population gradually moves toward favourable regions.

Yet the genealogy of the survivors does not necessarily become simple. Several competing ancestral branches can remain relevant because random fluctuations repeatedly alter which descendants are favoured. Noise plays a central role in this process. In a perfectly predictable environment, strong selection would often allow a small number of highly successful lineages to dominate. Over successive generations, this could lead to rapid coalescence, meaning that many present-day individuals would trace their ancestry to only a few recent predecessors. Genetic diversity would then decline as alternative branches disappear. With substantial environmental or movement noise, however, the ranking of descendants can change from one

generation to another. A lineage that performs poorly at one moment may become advantageous after a random displacement, while another lineage that previously appeared dominant may lose its position. This continual reshuffling can delay genealogical collapse.

Stronger selection introduces an additional layer of complexity. At first glance, stronger filtering should always decrease diversity because fewer individuals are allowed to contribute to the next generation. That conclusion overlooks the role of noise. When selection is sufficiently intense, descendants must repeatedly compete for narrow regions of favorable positions. Small random differences can therefore have large consequences. Rather than allowing a single lineage to remain permanently superior, strong selection can amplify fluctuations and create frequent changes in reproductive success. The population may consequently pass through a succession of temporary dominant families rather than settling around one persistent ancestor. This mechanism can be understood through the balance between selection intensity and stochastic movement. If noise is weak relative to selection, the same advantageous lineage may remain near the leading edge for many generations.

Genealogical diversity then contracts rapidly. If noise is stronger, spatial fluctuations can continually rearrange the competitive landscape. Increasing selection may make these fluctuations more consequential because only individuals close to the favourable boundary contribute substantially to future generations. In this regime, selection acts not merely as a force eliminating variation but also as a mechanism that exposes the population to repeated genealogical turnover. The transition between these regimes is particularly significant. As selection strength changes, the ancestry of the population may shift from a relatively persistent branching structure toward rapid lineage replacement or, under sufficiently noisy conditions, toward repeated coexistence of several competing ancestral branches. Such transitions can be detected through quantities such as the time required for two

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randomly chosen individuals to share a common ancestor, the number of distinct ancestral families surviving after several generations and the distribution of reproductive contributions across lineages.

These measures reveal that genetic diversity is not determined by population size alone. The fixed population size N is also important. A larger N provides more opportunities for different branches to survive temporary disadvantages and recover through later fluctuations. A smaller N makes random loss more severe, increasing the probability that entire lineages disappear

by chance. Nevertheless, even in relatively small populations, strong selection combined with substantial noise may repeatedly replace dominant families and prevent genealogical history from becoming permanently concentrated in one ancestral line. The noisy N -branching random walk therefore offers a useful framework for examining how ancestry changes when deterministic selection is coupled with stochastic movement. Stronger selection can accelerate the loss of weak lineages, but under suitable levels of noise it can also increase the frequency of lineage replacement and preserve multiple ancestral pathways.