From environmental dynamics to species adaptation: linking hypotheses to a computational model

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Current evidence suggests a correlation between important events in the evolution of the human species and climatic conditions, which affected environmental properties such as resource availability and predator pressure. The conceptual framework introduced by Maslin et al. (2015) attempts to consolidate existing hypotheses in ecology regarding the relationship between climate and evolution. Under it, the effect of different eco-evo mechanisms is qualitatively captured by the frequency of the turnover events of speciation and extinction, as well as the emergence of species properties such as diversity and adaptability. Our first step in our proposed computational study of these hypotheses is to build a simple evolutionary model that will allow us to analyze the desired qualities. In a second step, we plan to evaluate the hypotheses in a complex sequential test-bed inspired by paleoclimatology data.

A simple model and preliminary results We define a population of N agents evolving in an environment where niches are characterized by a scalar value which we term the state s. The genome of an individual i consists of two scalar values: the mean μ_i and standard deviation σ_i describing a Gaussian that characterizes the fitness of the individual for different values of the environment state, as can be seen in Figure 1. This model, adapted from (Grove, 2014), captures the assumption that a specialist species (small σ) has an advantage over a generalist species (large σ) in its preferred niche.

To model environmental variability we simulate the climate model proposed by Maslin et al. (2015), where climate values correspond to lake depth levels. We adopt a simplified direct mapping from a climate value to an environmental state, so that a single environment exists at any point in time and its state periodically goes through five phases (hard environment, abrupt transition, easy environment, highly variable transition, hard environment) that repeats periodically, as appears in the top subplots in Fig 2.

At each generation, small mutations occur in the genomes (i.e. on μ_i and σ_i values), the fitness of each individual f_i is computed based on its genome and the current environmental state and reproduction occurs using fitness-based selection. We associate the environmental state with a carrying capacity, so that the hard environment can support less individuals than the easy

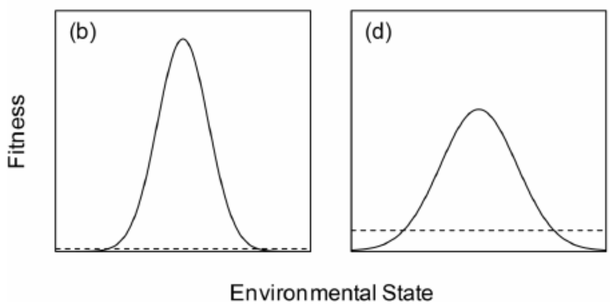

Figure 1: The Gaussian distribution describing how the fitness of an individual varies for different environmental states s. The individual on the left is a specialist (low σ), while the one on the right is a generalist (high σ). (Figure from (Grove, 2014))

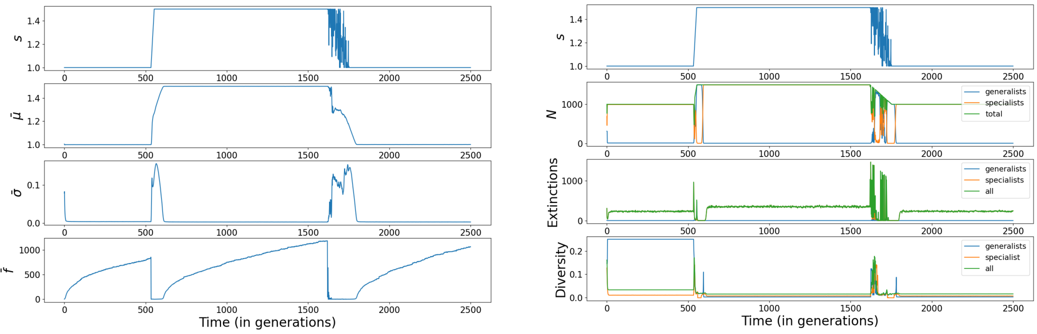

Figure 2: Measuring the effect of variability of the environmental state s on a population of agents (Upper) The average value of the genomes' mean $\bar{\mu}$, ($\bar{\sigma}$) and fitness ($\bar{f}$) across the population. (Lower) The number of alive individuals (N), the number of extinction events and the diversity of the population.

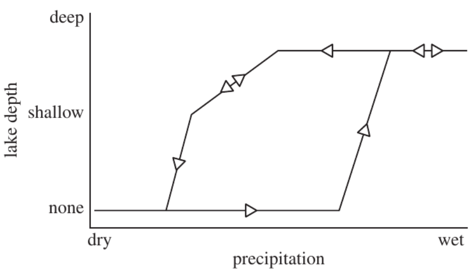

Figure 3: The relationship between lake depth and precipitation. (Figure from Maslin et al. (2015))

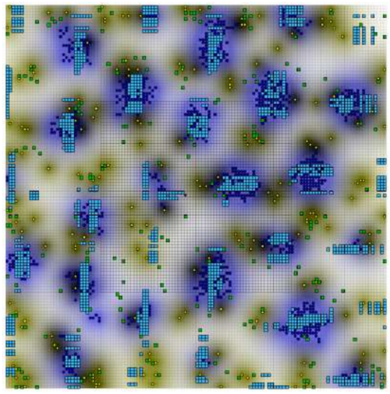

Figure 4: A bird's-eye view of our playground. The clustered blue tiles correspond to lakes, around which grow resources. A moving agent observe's a finite area of the grid around him and perceives it through scent and vision.

environment. Individuals may go extinct if the capacity of the environment is reached or if they experience an extinction, which occurs if the state s is sufficiently far from their μ_i. To evaluate the population we monitor the average $\bar{\mu}$, $\bar{\sigma}$ and $\bar{f}$ of the population and study two important properties, the ratio of specialists to generalists and the diversity within the population. In particular, we categorize an individual as a generalist if its σ_i exceeds a certain threshold and as a generalist otherwise. We measure diversity as the standard deviation of genome values and compute it across generalists, specialists and the whole population. Figure 2 presents the results of our simulations. Intuitively, the mean $\bar{\mu}$ of individuals continuously adapts to match the environment state s. When a change occurs in the climate, the population reacts by increasing its standard deviation $\bar{\sigma}$, which leads to the replacement of specialists by generalists. This pattern emerges from the evolutionary process, as variability creates a strong selection pressure in favor of individuals able to quickly adapt their optimal niche. Instead, during stable periods, the selection pressure favors specialization, thus individuals revert to being specialists.

Towards an eco-valid test-bed Due to its trivial genotype to phenotype matching, the simple model presented above does not allow the study of the mechanisms that allow adaptation and generalize its conclusions to more realistic setting. As a next step, we plan to ground our simulations in a test-bed where agents can navigate and forage resources, guided by deep reinforcement learning (Schulman et al., 2017) and neuroevolution algorithms (Lehman and Miikkulainen, 2015). We are currently implementing a test-bed that simulates the appearance and disappearance of lakes and resources in a simulated world according to the dynamics described in Fig 3. Our implementation is an extension of the jelly-bean world Platanios et al. (2020), a test-bed recently introduced for open-ended learning that allows the creations of a seemingly infinite world, as new terrains are created as agents move. Figure 4 contains a snapshot of a simulation.

References

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