

The Effect of Distinct Resource Pools on Genetic Diversity in Populations of Digital Organisms

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Abstract

Evolutionary theory has long held that genetic diversification can be driven by the presence of multiple distinct niches in an environment (Whittaker 1972). When organisms originally occupy the same niche, they can either outperform one another or evolve to take advantage of a different resource, the latter of which is predicted to be highly preferable. But establishing experimental control over environmental niches and accurately measuring genetic diversity are two great challenges for the field biologist. Instead, the present investigation makes use of a digital evolution simulation, which has been shown to demonstrate many of the same ecological traits as natural biology (Dorin et al. 2008; Johnson and Wilke 2004). The Avida framework is used to simulate digital organisms that evolve and execute logical functions (Adami 2006). Working from the preliminary results achieved by Cooper and Ofria (2002), we investigate if and how genetic diversity in populations of digital organisms changes as resources are increasingly limited. Genetic entropy - the number of bits required to store the genetic information present across the population - is used as a measure of diversity. The findings presented here demonstrate that there is a positive correlation between genetic diversity and the number of limited resources in the environment. This suggests that resource niches do drive diversification in species, as was previously conjectured.

Introduction/Motivation

In 2002 Cooper and Ofria measured the differences in diversity for two environments. Each environment drew from a pool of resources that were used to limit the rate of execution for logical tasks. In one environment the resources were all limited and depletable, in the other they were all unlimited. Cooper and Ofria found that the environment with limited resources was more genetically diverse than the environment with unlimited resources. We wish to expand upon this experiment and explore the nature of the relationship between the number of resources that are limited and the genetic diversity of a population. We hypothesize that as the number of resources with limited quantities increases, there will be higher genotypic diversity because

organisms will develop to fill the role of different niches. We do not anticipate a threshold or sudden peaks or valleys of diversity for intermediate numbers of limited resources.

For the purposes of this investigation, the null hypothesis states that there is no correlation between limited resources and genetic diversity, represented by constant values on boxplots graphing diversity with respect to the number of limited resources. When discounting the null hypothesis, it should be apparent whether there is a positive or negative correlation. However, further study would then be required to ascertain whether this relationship is linear, quadratic, or something else in nature.

Method

In order to test the relationship between limiting resources and diversity we conducted a series of treatments, each limiting a different number of resources from a predetermined resource pool. Each treatment consisted of 20 replicates in a 60 x 60 grid that ran for 100,000 updates. All mutation rates were set to 0 except for DIVIDE_MUT_PROB, which was set at 0.25. All other configuration values were left at their default setting. We created 9 different resources, each mapped to one of Avida's 9 logical functions. The inflow and outflow rates for each resource were set to 10 and 0.01 respectively. The value, min, and max fields were set to values corresponding to the reward for each logical task; 1 for NOT and NAND, 2 for AND and ORN, 3 for OR and ANDN, 4 for NOR and XOR and 5 for EQU. Resources were limited in pairs in accordance with their trophic levels. The table in Figure 1 details which resources were set to be depletable in each treatment, with an X denoting that resource being limited.

	NOT	NAND	AND	ORN	OR	ANDN	NOR	XOR	EQU
Control									
Treatment 1					X	X			
Treatment 2					X	X	X	X	
Treatment 3			X	X	X	X	X	X	
Treatment 4	X	X	X	X	X	X	X	X	

Figure 1. Table showing which resources were limited for each treatment.

Results

The results we received from our experiments support our hypothesis. There was clear evidence pointing to a positive correlation between how many resources are limited and the genetic diversity of the population.

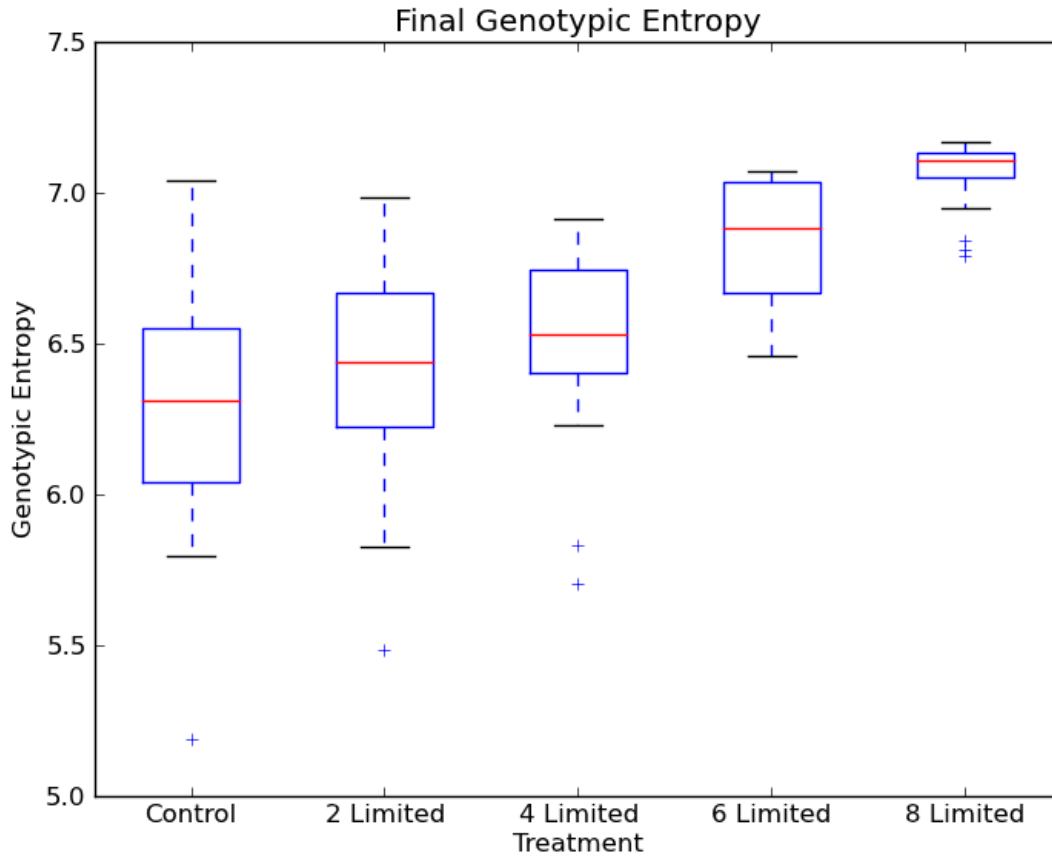


Figure 2. Box plot of genetic entropy at 100,000 updates across all replicates. Genetic entropy represents the number of bits needed to store the variety between genotypes in the population.

Figure 2 clearly shows the positive nature of the relationship. As more resources were limited, the overall genetic entropy went up. An initial Kruskal-Wallis test across all treatments demonstrated significant results. Then further u-tests identified a significant difference between the control and the 4-, 6-, and 8-limited resource treatments. However, the results from this figure are only based on the genetic entropy levels present at 100,000 updates.

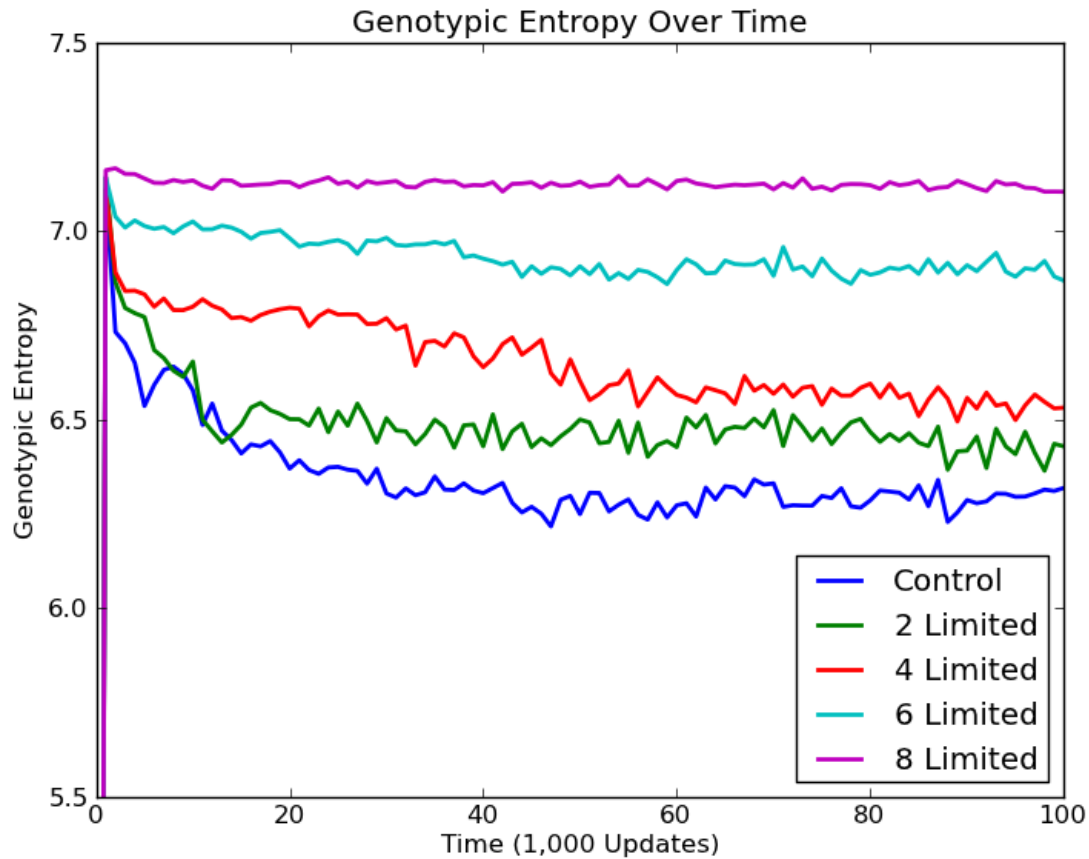


Figure 3. Line graph of median genetic entropy over time for each treatment

In order to get a better view of what happened to each treatment's genetic entropy throughout the course of the experiment we also decided to graph genetic entropy for each treatment over time, as shown in Figure 3. The results from this figure lend further support for our hypothesis. At the beginning of the run each treatment appears to jump to the same level of genetic entropy, but over time, depending on the number of resources, the genetic entropy for each population reaches a generally stable level as organisms evolve to fill various niches. The relationship between number of resources limited and genetic entropy is again clearly seen with the 8 limited resources treatment generally having the highest entropy, and the control having the lowest, with all the other treatments ranked accordingly.

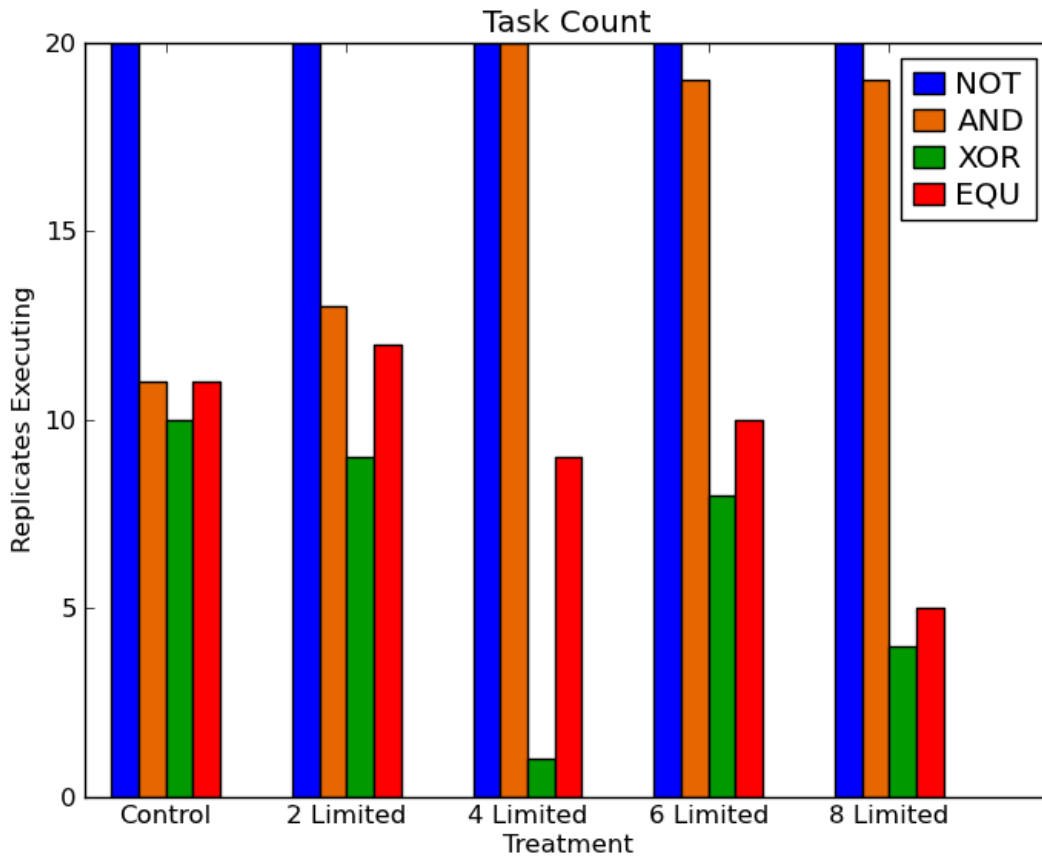


Figure 4. Bar graph of replicates performing various functions at 100,000 updates. A replicate is counted as performing a task if at least 10% of the population had developed it.

Finally, to leave room for further investigation, we considered the evolution of tasks across the various treatments. Of the nine tasks, four of the most interesting results are present in Figure 4 above. Most interesting is the occurrence of XOR in the five treatments. When XOR is first limited in the 4 limited treatment, it almost never evolves in the population. However, when additional resources are limited, this phenomenon disappears, at least temporarily. Also of note is decline in the performance of EQU. This was the one resource we did not limit, so it is interesting to see that in evolving to take advantage of limited resources, organisms appear to have increasingly ignored this valuable - if expensive - resource.

Discussion

As stated above, the results appear to support the initial hypothesis that genetic diversity would increase as resources were limited in the environment. This lends credence to the previously-conjectured belief that environmental niches can drive genetic diversification. However, there is insufficient data to state the nature of this relationship with confidence. Further study could not only confirm the results presented here, but also investigate whether this correlation is linear, exponential, or something else. Still, the result presented here is a significant step toward establishing the importance of limited resources for genetic diversity. It would be advised to extend the study to investigate all of the possible combinations of limited resources. It is possible that certain resources allow and/or preclude others; and eliminating the possibility of error for this reason would confirm the significance of these preliminary results.

Furthermore, the results presented in Figure 4 also leave room for further investigation. In particular, studying the immediate impact of limiting a resource in the environment could prove insightful, based on what occurred with XOR in our treatments. Perhaps the disappearance and subsequent reappearance of a limited task is anomalous, and therefore would not appear in subsequent tests. Or perhaps there is more at work in this scenario than is fully understood. Additionally, it could also be useful to investigate the effect of limited resources on the utilization of unlimited resources. It seems unusual that EQU would decrease in frequency in more limited environments, but perhaps this is related to EQU's unique position as the most valuable - and complex - task. Both recommended studies could be achieved using similar methods to ones presented here, and the results that come from them could further support the importance of limited resources for genetic diversity.

Literature Cited

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