

Some Techniques for the Measurement of Complexity in Tierra

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Abstract. Recently, Adami and coworkers have been able to measure the information content of digital organisms living in their *Avida* artificial life system. They show that over time, the organisms behave like Maxwell’s demon, accreting information (or complexity) as they evolve. In *Avida* the organisms don’t interact with each other, merely reproduce at a particular rate (their fitness), and attempt to evaluate an externally given arithmetic function in order win bonus fitness points. Measuring the information content of a digital organism is essentially a process of counting the number of genotypes that give rise to the same phenotype. Whilst Avidan organisms have a particularly simple phenotype, Tierran organisms interact with each other, giving rise to an ecology of phenotypes. In this paper, I discuss techniques for comparing pairs of Tierran organisms to determine if they are phenotypically equivalent. I then discuss a method for computing an estimate of the number of phenotypically equivalent genotypes that is more accurate than the “hot site” estimate used by Adami’s group. Finally, I report on an experimental analysis of a Tierra run.

1 Introduction

The issue of what happens to complexity in an evolving system is of great interest. In natural (biological) evolution, the naive view is that life started simple, and evolved ever more complex life forms over time, leading to that pinnacle of complexity, *homo sapiens*. The end points of that process are of course fixed. In the beginning, life must be simple. In our present era, there must exist intelligent organisms (namely us) pondering over the mystery of how we came to be. So the *anthropic principle* fixes the present day as having complex lifeforms. There is nothing within the *Modern Synthesis* of Darwinism that implies a steady interpolation between these two end points. In fact it is even plausible that more complex organisms than us existed in the past, but have since vanished into obscurity. However, examinations of the fossil record over the Phanerozoic (the last 550 million years of the Earth’s history) indicate almost no growth in complexity by a number of different measures over that period, apart from an initial large jump at the Cambrian explosion.[1]

The interesting thing is to ask what one might see if looking at another evolutionary system apart from the one in which we evolved. Would we see any growth in complexity at all? Since we don't have an extra terrestrial biology to observe (a few Martian meteorites aside), the only other systems available are Artificial Life systems evolving within a digital computer such as Tierra or Avida. The Avida group has reported measuring the information content (complexity) of individual avidan organisms[2], or rather a lower bound of the organism's complexity. Their results are that this lower bound increases over time for the maximally fit organism, thus showing information accumulating as time progresses. One important critique of this work, however, is that organisms do not interact directly with each other, and in order to prevent evolution stagnating, an externally imposed task (eg computing a logical operation) is added to the system. Organisms are given "fitness points" depending on how well they perform this task. This heavily weights the system in favour for accruing information.

By contrast, in the Tierra system, the organisms interact with each other, providing a rich array of possible (intrinsic) tasks for the organisms to exploit. Since this is an evolving ecology with no externally imposed task, the above critique does not apply. However, the downside is that determining whether two genotypes are phenotypically equivalent is considerably more complex. In some work a couple of years ago[3], I studied the phenotypic properties of Tierran organisms to build up a picture of the genotype to phenotype landscape. A Tierran organism's phenotype can be characterised by a couple of numbers for each possible pairwise interaction in the ecology. Multiway interactions are ignored in this study, as experience has shown them to be relatively rare.

2 Complexity of a Digital Organism

The information content of a string is given by the difference between the maximal Shannon entropy of that string (i.e. considering the string to be random, or devoid of information), and the entropy given by assuming that the string codes for some phenotype p : [2, 4]

$$I(g) = H(g) - H(g|p) = \ell - \log_{32} N \quad (1)$$

where ℓ is the length of the genotype (in instructions), and N is the number of genotypes that give rise to the same phenotype p . The base, 32, refers to the number of instructions in the Tierra instruction set. If $N \approx 32^\ell$ (ie a completely random sequence), then $I(g) = 0$. Similarly, if $N = 1$ (there is only one genetic sequence encoding a genotype, or no redundancy), then $I(g) = \ell$.

The most obvious way to compute N is to search all 32^ℓ genotypes for equivalent phenotypes. However, this is an enormous number of strings to check, and computationally infeasible. Adami recognised this problem, and took the approach of counting the number of volatile sites v (sites that vary amongst phenotypic equivalents), and approximating $N \approx 32^v$. In one sense this is an overestimate of N , so they argue that this gives a lower bound to the information $I(g)$. In another sense, however, it is not strictly a lower bound. If it turns

out that fixing one of the volatile sites to a particular value allows one of the fixed sites to vary without altering the phenotype, then this would be not be counted in the N . so what we have is really an overestimate of an underestimate.

The same criticism applies to this work. We can estimate the above mentioned estimate fairly accurately, more precisely we can find the size of the neutral network[5, 6, 7] connected by one-site neutral mutations to g . However, the possibility remains that there are other neutral networks of g that aren't connected by single site mutations to g . Probably the most efficient way of finding these is by using a genetic algorithm to explore genotype space, i.e. run Tierra for a long time to see what it discovers! The way we use this in our experiment is to keep a list of neutrally equivalent organisms that Tierra discovers. As we explore the neutral network connected to g , we eliminate items from the list that we come across. The remaining names on the list can then be used as seeds to start the process again.

In this work, we use two different techniques to measure N . The first is a Monte Carlo random sampling technique to estimate the proportion of the 32^v strings found by varying the volatile sites. The second technique, which we use in conjunction with the Monte Carlo approach mentioned above, is to walk the neutral net. The Monte Carlo technique works well when the density of neutral variants is fairly high, whereas the latter technique is best on sparse networks. A decision on which technique to use for which site is based on estimated densities of neutral variants.

3 Establishing Phenotypic Equivalence

Equation (4) of [3] presents the dynamical equations of two species of Tierran organisms interacting. The precise form of the dynamics is not important here, however the phenotype of the organism can be characterised by its interactions with all other possible Tierran phenotypes. Since it is impossible to have the complete set of all possible Tierran organisms, those organisms generated during a run of Tierra are used. Since Tierran organisms coevolve, the most important organisms should be contemporaneous with the test organism. The following characteristics are saved for each pair of organisms:

1. The outcome of the tournament. This may be one of the following:
 - infertile** The test organism never calls the divide instruction, or does not produce any recognisable progeny (essentially still born)
 - once** The organism produces progeny once, but then never repeats the act.
 - repeat** The organism continuously reproduces the same progeny. For this purpose we ignore what is produced first time around, as this will be swamped by number latter progeny.
 - nonrepeat** The organism continuously reproduces, but the progeny is either different each time, or the CPU is in a different state each time the divide instruction is called - thus can't be guaranteed to reproduce ad infinitum.
2. The name of the progeny organism. This is usually identical to the parent, but may another type in the case of symbiosis or parasitism.

3. The number of timesteps it takes to reach the first divide instruction (σ_{ij}), and the time it takes between successive divide steps after that (τ_{ij}).
4. The number of template matching operations made to the opposing organism prior to the first divide (μ_{ij}) and between successive divides (ν_{ij}).

Two organisms are neutrally equivalent if they have identical characteristics against all Tierran organisms. Once all organisms are paired with each other, we can produce a list of phenotypically unique organisms, which provides a smaller test list to pit trial mutants against. We may also eliminate some noninteractive pairings prior to simulation by trying to see if potential template matches could happen between organisms. This still produces a fairly large list of test organisms, so it is still computationally expensive. The high degree of parallelism in this problem allows it to be attacked in reasonable time on a parallel supercomputer.

A further refinement may be possible by producing an archetypal list, perhaps by ignoring the (μ, ν, τ and σ) parameters. The idea being that the archetypes contain a representative organism from each niche of the ecology, and ignoring minor differences such as reproductive rate. This would coarsen the approximation a little, but will probably give an acceptable result. At present this idea has not been tested.

4 Interim Results

Due to the time constraints of producing this paper, the analysis of a reasonable length Tierra run has not been completed. At the time of writing, a moderately large data set of 1660 organisms was generated from a 24 hour Tierra run. Tierra produces most of its diversity during the earliest stage of its running, so it becomes significantly more expensive to produce larger data sets. This data set was halved by removing every second organism, and then a phenotypic analysis was carried out. This set reduced to 103 distinct phenotypes, which formed the test list used for carrying out the complexity analysis. Each of these 103 organisms were then tested for phenotypic equivalence against their single site nearest neighbours. The number of sites on which no mutation resulted in a phenotypically equivalent organism (“nonvolatile sites”) is plotted against the time of speciation in figure 1.

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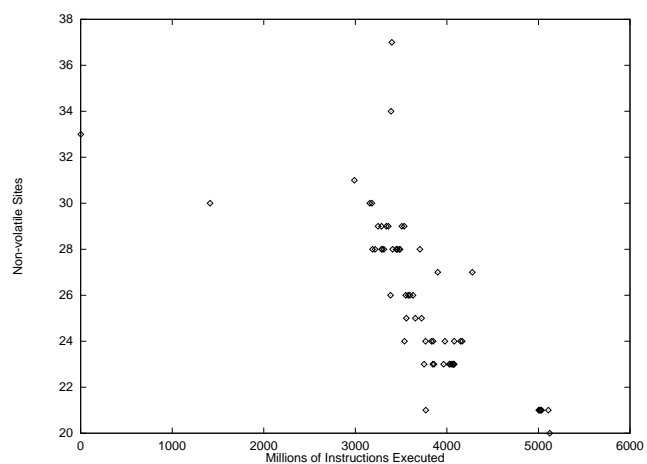


Fig. 1. Non-volatile site count (complexity estimate) for the set of phenotypic Tierran species, as a function of speciation time.

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