Scaling of Program Fitness Spaces

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Abstract

We investigate the distribution of fitness of programs concentrating upon those represented as parse trees, particularly how such distributions scale with respect to changes in size of the programs. By using a combination of enumeration and Monte Carlo sampling on a large number of problems from three very different areas we are lead to suggest, in general, once some minimum size threshold has been exceeded, the distribution of performance is approximately independent of program length. We proof this for linear programs and for simple side effect free parse trees. We give the density of solutions to the parity problems in program trees composed of XOR building blocks. We have so far only conducted limited experiments with programs including side effects and iteration. These suggest a similar result may also hold for this wider class of programs.

Keywords

stochastic search, genetic algorithms, genetic programming, tree fitness landscapes, nand gates, Monte Carlo sampling, symbolic regression, Santa Fe trail artificial ant

1 Introduction

The use of genetic algorithms and other stochastic search techniques to solve problems by automatically generating programs which solve them has become increasingly popular. Yet we know almost nothing about the distribution of solutions within these vast search spaces. They are neither continuous nor differentiable and so classical search techniques are incapable of solving our problems. Instead heuristic search techniques, principally stochastic search techniques, have been used. The term genetic programming (GP) is used for techniques which evolve suitable programs by stochastic search of the space of possible programs. The theoretical foundations of GP are at present weak. In particular little is known about the space which it searches, in particular how it scales. We suggest that in general above some problem dependent threshold considering all programs their fitness shows little variation with their size. The distribution of fitness levels, particularly the distribution of solutions, gives us directly the performance of random search. We can use this as a benchmark against which to compare GP and other techniques. We can also compare the density of solutions in parse trees with those in linear programs. Our analysis shows there is much more variation in big trees than in long linear programs. Some functions are much more common and some much rarer.

We test our claim using a combination of enumeration and Monte Carlo sampling (described in Section 2) on 66340 of the Boolean problems (Sections 3 and 4), on a continuous domain symbolic regression benchmark problem (Section 5) and finally on a commonly



Figure 1: Size of various search spaces (note log log scale)

used GP benchmark problem, the artificial ant problem, which includes both iteration and side effects (Section 6). This is followed by a proof for long linear programs (Section 7) and big random trees and deep random full trees where there are no side effects (Section 8). In Section 9 we give the fitness distribution and rate of convergence to it for arbitrary order XOR trees. (XOR is often considered a building block of solutions to the parity problems). This is followed by a discussion of these results and their implications (Section 10) and our conclusions (Section 11).

2 Experimental Method

For the very shortest programs it is feasible to generate and test every program of a given length. (The length of a tree program is the size of the tree, the number of internal nodes in the tree plus the number of leafs). However as Figure 1 makes clear the number of possible programs grows very quickly with their size and so we must fall back on randomly sampling programs. We use the random tree method given in (Alonso and Schott, 1995) to sample uniformly all the programs of a specific length. Typically we sample 10,000,000 programs of each length.¹

The ramped-half-and-half method (Koza, 1992, page 93) is commonly used to generate the initial population in genetic programming (GP). Half the random programs generated by it are full (i.e. every leaf is the same distance from the root). Therefore we also explicitly consider the subspace of full trees. In some cases this subspace is radically different from the whole space.

¹The C++ code used to generate random programs is available online at the following address ftp://ftp.cs.bham.ac.uk/pub/authors/W.B.Langdon/gp-code/rand_tree.cc).



Figure 2: Proportion of NAND trees which yield each 2 input logic function.

3 Boolean Functions

The Boolean functions have often been used as benchmark problems. The program trees we will consider are composed of n terminals (D0, D1, ... D_{n-1}) which are the Boolean inputs to the program and four sets of the Boolean logic functions NAND, XOR, {AND, OR, NAND and NOR} and {AND, OR, NAND, NOR and XOR}. There are 2^{2^n} Boolean logic functions of n inputs. NAND by itself is sufficient to construct any of them and therefore so are the last two sets. XOR by itself can only generate 2^n of them but as we shall see adding it to the function set can dramatically effect the whole search space. The fitness of each tree is given by evaluating it as a logical expression for each of the 2^n possible combinations of D_n inputs. Its fitness is the number of fitness cases when its output agrees with that of the target Boolean function (Koza, 1992).

There are $n^{(l+1)/2}|F|^{(l-1)/2} \times \frac{(l-1)!}{((l+1)/2)!((l-1)/2)!}$ different trees of length l (Koza, 1992; Alonso and Schott, 1995, page 213). |F| is one, four or five, depending which of the four function sets is used. This formula is simple as each function (internal node) has two arguments. The number of programs rises rapidly, approximately exponentially, with increasing program length l (see Figure 1). If no bounds are placed on the size or depth of programs then the number of them is unbounded, i.e. the search space is infinite.

4 Boolean Program Spaces

4.1 NAND Program Spaces

Due to the ease of manufacture of NAND gates in integrated semiconductors, and because any Boolean function can be constructed from a network of NAND gates, they are the principal active component in digital electronics. It is, therefore, an interesting function to study. The following sections give the number of different program trees composed only of NAND functions that are equivalent to each Boolean logic function. We specifically look at the programs trees composed only of NAND of various sizes for two, three and four inputs.

4.1.1 2 input NAND Program Spaces

There are $2^{2^2} = 16$ Boolean functions of two inputs. The proportion of NAND trees which evaluate to each is plotted in Figure 2.

Not surprisingly there are two peaks at size 1 of height 0.5 which correspond to the functions D0 and D1 and no other functions are possible. There is also a peak of the same height for size 3, which is NAND itself, and two smaller peaks for ND0 (not D0) and ND1 (not D1). Three functions can be constructed from trees of size 5, i.e., two NAND gates and three inputs. Seven from size 7 and so on. It is not until tree size 15 (7 NAND gates) that all of the 16 possible functions can be constructed from a tree of one length, although all can be constructed from trees of size 13 or less. XOR can be fabricated from 5 NAND gates and 6 terminals in a nearly full tree with 11 nodes and a height of 4.

Table 1: Proportion of Two Bit NAND Programs, and their fitness values (for two problems). Lower table gives proportion by fitness value (for the two problems)

Rule		Proportion	Fitness		
			Always on	Odd-2-Parity	
0	off	.00490	0	2	
1	nor	.00415	1	1	
2		.01689	1	3	
3	nd1	.10710	2	2	
4		.01696	1	3	
5	nd0	.10745	2	2	
6	xor	.01430	2	4	
7	nand	.15121	3	3	
8	and	.03695	1	1	
9	eq	.01088	1	0	
10	d0	.07727	2	2	
11		.10920	3	1	
12	d1	.07702	2	2	
13		.10898	3	1	
14	or	.04753	3	3	
15	on	.10922	4	2	
			Proj	portion	
		Fitness 0	.00495	.01088	
		1	.08583	.25928	
		2	.38314	.48296	
		3	.41692	.23259	
		4	.10922	.01430	

From Figure 2 we also see that each of the functions quickly converges towards some limiting proportion of the NAND trees of a given length. Thus we can give the proportion of the search space (formed by NAND, D0 and D1 trees) occupied by each of the sixteen



Figure 3: Proportion of NAND trees which yield each 3 input equivalence class.

functions, see Table 1.

Each of the $2^{2^n} = 16$ Boolean functions can be regarded as a problem with its own fitness function. As indicated in Section 3, each fitness function has $2^n + 1 = 5$ values. A simple problem is to find a tree which always returns 1 (the always on problem). This corresponds to function 15. Function 15 has, of course, the maximum fitness value (4). The fitness value of the other functions are given in column 4 of Table 1. (Column 5 gives their fitness values for the odd-2 parity (XOR) problem). The lower part of Table 1 give the fraction of the search space with a particular fitness value for the two example problems. Note the relationship between function and fitness (on a given problem) is fixed. Therefore (since the proportion of the search space occupied by each function does not change w.r.t. length above the threshold) the distribution of fitness values is independent of length above the same threshold. This is true for all possible (2 input) problems.

Functions 10 and 12 (D0 and D1) are equivalent to each other in the sense the other is produced by exchanging inputs. Function 10 and 12 are equally common in the search space. There are three other pairs of equivalent functions, 2 and 4, 3 and 5 (ND1 and ND0), and 11 and 13. It is also apparent that lexical ordering of functions is not the most convenient form for graphical presentation. In other plots they will be presented in order of decreasing frequency and only data for one function of an equivalent set will be plotted.

4.1.2 3 input NAND Program Spaces

There are $2^{2^3} = 256$ Boolean functions of three inputs. However, many of these are equivalent to each other. Taking this into account, these reduce to 80 classes. In Figure 3 we plot the proportion of NAND trees which evaluate to each of these classes using the class ordering given in (Koza, 1992, Table 9.2).

Comparing Figures 2 and 3 we see that they have several features in common. In



Figure 4: Proportion of NAND trees which yield each 4 input equivalence class (data with a signal to noise ratio of less than 3.0 are excluded)

particular the proportion of each function changes initially with increasing program length, but once some threshold has been exceeded, it changes scarcely at all with size. The variation between each function is far greater than when using just two inputs.

4.1.3 4 input NAND Program Spaces

There are $2^{2^4} = 65536$ Boolean functions of four inputs. Again many of these are equivalent to each other and so these reduce to 4176 classes. In Figure 4 we plot the proportion of NAND trees which evaluate to each of these classes. The ordering of the classes is given by their measured frequency in trees of size 255.

Comparing Figure 4 with the two earlier Figures (2 and 3) we see the same common features. While the proportion of each function changes initially (for clarity data for short programs are not plotted in Figure 4) if we look at programs containing 16 or more NAND gates (i.e. size 31 or more) the proportion scarcely changes with size. This appears to be true for all 65536 functions but as the data is based on Monte Carlo sampling the data for the rarer functions is correspondingly noisy.

Again the variation between each function is far greater than when using just two or three inputs. Indeed none of the functions in the 842 rarest equivalence classes where discovered in Monte Carlo sampling of 10,000,000 programs of length 255. This includes both the odd and even parity functions with 4 inputs. Neither of which were discovered in any of the 20 Monte Carlo runs (each sampling 10,000,000 points).



Figure 5: Proportion of functions in each equivalence class {AND, OR, NAND and NOR}

4.2 3 Input AND OR NAND NOR (XOR) Boolean Program Spaces

In this section we consider all the Boolean functions for n = 3 when using the larger function sets (i.e. {AND, OR, NAND and NOR} and {AND, OR, NAND, NOR and XOR}). As we said in Section 4.1.2 there are 256 of them but they can be split into 80 equivalence classes.

Comparing Figure 5 with Figure 3 we see the bigger search space shares many characteristics with that produced by NAND on its own. In particular it shows a certain minimum size is required before the problem can be solved and that the minimum size depends on the difficulty of the problem. Once this threshold size is exceeded the proportion of programs which belong to the equivalence class grows rapidly to a stable value which appears to be more-or-less independent of program size. Figure 6 shows these characteristics are retained if we extend the function set to include XOR. Note adding the XOR function radically changes the program space. In particular, as might be expected, the two parity functions (equivalence classes 79 and 80) are much more prevalent. Also the range of frequencies is much reduced. For example 68 of the 80 equivalence classes have frequencies between 0.1/256 and 10/256 rather than 28 with the standard function set.

While Figures 5 and 6 can be used to estimate the fitness space of each three input Boolean function across the whole space, there are some interesting parts of these spaces where certain functions are more concentrated than elsewhere. There are far more parity functions amongst the full trees than there are on average. When XOR is added to the function set, there are again a higher proportion of parity functions but the difference between the full trees and the rest of the search space is less dramatic.

4.3 6 Input Boolean Program Spaces

In this section we investigate the distribution of 6 input Boolean functions using the two larger function sets: AND, OR, NAND and NOR} and {AND, OR, NAND, NOR and



Figure 6: Proportion of functions in each equivalence class {AND, OR, NAND, NOR and XOR}



Figure 7: Proportion of 6-input Boolean functions {AND, OR, NAND and NOR} by number of ones returned by them (note linear scale)



Figure 8: Even-6-parity program space {AND, OR, NAND and NOR}

XOR}. It is difficult to analyse all the Boolean functions with more than four inputs. Instead we have concentrated the easiest and hardest Boolean functions of six inputs: the always-on-6 function and the even-6-parity function. Figures 7 and 8 show the proportion of programs of various lengths with each of the possible scores. Figure 9 shows the same when XOR is added to the function set. Always-on-6 and even-6-parity, both with and without XOR, have the same near independence of fitness from length.

The fitness distribution of the even-6-parity problem is much tighter than that of the binomial distribution produced by selecting Boolean functions uniformly at random from the 2^{2^n} available (centered on $\frac{n}{2}$ with variance of $\frac{n}{4}$ (Rosca, 1997, page 62). The measured variance is only 0.12 rather than 1.5. Such a tight fitness distribution and the absence of a high fitness tail suggests that the problem will be hard for adaptive algorithms. When discussing the evolution of evolvability, (Altenberg, 1994) assumes that high fitness tails exist and can be found by evolutionary search algorithms. We would hope that they would be better than random search at finding and exploiting such tails.

Adding XOR to the function set greatly increases the even-6-parity fitness distribution's width and it retains its near independence of program size (see Figure 9). The standard deviation is now 0.92 However, the more dramatic effect of the wider distribution, the more feasible it is for our Monte Carlo simulations to find solutions, i.e., programs scoring 64 hits. They occupy about 2 10^{-7} of the whole search space.

Figure 7 shows the distribution of number of trues returned is a saw-toothed curve. The proportion of programs which have one of the odd scores on the always-on-6 problem is about 0.3%. The proportion which have an even score, not divisible by four, is about 1%, scores divisible by 4 about 2%, those by 8 3%, those by 16 6% and those by 32 10%. Note the central peak in the even-6 parity fitness distribution (see Figure 8) is not solely due to a large number of programs which implement always-on-6 or always-off-6. Only 18.6% of programs are of these two types.



Figure 9: Even-6-parity program space {AND, OR, NAND, NOR and XOR}

The distribution of number of trues returned when XOR is added to the function set is a little changed but retains its saw toothed appearance and near independence of program size.

4.4 Even-6 Parity and Always-On-6 Full Trees

Restricting our search to just the full trees yields a similar fitness distribution for the even-6 parity problem, see Figure 10. In particular we have the convergence of fitness distribution once the tree size exceeds a threshold. There is a small variation with size but it does appear to decrease as we consider bigger trees. The distribution of fitness values observed is considerably wider with a range of 25–38 (twice that for the whole search space, see Figure 8) and a standard deviation of 0.68. Adding XOR to the function set further widens the distribution (the standard deviation becomes 1.8).

Searching just the full trees yields a similar fitness distribution for the always-on-6 problem as for the whole search space However the peaks corresponding to functions returning true multiples of 4, 8, 16 or 32 times are now far less prominent and instead always-on-6 itself and its compliment, always-off-6, now dominate and together represent 35% of all trees, compared to 18% when considering asymmetric trees as well. Also the troughs at odd numbers of hits are also less prominent, each representing about 0.5% rather than about 0.3% of all programs. Adding XOR to the function set has the effect of further smoothing the distribution. The peaks at either extreme are now 8% with a typical odd values near 32 being 1.4% and even being 1.8%. Both with XOR and without the distribution of the number of trues returned by full trees shows some dependence on depth of tree. However, as with even-6 parity, this appears to fade away as the programs become bigger.



Figure 10: Even-6-parity full tree program space {AND, OR, NAND and NOR}

5 Symbolic Regression

Symbolic regression is the problem of finding in a functional form a model of some dataset. This is a very common requirement and techniques such as linear regression are widely used. Often such models are used to predict values for unknown data points. Where data are complex more complex regression techniques are needed. We investigate a benchmark symbolic regression problem in this section.

We use the sextic polynomial regression problem (Koza, 1994, pages 110–122). The sextic polynomial is $x^6 - 2x^4 + x^2$, which can be rewritten as the product of three squares, i.e., $x^2(x-1)^2(x+1)^2$. The problem for GP is to match it over the range -1.0...1.0 using $+, -\times$, protected division, the input x and random constants. We used 250 random constants, chosen from the 2001 numbers between -1 and +1 with a granularity of 0.001. No constant was repeated and none of the three special values of -1, 0 or 1 where included. The 50 test points used were chosen uniformly at random from the range -1 and 1. No granularity was imposed. Again, none of the three special values of -1, 0 or 1 where included and no value was repeated. Apart from limiting ourselves to 250 constants, this is as described in (Koza, 1994, pages 110–122).

5.1 Sextic Polynomial Fitness Function

The fitness of each program is given by its absolute error over all the test cases (Langdon et al., 1999). This is as described by (Koza, 1994) except we divide by the number of test cases (50) to yield the average discrepancy between the value it returns and the target value. All calculations were performed in standard floating point representations.



Figure 11: Distribution of fitness in Sextic Polynomial (constants and input equally sampled)

5.2 Sextic Polynomial Fitness Distribution

The distribution of fitness is given in Figure 11. It is apparent that symbolic regression shares many of the characteristics of the more difficult Boolean problems. The proportion of good programs is very small (as expected) but again we see above a small threshold the proportion of good programs in a given fitness range converges to a value which is independent of their size. (Figure 11 shows the proportion of very bad programs does show variation w.r.t. length. However it appears to reach a stable value but the threshold length is bigger. Each test case where a floating point exception occurs is given a penalty of about 2,000 (Langdon et al., 1999). Figure 11 suggests bigger programs are more likely to cause floating point exceptions but when programs are big enough this proportion also converges to a limit. In practice such programs have little effect as they are never selected to be parents of the next generation).

6 Artificial Ant

Our last example is in some ways the most complex. We report the distribution of fitness in a benchmark GP problem, which combines both side effects and iteration. The problem chosen is the artificial ant following the Santa Fe trail. The program tree is repeatedly executed during which it controls an artificial ant using the side effects of special leafs. The value returned by the root node is ignored. It also includes functions with more than two arguments. (A more complete description of this particular problem search space may be found in (Langdon and Poli, 1998), including schema analysis. Here we concentrate upon variation w.r.t. length).

Figure 12 again suggests that, provided programs exceed some small fitness dependent threshold, the distribution of program fitnesses is roughly independent of their size. Much of the fluctuation seen at the higher fitness levels is due to sampling noise inherent in



Figure 12: Proportion of Artificial Ant programs of a given length by their fitness. Values for lengths 15 and above are based on Monte Carlo sampling and so are subject to noise.

Monte Carlo measurements.

In Figure 13 (solid line) we present the data for just one fitness value (the solutions). There are no solutions with less than ten nodes. From 11 to 18 nodes the proportion of solutions in the search space rises rapidly (but not monotonically) to a peak from which it falls. For programs with more than 30 nodes, the concentration of solutions appears to change only slowly with program size. It appears to eventually falls to near zero.

In the standard Santa Fe problem the function set includes both Prog2 and Prog3, however it is not necessary to have both to solve the problem. The two dashed lines in Figure 13 show the density of solutions when only one of them is included. While the data are subject to sampling noise, it appears that both subspaces formed by excluding one or other of the Prog functions are richer in solutions than the original one. Again in both subspaces it appears there is only very slow variation in the density of the maximum fitness value w.r.t. length above some threshold (about 50 or 100 nodes).

7 Long Random Linear Programs

In this section we will proof that, provided certain assumptions hold, each output generated by long random linear programs is equally likely and that this is true regardless of the program's inputs and its length. Consequently the chance of finding at random a solution reduces exponentially with the size of the test set.

The state of a computer is determined by the contents of its memory. For our purposes, registers, condition flags, etc. within its CPU and input and output registers, are regarded as part of its memory but we exclude the program counter (PC). If it has N bits of memory it can be in up to 2^N states. Program execution starts with all memory initialised. Execution of each program instruction moves the computer from one state to another.



Figure 13: Proportion of Artificial Ant programs of a given length which solve the Santa Fe trail problem, using three different function sets. Error bars indicate the standard error. With the two new function sets, there is little variation with length (note log scale) for longer programs. There may be some variation when using the combined function set (solid line) above 400.

Usually the next state will be different but it need not be. For example an instruction which sets a register to zero will not change the state if the register is already zero. We will assume there is at least one such state and instruction.

We assume the designer of the computer (or GP experiment) has ensured that it is possible to reach every state. This is done since 1) inaccessible states correspond to unusable memory, i.e. to inefficient use of hardware and, 2) it makes it is possible to transform any input to any output.

Finally we will assume the instruction set is symmetric in that if there is one instruction which moves the computer from one state to another there is also an instruction which moves it in the other direction.

Consider a program as a sequence of instructions each of which transforms the computer's state. In particular consider the case where the program contains l instructions chosen at random. The computer starts from an initial state (given by the program's inputs) and terminates l states later. The program's output is then the state of the computer's outputs. Note: the program itself need not be linear, it can contain branches, loops, function calls etc. provided it executes state changing instructions at random and terminates after l of them. We exclude the program counter (PC) from the machine's state so its contents and thus the address of the next instruction need not be random. Program termination could be forced by an external event or by fixing a path l instruction long for the program counter, cf. linear GP (Nordin, 1997).

We can represent the computer by a probability vector of length 2^N . When executing a fixed program, the computer will be in exactly one state at a time, i.e., its probability vector will contain one element of 1.0 and the rest will be zero. We can view each instruction as an $2^N \times 2^N$ matrix which when multiplied by the current probability vector (state) yields the next probability vector (next state). The elements of the matrix are either zero or one and there is exactly one "1" in each row. Therefore it is a stochastic matrix (Feller, 1970, 375).

If we consider all possible programs of length l we can define the average state at a particular time as the mean probability vector u at that time. In a particular program the next state is given by the current state vector multiplied by a particular matrix. When considering all programs, we can say the average next state is given by mean probability vector when multiplied by the average instruction matrix. Note the next state is given by the current state alone. It does not depend upon earlier events. Thus, on average, the state of the computer can be represented by a Markov process. The Markov transition probability matrix M is the mean of all the instruction state matrices.

Since M is the mean of stochastic matrices, it too will be stochastic. At least one of the elements on its diagonal will be greater than zero. The period of this state will therefore be 1, i.e. it will be aperiodic (Feller, 1970, page 387). Therefore the greatest common divisor (g.c.d) of all the states is 1. Since any state can be reached, M is irreducible. Thus M corresponds to an irreducible ergodic Markov chain so u will tend to a limit u_{∞} independent of the starting state (i.e. the program's inputs) as the length l of the program is increased (Feller, 1970, page 393).

Because the instruction set is symmetric, M will be symmetric and both its rows and columns will each sum to 1.0 (M is doubly stochastic). Therefore, in the limit all states are equally probable (Feller, 1970, 399), i.e., there is a limiting probability distribution for the states of the computer and at the limit each state is equally likely. If the instruction set is asymmetric, there is still a limit but the states are no longer equally likely.

7.1 The Chance of Finding a Solution

We define a solution to mean that the program passes all the test conditions. As an example, suppose there are T non-overlapping tests. Each test specifies a number of input bits and a target output pattern of n bits. After executing a long random program each final state is equally likely. In particular each combination of bits in the output registers are equally likely. I.e. each function of the inputs is equally likely. Thus the chance of generating exactly the target bit pattern is 2^{-n} . There are many functions which implement this transformation, there is equal chance of selecting at random any of them. In particular, if the test cases don't overlap, the chance of having selected one of them which also passes the second test case is also 2^{-n} . Therefore the chance of finding a program which passes all T tests (i.e. of solving the problem) is 2^{-nT} . This can be viewed as the chance of finding a solution is given by the information content of the test set (nT bits).

7.2 An Illustrative Example

Consider a system with two Boolean registers R_0 and R_1 . At the start of program execution each is loaded with an input. When the program terminates its answer is given by R_0 . There are eight instructions:

$R_0 \leftarrow \text{AND}$	(R_0, R_1)	$R_1 \leftarrow \text{AND}$	(R_0, R_1)
$R_0 \leftarrow \text{NAND}$	(R_0, R_1)	$R_1 \leftarrow \text{NAND}$	(R_0, R_1)
$R_0 \leftarrow OR$	(R_0, R_1)	$R_1 \leftarrow OR$	(R_0, R_1)
$R_0 \leftarrow \text{NOR}$	(R_0, R_1)	$R_1 \leftarrow \text{NOR}$	(R_0, R_1)

There are $2^2 = 4$ states $(R_0 R_1 = 00, 01, 10, 11)$.

$R_0 \leftarrow \text{AND}$	$R_1 \leftarrow \text{AND}$	$R_0 \leftarrow \text{NAND}$	$R_1 \leftarrow \text{NAND}$
$1 \ 0 \ 0 \ 0$	$1 \ 0 \ 0 \ 0$	$0 \ 1 \ 0 \ 0$	$0 \ 0 \ 1 \ 0$
$1 \ 0 \ 0 \ 0$	$0 \ 1 \ 0 \ 0$	$0 \ 1 \ 0 \ 0$	$0 \ 0 \ 0 \ 1$
$0 \ 0 \ 1 \ 0$	$1 \ 0 \ 0 \ 0$	$0 \ 0 \ 0 \ 1$	$0 \ 0 \ 1 \ 0$
$0 \ 0 \ 0 \ 1$	$0 \ 0 \ 0 \ 1$	$0 \ 0 \ 1 \ 0$	$0 \ 1 \ 0 \ 0$
$R_0 \leftarrow \mathrm{OR}$	$R_1 \leftarrow \mathrm{OR}$	$R_0 \leftarrow \text{NOR}$	$R_1 \leftarrow \text{NOR}$
$\begin{array}{c} R_0 \leftarrow \mathrm{OR} \\ 1 0 0 0 \end{array}$	$\begin{array}{c} R_1 \leftarrow \text{OR} \\ 1 0 0 0 \end{array}$	$\begin{array}{c} R_0 \leftarrow \text{NOR} \\ 0 1 0 0 \end{array}$	$\begin{array}{c} R_1 \leftarrow \text{NOR} \\ 0 0 1 0 \end{array}$
$\begin{array}{c} R_0 \leftarrow \text{OR} \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \end{array}$	$\begin{array}{c} R_1 \gets \text{OR} \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \end{array}$	$\begin{array}{rrrr} R_0 \leftarrow \text{NOR} \\ 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \end{array}$	$R_1 \leftarrow \text{NOR} \\ 0 0 1 0 \\ 0 1 0 0 \end{cases}$
$\begin{array}{c} R_0 \leftarrow \text{OR} \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 \end{array}$	$\begin{array}{c} R_1 \leftarrow {\rm OR} \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 \end{array}$	$\begin{array}{rrrrr} R_0 \leftarrow \text{NOR} \\ 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \end{array}$	$\begin{array}{rrrrr} R_1 \leftarrow \text{NOR} \\ 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \end{array}$

If we use each of the instructions with equal probability the Markov transition matrix is the average of all 8, i.e.

	1	4	2	2	0 \
M 1/0		2	4	0	2
M = 1/8		2	0	4	2
	ĺ	0	2	2	4 /

We can see $u_{\infty} = 1/4(1, 1, 1, 1)$ satisfies $u_{\infty}M = u_{\infty}$ so it is the limiting probability distribution. Alternatively we can proof this by noting M is symmetric and hence doubly stochastic, it has at least one non-zero diagonal term thus the theorem from (Feller, 1970, 399) holds and so in the limit all states are equally probable.

The eigenvalues λ and corresponding eigenvectors E of M are

$\lambda_{00} = 1/2$	(0	-1	1	0)
$\lambda_{01} = 1/2$	(-1)	0	0	1)
$\lambda_{10}=1$	(1	1	1	1)
$\lambda_{11}=0$	(1	-1	-1	1)

Note since M is symmetric the other eigenvalues are also real.

7.3 Rate of Convergence and the Threshold

The eigenvectors E form an orthonormal set and so any vector can be expressed as a linear combination w of them u = wE ($w = uE^{-1}$). Where E is the $n \times n$ matrix formed by the n eigenvectors of M and E^{-1} is its inverse. So $EM = \lambda E$, where λ is the $n \times n$ diagonal matrix formed from the eigenvalues of M. Thus the probability vector of the next state is

 $u_1 = uM$ wEM $w\lambda E$ w_1E

Where $w_1 = w\lambda$. The new probability vector u_1 can also be re-expressed as a linear combination of the eigenvectors of M. It is actually w_1 . Note that the components have been shrunk by a factor given by the corresponding eigenvalue.

The probability distribution of the second state is $u_2 = u_1 M = w \lambda E M = w \lambda^2 E$ and so that of the i^{th} state is $u_i = w \lambda^i E$.

As *i* increases only the components with the largest eigenvalues will survive, other components will vanish exponentially quickly. I.e. the probability distribution will converge to the limit. The slowest terms to be removed that are not part of the limiting distribution are given by the eigenvectors corresponding to the second largest eigenvalue λ_2 . The number of steps, i.e. the threshold size, is dominated by the magnitude of this eigenvalue.

If we require the largest transient term to be less than some e > 0 then

$$\lambda_2^n < e$$

$$h \log(\lambda_2) < \log(e)$$

$$h > \log(e) / \log(\lambda_2)$$
Threshold size = O(1 / \log(\lambda_2))

Returning to our example. Suppose both inputs are 0. Then u = (1, 0, 0, 0). From M we can calculate $\lambda = (1/2, 1/2, 1, 0)$, E and E^{-1} .

$$E = \begin{pmatrix} 0 & -1 & 1 & 0 \\ -1 & 0 & 0 & 1 \\ 1 & 1 & 1 & 1 \\ 1 & -1 & -1 & 1 \end{pmatrix} \qquad E^{-1} = 1/4 \begin{pmatrix} 0 & -2 & 1 & 1 \\ -2 & 0 & 1 & -1 \\ 2 & 0 & 1 & -1 \\ 0 & 2 & 1 & 1 \end{pmatrix}$$

$$w = uE^{-1} = (0, -1/2, 1/4, 1/4)$$

$$w_1 = w\lambda = (0, -1/4, 1/4, 0)$$

$$u_1 = w_1E = (1/2, 1/4, 1/4, 0)$$

$$u_2 = w\lambda^2E = (0, -1/8, 1/4, 0)E$$

$$= (3/8, 1/4, 1/4, 1/8)$$

Note all elements of u_2 are already with 50% of their limit values. In this example the other eigenvalues are not close to 1.0, so convergence is rapid. $-1/\log(\text{next largest eigenvalue}) = -1/\log(1/2) = 1.442695$.



Figure 14: The expression $(x - y/3) \times (10 + 2)$ represented as a tree

8 Big Random Tree Programs

In this section we will proof that, provided certain assumptions hold, there is a limiting distribution for functionality implemented by large binary tree programs. Initially we allow functions with any number of inputs but later sub-sections simplify this by only considering binary functions.

8.1 Introduction

We wish to establish a similar result for trees that we have already shown for linear programs. We will start by assuming that all the state information is held within the tree (i.e. the functions have no side effects) and that the output of the program is returned only via its root. It should be possible to combine the two results to include trees with external memory. We start with an example tree.

Consider the expression $(x - y/3) \times (10 + 2)$. It has four functions $(-, /, \times \text{ and } +)$ and five leafs (x, y, 3, 10 and 2). We represent it as a tree, see Figure 14. It would usually be interpreted depth first, i.e. by evaluating x, then y/3, then (x - y/3), then 10 + 2 and finally multiplying them together. However, as there are no side effects the expression can be evaluated in a variety of different orders all of which yield the same answer. In particular the tree can be evaluated from the deepest node upwards. E.g. evaluate y first, then y/3. As we reach each new function node in the tree we have to stop and save the value we have calculated until the value of the function's other arguments have also been calculated. When one execution thread is blocked we create a new one from the next unprocessed leaf. In this case 10 and then 2, so we can calculate 10+2 but when this new thread reaches the \times node it also has to stop. So we start a new thread from x. When it reaches the - node, all its arguments are known and so we can restart the deepest path thread. It calculates x - y/3 and moves up the tree. On reaching the root (×) all its arguments are now known so we can perform the final multiplication using the current value and the previously stored result of 10+2. This is the value of the tree and evaluation halts.

We will now repeat the analysis used for linear programs. Instead of having a linear execution path the program is a tree but we will concentrate on the longest path within the tree (shown with thick lines in Figure 14).

The state of the program at each point in this path is determined by the current value (we are excluding additional memory in this paper). Its initial value is given by the leaf we start from. Each function along the way to the root will potentially change it and then the new value will be propergated towards the root. If the function has more than one argument then, in general, before we can determine the transformation the function will make, we will have to evaluate all its other arguments.

In our example the first function we reach is *divide*. *Divide* has two arguments.

However once we have calculated the value of its other argument (it is 3 in our example) we can treat *divide* as a function with one argument. Note the transformation at a given step will change each time the program is executed with different inputs.

This framework is similar to the linear case in that in random trees we can view each function along the longest path (in conjunction with its other inputs) as causing a random transformation of the current value. However the process is not, in general, a Markov chain because even for random trees the transformation matrices change as we get further from the leaf.

Let u be a vector whose elements correspond to each of the possible values. For example if we are dealing with an integer problem then there are 2^{32} possible values $(n = 2^{32})$ and u has 2^{32} elements. u is the probability density vector of the current value. For a given program at a given time, one element of u will be 1.0 and all the others will be zero.

For each function of arity a there is n^{a+1} hypercube transformation matrix. When all the inputs to the function are known they are converted to a probability vectors like u. By multiplying the transformation matrix by each of them in turn we get the output probability vector. The output of the function is given by the non-zero element in the output probability vector.

Since we wish to treat the current path separately from the function's other inputs we split its n^{a+1} hypercube transformation matrix into a n^{a+1} transformation matrices, one for each argument. Firstly we determine which argument of the function the current path is. We then choose the corresponding transformation matrix and multiply it by each input in turn but excluding the current path. This yields an $n \times n$ matrix which when multiplied by the current probability vector yields the next probability vector. E.g. each binary function has $2 n \times n \times n$ transformation matrices. If the current path is its first argument, we use the first, otherwise we use the second.

We now start the analysis of random programs. Starting from a leaf the non-zero element of u will correspond to one of the inputs to the program. (For simplicity we will treat constant values as being inputs to the program). We define the average value of u as being the mean of its values across all possible programs. Thus initially all the elements of u which correspond to one of the input values will be non-zero and all other elements will be zero. Call this u_0 .

We then come to a particular arity a function as its i^{th} input. The probability distribution u_1 after the first function is given by u_0M_1 where M_1 is the transformation matrix corresponding to the i^{th} input of the first function. Since this is the deepest function the other branches must also be random leafs and so their probability distributions will also be u_0 . Thus $M_1 = u_0^{a-1}N_{afi}$ where N_{afi} is the n^{a+1} hypercube transformation matrix for function f input i (a indicates its arity). On average the new probability density function will be the mean of all functions of arity a. Also on average the path we have chosen is equally likely to reach any of the inputs of f, so we can also average across all value of i. Let $N_a = 1/f_a \sum_{j=1}^{j=f_a} 1/a \sum_{k=1}^{k=a} N_{ajk}$ where f_a is the number of functions of arity a in the function set. So on average $M_1 = u_0^{a-1}N_a$ and $u_1 = u_0M_1$.

8.2 Large Binary Trees

To avoid the complexity associated with considering multiple function arities we will assume that all internal nodes are binary. We define $N = N_2$. So $M_1 = u_0 N$.

The probability vector u_1 is now propergate up the tree to the next function. Its other argument is determined, N_{2jk} is multiplied by them to yield M_2 . Again we have to average across all programs so we use the mean N transformation matrix. The functions' arguments may be either leafs or trees of height one. If they are leafs, their probability vector will be identical to u_0 (since they are also random). If they are functions, the probability vector is the same as in the longest path because the same functions are equally probable in each branch. So $u'_1 = u_1 = u_0 M_1$. Let p'_{20} be the average number of functions which are children of the function at distance 2 from the leaf along the longest path (excluding those on the longest path). Also $p'_{00} = 1 - p'_{20}$ is the average number of children which are leafs. Thus $M_2 = p'_{00}u_0N + p'_{20}u_1N$. Note $M_2 \neq M_1$ and so the process is not Markov.

$$M_{1} = u_{0}N$$

$$u_{1} = u_{0}u_{0}N$$

$$M_{2} = p'_{00}u_{0}N + p'_{20}u_{1}N$$

$$M_{2} = p'_{00}u_{0}N + p'_{20}u_{0}u_{0}NN$$

At the third level,

$$M_3 = p'_{000}u_0N + p'_{200}u_0^2NN + p'_{220}(u_0^2N)(u_0N)N + p'_{222}(u_0^2N)(u_0^2N)N$$

where p'_{iii} refer to the proportion of children of the fourth node along the longest path (but excluding those on the longest path). p'_{000} is the proportion of programs where there is only one child (so it is a leaf). p'_{200} is the fraction where the child is a function but both its children are leafs. p'_{220} is the fraction where the child has one child which is a function and p'_{222} is the remainder. I.e. p'_{222} is the fraction of programs where the other child of the fourth node is a full subtree as deep as the child on the longest path.

The $n \times n$ sub matrices of N are stochastic. $u_0 N$ for arbitrary u_0 will also be stochastic. $u_0 = \sum we$ where e are the eigenvectors of $u_0 N$ with corresponding eigenvalues λ . Note $|\lambda| \leq 1$. Thus, v_1 , the probability distribution produced by a random full binary tree of depth 1 is:

$$v_1 = u_0 u_0 N$$

= $\sum weu_0 N$
= $\sum w\lambda e$

 v_1 is closer to (or at least no further away from) the limiting distribution of u_0N than u_0 itself. Similarly v_2 the distribution produced by full trees of depth 2 is

$$v_{2} = v_{1}v_{1}N$$

= $\sum_{i} w_{i}\lambda_{i}e_{i}v_{1}N$
= $\sum_{i} w_{i}\lambda_{i}e_{i}u_{0}u_{0}NN$

$$= \sum_{i} w_{i}\lambda_{i}e_{i}\sum_{j} w_{j}e_{j}u_{0}NN$$
$$= \sum_{i} w_{i}\lambda_{i}e_{i}\sum_{j} w_{j}\lambda_{j}e_{j}N$$
$$= \sum_{i}\sum_{j} w_{i}\lambda_{i}w_{j}\lambda_{j}e_{i}e_{j}N$$

Since $|\lambda| \leq 1 v_2$ is also closer (or at least no further away) to the limiting distribution eeN (where e is the eigenvector of u_0N with the largest eigenvalue. If u_0N has a diagonal element greater than zero, there will be just one eigenvalue with a modulus of 1 and the limiting distribution v_{∞} will not cycle. (The matrix components corresponding to asymmetric subtrees are similarly bounded). Thus as we go higher in the tree the matrix elements of the higher order components of M_i will be bounded.

As we go higher in the tree the number of branches we encounter that are the same length as the longest one falls rapidly. I.e. the higher coefficients p' are not only bounded (they are non-negative but sum to 1.0) but the higher order ones vanish. In fact in large random binary trees the chance that the other subtree is empty tends to a constant value of approximately 0.5 (Sedgewick and Flajolet, 1996, page 241). I.e. $p'_{0...0}$ tends to 0.5 as we get further from the leaf, i.e. as *i* increases, so M_i is dominated by the first few terms. Hence while $M_i \neq M_1$, $M_{i+1} = M_i$ and so the current value along the longest path will become Markovian. Therefore the probability distribution of the output of large random trees does not depend upon their size. From the eigenvalues and eigenvectors of M_{∞} we can calculate the probability distribution of the output of large random trees and how big the threshold size is. Note that unlike linear programs, these may depend upon the programs inputs.

8.3 An Illustrative Example

We take the same four Boolean functions as before (i.e. AND, NAND, OR and NOR) and apply them to a Boolean regression problem of n-bits. Each is a binary function of one bit input and so has two $2 \times 2 \times 2$ transition matrices. Since each function is symmetric, in each case the two matrices are the same.

As for each function, we also include the function with the opposite output (AND and NAND). The mean matrix has the same value at every element. This means M_1 is independent of u_0 with every element being the same $-M_1$ is irreducible, doubly stochastic, with non-zero diagonal elements. Thus, the output of the first random function is independent of its inputs and is equally likely to be 0 as 1. Since the coefficients p' sum to 1, this is true for every M_i . The output of the whole tree is independent of its inputs and is equally likely to be 0 as 1 regardless of the size of the tree.

8.4 The Chance of Finding a Solution

Because random trees have some inputs near their root, they are more likely to implement program functionality which needs few operations on the inputs compared to functions chosen at random. We can repeat the analysis in Section 8.1–8.2 but replace the current value with the current functionality. Instead of considering the value output at each node in the tree, we use an index number of the function implemented by the subtree rooted at that node. For example, in an *i*-bit-input *m*-bit-output problem there are 2^{m2^i} possible



Figure 15: Distribution of 2 input functions produced by random trees comprised of AND, NAND, OR and NOR. The solid line give the measured. Dotted lines are numerical predictions based on simplified models of random trees.

functions and each can be given an $m2^i$ bit index number. So the number of possible values $n = 2^{m2^i}$. The n^{a+1} hypercube transformation matrices N_{ajk} now operate on function index values rather than actual values but we can define average behaviour etc. as before and the analysis follows through. I.e. the functionality of large random trees tends to a distribution which is independent of the tree size. The distribution and the threshold size are again given by the eigenvalues and eigenvectors of the limit value of M.

8.5 A Second Illustrative Example

Returning to the example in Section 8.3, The transformation matrices now depend upon the order of the problem. If we take the case where there are two inputs then there are a $2^{1^{2^2}} = 16$ possible functions. So each function has two $16 \times 16 \times 16$ transition matrices. The functions are still symmetric so again we need only consider one of each pair.

However this does not mean each function is equally likely. When we consider the average function transition matrix it is irreducible, stochastic, with non-zero diagonal elements but not symmetric. Thus there is a limiting distribution independent of the inputs but is not uniform. Also it has several non-zero eigenvalues, so while convergence is rapid it is not instantaneous. Thus M_{∞} depends on the distribution of p', i.e. of subtree sizes. In Figure 15 the function distribution produced assuming a simple model in which functions within the trees have one branch which is a leaf is compared with the measured distribution. The distribution for full trees is shown for comparison.

It is clear that the simple mode is approximately correct. A full model would need to consider the distribution of subtree sizes (i.e. p') more carefully. In the case of trees containing only XOR the output of a tree does not depend upon its shape and we can give an exact theoretical result for the limiting distribution.

9 XOR Program Spaces

In this section we give a theoretical analysis which shows in the limit as program size grows the density of parity solutions when using EQ or XOR is independent of size but falls exponentially with number of inputs (Section 9.2). But first we start with the functions which can be created using EQ and XOR and in particular the form of the solutions to the parity problems.

9.1 Parity and Always-on/off Program Spaces

Even parity solutions, where n is even, are of the form $D0 = D1 = D2 = \ldots = D_{n-1}$. However given the symmetry of the EQ building block the inputs to the program can occur in any order. Further $D_x = D_x$ is true so $(D_y = D_x = D_x) = D_y$ therefore any pair of repeated inputs can be removed from the program without changing its output.

Odd parity solutions, where n is odd, are of the form $D0 \neq D1 \neq \ldots \neq D_{n-1}$. Again given the symmetry of the XOR building block the inputs to the program can occur in any order. Further $D_x \neq D_x$ is false but $(D_x \neq \text{false}) = D_x$ so $(D_y \neq D_x \neq D_x) = D_y$. Therefore again any pair of repeated inputs can be removed from the program without changing its output.

Therefore any program will be a solution to the parity problem provided it contains an odd number of all n terminals. Thus all solutions contain t = n + 2i terminals, where i = 0, 1, 2, ... Both EQ and XOR are binary functions, so programs are of odd length l = 2t - 1 and solutions are of length l = 2t - 1 = 2n + 4i - 1.

Any program with an even number of one or more inputs effectively ignores those inputs. Given the nature of the parity function, such a program will pass exactly half the fitness cases.

Note while XOR (or EQ) may more readily create solutions to the parity problems they are considerably more limited than NAND and can only generate 2^n of the possible 2^{2^n} functions (NAND can generate them all, thus the results of Section 7 do not directly apply). Unlike NAND they show long range periodicity generating 2^{n-1} functions in trees of length l = 2n + 4i - 1 (for large *i*) and the other 2^{n-1} functions in trees of length l = 2n + 4i + 1.

9.2 **Proportion of Solutions**

If a program's length does not obey l = 2n + 4i - 1 then it cannot be a solution to the order n parity problem and will score exactly half marks on the parity problems. If l = 2n + 4i - 1 is true, there is a chance that a randomly generated program will contain an odd number of each input and so be a solution. When calculating the fraction of programs of a given length that are solutions we can ignore the number of different tree shapes. This is because the output of an XOR tree is determined only by how we label its leafs and not by its shape.

To apply our Markov analysis we consider the current state to be given by the oddness



Figure 16: Fraction of programs that solve Even-6-parity or Always-on-6 problems, using EQ (note log scale). Error bars show standard error.

or evenness of the number of each of n-1 inputs. (Given these and that we are only considering programs which obey l = 2n + 4i - 1 the oddness or evenness of the remaining input is fixed. Therefore we need only consider n-1 rather than n inputs). The distribution of solutions to the parity problem is given by the chance of selecting a solution at random, i.e. of all n-1 inputs having the right parity. Suppose we create long random programs by adding two randomly chosen inputs i, j at a time. I.e. the number of inputs of types i and j will both increase by one and so will change from an odd to and even number or vice versa. (If both inputs are of the same type (i = j) then it will swap back and there is no change of state). The chance of moving from one state to another does not depend upon how we got to that state, i.e. the process is Markovian and can be described by a stochastic state transition matrix. The chance of moving from one state to another is equal to the chance of moving in the opposite direction, i.e. the state transition matrix is symmetric. There is a 1/(n-1) > 0 chance of remaining in the same state after selecting the next pair of inputs. Thus there is an acyclic limiting distribution and in it each of the states is equally likely (Feller, 1970, page 399). There are 2^{n-1} states, one of which corresponds to a solution to the parity problem. I.e. in the limit of large programs the chance of finding a solution to the parity problem of order n in a parse tree composed of XOR (or EQ) is $1/(2^{n-1})$ provided the tree is the right size (and zero other wise). In fact at the large program limit this is true for each of the possible functions.

Figure 16 shows the fraction of 100,000 random programs which are solutions to the Even-6 parity or always-on-6 problems, for a variety of lengths. Figure 16 shows measurement approaches the theoretical large program limit for $t \ge 16$, i.e. $l \ge 31$. This is to be expected as the second largest eigenvalue of the Markov transition matrix is 0.36



Figure 17: Fraction of programs that solve parity problems given appropriate building block. Length of programs increases with number of inputs to ensure leafs $\geq 2\frac{2}{3}$ inputs. Measurement and theory agree within 2 standard errors (error bars show standard error).

which is far from the first. This means transient terms decrease by about e^{-1} every time the program length increases by 2 leafs.

Figure 17 shows the fraction of random programs which are solutions to the Even or Odd parity problems (100,000 or a million random trials). The lengths of the programs were chosen so that l = 2n + 4i - 1 is true and the number of leafs exceeds 6n/16. (6n/16 was chosen as a linear variation of threshold with number of inputs was assumed and 2.33*n* was sufficient for n = 6. While the second eigenvalue changes only slowly with the number of inputs in the problem, the threshold appears to rise linearly with it. The threshold length $\approx n - 2$). Figure 17 again shows agreement between measurement and the theoretical large program limit.

As the Markov analysis predicts, we have observed (for n = 4) the proportion of all possible functions generated by XOR and EQ rapidly converges to the same value with increasing tree size.

10 Discussion

In the previous sections we have shown 66344 examples from diverse problems where our claim appears to be justified and we have proved it for linear programs and standard GP. In the case of the XOR trees, we have given the limiting distribution for each fitness level. In the more difficult problems at the extremes of the fitness range (solutions to the parity and the sextic polynomial problems), even sampling huge numbers of random trees, we

have not be able to amass enough examples to demonstrate our claim. However, our proof covers such cases. We next consider extending our claim.

10.1 Automatically Defined Function

We can extend our argument to cover programs evolved using Automatically Defined Functions (ADFs) (Koza, 1994). Each ADF can be viewed as a tree in its own right and so, if the ADF exceeds the threshold size, the distribution of possible functions the ADF can implement will also converge to a limiting distribution as the ADF gets bigger. For each function its value is determined by its input(s). The value of each of its inputs is given by a subtree in the calling ADF or main program. When the subtree exceeds the threshold size, the distribution of values used when calling the ADF will also converge and thus the distribution of values returned by the ADFs will also converge and so, finally, will be the distribution of values returned by the program as a whole.

10.2 Memory

It should be possible to produce a combined proof based on Sections 7 and 8 which covers tree programs which have additional state (i.e. memory) outside the tree. We have not measured the distribution of programs with external memory. It may be memory radically changes the threshold size. However we suggest that our claim will hold for non-recursive programs which include memory and subroutines.

10.3 Turing Complete Programs

Finally to consider all programs we need to consider Turing completeness. This requires the addition of either recursion or iteration. The proof advanced in Section 7 for long linear programs can be extended to Turing complete programs provided they halt. Firstly we note Section 7 requires the programs complete l instructions. But if l is big enough, programs longer than l have the same distribution. So exactly when the program halts is not crucial. Secondly it is assumed each instruction is independent of the previous one. In program loops, the instructions are executed in an ordered sequence. However if each loop is small compared to the program it is reasonable to treat a repeated sequence of random instructions as if it was just a random sequence.

It seems to reasonable that a similar result will also apply to big trees including iteration or recursion and memory. However in both cases we anticipate the greater complexity available may radically effect the threshold length. Perhaps to such an extent that it is thus not obvious that our claim will hold in general to Turing complete programs.

10.4 Parity Problems Landscapes and Building Blocks

Section 9 describes the program space of the parity functions when given the appropriate functional building block (i.e. XOR or EQ). For all but the simplest problems at all program lengths the fitness space is dominated by a central spike indicating almost all programs score exactly half marks. However a small fraction of programs do solve the parity problems. We have derived a simple analytical expression for the case of large programs which shows, the proportion of solutions falls exponentially with increasing number of inputs. However for modest numbers of inputs the proportion is not so small as to be infeasible to find using modern computers. To derive a fitness landscape, we would also need to consider how genetic or other operators move between points in the search space, as well as the fitness of those points. This is unnecessary in this case, because either we have found a solution or the point in the search space scores half marks. That is, the program space contains no gradient information. Search techniques such as GP, which rely on gradient information will be unable to out-perform random search on such a landscape. We might anticipate population based search without mutation performing worse than random search as genetic drift in a small population means the population may loose one or more primitives. If this happens, then it becomes impossible to construct a solution.

This suggests techniques which seek to solve the parity problems by evolving the appropriate building blocks are unlikely to find minimal solutions directly. Such evolutionary techniques will probably have found programs with fitness well above half marks and so will reject any partial solution only composed of the discovered building blocks since these will score less than the partial solutions it has already discovered. It is possible impure solutions to the problem may be found which subsequent evolution, perhaps under the influence of parsimony or beauty pressures, may evolve into a solution comprised only of building blocks.

It is worth noting that we have only considered the case where all components of the programs are of the same type. So there are no restrictions on how functions work with each other. Performance gains for GP have been reported by using strong typing (Montana, 1995) or grammars (Whigham, 1996) which control program components' interactions. In the case of the Boolean problems, examples include (Janikow, 1996) who gainfully employed typed inputs, while (Yu and Clack, 1998) structures their inputs as a list. Work is continuing to understand the role of different function sets and search operators on the Boolean problems (Page et al., 1999; Poli et al., 1999).

10.5 "Random Trees"

On average half the random trees sampled using the ramped-half-and-half method (Koza, 1992, page 93) are full. Therefore, particularly if the depth parameter is increased beyond the usual 6 (equivalent to maximum size of 63), the chances of finding at random both the even-3 and the odd-3 parity functions are considerably higher using it than using uniform search. In contrast ramped-half-and-half is less likely to find solutions to the Santa Fe ant trail problem than uniform search. See (Langdon and Poli, 1998, Table 3). This suggests that the best method to use to create the initial random population is problem dependent.

In large binary random trees about half the functions have one or more terminals as their arguments (Sedgewick and Flajolet, 1996, page 241). I.e. not only are they relatively sparse (their average height is $2\sqrt{\pi(l-1)/2} + O(l^{1/4+\epsilon})$ (Sedgewick and Flajolet, 1996, page 256), which is greater than the height of full binary trees $\lceil \log_2 l + 1 \rceil$) but so too are the subtrees within them. I.e. the whole search space contains a lower proportion of full or nearly full subtrees than do full trees. Since nearly full subtrees can be used to form XOR from NAND gates, this may be a partial explanation for why the parity functions are so rare in the whole search space but are comparatively more frequent in full trees.

Our studies of the "bloating" phenomena (Langdon et al., 1999) in GP and other search techniques indicate that, in the absence of parsimony or size or depth restrictions, GP populations tend to evolve towards these large relatively sparse trees which may have few full subtrees within them. This suggests problems may arise if the problem (and function set used) needs full or nearly full subtrees to solve it. The use of a depth limit rather than size limit on the evolution of the program trees may encourage the formation of nearly full trees of the maximum permitted depth. These will contain more full subtrees. A depth limit may ease the solution of problems in which full trees contain a higher proportion of solutions. A size limit will discourage the formation of full trees and may help in problems where the density of solutions is lower in full trees.

10.6 GP and Random Search

We have discussed the number of programs which implement each function as a fraction of the total number of programs. Particularly the proportion of solutions. This corresponds directly to the difficulty of the problem for random search and establishes a benchmark with which to compare GP and other techniques. In (Koza, 1992, Chapter 9) GP performance is shown not to be the same as random search. Indeed in the case of all but a few of the simplest problems, which both GP and random search easily solve, GP performance is shown to be superior to random search. It is commonly assumed that problems that are harder for random search will also be harder for any search technique. There is a little evidence to support this. For example (Koza, 1992, Figure 9.2) shows a strong correlation in the 3 input Boolean problems between difficulty for random search and difficulty for GP. Thus the distribution of solutions in the search space can give an indication of problem difficulty for GP.

10.7 Searching Long Programs

As the density of solutions changes little with program size then there is no intrinsic advantage in searching programs longer than the threshold. It may be that some search techniques perform better with longer programs, perhaps because together they encourage the formation of smoother more correlated or easier to search fitness landscapes (Poli and Langdon, 1998). However in practice searching at longer lengths is liable to be more expensive both in terms of memory and also time (since commonly the CPU time to perform each fitness evaluation rises in proportion to program size).

At present we do not know in advance where the threshold is. A line of research would be devise a means of predicting it. This could be of practical value by replacing existing ad-hoc measures to preset the upper bound on the size of programs with a more principled approach.

11 Conclusions

In Section 7 we proved that the distribution of functions implemented by linear programs converges in the limit of long programs, and at that limit each is equally likely. While convergence to the limit is exponentially fast with the size of the program the number of functions is exponential in the sizes of both input and output registers. The chance of finding a long solution at random falls exponentially with the problem size.

Section 8 gives the corresponding proof for binary parse trees. Most parse trees are asymmetric and even if the function set is symmetric the limiting distribution is asymmetric. I.e. there is a much higher number of some functions than others. Functions that can be produced by small trees are frequent not only in short programs but also in very big ones.

In Section 9 we showed trees composed of only XOR or EQ functions can be treated

as special cases of linear programs. This yields a limiting proportion of solutions to the n input parity problems of $1/2^{n-1}$. This was confirmed by experiment. An empirical measure for the rate of convergence is also given. Together with the fitness function, these give the complete fitness landscape.

In three very different classes of problems (the Boolean problems, symbolic regression, evolving agent) we have now shown that the fitness space is in a gross manner independent of program length. In general the number of programs of a given length grows approximately exponentially with that length. Thus the number of programs with a particular fitness score or level of performance also grows exponentially, in particular the number of solutions also grows exponentially.

Acknowledgments

I would like to thank, Trevor Fenner for suggesting the Markov analysis of XOR parity problems, Tom Westerdale for help and inspiration, Paul Vitanyi and finally I would like to thank the anonymous referees for particularly helpful comments and suggestions.

References

- Alonso, L. and Schott, R. (1995). Random Generation of Trees. Kluwer Academic Publishers.
- Altenberg, L. (1994). The evolution of evolvability in genetic programming. In Kinnear, Jr., K. E., editor, Advances in Genetic Programming, chapter 3, pages 47–74. MIT Press.
- Feller, W. (1970). An Introduction to Probability Theory and Its Applications, volume 1. Wiley, 3rd edition.
- Janikow, C. Z. (1996). A methodology for processing problem constraints in genetic programming. Computers and Mathematics with Applications, 32(8):97–113.
- Koza, J. R. (1992). Genetic Programming: On the Programming of Computers by Means of Natural Selection. MIT Press, Cambridge, MA, USA.
- Koza, J. R. (1994). Genetic Programming II: Automatic Discovery of Reusable Programs. MIT Press, Cambridge Massachusetts.
- Langdon, W. B. and Poli, R. (1998). Why ants are hard. In Koza, J. R., Banzhaf, W., Chellapilla, K., Deb, K., Dorigo, M., Fogel, D. B., Garzon, M. H., Goldberg, D. E., Iba, H., and Riolo, R., editors, *Genetic Programming 1998: Proceedings of the Third Annual Conference*, pages 193–201, University of Wisconsin, Madison, USA.
- Langdon, W. B., Soule, T., Poli, R., and Foster, J. A. (1999). The evolution of size and shape. In Spector, L., Langdon, W. B., O'Reilly, U.-M., and Angeline, P. J., editors, *Advances in Genetic Programming 3*, pages 163–190. MIT Press.
- Montana, D. J. (1995). Strongly typed genetic programming. *Evolutionary Computation*, 3(2):199–230.
- Nordin, P. (1997). Evolutionary Program Induction of Binary Machine Code and its Applications. PhD thesis, der Universitat Dortmund am Fachereich Informatik.
- Page, J., Poli, R., and Langdon, W. B. (1999). Smooth uniform crossover with smooth point mutation in genetic programming: A preliminary study. In Poli, R., Nordin, P., Langdon, W. B., and Fogarty, T. C., editors, *Genetic Programming, Proceedings of EuroGP'99*, volume 1598 of *LNCS*, pages 39–49, Goteborg, Sweden. Springer-Verlag.

- Poli, R. and Langdon, W. B. (1998). On the search properties of different crossover operators in genetic programming. In Koza, J. R., Banzhaf, W., Chellapilla, K., Deb, K., Dorigo, M., Fogel, D. B., Garzon, M. H., Goldberg, D. E., Iba, H., and Riolo, R., editors, *Genetic Programming 1998: Proceedings of the Third Annual Conference*, pages 293–301, University of Wisconsin, Madison, Wisconsin, USA. Morgan Kaufmann.
- Poli, R., Page, J., and Langdon, W. B. (1999). Smooth uniform crossover, sub-machine code GP and demes: A recipe for solving high-order boolean parity problems. In Banzhaf, W., Daida, J., Eiben, A. E., Garzon, M. H., Honavar, V., Jakiela, M., and Smith, R. E., editors, *GECCO-99: Proceedings of the Genetic and Evolutionary Computation Conference*, Orlando, Florida, USA. Morgan Kaufmann. Forthcoming.
- Rosca, J. P. (1997). Hierarchical Learning with Procedural Abstraction Mechanisms. PhD thesis, University of Rochester, Rochester, NY 14627.
- Sedgewick, R. and Flajolet, P. (1996). An Intoduction to the Analysis of Algorithms. Addison-Wesley.
- Whigham, P. A. (1996). Search bias, language bias, and genetic programming. In Koza, J. R., Goldberg, D. E., Fogel, D. B., and Riolo, R. L., editors, *Genetic Programming* 1996: Proceedings of the First Annual Conference, pages 230–237, Stanford University, CA, USA. MIT Press.
- Yu, T. and Clack, C. (1998). Recursion, lambda abstractions and genetic programming. In Koza, J. R., Banzhaf, W., Chellapilla, K., Deb, K., Dorigo, M., Fogel, D. B., Garzon, M. H., Goldberg, D. E., Iba, H., and Riolo, R., editors, *Genetic Programming 1998: Proceedings of the Third Annual Conference*, pages 422–431, University of Wisconsin, Madison, Wisconsin, USA. Morgan Kaufmann.