

# Evolution of Tail-Call Optimization in a Population of Self-Hosting Compilers

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## ABSTRACT

We demonstrate the evolution of a more complex and more efficient self-replicating computer program from a less complex and less efficient ancestor. Both programs, which employ a novel method of self-replication based on compiling their own source code, are significantly more complex than programs which reproduce by copying themselves, and which have only exhibited evolution of degenerate methods of self-replication.

## Categories and Subject Descriptors

I.2.2 [Artificial Intelligence]: Automatic Programming—*Program modification*

## General Terms

Experimentation

## Keywords

Artificial life, genetic programming, quine, self-hosting compiler, self-replicating program, tail-call optimization

## 1. INTRODUCTION

Among living organisms, which employ many and varied mechanisms in the process of reproduction, examples of evolved mechanisms which are both more complex and more efficient than ancestral mechanisms, abound. Yet, nearly twenty years after Ray's groundbreaking work on the Tierra system[14], in which the evolution of many novel (but degenerate) methods of self-replication was first demonstrated, there is still no example of a more complex and more efficient self-replicating computer program evolving from a less complex and less efficient ancestor.

This is not to say that there has been no progress in the field of artificial life since Tierra. Nor are we suggesting that increased reproductive efficiency is the only evolutionary path to increased complexity. The evolution of self-replicating programs of increased complexity has been demonstrated many times[7, 9, 12, 15, 17], and perhaps most convincingly in the Avida system[1, 2]. However, more complex programs evolved in Avida only because complexity was artificially equated with efficiency in the sense that programs

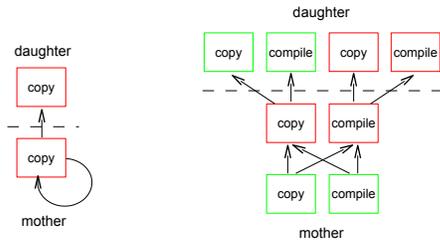
which learned to solve problems unrelated to self-replication were rewarded with larger rations of CPU time. No program in Avida (or in any other system known to us) has ever evolved a method of self-replication that is both more complex and more efficient than the method employed by its ancestor.

Self-replicating programs have been written in both high-level languages and in machine language. We define a machine language program to be *interesting* if it prints a string at least as long as itself and halts when executed, and observe that the Kolmogorov complexity of interesting programs is significantly lower than that of random strings of equal length. Consequently, if we were to train an adaptive compression algorithm, such as Lempel-Ziv[20], on a large set of interesting programs, then the compressed programs would not only be shorter, they would also look more random. Furthermore, because there are fewer random strings of equal length, the compressed programs are relatively more numerous. It follows that compression, which *decreases* redundancy by replacing recurring sequences of instructions with invented names, *increases* the density of interesting programs.

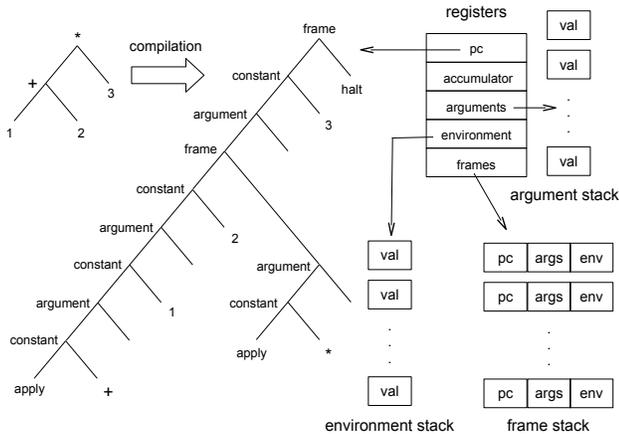
Since both processes increase redundancy and output machine language programs, it is natural to identify *decompression* with *compilation*, which increases redundancy by repeatedly generating similar sequences of instructions while traversing a parse tree. Viewed this way, programs written in (more expressive) high-level languages are compressed machine language programs, and compiling is the process of decompressing source code strings into object code strings which can be executed by a CPU.

If the density of interesting programs increases with the expressiveness of the language in which they are encoded (as the above implies), then this argues for using the most expressive language possible for any process, like genetic programming, which involves searching the space of interesting programs. However, if the goal is building artificial organisms, then high-level languages have a very serious drawback when compared to machine language. Namely, programs in high-level languages must be compiled into machine language before they can be executed by a CPU or *reified* as a *distributed virtual machine*[19]. Given that we want our artificial organisms to be both (potentially) reifiable and to evolve into self-replicating programs of greater complexity and efficiency, we must ask: How can the advantages which derive from the use of a high-level language for genetic programming be reconciled with the fact that only machine language programs can be reified?

To address this question, we introduce a new and significantly more complex kind of artificial organism—a machine language program



**Figure 1: Conventional self-replicating program (left) copies itself by exploiting program-data equivalence of von Neumann architecture. Compiling quine self-replicating program (right) with source code genotype (green) and object code phenotype (red). Because the shortest correct implementation of copy is optimal, only the compiling quine is capable of non-degenerate evolution.**



**Figure 2: Dybvig's[5] virtual machine for evaluating compiled Scheme expressions showing its registers and associated heap-allocated data structures.**

which reproduces by compiling its own source-code. See Figure 1. Conventional self-replicating programs reproduce by copying themselves. Optimum copiers accomplish this in time proportional to their length, and it not very hard to write a copier which is optimum in this sense (or to evolve one). It follows that shorter implementations are always more efficient, which leads to degenerate evolution, absent other factors. The possible variation in the implementation of a compiler is far larger. Even if the definition of the object language is stipulated, there is still a huge space of alternative implementations, including the syntax and semantics of the source language, the ordering of the decision tree performing syntactic analysis, and the presence (or absence) and effectiveness of any object code optimizing procedures.

In this paper we describe a machine language program which reproduces by compiling its own source code and use genetic programming to demonstrate its capacity for non-degenerate evolution. In the process we address questions such as: How can a complex lexically scoped computer program like a compiler evolve without breaking? How can a more efficient self-replicating program evolve when all mutations initially yield higher self-replication cost?

## 1.1 A Simple Programming Language

Because a self-hosting compiler compiles the same language it is written in, it can compile itself. The language we used to construct our self-hosting compiler is a pure functional subset of Scheme which we call *Skeme*. Because it is purely functional, *define*, which associates values with names in a global environment using mutation, and *letrec*, which also uses mutation, have been excluded. The global environment itself is eliminated by making primitive functions constants. For simplicity, closures are restricted to one argument; user defined functions with more than one argument must be written in a curried style. This simplifies the representation of the lexical environment which is used at runtime by making all variable references integer offsets into a flat environment stack. These offsets are termed de Bruijn indices[3] and can be used instead of symbols to represent bound variables. For example, in the following expression, a closure which squares its argument is applied to the number five:

```
> ((lambda (* %0 %0)) 5)
25
```

where *%0* is a reference to the closure's argument. One feature peculiar to *Skeme* is the special-form, *lambda+*. When a closure created by *lambda+* is applied to a value, the address of the closure is pushed onto the environment stack after the address of the value; the de Bruijn index for this address can then be used for recursive function calls. For example, the following expression computes ten factorial:

```
> ((lambda+ (if (= %1 0) 1 (* %1 (%0 (- %1 1)))) 10)
3628800
```

where *%0* is the closure and *%1* is the closure's argument.

## 1.2 Tail-Call Optimization

The very first self-hosting compiler was written in Lisp and so it is not surprising that it is possible (by including primitive functions which construct bytecode types) to write a very small self-hosting compiler in *Skeme*. See Figures 2, 3 and 4.

The cost of compiling a given source code depends not only on its size, but also on the complexity of the source language, the efficiency of the compiler, and the cost of any object code optimizations it performs. Common compiler optimizations include constant folding, loop unrolling, function inlining, and dead code elimination. Since a self-hosting compiler compiles itself, the efficiency of the object code it generates also affects compilation cost; it follows that minimizing the cost of self-compilation involves a complex set of tradeoffs. The most important of these is that object code optimizations have to pay for themselves by yielding an increase in object code efficiency large enough to offset the additional cost of compiling the source code implementing the optimization.

Most of the overhead associated with a function call involves the saving and restoration of evaluation contexts. In *Skeme*, these operations are performed by the *frame* and *return* bytecodes which push and pop the frame stack. However, when one function calls another function in a *tail position*, there is no need to save an evaluation context, because the restored context will just be discarded when the first function returns. A compiler which performs *tail-call optimization* recognizes when a function is called in a tail position and does not generate the code which saves and restores evaluation contexts. This not only saves time, it also saves space, since tail recursive function calls will not increase the size of the frame stack at runtime.

### 1.3 A Quine which Compiles Itself

A *quine* is a program which prints itself. It is possible to write a quine in any programming language but Skeme's list-based syntax makes it possible to write especially short and simple quines. For example, in the following Skeme quine, an expression `(lambda (list %0 (list quote %0)))` which evaluates to a closure which appends a value to the same value quoted is applied to the same expression quoted:

```
((lambda (list %0 (list quote %0)))
 (quote (lambda (list %0 (list quote %0)))))
```

It is possible to define an expression  $\phi$  in Skeme which can compile any Skeme expression. The expression  $\phi$  evaluates to a curried function which takes a compiled expression and an uncompiled expression as arguments. The compiled expression is a continuation; the uncompiled expression is the source code to be compiled; applying the curried function to the halt bytecode yields a function which can compile top-level expressions. Inserting a copy of  $(\phi$  (make-halt)) into the unquoted half of the quine so that it compiles its result (and mirroring this change in the quoted half) yields

```
((lambda ((phi (make-halt))
 (list %0 (list quote %0))))
 (quote (lambda ((phi (make-halt))
 (list %0 (list quote %0)))))
```

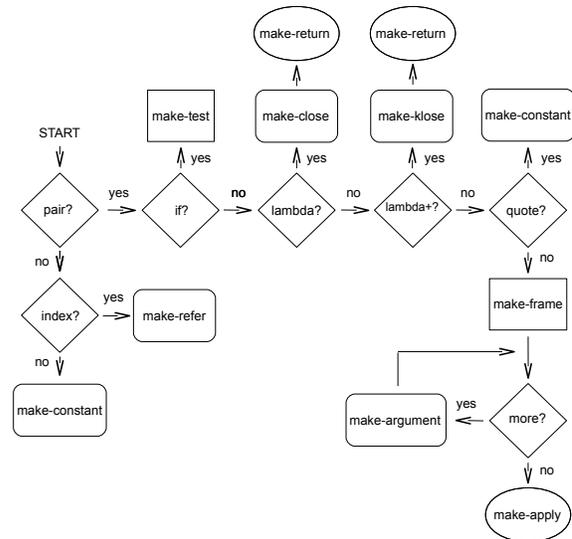
which, although not a quine itself, returns a quine when evaluated. Significantly, this quine is not a source code fixed-point of the Skeme interpreter but an object code fixed-point of Dybvig's virtual machine. In effect, it is a quine in a low-level language (phenotype) which reproduces by compiling a compressed self-description written in a high-level language (genotype).

In prior work on evolution of self-replicating programs there has been no distinction between phenotype and genotype; mutations are made on the same representation which is evaluated for fitness. In contrast, in living organisms, small changes in genotype due to mutation can be amplified by a development process and result in large changes in phenotype; it is phenotype which is then evaluated for fitness. In a compiling quine, small changes in source code (genotype) are amplified by compilation (development) yielding much larger changes in object code (phenotype) and it is object code which determines fitness, since it is the execution of object code which consumes the physical resources of space and time.

## 2. RELATED WORK

Stephenson *et al* describe a genetic programming system which learns priority functions for compiler optimizations including hyperblock selection, register allocation, and data prefetching[16]. D'Haeseleer described and experimentally evaluated a method for context preserving crossover[4]. Kirshenbaum demonstrated a genetic programming system where crossover was defined so that it respected the meaning of statically defined local variables[8]. Weimer *et al.* describe a system for finding and fixing bugs in large programs[18].

Several authors have explored the idea of staged or alternating fitness functions. Koza *et al.* used a staged fitness function as a method for multi-objective optimization[10]. Pujol describes a system where the fitness function is switched after a correct solution is discovered to a function which minimizes solution size[13]. Zou[21] and Offman[11] used alternating fitness functions to preserve diversity in genetic algorithm derived solutions to problems in water quality model calibration and protein model selection.



**Figure 3: A flowchart illustrating the Skeme compilation process. Not explicitly shown is the fact that the process calls itself recursively at many points—once in each box with rounded corners (for bytecodes with one continuation) and twice in each box with sharp corners (for bytecodes with two continuations).**

## 3. GENETIC PROGRAMMING

Our approach to genetic programming is motivated by the fact that gene duplication followed by specialization of one or both copies is a common route to increased complexity in biological evolution[6]. We introduce two mutation operators called *bloat* and *shrink* which play roles analogous to gene duplication and specialization and employ these in a genetic programming system where fitness alternates between object code based definitions of complexity and self-replication efficiency. In teleological terms, the bloat operator attempts to increase effective complexity by adding source code while the shrink operator attempts to increase self-replication efficiency by removing it.

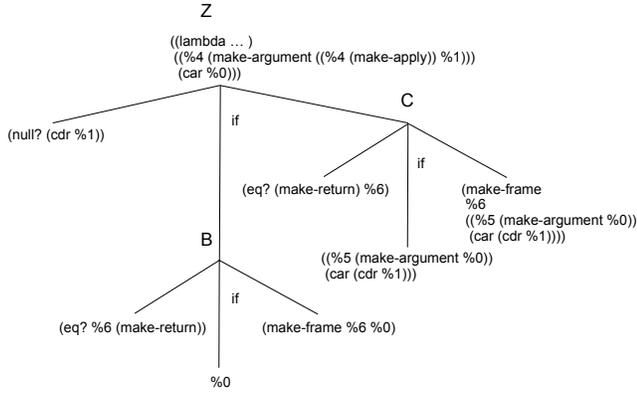
### 3.1 Alternating Fitness Function

Time is divided into ten generation periods termed *epochs* which alternate between two types, *flush* and *lean*. In flush epochs, fitness is defined as *effective complexity* while in lean epochs it is defined as *self-replication efficiency*.

A test bytecode is defined to be *non-trivial* if both of its continuations are exercised in the course of self-replication. This will only happen if the predicate expression in the *if* special-form from which the test bytecode is compiled sometimes evaluates to *#t* and sometimes to *#f*. The number of non-trivial test bytecodes in the object code is a good measure of the source code's effective complexity. Consequently, in flush epochs the number of non-trivial test bytecodes in the object code is *maximized*.

Because frame stack pushes and pops are the most expensive operation performed by the virtual machine, they are an excellent proxy for overall self-replication cost. Consequently, in lean epochs, the number of frame stack pops, which are implemented by the return bytecode, is *minimized*.





**Figure 6: Evolved subtrees implementing the tail-call optimizations which characterize the *B* and *C* genotypes. The *A* genotype performs neither optimization while the *D* genotype performs both. Both optimizations check to see if the continuation is a return bytecode, which performs a frame stack pop. If so, the push-pop sequence is not generated, resulting in significant savings in time and space usage.**

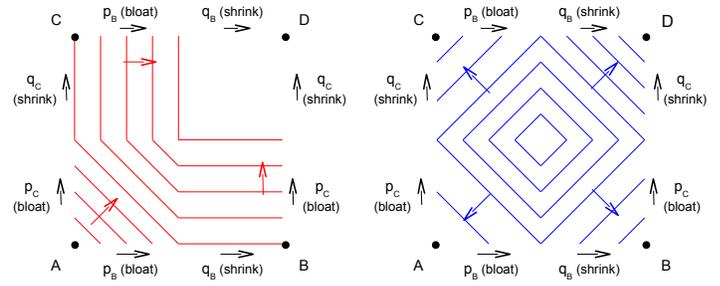
simplify function applications; the last shrink rule replaces expressions where a function is applied to one or more values with just one of those values. Because these rules also remove the identity function tags inserted by the bloat operator, the expression which results from a shrink mutation is again subject to bloating.

The five rules which define the shrink operator are

1.  $(\text{lambda}[+] e_0) \rightarrow (\text{lambda}[+] e'_0)$
2.  $((\text{lambda}[+] e_0) e_1) \rightarrow ((\text{lambda}[+] e'_0) e'_1)$
3.  $(\text{if } e_0 e_1 e_2) \rightarrow (\text{if } e_0 e'_1 e'_2)$
4.  $(\text{if } e_0 (\text{id } e_1) e_2) \rightarrow (\text{if } e_0 (\text{id } e'_1) e'_2) \parallel e_1 \mid e_2$
5.  $(f e_0 \dots e_N) \rightarrow (f e_0 \dots e_N) \parallel e_0 \mid \dots \mid e_N$

where  $f$  is a primitive function,  $\text{id}$  is the identity function, and primes mark expressions which are recursively expanded. Alternative right hand sides are separated by vertical bars; the alternative to the left of the  $\parallel$  is chosen with 95% probability; one of the remaining alternatives is chosen otherwise (each with equal probability). Unlike the bloat operator, which is value neutral, the shrink operator changes the object code generated by the compiler when it modifies an expression which is evaluated during self-replication. In the case of the fourth shrink rule, this often reverses a harmful bloat mutation, in which case the shrink mutation is beneficial. However, in the case of the last shrink rule, the mutation most often breaks the compiler. Very rarely, the shrink mutation does not break the compiler but instead results in a decrease in self-replication cost.

The problem which plagues many genetic programming systems, in which code trees grow larger with increasing time, does not occur for two reasons. First, the use of the  $\text{id}$  function as a tag prevents the bloat operator from being applied within  $\text{if}$  expressions which were themselves just created. Second, the shrink operator reverses bloat mutations, and bloat mutations not yielding a decrease in self-replication cost are strongly selected against during lean epochs.



**Figure 7: Contour plots of fitness landscapes during flush (left) and lean (right) epochs. Colored arrows point in directions of increased fitness. In lean epochs, the four genotypes *A*, *B*, *C*, and *D* occupy islands separated by valleys of decreased fitness; the bloat mutations necessary for *A* to evolve into any of the other genotypes are harmful since they increase the cost of self-replication. In contrast, the shrink mutations required for *A* to evolve into any of the other genotypes are beneficial. In flush epochs, the situation is reversed—the bloat mutations are beneficial and the shrink mutations are harmful since they increase and decrease effective complexity respectively. Alternating between the two fitness functions creates paths between the *A* and *D* genotypes consisting solely of beneficial mutations.**

### 3.4 Crossover

The self-hosting compiler is a relatively complex lexically scoped program. Variables which are defined in one scope will not necessarily be defined in other scopes. If we employed the standard method of non-homologous crossover used in most work on genetic programming, then subtrees could be inserted into scopes where one or more variables might not be defined, and this would break the compiler. We address this problem by employing the *homologous* crossover method described by D’Haeseleer[4]. D’Haeseleer’s crossover operator descends into both parent trees in parallel. Points where the two parent trees differ are subject to crossover, with the child receiving the subtree of either parent with equal probability. D’Haeseleer also notes that his method of crossover facilitates convergence (fixation) since children resulting from the crossover of identical parents will be identical to both parents.

## 4. GENOTYPES

Function applications involving one and two arguments are compiled at two different points in the  $\varphi$  expression and each of these points is a potential target for a pair of bloat and shrink mutations which would partially implement tail call optimization. We call the genotype of programs which perform neither optimization *A*, one (or the other) optimization *B* (or *C*), and both optimizations, *D*. Both optimizations check to see if the continuation is a return bytecode, which performs a frame stack pop. If so, the push-pop sequence is not generated, resulting in significant savings in time and space usage. See Figure 6. Lower bounds for the complexity and self-replication cost of each of the four genotypes are shown in Table 1. Finally, the relative fitnesses of the four genotypes are shown graphically, in the context of the fitness landscapes for the flush and lean epochs, in Figure 7.

Otherwise impassable valleys in a fitness landscape can sometimes be traversed if multiple mutations occur in a single individual. Even when one or more mutations would be harmful separately, the combination can still be beneficial. This is termed *stochastic tunneling*.

**Table 1: Complexities and self-replication costs.**

|                   | A   | B   | C   | D   |
|-------------------|-----|-----|-----|-----|
| non-trivial tests | 8   | 9   | 9   | 10  |
| returns           | 551 | 333 | 432 | 183 |

Because bloat mutations introduce dead code which does nothing but must still be compiled, and because they are easily reversed by shrink mutations, stochastic tunneling is the only way in which the  $B$  and  $C$  genotypes can evolve if fitness is based solely on self-replication efficiency. Assuming that mutation is a Poisson process, we can derive an expression for the expected number of trials required for an individual with the  $D$  genotype to evolve

$$\begin{aligned} \langle t_D \rangle &= \int_0^\infty \int_0^\infty \max(t_B, t_C) \frac{p_B q_B}{e^{p_B q_B t_B}} \frac{p_C q_C}{e^{p_C q_C t_C}} dt_B dt_C \\ &= \frac{1}{p_B q_B} + \frac{1}{p_C q_C} - \frac{1}{p_B q_B + p_C q_C} \end{aligned}$$

where  $p_X$  and  $q_X$  are the probabilities of the bloat and shrink mutations which characterize genotype  $X$  and  $t_X$  is the trial in which genotype  $X$  first evolves. Because the combination of mutations is (in both cases) strongly beneficial, we assume that once the  $B$  (or  $C$ ) genotype evolves, the population quickly converges to individuals of that genotype.

The median number of trials required for the  $D$  genotype to evolve is the value  $\tilde{t}_D$  where the joint cumulative distribution function for  $t_B$  and  $t_C$  equals one half:

$$1 - e^{-p_B q_B \tilde{t}_D} - e^{-p_C q_C \tilde{t}_D} + e^{-(p_B q_B + p_C q_C) \tilde{t}_D} = 1/2.$$

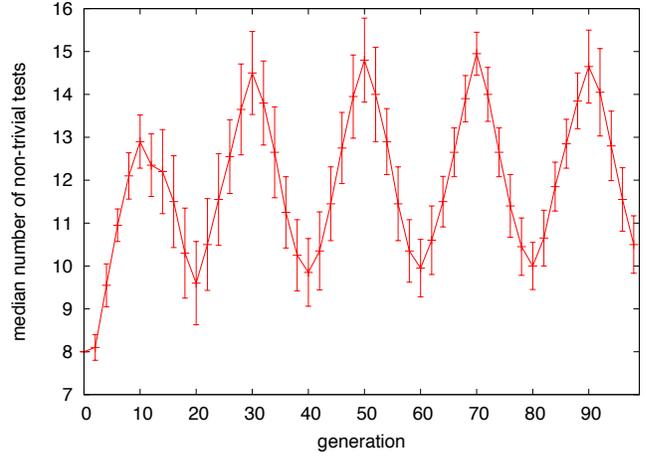
The mean and median generation in which an individual with the  $D$  genotype first appears can be computed by dividing  $\langle t_D \rangle$  and  $\tilde{t}_D$  by population size.

In order to estimate  $p_B q_B$  and  $p_C q_C$ , the bloat and shrink operators were applied to  $10^6$  individuals with genotype  $A$ . Approximately 59% of the resulting mutants were viable. Of the viable mutants, 15 possessed the  $B$  genotype and 15 possessed the  $C$  genotype, so that  $p_B q_B \approx p_C q_C \approx 15 \times 10^{-6}$ . Using these values in the expressions for mean and median trial and assuming a population size of 200 yields estimates of the expected (and median) number of generations for the  $D$  genotype to evolve by stochastic tunneling of 667 generations (expected) and 462 generations (median).

## 5. EXPERIMENTAL RESULTS

The initial population consisted of two hundred identical individuals of genotype  $A$  at the beginning of a flush epoch (in which fitness is equated with effective complexity). In the first step of the genetic algorithm, the bloat and shrink operators are applied to all individuals in the population and the mutants which result are tested for viability. To test for viability, the mutant is evaluated to produce a daughter, and the daughter is evaluated to produce a granddaughter. The mutant is classified as viable if the daughter and granddaughter contain the same number (greater than zero) of bytecodes (this is done in lieu of a much more expensive test of actual structural equivalence). Viable mutants replace their progenitors in the population.

The population is then subjected to crossover using tournament selection. In each tournament, four individuals are chosen at random (with replacement). The winners of two tournaments are then combined using crossover, and the resulting individual is tested for



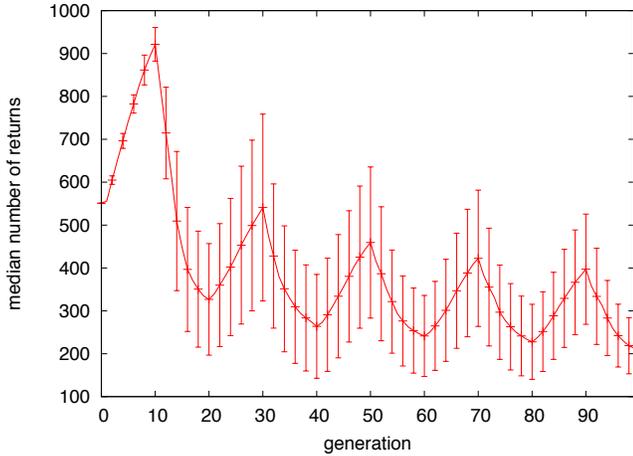
**Figure 8: The median number (in a population of size 200) of non-trivial test bytecodes averaged over 20 runs (error bars show plus or minus one standard deviation).**

viability. The crossover operation is repeated until it yields two hundred viable individuals which comprise the population of the next generation.

The above process is repeated for nine more generations, then the epoch is switched to lean (in which fitness is equated with self-replication efficiency). The genetic algorithm is run for a total of 100 generations (five flush epochs interrupted by five lean epochs).

In an initial experiment, the system was run twenty times. The median number of interesting test bytecodes contained in the compiled  $\phi$  expression and the median number of return bytecodes executed during self-replication were then plotted as a function of generation; see Figures 8 and 9. As expected, both complexity and self-replication cost increase in flush epochs and decrease in lean epochs. We observe that after 40 generations (two flush-lean cycles), the median complexity at the end of flush epochs is nearly double its initial value, which means that the majority of individuals contain 7 or more predicates which compile to non-trivial test bytecodes not present in the initial population. Furthermore, the median complexity at the end of lean epochs is always 10 or more, which suggests that either 1) the shrink operator is not fully able to reverse the effects of the bloat operator so that one or more bloat mutations (on average) survive through lean epochs; or 2) one (or both) of the  $B$  and  $C$  alleles is fixed in the population. Examination of Figure 9 shows that after 40 generations, the median self-replication cost at the end of lean epochs is slightly more than half of its initial value. This is consistent with evolution of one or both of the  $B$  and  $C$  genotypes. Self-replication cost continues to increase and decrease (depending on epoch) eventually reaching a point where the median value at the end of the fifth lean epoch is nearly three times smaller than the initial value. This is consistent with the evolution of the  $D$  genotype.

After running the system 100 times, the probabilities of the  $B$ ,  $C$ , and  $D$  genotypes evolving and for the mutations becoming fixed in the population were estimated. See Table 2. Notably, the most complex and most efficient genotype,  $D$ , evolved within 100 generations 81 times. Additionally, the average and median number of



**Figure 9: The median number (in a population of size 200) of return bytecodes executed during self-replication averaged over 20 runs (error bars show plus or minus one standard deviation).**

generations required for each genotype to evolve and for the mutations to become fixed were also estimated. Considering only the 81 runs in which the *D* genotype evolved, the average number of generations required was approximately 36 and the median number was 29. This is over 15 times faster than if fitness were based on efficiency alone, which clearly demonstrates the utility of the alternating fitness function.

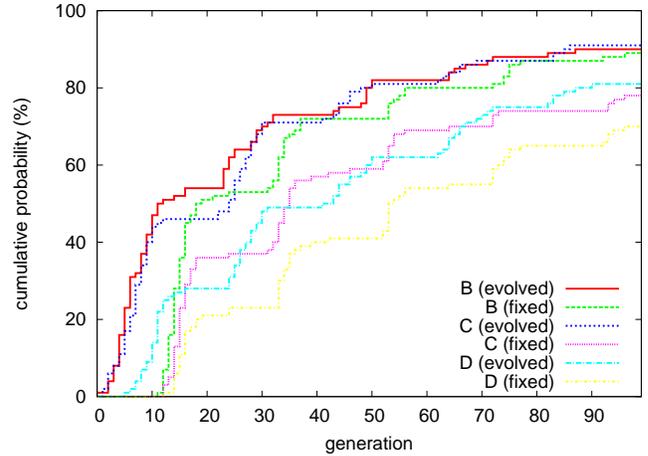
**Table 2: Generation of initial evolution and fixation.**

|             | B    | C    | D    | B'   | C'   | D'   |
|-------------|------|------|------|------|------|------|
| probability | 0.90 | 0.91 | 0.81 | 0.89 | 0.78 | 0.70 |
| mean        | 21.8 | 24.5 | 35.8 | 29.9 | 34.3 | 43.3 |
| std. dev.   | 21.0 | 22.0 | 24.5 | 21.1 | 22.2 | 24.5 |
| median      | 11   | 13   | 29   | 17   | 33   | 36   |

If we know the average numbers of individuals of a given genotype in each generation, then we can compute cumulative distribution functions (c.d.f.'s) for evolution and fixation of that genotype; see Figure 10. If we examine the c.d.f.'s, which look like step functions, we see several interesting things.

First, the c.d.f.'s for evolution of genotypes have zero slope during lean epochs, which suggests that new genotypes typically appear during flush epochs, when fitness is equated with effective complexity. Conversely, the c.d.f.'s for genotype fixation have zero slope during flush epochs, which leads us to conclude that fixation of genotypes typically occurs during lean epochs, when fitness is equated with efficiency. This is consistent with an increase in diversity during flush epochs and a decrease during lean epochs.

Second, there is always a lag between the generations of evolution and fixation, and the size of the lag depends on the improvement in self-replication efficiency—the greater the improvement, the shorter the lag. The C allele (which confers an advantage of 119 returns relative to the A allele) requires more time for fixation than the B allele (which confers an advantage of 218 returns).



**Figure 10: Cumulative distribution functions representing the probabilities that genotypes B, C, and D have evolved and are fixed by the given generation.**

**Table 3: Probabilities of pathways to D genotype.**

| $t_B < t_C = t_D$ | $t_C < t_B = t_D$ | $t_B < t_C < t_D$ | $t_C < t_B < t_D$ |
|-------------------|-------------------|-------------------|-------------------|
| 0.33              | 0.31              | 0.26              | 0.09              |

If we know the generation in which each genotype evolved, it is possible to estimate probabilities for each of the pathways leading from the (least complex and least efficient) A genotype to the (most complex and most efficient) D genotype; see Table 3. This analysis shows that in 64% of the runs in which D evolved, one of the B or C alleles evolved and was fixed prior to the evolution of the other; the D genotype then evolved by mutation from an ancestral program of the B or C genotype. However, in 35% of the runs in which D evolved, something (arguably) more interesting happened. Namely, the B and C alleles evolved in distinct lineages before either was fixed. The D genotype then evolved when an individual with the B allele and an individual with the C allele were combined by crossover. Stated differently, in 35% of the runs where D evolved, beneficial traits which evolved separately were combined by crossover to produce a child program more complex and more efficient than either parent program.

## 6. FUTURE WORK

This paper describes work that, although preliminary, opens many avenues for further exploration, including

- Determining whether or not a self-replicating program which reproduces by compiling itself can evolve the optimum order for the tests comprising the decision tree which performs syntactic analysis; this would require a new mutation operator which could reorder nested-*if* expressions.
- Determining whether or not it is possible to evolve dead code elimination, which would be a useful optimization in a system which includes mutation operators (like bloat) which (in effect) introduce dead code; to accomplish this, the bloat operator would have to generate a much larger set of  $\phi$  expressions, including dereferencing source code with *car* and *cdr* combinations.

- In the present system, de Bruijn indices are used mainly to simplify the compilation process by eliminating the need for static analysis; however, it is difficult to see how new lexical scopes could evolve (via a new mutation operator which introduces *lambda* expressions) unless bound variables are represented by symbols, and this would mean that the self-hosting compiler must be generalized so that it performs static analysis.
- Demonstration of *auto-constructive evolution* as described by Spector and Robinson[15], in which artificial organisms possess not only their own means of self-replication, but also of producing variation; this would require coding all mutation operators in Skeme and including this code in the subtree of the self-hosting compiler which copies quoted expressions.
- Reification of the compiling quine as a self-replicating distributed virtual machine and demonstration of evolution of increased complexity and self-replication efficiency.

## 7. CONCLUSION

We introduced a new type of self-replicating program which (unlike previous self-replicating programs) includes distinct phenotype and genotype components. Although the program is encoded in machine language, and (for this reason) can be executed on a CPU, it reproduces by compiling itself from its own source code, which is written in a more expressive high-level language. Because compiling is an intrinsically more complex process than copying, there is a much larger space of implementations to be explored by an evolutionary process; because its genotype is encoded in a high-level language, the space of neighboring self-replicating programs can be more efficiently probed.

To address the problem of how a complicated lexically scoped program like a compiler can evolve into a more complex and efficient program without breaking, we designed, implemented and tested a novel genetic programming system, which uses a pair of mutation operators analogous to gene duplication and specialization, together with homologous crossover and an alternating fitness function which selects for complexity or efficiency depending on epoch. Using this system, we experimentally demonstrated the evolution of several self-replicating programs of increased complexity and efficiency from a less complex and less efficient ancestor. We were able to show that in a population of 200 individuals, the most complex and efficient self-replicating program evolved within 100 generations in over three quarters of all trials, and by crossover of less complex and less efficient parent programs a significant fraction of the time.

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