Tree-Adjunct Grammatical Evolution

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***Abstract*— In this paper we investigate the application of tree-adjunct grammars to grammatical evolution. The standard type of grammar used by grammatical evolution, context-free grammars, produce a subset of the languages that tree-adjunct grammars can produce, making tree-adjunct grammars, expressively, more powerful. In this study we shed some light on the effects of tree-adjunct grammars on grammatical evolution, or tree-adjunct grammatical evolution. We perform an analytic comparison of the performance of both setups, i.e., grammatical evolution and tree-adjunct grammatical evolution, across a number of classic genetic programming benchmarking problems. The results firmly indicate that tree-adjunct grammatical evolution has a better overall performance (measured in terms of finding the global optima).**

I. Introduction

Grammatical evolution (GE) [21], [2], since its inception, has had much success. A large proportion of this success can be attributed to how easily GE can be extended. Many different grammars have been explored with GE, including shape grammars[22], attribute grammars[1] and logic grammars[14]. In this paper we explore the utility of tree-adjunct grammars (TAGs) in GE.

The goal of this study is to introduce tree-adjunct grammatical evolution (TAGE), which extends standard GE by incorporating TAGs in its operation. We show how the incorporation of TAGs in GE translates into a more effective GE to find solutions on a number of problems with very different landscape features.

As outlined in [13], the set of languages produced by context-free grammars (CFGs), known as context-free languages (CFLs), are strictly included in the set of languages produced by TAGs, known as tree-adjunct languages (TALs), which in turn are strictly included in indexed languages, which are finally strictly included in context-sensitive languages. Consequently, this indicates that TAGs are the next step for GE in terms of choice of grammar type.

The rest of the paper is structured as follows. A brief overview of GE and it's genotype to phenotype mapping process is given in the following section, including an introduction into TAGs. The approach taken in this study to utilise TAGs in GE is outlined in Section III. The paper continues by describing the experimental setup in Section IV. The results and discussion are presented in Section V, before closing with some conclusions and future work in Section VI.

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II. Background

A. Grammatical Evolution

GE is a grammar-based approach to genetic programming (GP) [15], [24]. GE combines principles from genetics and molecular biology, the genotype to phenotype mapping, with the representational power of formal grammars, the ability to change the behaviour of the algorithm by simply changing the structure of the grammar. The grammar, a CFG which is usually written in Backus-Naur form, can be easily modified to output programs of an arbitrary language, something that is not a trivial task in other forms of GP. In addition to this, GE's genotype to phenotype mapping means that search operators can be applied to the genotype (usually an integer or binary chromosome), as well as the ability to apply standard GP search operations to the phenotype as well, therefore extending the search capabilities of standard GP.

1) Genotype to Phenotype Map: GE's genotype to phenotype mapping constructs a derivation tree using a chromosome and a grammar; it operates as follows (see Figure 1 for the grammar and chromosome used for this example): Mapping begins with the start symbol, usually the first symbol declared in the grammar, `<e>`. The first codon (or integer value) is read from the chromosome, in this case it is the value `12`. The number of production rules for the start symbol are counted, `2`, `<e><o><e>` and `<v>`. Which rule to choose is decided according to the mapping function `i mod c`, where `i` is the value of the codon read from the chromosome and `c` is the number of choices available, e.g, `12 mod 2 = 0`, therefore we chose the zero-th rule and `<e>` is expanded to `<e><o><e>`. This expansion forms a partial derivation tree with the start symbol as the root, attaching each of the new symbols as child nodes of this root. The next symbol to expand is the first non-terminal leaf node discovered while traversing the tree in a depth first manner. However, it should be noted that there is on-going study into variations on the method used to choose which node to expand next [18], [19]. In standard GE this will be the left-most `<e>` in the tree. The next codon is read and has a value of `3`, expanding this `<e>` to `<v>` and growing the tree further. The next symbol is the `<v>` previously expanded and the next codon has a value of `7`, `7 mod 2 = 1`, so the rule at index 1, `Y`, is chosen, and so on.

This continues until either there are no more non-terminal leaf nodes left to expand, or until there are no codons left to read, i.e., the end of the chromosome has been reached. If there are no codons left to read and derivation is not complete, with non-terminal leaf nodes still in the derivation tree, derivation can proceed in one of a few different manners. For example, assign a bad fitness to the individual, so it is highly

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```
Grammar:
<e> ::= <e> <o> <e> | <v>
<o> ::= + | -
<v> ::= X | Y

Chromosome: 12,3,7,15,9,10,14
```

Fig. 1. Example context-free grammar and integer chromosome.

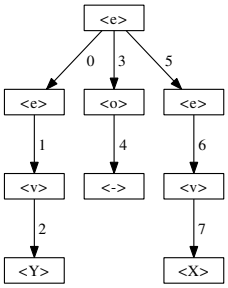


Fig. 2. GE derivation tree - The nodes are labeled with symbols from the grammar and the edges are labeled with the order of expansion.

unlikely that this individual will survive the selection process to the next generation. Another approach can be the use of wrapping. The chromosome maybe reused for a predefined number of times or wrappings. If after the wrapping limit is reached and we still have an invalid individual, we could then assign it a bad fitness.

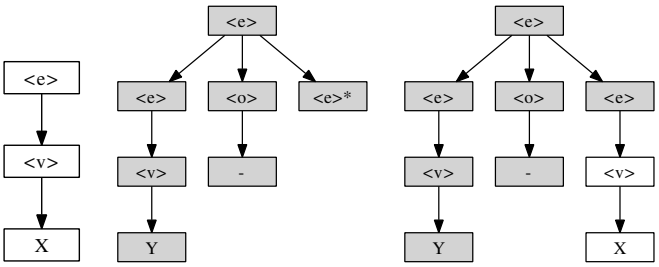
It should be noted that other approaches might be employed, such as choosing only those rules which produce terminals from the grammar when a specific derivation tree depth [4] or number of wrappings has been reached. Ensuring that the individuals are valid, i.e., they have no non-terminal leaf nodes. The complete derivation tree for this example is shown in Figure 2.

B. Tree-Adjunct Grammars

TAGs, which were introduced first in [12], are a tree generating system. Originally making use of only one composition operation, adjunction, TAGs have since been renamed as tree-adjoining grammars and extended to use a second composition operation, substitution. TAGs have been utilised with much success (see [11], [16] and more recently [13]). In particular, in the field of GP in the form of TAG3P [6], [7], [9], [17], [5], [8]. It should be noted that TAGs (only adjunction) and tree-adjoining grammars (substitution also) are, formally, as powerful as each other, that is to say, they produce the same set of languages [6]. The inclusion of substitution allows for a more compact formalism, i.e., less trees [13].

This paper is concerned primarily with the original definition of TAGs as outlined in [12], with adjunction as the only composition operation. With this in mind, married with the clearer definition of tree-adjoining grammars presented in [13], we present the following definition of TAGs.
A TAG is defined by a quintuple (T, N, I, A, S) where:

1) T is a finite set of terminal symbols;
2) N is a finite set of non-terminal symbols: $T \cap N = \emptyset$;
3) S is the start symbol: $S \in N$;



(a) α_0 (b) β_7 (c) Derived Tree

Fig. 3. Composition operation: Adjunction. β_7 is adjoined to α_0 at α_0's root node, or address 0.

4) I is a finite set of finite trees. The trees in I are called *initial trees* (or α trees). An initial tree has the following properties:
   - the root node of the tree is labelled with S;
   - the interior nodes are labeled with non-terminal symbols;
   - the leaf nodes, or the nodes along the frontier are labeled with terminal symbols;
5) A is a finite set of finite trees. The trees in A are called *auxiliary trees* (or β trees). An auxiliary tree has the following properties:
   - the interior nodes are labeled with non-terminal symbols;
   - the leaf nodes, or the nodes along the frontier are all labeled with terminal symbols apart from one node; this node is labeled with the same non-terminal symbol as the root node and is known as the foot node; the convention outlined in [13] is followed and foot nodes are marked with an asterisk (*).

An initial tree is meant to represent a minimal non-recursive structure or derivation tree produced by the grammar, i.e., it contains no recursive non-terminal symbols. Inversely, an auxiliary tree of type X represents a minimal recursive structure, which allows recursion upon the non-terminal X during derivation [16]. The set of initial trees and the set of auxiliary trees together form the set of *elementary trees*, E; where $I \cap A = \emptyset$ and $I \cup A = E$.

During derivation, composition operations are used to join elementary trees together. The adjunction operation takes an initial or derived tree a, creating a new derived tree, d by combining a with an auxiliary tree, b. A subtree, c is selected from a. The type of the subtree (the symbol at its root), X, is used to select an auxiliary tree, b, of the same type. c is removed temporarily from a. b is then attached to a as a subtree in place of c and c is attached to b by replacing c's root with b's foot node (Figure 3 depicts this idea). An example of TAG derivation is provided in Section III.

III. Tree-Adjunct Grammatical Evolution

TAGs are more powerful than CFGs [13] which are currently used in standard GE since the set of languages produced by TAGs, TALs, is a super-set of CFLs, those

produced by CFGs [13]. Unlike CFGs, TAGs can also generate some context-sensitive languages [6], [13]. In addition to this, it has been shown that for every CFG there is a TAG that is both weakly and strongly equivalent to it[10]. A grammar is weakly equivalent to another if it can produce the same language as the other, whereas a grammar is strongly equivalent only if it can represent each of the words in that language using the same structures as the other, i.e., derivation trees.

In order to incorporate the power of TAGs into GE, TAGE was developed. A number of steps were to be taken in order to achieve this. The first was to translate current CFGs used by GE into TAGs which could be used by TAGE. Secondly, an algorithm for derivation had to be developed in order to successfully map from genotype to phenotype using a TAG.

A. CFG to TAG

There is a special type of TAG called a lexicalised TAG (LTAG). A lexicalised grammar has two defining properties:

- it consists of a finite set of structures, each with at least one terminal symbol, known as the anchor;
- it has at least one operation for composing the structures together.

The TAGs referenced in this study are LTAGs since all the leaf nodes of the elementary trees are labeled with terminal symbols (apart from the foot nodes). The phrases TAGs and LTAGs will be inter-changeable throughout the remainder of this paper and will both represent lexicalised tree-adjunct grammars.

In [13], Joshi and Schabes state that for a *"finitely ambiguous CFG*[1] *which does not generate the empty string, there is a lexicalised tree-adjunct grammar generating the same language and tree set as that CFG"*. Joshi and Schabes also provided an algorithm for generating such a TAG. This algorithm is outlined below.

Take a finitely ambiguous CFG, $G = \{N, T, P, S\}$, where: N is the set of non-terminal symbols; T is the set of terminal symbols; P is the set of production rules; and S is the start symbol. Construct a directed graph, g, from G, where the nodes of the graph are labeled with symbols from N and the edges of the graph are labeled with the productions from P which map between them. Then find the set of minimal cycles, c, in the graph such that they contain no other cycles within them. The productions in P must then be divided into two separate sets; R is the set of recursive productions (a production is recursive if it is part of a cycle, c_i); and NR is the set of non-recursive productions in the grammar.

Using S as the root node, create the set of all possible derivation trees using only the productions in NR. This is the set of initial trees, I. Then create A, the set of auxiliary tree, as an empty set. $A = \emptyset$.

For each node n_j, in each of the cycles c_i, if there is a tree in $I \cup A$ that contains a node which has the same label as n_j, create the set of all possible derivation trees, using only the productions in NR and the current cycle, where the n_j is the root node, and the leaf node which has the same label, as the foot node. Add this set of trees to A. See Algorithm 1 for a summary of this algorithm.

[1]A grammar is said to be *finitely ambiguous* if all finite length sentences produced by that grammar cannot be analysed in an infinite number of ways.

Algorithm 1 Generating a TAG from a CFG

Require: $G = \{N, T, P, S\}$
  $g = createDiGraph(G)$;
  $c = findBaseCycles(g)$;
  $R = getRecursiveProductions(P, g)$;
  $NR = P - R$;
  $I = generateInitialTrees(S, NR)$;
  $A = \emptyset$
  for all c_i in c **do**
    for all n_j in c_i **do**
      $E = I \cup A$;
      if a tree in E has a node labeled the same as n_j **then**
        $A = A \cup generateAuxiliaryTrees(n_j, c_i, NR)$
      end if
    end for
  end for

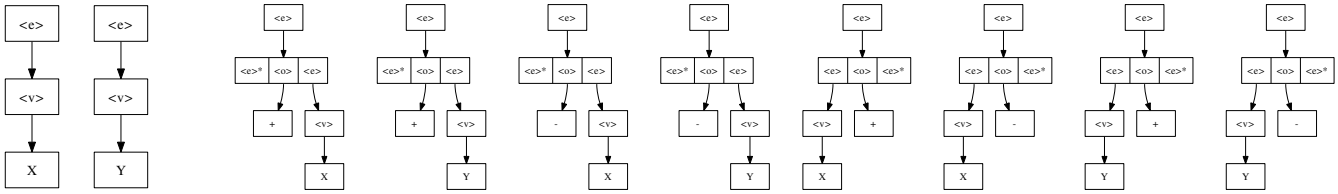
An example of a TAG produced by Algorithm 1 can be seen in Figure 4, and was generated from the CFG shown in Figure 1.

B. Derivation in TAGE

Derivation in TAGE is different from derivation in GE in that it is a two step process, first a derivation tree is formed, and from that the derived tree is produced. The derivation tree is different to that of standard GE, as it is a tree where each node itself is representative of an elementary tree. The edges of this derivation tree are labeled with node addresses. These addresses lead to nodes in the elementary trees which label the tail nodes of the edges. It is on these nodes that composition operations are to be applied using the trees represented by the head nodes of the edges. The derived tree in TAGE is the same as standard GE's derivation tree. It is the tree of symbols resulting from the composition operations listed in the derivation tree. Examples of both types of trees can be seen in Figure 5.

The derivation tree in TAGE, the tree of trees, is important when dealing with TAGs if you intend to do any operations on the tree itself. For example, sub-tree crossover on the derived tree could result in altering an elementary tree, the most basic structure in a TAG. These operations should instead be used on the derivation tree, allowing whole elementary trees to be moved.

1) Example Derivation: An example of derivation in TAGE follows. It is similar to the algorithm used in [7]. Given the TAG G, where
$T = \{x, y, +, -\}$, $N = \{< e >, < o >, < v >\}$, $S =< e >$ and I and A are shown Figure 4, derivation proceeds using the chromosome from Figure 1 and operates as follows. First an initial tree must be chosen to start the derivation. The first codon value is read, `12`, and is used to choose an initial tree based on the number of trees in I using the same mapping



(a) α_0 (b) α_1 (c) β_0 (d) β_1 (e) β_2 (f) β_3 (g) β_4 (h) β_5 (i) β_6 (j) β_7

Fig. 4. I (α) and A (β) sets of the TAG produced from the CFG shown in Figure 1 using Algorithm 1 described previously.

function as GE, `i mod c`. From I, the set of α trees, `12 mod 2 = 0`, the zero-th tree is chosen, α_0, and set as the root node of tree, `t`, the derivation tree, see Figure 5(a).

Next we enter the main stage of the algorithm. A location to perform adjunction must be chosen. The set `N` is created of the adjunctable addresses[2] available within all nodes(trees) contained within `t`. In this case `N` = $\{\alpha_0 0\}$, so a codon is read and an address is selected from `N`, `2 mod 1 = 0` indicates which address to choose, `N[0]`. Adjunction will be performed at $\alpha_0 0$, or index `0` of tree α_0, `<e>`. An auxiliary tree is now chosen from the set of trees in A that are of the type `l`, i.e., the label of their root node is `l`, where `l` is the label of the node adjunction is being performed at. In this case `l = <e>`. Since there are 8 such trees in A, `3 mod 8 = 3`, β_3 is chosen. This is added to `t` as a child of the tree being adjoining to, labeling the edge with the address `0`, see Figure 5(b). The adjunctable addresses in β_3 will be added to `N` on the next pass of the algorithm. This process, the main part of the algorithm, is repeated until all remaining codons have been read. The resulting derivation and derived trees from each stage of this process can be seen in Figure 5.

If the end of the chromosome is reached mid-execution, the operation is aborted and the individual is marked as valid since the derived tree has no non-terminal leaf nodes and the resulting program can always be evaluated.

IV. Experimental Setup

The focus of this study is to compare the performance of standard GE to TAGE, and to analyse the results in order to discover whether TAGs affect the ability of GE to find correct solutions.

The GEVA v1.1 software [20] was used to conduct the experiments for this study. It was extended to allow the use of TAGs. The evolutionary parameters adopted for all the benchmark problems described below are presented in Table I. A short initial chromosome length was selected (15 was a randomly selected value) due to TAGE's use of the entire chromosome during derivation, unlike standard GE where the amount of the chromosome used varies. This provides TAGE with the ability to attempt to find short solutions to the problems if they exist. Each run was evolved for 200 generations, enabling longer solutions to be explored if needed through chromosome growth by means of single-point crossover. Wrapping, as described in Section II-A, was disabled for all experiments.

[2]An adjunctable address in a tree is the breadth first traversal index of a node labeled with a non-terminal symbol, of which there is an auxiliary tree of that type, and that there is currently no auxiliary tree already adjoined to the tree at that index

TABLE I

GE parameters adopted for each of the benchmark problems.

Parameter	Value
Generations	200
Population Size	100
Initialisation	Random
Initial Chromosome Size	15
Max Chromosome Wraps	0
Replacement Strategy	Generational
Elitism	10 Individuals
Selection Operation	Tournament
Tournament Size	3
One Point Crossover Probability	0.9
Integer Mutation Probability	0.02

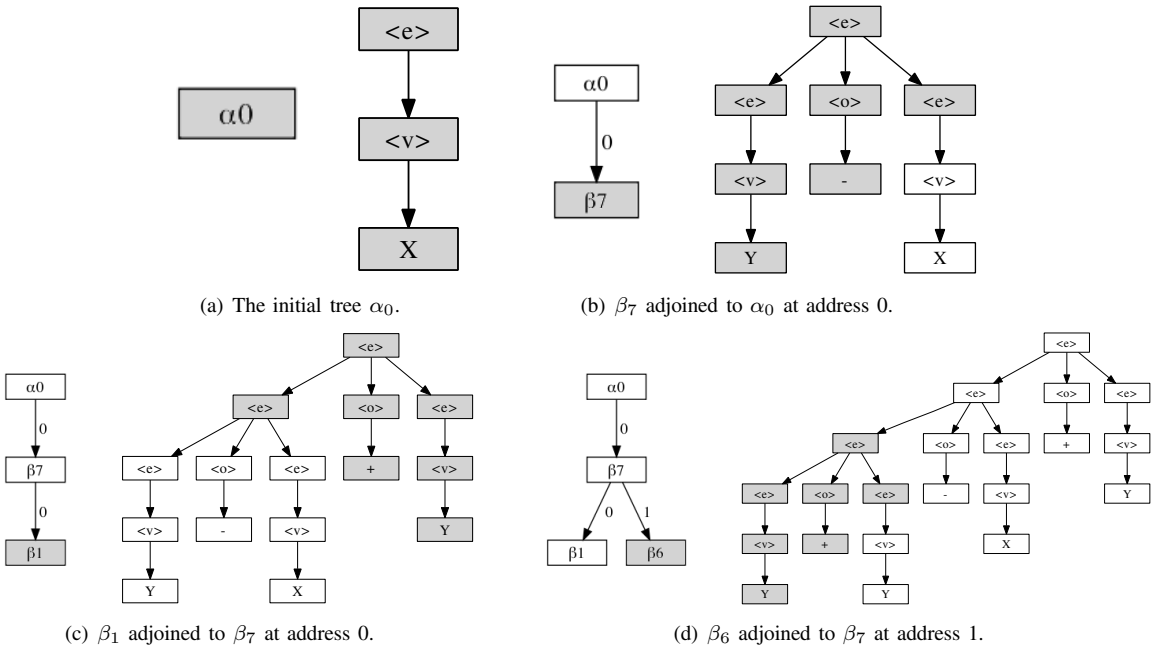
A. Benchmark Problems

Standard GE was compared to TAGE using five classic benchmark problems taken from specialised GP literature. 100 independent runs were performed for each of the problems listed below using each setup. The CFGs used in standard GE and in TAGE to generate TAGs for each problem are shown in Figure 6.

Even-5-parity: This problem attempts to evolve the five input even-parity boolean function, in which the best fitness is obtained when the correct output is returned for each of the 2^5 test cases.

Santa Fe ant trail: In this problem a control program is evolved to control the movements of an artificial ant on a 32x32 toroidal grid. The ant has use of several operations to collect 89 pieces of food located along a broken trail: foodAhead(), enabling the ant to check if there is food in the tile directly facing it, as well as right(), left() and move(). The latter three operations consume one unit of energy.

Symbolic Regression: The objective is to evolve the classic quartic function, $x + x^2 + x^3 + x^4$. Fitness is measured by the sum of the error across 20 test cases drawn from the range $[-1, 1]$. A successful solution is where the error is less than a certain threshold, or hits criterion, as described in [15]. In our study, we set this threshold at 0.01.



(a) The initial tree α_0.

(b) β_7 adjoined to α_0 at address 0.

(c) β_1 adjoined to β_7 at address 0.

(d) β_6 adjoined to β_7 at address 1.

Fig. 5. The derivation tree and corresponding derived tree at each stage of derivation in TAGE. The shaded areas indicate the new content added to the tree at each step.

Six Multiplexer: This classic GP boolean function problem in which evolution attempts to find correct two input and four output line boolean function. A perfect solution generates the correct output for a given input for all 64 test cases. Fitness is measured by how many test cases generate correct outputs.

Max: This problem, as described in [3], aims to evolve a tree whose growth is constrained by a depth limit, that when the tree's phenotype is executed, returns the largest value possible. A function set of addition and multiplication operators are used as well as a terminal set of $\{0.5\}$. A max tree depth of 8 was used for the purposes of these experiments.

V. Results and Discussion

A. Performance

Compared to standard GE, TAGE performs better at finding the global optimum. Table II shows that for four out of the five problems tested TAGE finds more solutions than GE which achieve perfect fitness values across the 100 runs. This is reinforced by the fact that the mean best fitness at the final generation in each case is lower for TAGE than GE[3]. This is reflected in Figure 7, plotting the mean best fitness values at each generation. TAGE repeatedly shows an ability to find fitter solutions in fewer generations than GE, effectively searching the solution space more efficiently.

TAGE fails to improve upon the results found by GE for the Max problem. The plots in Figure 9 show a repeated trend across the Even-5 parity, Santa Fe Ant Trail and Symbolic Regression problems, the Six Multiplexer problem

[3]It is important to point out that GEVA minimises, so the lower the fitness, the better.

TABLE II

A comparison of results obtained by GE and TAGE across the five benchmark problems - The best and average fitness values averaged across 100 runs for the final generation. The numbers in bold indicate the best performance in terms of finding the global optimum.

	Best Fitness Mean (SD)	Average Fitness Mean (SD)	Successes (/100)
Even-5			
GE	2.08 (4.57)	6.15 (3.58)	79
TAGE	**0.64 (1.90)**	**13.12 (0.67)**	**88**
Santa Fe			
GE	32.42 (10.59)	42.13 (9.76)	3
TAGE	**16.53 (10.99)**	**69.32 (3.96)**	**12**
Sym.Reg.			
GE	0.253 (0.394)	8.700 (13.689)	44
TAGE	**0.054 (0.171)**	**29.053 (9.145)**	**76**
6 Multi.			
GE	9.14 (4.19)	11.65 (3.69)	6
TAGE	**1.77 (2.66)**	**16.87 (1.83)**	**63**
Max			
GE	2.31 (4.22)	199.88 (125.46)	0
TAGE	2.04 (1.52)	579.79 (335.25)	0

was omitted due to space restictions. The derived trees produced by TAGE are consistently deeper and larger in size than the derivation trees produced by GE. It is believed that larger trees are more likely to find a better solution [23]. The equivalent plots for the Max problem, shown in Figure 8, display the opposite of this trend, with deeper and larger trees being produced by GE than those produced by TAGE. With respect to this, it is not surprising that a similar increase in performance was not seen for the Max problem as was for the other four problems.

In addition, TAGE increases the connectivity of the search

```
Even-5 parity grammar:
<prog>   ::= <expr>
<expr>   ::= <expr> <op> <expr>
          | ( <expr> <op> <expr> )
          | <var>
          | <pre-op> ( <var> )
<pre-op> ::= not
<op>     ::= "|" | & | ^
<var>    ::= d0 | d1 | d2 | d3 | d4
```

```
Santa Fe ant trail grammar:
<prog>      ::= <code>
<code>      ::= <line> | <code> <line>
<line>      ::= <condition> | <op>
<condition> ::= if(food\_ahead()==1)
                { <opcode> }
                else
                { <opcode> }
<op>        ::= left(); | right(); | move();
<opcode>    ::= <op> | <opcode> <op>
```

```
Max grammar:
<prog> ::= <expr>
<expr> ::= <op> <expr> <expr>
         | <var>
<op>   ::= + | *
<var>  ::= 0.5
```

```
Symbolic Regression grammar:
<expr> ::= ( <op> <expr> <expr> )
         | <var>
<op>   ::= + | - | *
<var>  ::= x0 | 1.0
```

```
Six Multiplexer grammar:
<B> ::= (<B>) &&(<B>)
      | (<B>) "||"(<B>)
      | !(<B>)
      | (<B>) ? (<B>) : (<B>)
      | a0 | a1 | d0| d1 | d2 | d3
```

Fig. 6. Grammars in Backus-Naur form used for all the benchmark problems.

space. Operations applied to the genotype in TAGE, such as crossover and mutation, affect larger changes in the resulting phenotype than in GE, since the building blocks employed by TAGE, elementary trees, are larger than those employed by GE, individual symbols. As a result of this, TAGE allows access to new kinds of tree transformations that are not readily available with standard GE. This is evident when examining the mean average fitness values in Table II. The values for TAGE are much larger than those of GE, and in contrast to GE, they are much further away from their respective mean best fitness values. This indicates that while GE begins to converge when a local optimum is found, TAGE promotes diversity, and as such, deters convergence.

B. Chromosome Length

A common problem with GE is that while the number of codons used for derivation can remain quite small, the length of the chromosome, i.e., the total number of codons in the chromosome, can grow uncontrollably. This can sometimes cause applications to run out of memory. An unforeseen result of TAGE is that the chromosome length does not grow as it does in standard GE. This can be seen in the chromosome length plots in Figure 8 and Figure 9. One argument for why this occurs is that derivation in GE might only use a certain percentage of the chromosome, whereas derivation in TAGE uses the entire chromosome. As a result of this, every operation on the chromosome that affects its length has an effect on the fitness of that individual in TAGE, but in standard GE this might not always be the case. If the fitness of an individual is adversely affected by the operation in TAGE, then evolution might discard this new individual, preserving the original chromosome length. In standard GE if the fitness is not affected, i.e., the operation only affects an unused section of the chromosome, then this individual will survive on to the next generation where the probability that a chromosome lengthening operation that will not affect fitness is increased.

C. Limitations

As a result of making use of adjunction as the only composition operation, it was discovered that TAGE could not operate on complex grammars. During the translation process from CFG to TAG, the number of elementary trees grows exponentially with the complexity of the CFG, due to all possible derivations being explored, see Algorithm 1. With the introduction of substitution as a composition operation, this limitation could be overcome, since it allows for a much more compact grammar.

VI. Conclusions

This study presents a new form of GE called TAGE, which adopts TAGs in place of CFGs. It demonstrates that the use of TAGs in GE has a beneficial effect on GE's ability to move through the solution search space and to find successful solutions.

In [7], [17] TAGs were found to have a positive effect on the performance of GP, results which are shown by this study to carry over into the field of GE, with interesting results and properties of its own, such as minimal growth of the chromosome, and the increase of connectivity of the search space which helps TAGE maintain diversity.

Plans for future work include continuing this study by extending TAGE to work with tree-adjoining grammars and the substitution composition operation, allowing more complex grammars and problems to be explored, and to investigate further the implications of using TAGs in GE and for what reasons they perform better than CFGs in GE.

Acknowledgments

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References

[1] R. Cleary. Extending Grammatical Evolution with Attribute Grammars: An Application to Knapsack Problems, M.Sc. Thesis, University Of Limerick, 2005.

[2] I. Dempsey, M. O'Neill, and A. Brabazon. *Foundations in Grammatical Evolution for Dynamic Environments, 1st edition*. Springer, 2009.

[3] C. Gathercole and P. Ross. An adverse interaction between crossover and restricted tree depth in genetic programming. In *GECCO '96: Proceedings of the First Annual Conference on Genetic Programming*, pages 291–296, Cambridge, MA, USA, 1996. MIT Press.

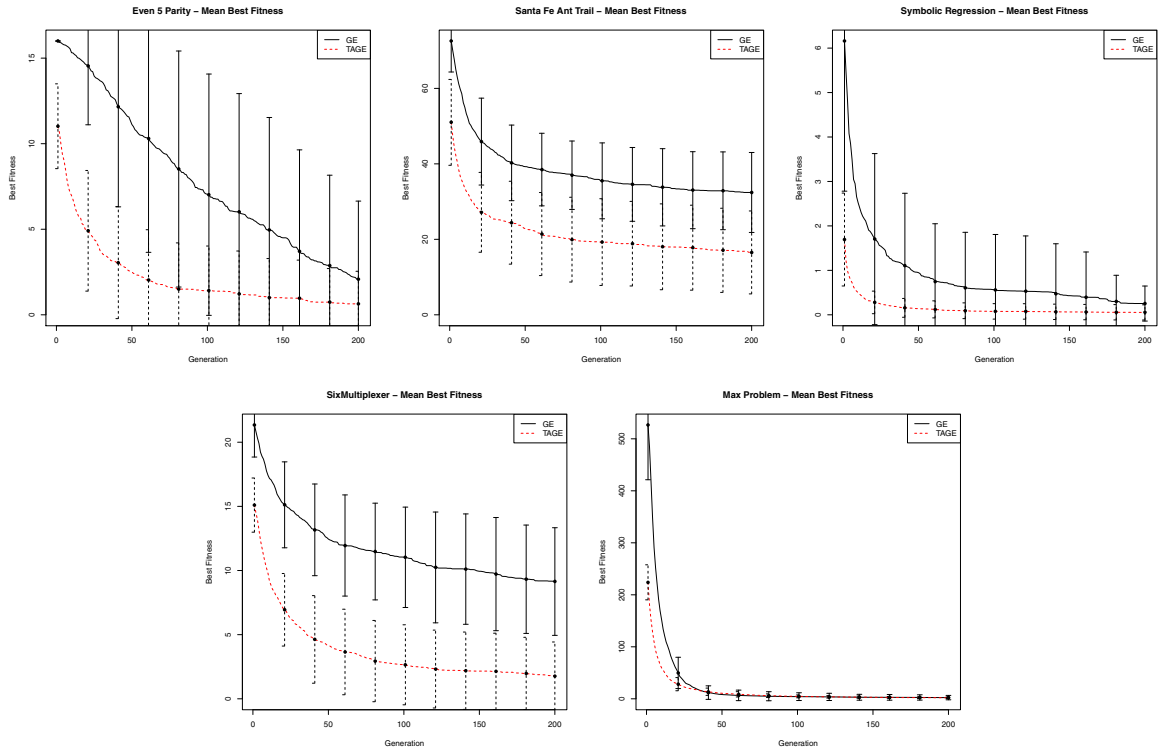

Fig. 7. Mean best fitness plots (minimising) across 100 runs at each generation with error bars of one standard deviation - From left-right, top-bottom: Even-5 parity, Santa Fe Ant Trail, Symbolic Regression, Six Multiplexer and Max.

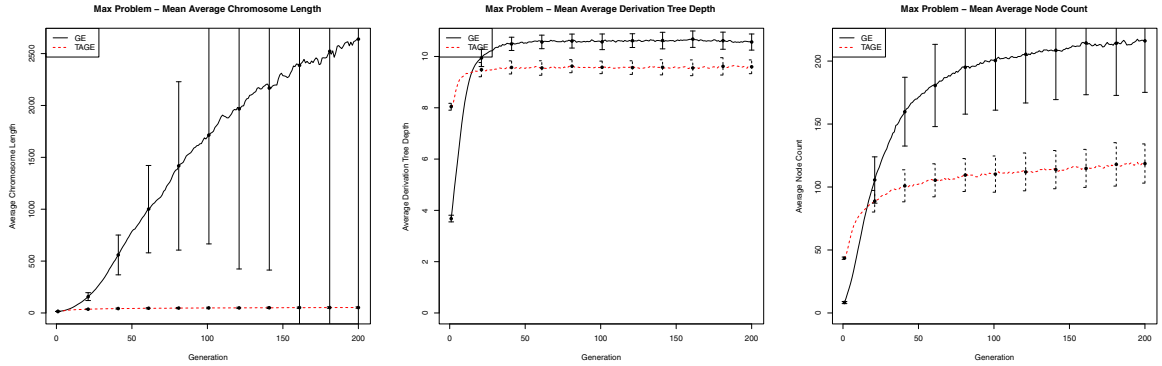

Fig. 8. Chromosome length, derivation tree depth and derivation tree size plots for the Max problem.

[4] M. Hemberg and U. OReilly. Extending Grammatical Evolution to Evolve Digital Surfaces with Genr8. In *Genetic Programming*, pages 299–308. Springer Berlin / Heidelberg, 2004.

[5] N. Hoai. A Flexible Representation for Genetic Programming: Lessons from Natural Language Processing, PhD Thesis, University of New South Wales, 2004.

[6] N. Hoai and R. McKay. A framework for tree adjunct grammar guided genetic programming. pages 93–99. ADFA, 2001.

[7] N. Hoai, R. McKay, and D. Essam. Some experimental results with tree adjunct grammar guided genetic programming. *Lecture notes in computer science*, pages 228–237, 2002.

[8] N. Hoai, R. McKay, and D. Essam. Representation and structural difficulty in genetic programming. *IEEE Transactions on Evolutionary Computation*, 10(2):157–166, April 2006.

[9] N. Hoai, R. McKay, D. Essam, and R. Chau. Solving the symbolic regression problem with tree-adjunct grammar guided genetic programming: the comparative results. *Proceedings of the 2002 Congress on Evolutionary Computation. CEC'02 (Cat. No.02TH8600)*, pages 1326–1331, 2002.

[10] A. Joshi. *Tree adjoining grammars: How much context-sensitivity is required to provide reasonable structural descriptions*, chapter 6, pages 205–250. Cambridge University Press, New York, 1985.

[11] A. Joshi. An Introduction to Tree Adjoining Grammars. In *Mathematics of Language*, pages 87–114, Amsterdam, 1987. John Benjamins.

[12] A. Joshi, L. Levy, and M. Takahashi. Tree adjunct grammars. *Journal of Computer and System Sciences*, 10(1):136–163, 1975.

[13] A. Joshi and Y. Schabes. Tree-Adjoining Grammars. *Handbook of Formal Languages, Beyond Words*, 3:69–123, 1997.

[14] M. Keijzer, C. Ryan, M. O'Neill, M. Cattolico, and V. Babovic. Adaptive Logic Programming. In *Genetic and Evolutionary Computation Conference*, 2001.

[15] J. Koza. *Genetic Programming*. MIT Press, 1992.

[16] A. Kroch and A. Joshi. The Linguistic Relevance of Tree Adjoining Grammar, Technical Report, University Of Pennsylvania, 1985.

[17] R. McKay, N. Hoai, and H. Abbass. Tree adjoining grammars,

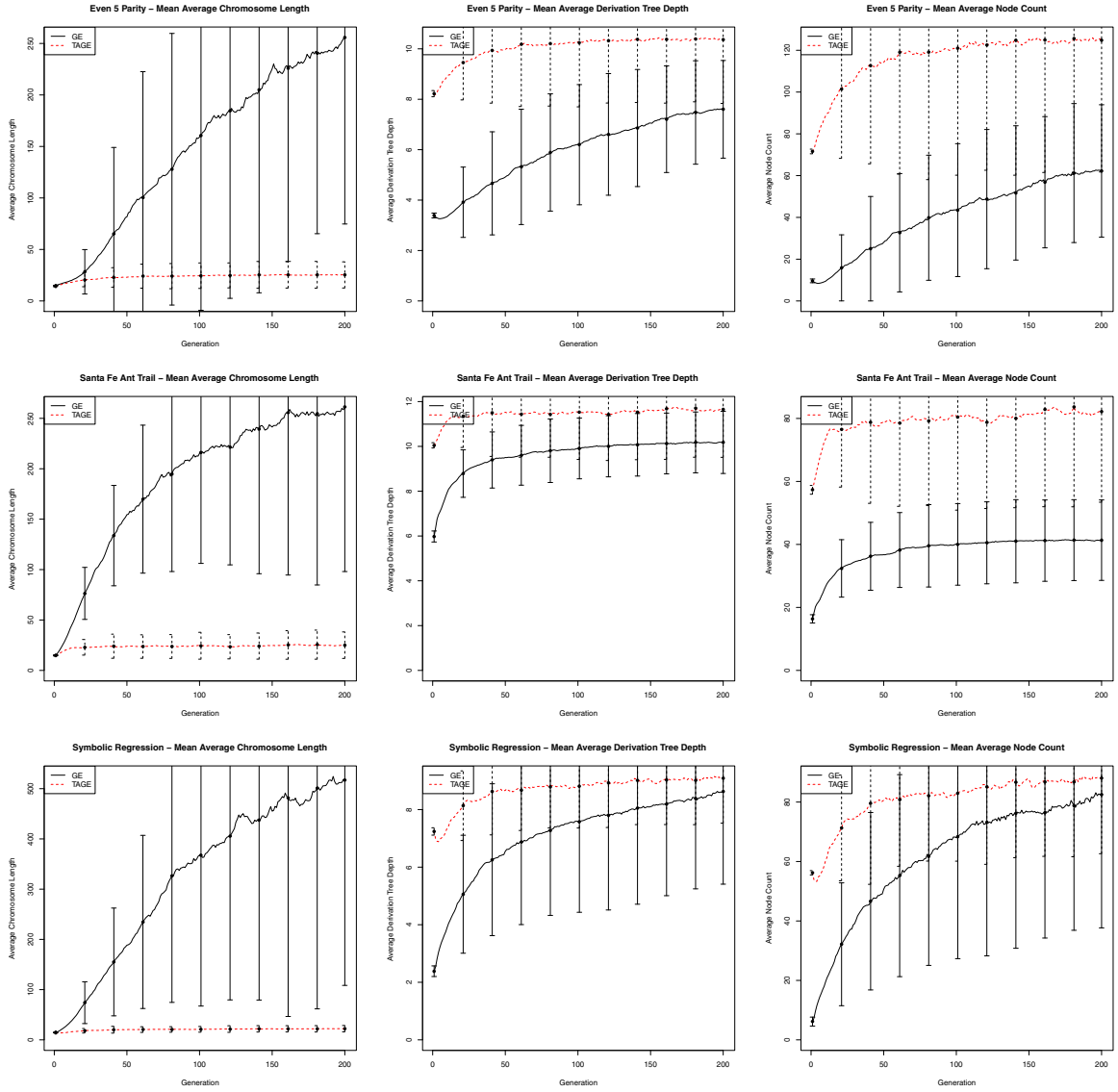

Fig. 9. From left-right: chromosome length, derivation tree depth and derivation tree size plots for the Even Five Parity, Santa Fe Ant Trail and Symbolic Regression problems (top-bottom). Plots for the Six Multiplexer problem were omitted due to space restrictions, but displayed similar trends to those above.

language bias, and genetic programming. In *Genetic Programming*, pages 335–344. Springer, 2003.

[18] M. O'Neill, A. Brabazon, M. Nicolau, S. Garraghy, and P. Keenan. πGrammatical Evolution. In *Genetic and Evolutionary Computation GECCO 2004*, pages 617–629. Springer Berlin / Heidelberg, 2004.

[19] M. O'Neill, D. Fagan, E. Galvan, A. Brabazon, and S. McGarraghy. An analysis of Genotype-Phenotype Maps in Grammatical Evolution. In *EuroGP 2010*, 2010.

[20] M. O'Neill, E. Hemberg, C. Gilligan, E. Bartley, J. McDermott, and A. Brabazon. GEVA: Grammatical Evolution in Java. *ACM SIGEVOlution*, 3(2):17–23, 2008.

[21] M. O'Neill and C. Ryan. *Grammatical Evolution: Evolutionary Automatic Programming in an Arbitrary Language*. 2003.

[22] M. O'Neill, J. Swafford, J. McDermott, J. Byrne, A. Brabazon, E. Shotton, C. McNally, and M. Hemberg. Shape grammars and grammatical evolution for evolutionary design. In *Genetic And Evolutionary Computation Conference*, 2009.

[23] R. Poli, W. Langdon, and S. Dignum. On the limiting distribution of program sizes in tree-based genetic programming. In M. Ebner, M. O'Neill, A. Ekárt, L. Vanneschi, and A. Esparcia-Alcázar, editors, *Proceedings of the 10th European Conference on Genetic Programming*, pages 193 – 204, Valencia, Spain, 2007. Springer.

[24] R. Poli, W. Langdon, and N. McPhee. *A Field Guide To Genetic Programming*. lulu, 2008.