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<th><strong>Title</strong></th>
<th>Tree-adjunct grammatical evolution</th>
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Tree-Adjunct Grammatical Evolution

Eoin Murphy, Michael O’Neill, Edgar Galván-López and Anthony Brabazon

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.

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).

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
are, formally, as powerful as each other, that is to say, they adjunction) and tree-adjoining grammars (substitution also).

In particular, in the field of GP in the form of TAG3P [6], [7], [12], [6], [8]. It should be noted that TAGs (only composition operation, substitution) have been utilised as tree-adjoining grammars and extended to use a second adjunction operation. TAGs have since been renamed by replacing the convention outlined in [12] with adjunction as 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 [12] which are currently used in standard GE since the set of languages produced by TAGs, TALs, is a super-set of CFLs, those

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], [12] 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: \(S \in N\);
4) \(I\) is a finite set of finite trees. The trees in \(I\) are called initial trees (or \(\alpha\) trees). An initial tree has the following properties:
   - the root node of the tree is labelled with \(S\);
   - the interior nodes are labelled with non-terminal symbols;
   - the leaf nodes, or the nodes along the frontier are labelled with terminal symbols;
5) \(A\) is a finite set of finite trees. The trees in \(A\) are called auxiliary trees (or \(\beta\) trees). An auxiliary tree has the following properties:
   - the interior nodes are labelled with non-terminal symbols;
   - the leaf nodes, or the nodes along the frontier are all labelled with terminal symbols apart from one node; this node is labelled 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.
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 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.

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

---

**Algorithm 1 Generating a TAG from a CFG**

**Require:** $G = \{N, T, P, S\}$

```plaintext
g = createDiGraph(G);
c = findBaseCycles(g);
R = getRecursiveProductions(P, g);
NR = P − R;
I = generateInitialTrees(S, NR);
A = ∅
for all $c_i$ in $c$
do 
   for all $n_j$ in $c_i$
do 
      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
```

---

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.
function as GE, i.e., mod 3. From I, the set of $\alpha$ trees, 12 mod 2 = 0, the zero-th tree is chosen, $\alpha_0$, 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 available within all nodes(trees) contained within $t$. In this case $N = \{ \alpha_0 \}$. A codon is read and an address is selected from $N$. This indicates which address to choose, $N[0]$. Adjunction will be performed at $\alpha_0$, or index 0 of tree $\alpha_0$. An auxiliary tree is now chosen from the set of trees in $A$ that are of the type 1, i.e., the label of their root node is 1, where 1 is the label of the node adjunction is being performed at. In this case $1 = 2$. Since there are 8 such trees in $A$, 3 mod 8 = 3, $\beta_3$ 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 $\beta_3$ 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 GEV 1.1 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.

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.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
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<tr>
<td>Generations</td>
<td>200</td>
</tr>
<tr>
<td>Population Size</td>
<td>100</td>
</tr>
<tr>
<td>Initialisation</td>
<td>Random</td>
</tr>
<tr>
<td>Initial Chromosome Size</td>
<td>15</td>
</tr>
<tr>
<td>Max Chromosome Wraps</td>
<td>0</td>
</tr>
<tr>
<td>Replacement Strategy</td>
<td>Generational</td>
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<tr>
<td>Elitism</td>
<td>10 Individuals</td>
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<tr>
<td>Selection Operation</td>
<td>Tournament</td>
</tr>
<tr>
<td>Tournament Size</td>
<td>3</td>
</tr>
<tr>
<td>One Point Crossover Probability</td>
<td>0.9</td>
</tr>
<tr>
<td>Integer Mutation Probability</td>
<td>0.02</td>
</tr>
</tbody>
</table>
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 was omitted due to space restrictions. 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.

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

### Table II

<table>
<thead>
<tr>
<th>Problem</th>
<th>Best Fitness Mean (SD)</th>
<th>Average Fitness Mean (SD)</th>
<th>Successes (/100)</th>
</tr>
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<tbody>
<tr>
<td>Even-5</td>
<td>GE</td>
<td>2.08 (4.57)</td>
<td>6.15 (3.58)</td>
</tr>
<tr>
<td></td>
<td>TAGE</td>
<td>0.64 (1.90)</td>
<td>13.12 (0.67)</td>
</tr>
<tr>
<td>Santa Fe</td>
<td>GE</td>
<td>32.42 (10.59)</td>
<td>42.13 (9.76)</td>
</tr>
<tr>
<td></td>
<td>TAGE</td>
<td>16.53 (10.99)</td>
<td>69.32 (3.96)</td>
</tr>
<tr>
<td>Sym.Reg.</td>
<td>GE</td>
<td>0.253 (0.394)</td>
<td>8.700 (13.689)</td>
</tr>
<tr>
<td></td>
<td>TAGE</td>
<td>0.054 (0.171)</td>
<td>29.053 (9.145)</td>
</tr>
<tr>
<td>6 Multi.</td>
<td>GE</td>
<td>9.14 (4.19)</td>
<td>11.65 (3.69)</td>
</tr>
<tr>
<td></td>
<td>TAGE</td>
<td>1.77 (2.66)</td>
<td>16.87 (1.83)</td>
</tr>
<tr>
<td>Max</td>
<td>GE</td>
<td>2.31 (4.22)</td>
<td>199.88 (125.46)</td>
</tr>
<tr>
<td></td>
<td>TAGE</td>
<td>2.04 (1.52)</td>
<td>579.79 (335.25)</td>
</tr>
</tbody>
</table>
### Even-5 parity grammar:

```plaintext
<prog> ::= <expr> <prog> ::= <code> <code> ::= <line> | <code> <line> ::= <condition> | <op> | <var> <condition> ::= if(food\_ahead()==1) <op> ::= + | * <var> ::= d0 | d1 | d2 | d3 | d4 <code> ::= <op> | <opcode> <op> ::= left(); | right(); | move(); <opcode> ::= <op> | <opcode> <op>
```

### Santa Fe ant trail grammar:

```plaintext
<prog> ::= <expr> <prog> ::= <code> <code> ::= <line> | <code> <line> ::= ( <expr> <op> <expr> ) | <var> <condition> ::= if(food\_ahead()==1) <op> ::= + | * <var> ::= d0 | d1 | d2 | d3 | d4
```

### Max grammar:

```plaintext
<prog> ::= <expr> <prog> ::= <code> <code> ::= <line> | <code> <line> ::= ( <expr> <op> <expr> ) | <var> <condition> ::= if(food\_ahead()==1) <op> ::= + | * <var> ::= d0 | d1 | d2 | d3 | d4
```

### Symbolic Regression grammar:

```plaintext
<expr> ::= ( <op> <expr> <expr> ) <var> ::= x0 | 1.0 | (<B>) ? (<B>) : (<B>) <op> ::= + | - | * | !(<B>) <B> ::= (<B>) & (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>) | (<B>...
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.

[17] R. McKay, N. Hoai, and H. Abbass. Tree adjoining grammars,
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<th>Figures</th>
<th>Description</th>
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**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.

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