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Abstract. In this paper we present a new Estimation-of-Distribution Algorithm (EDA) for Genetic Programming (GP). We propose a probability distribution for the space of trees, based on a grammar. To introduce dependencies into the distribution, grammar transformations are performed that facilitate the description of specific subfunctions. We present some results from experiments on two benchmark problems and show some of the subfunctions that were introduced during optimization as a result of the transformations that were applied.

1 Introduction

GP [4, 6] offers algorithms to search highly expressive classes of functions, and has been applied to a diverse range of problems including circuit design, symbolic regression, and control. Most GP methods employ the subtree-crossover operator, which exchanges randomly selected subtrees between individuals. Due to the particular structure of trees, subtrees (rather than e.g. any combination of nodes and arcs) appear a reasonable choice as the form of the partial solutions that will be exchanged since the functionality of a subtree is independent of its place within the tree. However, basic GP does not make informed choices as to *which* partial solutions will be exchanged; both the size of the removed subtree and the position where it will be inserted are chosen randomly.

Several subtree encapsulation methods exist that make more specific choices as to which partial solutions are selected to be further propagated, e.g. GLiB [1], ADFs [7], and ARL [13]. Subtree encapsulation methods have been found to substantially improve performance on a variety of problems. Yet, the criteria for the selection of partial solutions they employ are still heuristic; typically, either the fitness of the tree in which a subtree occurs is used as an indication of its value, or the partial solution is itself subject to evolution.

Here, we explore whether a more principled approach to the selection of partial solutions and their recombination is possible. If the distribution of high-fitness trees can be estimated, this would directly specify which combinations of elements are to be maintained in the creation of new individuals and thus which combinations of partial solutions may be fruitfully explored. We investigate how the principle of distribution estimation may be employed in the context of tree-based problems. In GAs, the development of EDAs and other linkage learning techniques has yielded a better insight into the design of competent GAs by rendering the assumptions implicitly made by algorithms explicit. Our aim is that

the application of distribution estimation techniques to tree-based problems may likewise clarify the design of principled methods for GP. This paper represents a first step in that direction.

To estimate distributions over the space of trees, a representation must be chosen. In Probabilistic Incremental Program Evolution (PIPE) [14], trees are matched on a fixed-size template, such that the nodes become uniquely identifiable variables. The size of the template may increase over time however as trees grow larger. Using this representation, all nodes are treated equally. While this permits the encapsulation of any combination of nodes, it does not exploit the particular non-fixed-size and variable-child-arity structure of trees. The complexity of such an algorithm is determined by the maximally allowed shape for the trees, which must be chosen in advance. In PIPE the distribution is the same for each node, which corresponds to a univariately factorized probability distribution over all nodes. In Extended Compact Genetic Programming (ECGP) [15], trees are represented in the same way as in PIPE. However, the probability distribution that is estimated is a marginal-product factorization that allows the modelling of dependencies between multiple nodes that are located anywhere in the fixed-size template. Moreover, the size of the template is fixed beforehand in ECGP and does not increase over time. In this paper, a method will be employed that estimates the distribution of trees based on the subtrees that actually occur. The representation specifies a set of rules whose expansion leads to trees. The rules capture local information, thereby offering a potential to exploit the specific structure of trees, while at the same time their use in an EDA offers a potential for generalization that is not provided by using fixed-size templates. Shan *et al.* [16] use a similar approach (based on stochastic grammars). The main difference is that their approach starts from an explicit description of a specific set of trees and then generalizes the description to represent common subtrees. In our approach we do the reverse. Our approach starts from a description of all possible trees and then tunes it to more specifically describe the set of trees.

The remainder of this paper is organized as follows. In Section 2 we introduce basic notation and terminology. In Section 3 we describe how we allow the grammar to be transformed to introduce more specific subfunctions. Next, in Section 4 we define the probability distribution over trees that we work with. In Section 5 we perform experiments on two benchmark problems and compare the performance of standard GP and an EDA based on the proposed distribution. We also show some of the subfunctions that were introduced during optimization as a result of the grammar transformations that were applied. We present our conclusions and a discussion of future research in Section 6.

2 Terminology

A grammar \mathbf{G} is a vector of l_r production rules $R_j, j \in \{0, 1, \dots, l_r - 1\}$, that is, $\mathbf{G} = (R_0, R_1, \dots, R_{l_r-1})$.

A production rule is denoted by $R_j : \mathcal{S}_k \rightarrow E_j$, where \mathcal{S}_k is a symbol that can be replaced with the expansion E_j of the production rule. Let K be the number of available symbols, then $k \in \{0, 1, \dots, K - 1\}$. We will use only one symbol and allow ourselves to write \mathcal{S} instead of \mathcal{S}_k .

An expansion E_j of production rule R_j is a tree. We will therefore generally call E_j an expansion tree. The internal nodes of an expansion tree are functions with at least one argument. The leaves are either symbols, constants or input variables. An example of an expansion tree is $E_j = +(\sin(\mathcal{S}), (-\log(\mathcal{S}), \cos(\mathcal{S})))$ which, in common mathematical notation, represents $\sin(\mathcal{S}) + (\log(\mathcal{S}) - \cos(\mathcal{S}))$.

A sentence is obtained from a grammar if a production rule is chosen to replace a symbol repeatedly until all symbols have disappeared. Sentences can therefore be seen as trees. We denote a sentence by s . We will denote a subtree of a sentence by t and call it a sentence subtree.

A sentence subtree t is said to be matched by an expansion tree E_j , denoted $t \in E_j$ if and only if all nodes of E_j coincide with nodes found in t following the same trails, with the exception of symbol nodes, which may be matched to any non-empty sentence subtree.

The following grammar $\mathbf{G} = (R_0, R_1, \dots, R_{5+n})$ with $l_r = 6+n$ is an example of a grammar that describes certain n -dimensional real-valued functions:

$$\begin{array}{ll}
 R_0 : \mathcal{S} \rightarrow c \text{ (a constant } \in \mathbb{R}) & R_{n+1} : \mathcal{S} \rightarrow +(\mathcal{S}, \mathcal{S}) \\
 R_1 : \mathcal{S} \rightarrow i_0 \text{ (input variable 0)} & R_{n+2} : \mathcal{S} \rightarrow \cdot(\mathcal{S}, \mathcal{S}) \\
 R_2 : \mathcal{S} \rightarrow i_1 \text{ (input variable 1)} & R_{n+3} : \mathcal{S} \rightarrow -(\mathcal{S}) \\
 \vdots & \vdots \\
 R_n : \mathcal{S} \rightarrow i_{n-1} \text{ (input variable n-1)} & R_{n+4} : \mathcal{S} \rightarrow \sin(\mathcal{S}) \\
 & R_{n+5} : \mathcal{S} \rightarrow \cos(\mathcal{S})
 \end{array}$$

3 Grammar transformations

The grammar that is initially supplied describes the space of all possible sentences in which to search for the optimal sentence. As the search progresses, the subspace of sentences that we are still interested in becomes smaller as the sentences become more specific and have more parts in common. To be able to reproduce these commonalities as much as possible and remain within the subspace that we are interested in when drawing new solutions, the probability distribution must be able to represent these commonalities with a large-enough density. One of the most important features of the probability distribution based on a grammar that we will propose in Section 4 is that a probability will be associated with each production rule to represent the probability of that specific subfunction to appear in a sentence. These probabilities can be changed to make certain combinations of subfunctions more probable. For instance, subfunction $f(\mathcal{S}, \mathcal{S})$ can be estimated to occur more frequently than subfunction $g(\mathcal{S}, \mathcal{S})$ by increasing the probability associated with production rule $\mathcal{S} \rightarrow f(\mathcal{S}, \mathcal{S})$. However, these individual probabilities do not allow us to say anything about the combination of functions f and g , i.e. for instance the frequency of $f(g(\mathcal{S}, \mathcal{S}), \mathcal{S})$ versus $g(f(\mathcal{S}, \mathcal{S}), \mathcal{S})$. To allow for such dependencies regarding subfunctions to be described in the probability distribution, we propose the use of grammar transformations. In the remainder of this section we describe a specific transformation that we have used. Examples of results of using these transformations in an actual EDA are given in Section 5.3.

3.1 Substitution transformation

In this paper, the only transformation that we allow is the substitution of one symbol of an expansion tree with one expansion tree from the base grammar. The base grammar is the grammar that is initially provided. This substitution transformation will allow the probability distribution to model some sentences more specifically than others. To ensure that after a transformation any sentence subtree can be matched by only one expansion tree we assume that the base grammar has this property. To transform the grammar we only allow to substitute symbols with expansion trees of the base grammar. Here is an example of expanding the base grammar (first column) using a single expansion (second column):

<u>Base grammar</u>	<u>Single expansion</u>	<u>Full expansion</u>
$R_0 : \mathcal{S} \rightarrow c$	$R_0 : \mathcal{S} \rightarrow c$	$R_0 : \mathcal{S} \rightarrow c$
$R_1 : \mathcal{S} \rightarrow i$	$R_1 : \mathcal{S} \rightarrow i$	$R_1 : \mathcal{S} \rightarrow i$
$R_2 : \mathcal{S} \rightarrow f(\mathcal{S}, \mathcal{S})$	$R_2 : \mathcal{S} \rightarrow f(\mathcal{S}, \mathcal{S})$	$R_2 : \mathcal{S} \rightarrow f(\mathcal{S}, \mathcal{S})$
$R_3 : \mathcal{S} \rightarrow g(\mathcal{S}, \mathcal{S})$	$R_3 : \mathcal{S} \rightarrow g(\mathcal{S}, \mathcal{S})$	$R_3 : \mathcal{S} \rightarrow g(c, \mathcal{S})$
	$R_4 : \mathcal{S} \rightarrow g(f(\mathcal{S}, \mathcal{S}), \mathcal{S})$	$R_4 : \mathcal{S} \rightarrow g(i, \mathcal{S})$
		$R_5 : \mathcal{S} \rightarrow g(f(\mathcal{S}, \mathcal{S}), \mathcal{S})$
		$R_6 : \mathcal{S} \rightarrow g(g(\mathcal{S}, \mathcal{S}), \mathcal{S})$

Note that the set of expansion trees can now no longer be matched uniquely to all sentence trees. For instance, sentence $g(f(c, c), c)$ can at the top level now be matched by expansion trees 3 and 4. To ensure only a single match, we could expand every expansion tree from the base grammar into a production rule and subsequently remove the original production rule that has now been expanded (third column in the example above). However, this rapidly increases the number of production rules in the grammar and may introduce additional rules that aren't specifically interesting for modelling the data at hand. To be able to only introduce the rules that are interesting, we equip the symbols with a list of indices that indicate which of the production rules in the base grammar may be matched to that symbol. Once a substitution occurs, the symbol that was instantiated may no longer match with the expansion tree that was inserted into it. For example:

<u>Base grammar</u>	<u>Expanded grammar</u>
$R_0 : \mathcal{S} \rightarrow c$	$R_0 : \mathcal{S} \rightarrow c$
$R_1 : \mathcal{S} \rightarrow i$	$R_1 : \mathcal{S} \rightarrow i$
$R_2 : \mathcal{S} \rightarrow f(\mathcal{S}^{0,1,2,3}, \mathcal{S}^{0,1,2,3})$	$R_2 : \mathcal{S} \rightarrow f(\mathcal{S}^{0,1,2,3}, \mathcal{S}^{0,1,2,3})$
$R_3 : \mathcal{S} \rightarrow g(\mathcal{S}^{0,1,2,3}, \mathcal{S}^{0,1,2,3})$	$R_3 : \mathcal{S} \rightarrow g(\mathcal{S}^{0,1,3}, \mathcal{S}^{0,1,2,3})$
	$R_4 : \mathcal{S} \rightarrow g(f(\mathcal{S}^{0,1,2,3}, \mathcal{S}^{0,1,2,3}), \mathcal{S}^{0,1,2,3})$

A sentence can now be preprocessed bottom-up in $\mathcal{O}(n)$ time to indicate for each node which expansion tree matches that node, where n is the number of nodes in the tree. The sentence can then be traversed top-down to perform

the frequency count for the expansion trees. It should be noted that this approach means that if a symbol list does not contain all indices of the base grammar, then it represents only the set of the indicated rules from the base grammar. In the above example for instance $\mathcal{S}^{0,1,3}$ represents $\mathcal{S} \rightarrow c$, $\mathcal{S} \rightarrow i$ and $\mathcal{S} \rightarrow g(\mathcal{S}^{0,1,2,3}, \mathcal{S}^{0,1,2,3})$. Therefore, the probability associated with this particular symbol is not the recursive application of the distribution in equation 2, but is uniform over the indicated alternatives. This is comparable to the approach of default tables for discrete random variables in which instead of indicating a probability for all possible combinations of values for the random variables, only a subset of them is explicitly indicated. All remaining combinations are assigned an equal probability such that the distribution sums to 1 over all possible values.

4 Probability distribution

To construct a probability distribution over sentences, we introduce a random variable S that represents a sentence and a random variable T that represents a sentence subtree. Because sentence subtrees are recursive structures we define a probability distribution for sentence subtrees recursively. To do so, we must know where the tree terminates. This information can be obtained by taking the depth of a sentence subtree into account. Let $P^{\mathcal{G}}(T = t|D = d)$ be a probability distribution over all sentence subtrees t that occur at depth d in a sentence. Now, we define the probability distribution over sentences s by:

$$P^{\mathcal{G}}(S = s) = P^{\mathcal{G}}(T = s|D = 0) \quad (1)$$

Since sentence subtrees are constructed using production rules, we can define $P^{\mathcal{G}}(T = t|D = d)$ using the production rules. Since there is only one symbol, we can also focus on the expansion trees. Although depth can be used to model the probability of terminating a sentence at some node in the tree, sentences can be described more precisely if depth is also used to model the probability of occurrence of functions at specific depths. Preliminary experiments indicated that this use of depth information leads to better results.

We define $P_j^E(J = j|D = d)$ to be a discrete conditional probability distribution that models the probability of choosing expansion tree E_j , $j \in \{0, 1, \dots, l_r\}$ at depth d when constructing a new sentence.

We assume that the values of the constants and the indices of the input variables in an expansion tree are not dependent on the depth. Conforming to this assumption we define $2l_r$ multivariate probability distributions that allow us to model the use of constants and inputs inside production rules other than the standard rules $\mathcal{S} \rightarrow c$ and $\mathcal{S} \rightarrow i_k$, $k \in \{0, 1, \dots, n-1\}$:

- $P_j^C(\mathbf{C}_j)$, $j \in \{0, 1, \dots, l_r - 1\}$, a probability distribution over all constants in expansion tree E_j , where $\mathbf{C}_j = (C_{j0}, C_{j1}, \dots, C_{j(n_{C_j}-1)})$. Each C_{jk} is a random variable that represents a constant in E_j .
- $P_j^I(\mathbf{I}_j)$, $j \in \{0, 1, \dots, l_r - 1\}$, a probability distribution over all inputs in expansion tree E_j , where $\mathbf{I}_j = (I_{j0}, I_{j1}, \dots, I_{j(n_{I_j}-1)})$. Each I_{jk} is a random variable that represents all input variables, i.e. $I_{jk} \in \{0, 1, \dots, n-1\}$.

The above definition of $P_j^I(\mathbf{I}_j)$ enforces a single production rule $\mathcal{S} \rightarrow i$, where i represents all input variables, instead of n production rules $\mathcal{S} \rightarrow i_j$, $j \in \{0, 1, \dots, n-1\}$. This reduces the required computational complexity for estimating the probability distribution, especially if n is large. However, it prohibits the introduction of production rules that make use of specific input variables.

We will enforce that any sentence subtree t can be matched by only one expansion tree E_j . The probability distribution over all sentence subtrees at some given depth $D = d$ is then the product of the probability of matching the sentence subtree with some expansion tree E_j and the product of all (recursive) probabilities of the sentence subtrees located at the symbol-leaf nodes in E_j .

Let \mathcal{S}_{jk} be the k -th symbol in expansion tree E_j , $k \in \{0, 1, \dots, n_{\mathcal{S}_j} - 1\}$. Let $stree(\mathcal{S}_{jk}, t)$ be the sentence subtree of sentence subtree t at the same location where \mathcal{S}_{jk} is located in the expansion tree E_j that matches t . Let $depth(\mathcal{S}_{jk})$ be the depth of \mathcal{S}_{jk} in expansion tree E_j . Finally, let $match(t)$ be the index of the matched expansion tree, i.e. $match(t) = j \Leftrightarrow t \in E_j$. We then have:

$$P^G(T = t | D = d) = \tag{2}$$

$$P^E(J = j | D = d) P_j^C(\mathbf{C}_j) P_j^I(\mathbf{I}_j) \prod_{k=0}^{n_{\mathcal{S}_j} - 1} P^G(T = stree(\mathcal{S}_{jk}, t) | D = d + depth(\mathcal{S}_{jk}))$$

where $j = match(t)$

Drawing new samples from the probability distribution is a recursive procedure just as the definition of the distribution is recursive itself. To draw a new sentence subtree at depth d , first a production rule is drawn according to the probabilities associated with the production rules at the specified depth. Second, values are drawn for the constants and input variables in the expansion tree of the selected production rule, after which sentence subtrees are drawn recursively for the symbols in the expansion tree of the selected production rule.

To estimate $P^G(T)$ from a set \mathcal{S} of sentences we choose a greedy approach, similar to what has been done in most EDAs so far [2, 8–10]. The algorithm starts from the initial grammar and performs all possible transformations. From all so-obtained candidate grammars, the best one is selected if the associated probability distribution is better than the distribution associated with the current grammar. The greedy algorithm terminates if no further improvement can be made. The performance measure used to score distributions is the MDL metric [3, 12]. The penalty term in the MDL metric consists of a parameter-complexity term and a structure-complexity term. The number of parameters to be estimated can be determined in a straightforward manner from the probability distribution. The value of the structure-complexity term comes from the production rules. The more production rules, the more bits are required. Moreover, longer production rules require more bits. The number of bits required to store a production rule is $\ln(l_{r_{base}})$ times the number of internal nodes in the expansion tree where $l_{r_{base}}$ is the number of production rules in the base grammar. Finally, symbols have lists of production-rule indices. To store one such list, the number of required bits equals $\ln(l_{r_{base}})$ times the length of that list.

5 Experiments

We have performed experiments with our approach to estimating a probability distribution over sentences by using it in an EDA. We applied the resulting EDA as well as a standard GP algorithm that only uses subtree–swapping crossover to two GP–benchmarking problems, namely the royal tree problem by Punch, Zongker and Goodman [11] and the tunable benchmark problem by Korkmaz and Üçoluk [5], which we will refer to as the binary–functions problem. Both problems are non–functional, which means that fitness is defined completely in terms of the structure of the sentence and input variables have an empty domain.

5.1 Benchmark problems

In the royal tree problem, there is one function of arity n for each $n \in \{0, 1, 2, \dots\}$. The function with arity 0 is i_0 . The other functions are labeled A for arity 1, B for arity 2 and so on. The fitness function is defined recursively and in terms of “perfect” subtrees. A subtree is perfect if it is a full tree, i.e. all paths from the root to any leaf are equally long and the arity of any function is $n - 1$ where n is the arity its parent function. Figure 1 gives an example of a perfect tree of height 4. The fitness of a sentence is the fitness of the root. The fitness of a node is a weighted sum of the fitness values of its children. The weight of a child is

- *Full* if the child is a perfect subtree with a root function of arity $n - 1$ where n is the arity of the function in the current node.
- *Partial* if the child is not a perfect subtree but it has the correct root function.
- *Penalty* otherwise.

If the node is itself the root of a perfect tree, the final sum is multiplied by *Complete*. In our experiments, we follow the choices of Punch, Zongker and Goodman [11] and set $Full = 2$, $Partial = 1$, $Penalty = \frac{1}{3}$ and $Complete = 2$. The structure of this problem lies in perfect subtrees and child nodes having a function of arity that is one unit smaller than the function of their parent. Coincidentally, this results in a very strong dependence on the depth, since the optimal sentence subtree of height d has one function of arity $d - 1$ in the root, $d - 1$ functions of arity $d - 2$ on the second level and so on (see figure 1).

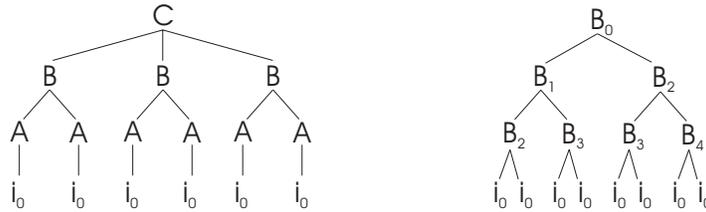


Fig. 1. Examples of sentences for the royal tree problem (left) and the binary–functions problem (right).

In the binary-functions problem there are various functions B_i , all of which have arity two. Similar to the royal tree problem, there is only one input variable i_0 . The fitness of a sentence is again the fitness of the root. The fitness of a node is 1 if the node is an input variable. Otherwise the fitness is a combination of the fitness values of its two children C_1 and C_2 ; it is computed according to:

$$\left\{ \begin{array}{ll} f(C_1) + f(C_2) & \text{if both children are inputs or no constraints violated} \\ \eta f(C_1) + f(C_2) & \text{if } C_1 \text{ violates first constraint, } C_2 \text{ doesn't violate first} \\ & \text{constraint and second constraint not violated} \\ f(C_1) + \eta f(C_2) & \text{if } C_2 \text{ violates first constraint, } C_1 \text{ doesn't violate first} \\ & \text{constraint and second constraint not violated} \\ \eta f(C_1) + \eta f(C_2) & \text{if both children violate first constraint or the second} \\ & \text{constraint is violated} \end{array} \right.$$

where the indicated constraints are:

1. The index of the parent function is smaller than the indices of its children.
2. The index of the left child is smaller than the index of the right child.

In our experiments we have used $\eta = 0.25$. The structure of this optimization problem is both local and overlapping. The local aspect lies in the fact that only a node and its direct descendants are dependent on each other. However, since these dependencies hold for each node, the structure is recursive throughout the tree and thus the dependencies are inherently overlapping.

5.2 Results

For both problems, we have computed convergence graphs for both algorithms and three different population sizes. The curves in the graphs are averaged over 25 runs. For the Royal Tree problem (see Fig. 2, left), GP achieves reasonable results for population sizes 500 and 1000, but does not reliably find the optimum. The EDA identifies the optimal solution in every single run and for all population sizes. The Royal Tree problem is a benchmark problem for GP that features a depth-wise layered structure. Clearly, the use of depth information therefore renders the EDA particularly appropriate for problems of this kind. Still, this result demonstrates the feasibility of our EDA to GP. Figure 2 (right) shows the results when recombination is performed in only 90% of the cases, and copying a random parent is performed in the remaining 10%. Although GP is in this case also able to reliably find the optimum this is only the case for a population size of 1000 whereas the EDA is still able to reliably find the optimum for all population sizes. Although lowering the probability of recombination normally speeds up convergence, in this case the EDA is only hampered by it because the distribution can perfectly describe the optimum and therefore using the distribution more frequently will improve performance. Moreover, copying introduces spurious dependencies that are estimated in the distribution and will additionally hamper optimization.

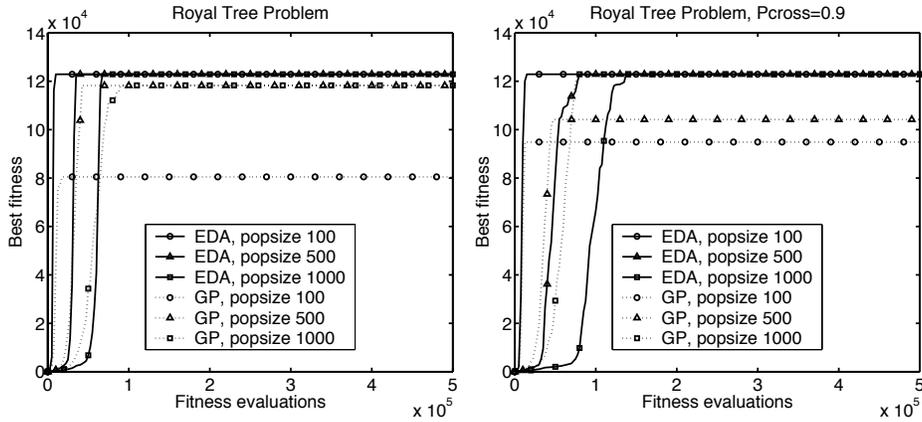


Fig. 2. Results for the Royal Tree problem.

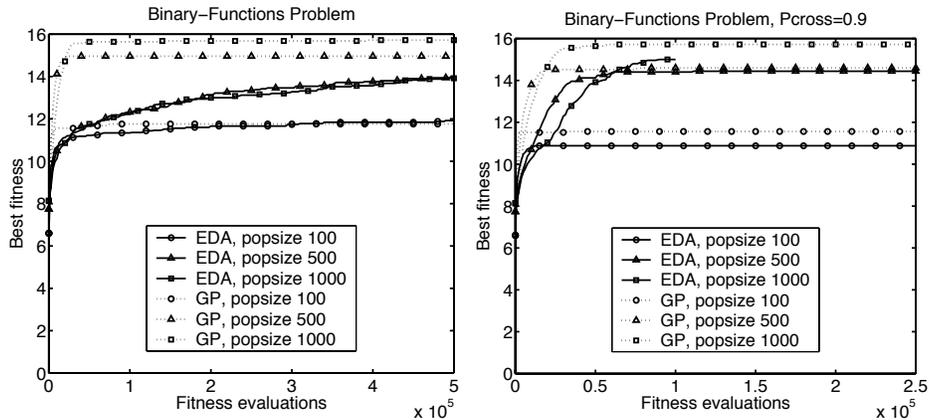


Fig. 3. Results for the binary-functions problem.

Figure 3 shows the results for the binary-functions problem (maximum fitness is 16). This problem has dependencies that are much harder for the distribution to adequately represent and reliably reproduce. Very large subfunctions are required to this end. Moreover, the multiple (sub)optima slow down convergence for the EDA as can be seen in Figure. 3 on the left. Crossover in GP is much more likely to reproduce large parts of parents. Hence, crossover automatically biases the search towards one of these solutions, allowing for faster convergence. The use of copying leads to faster convergence of the EDA. However, the deficiency of the distribution with respect to the dependencies in the problem still hamper the performance of the EDA enough to not be able to improve over standard GP. Additional enhancements may be required to make the distribution used more suited to cope with dependencies such as those encountered in the binary-functions problem, after which an improvement over standard GP may be expected similar to the improvement seen for the Royal Tree problem.

5.3 Examples of learned production rules

In Figure 4 the learned probability distributions during a run of the EDA on the Royal Tree problem are presented in a tabulated fashion. The figure shows the distributions at the beginning, in generation 50, and at the end of the run. A population of size 100 was used and the probability of recombination was set to 1.0. Clearly, the distribution can already be made specific enough by setting the probabilities because of the perfect dependency on the depth of the Royal Tree problem. Hence, no new production rules are introduced into the grammar at any point during the run and the probabilities converge towards a configuration that uniquely describes the optimal sentence.

In Figure 4 the learned probability distribution in generation 35 during a run of the EDA on the binary-functions problem is also presented in a tabulated fashion. The population size used in this experiment is 10000 and the probability of recombination is set to 0.9. In generation 35, the average fitness was 10.1379 whereas the best fitness was 13 (optimal fitness is 16). Clearly in this case the probability distribution based on the initial grammar cannot be made specific enough to describe the features of good sentences nor can it perfectly describe the optimal sentence. Therefore, additional production rules are added by the greedy search algorithm. As can be seen, the most important rules are added first and they have a high probability for at least one depth. The rules that are added afterwards mainly serve to make the distribution more specific by reducing the size of the default tables that have been created by the substitution transformations. The rules themselves have only a very low probability. One of the most important rules regarding the root of the tree has already been established (i.e. $B_0(B_1(S, S), S)$). Although other important rules have been discovered, they have not yet received high probabilities as they do not occur frequently in the population. As the search progresses towards the optimum, other important rules such as $B_2(B_3(S, S), S)$ will obtain more prominent probabilities as well to more specifically describe a smaller subset of high-quality sentences.

6 Discussion and conclusions

In this paper we have proposed a probability distribution over trees to be used in an EDA for GP. The distribution basically associates a probability with each production rule in a context-free grammar. More involved production rules or subfunctions can be introduced using transformations in which one production rule is expanded into another production rule. This allows the probability distribution to become more specific and to express a higher order of dependency. We have performed experiments on two benchmark problems from the literature. The results indicate that our EDA for GP is feasible. It should be noted however that learning advanced production rules using the greedy algorithm proposed in this paper can take up a lot of time, especially if the number of production rules and the arity of the subfunctions increase. To speed up this greedy process, only a single rule can be randomly selected into which to expand each production rule from the base grammar instead of expanding each production rule

		D					
		0	1	2	3	4	5
i_0		0.167	0.167	0.167	0.167	0.167	1.000
$A(S)$		0.167	0.167	0.167	0.167	0.167	0.000
$B(S, S)$		0.167	0.167	0.167	0.167	0.167	0.000
$C(S, S, S)$		0.167	0.167	0.167	0.167	0.167	0.000
$D(S, S, S, S)$		0.167	0.167	0.167	0.167	0.167	0.000
$E(S, S, S, S, S)$		0.167	0.167	0.167	0.167	0.167	0.000

		D					
		0	1	2	3	4	5
i_0		0.000	0.000	0.029	0.140	0.158	1.000
$A(S)$		0.000	0.000	0.027	0.131	0.318	0.000
$B(S, S)$		0.000	0.000	0.079	0.362	0.146	0.000
$C(S, S, S)$		0.000	0.000	0.642	0.143	0.121	0.000
$D(S, S, S, S)$		0.000	0.992	0.011	0.106	0.133	0.000
$E(S, S, S, S, S)$		1.000	0.008	0.011	0.116	0.123	0.000

		D					
		0	1	2	3	4	5
i_0		0.000	0.000	0.000	0.000	0.000	1.000
$A(S)$		0.000	0.000	0.000	0.000	1.000	0.000
$B(S, S)$		0.000	0.000	0.000	1.000	0.000	0.000
$C(S, S, S)$		0.000	0.000	1.000	0.000	0.000	0.000
$D(S, S, S, S)$		0.000	1.000	0.000	0.000	0.000	0.000
$E(S, S, S, S, S)$		1.000	0.000	0.000	0.000	0.000	0.000

		D				
		0	1	2	3	4
i_0		0.000	0.000	0.185	0.346	1.000
$B_0(S, S)$		0.082	0.000	0.020	0.000	0.000
$B_1(S, S)$		0.002	0.000	0.009	0.000	0.000
$B_2(S, S)$		0.002	0.002	0.027	0.000	0.000
$B_3(S, S)$		0.006	0.011	0.059	0.000	0.000
$B_4(S, S)$		0.001	0.097	0.106	0.110	0.000
$B_5(S, S)$		0.000	0.158	0.105	0.185	0.000
$B_6(S, S)$		0.000	0.000	0.000	0.000	0.000
$B_0(B_1(S, S), S)$		0.582	0.000	0.032	0.000	0.000
$B_0(i_0, S)$		0.000	0.000	0.004	0.000	0.000
$B_6(i_0, S)$		0.000	0.412	0.114	0.000	0.000
$B_6(S, i_0)$		0.000	0.295	0.121	0.000	0.000
$B_6(i_0, i_0)$		0.000	0.000	0.000	0.249	0.000
$B_1(B_2(S, S), S)$		0.189	0.000	0.034	0.000	0.000
$B_1(i_0, S)$		0.000	0.000	0.001	0.018	0.000
$B_3(i_0, S)$		0.000	0.013	0.092	0.000	0.000
$B_3(i_0, i_0)$		0.000	0.000	0.000	0.058	0.000
$B_2(i_0, S)$		0.000	0.003	0.026	0.000	0.000
$B_2(B_3(S, S), S)$		0.018	0.010	0.046	0.000	0.000
$B_2(i_0, i_0)$		0.000	0.000	0.000	0.019	0.000
$B_0(B_2(S, S), S)$		0.096	0.000	0.011	0.000	0.000
$B_1(B_3(S, S), S)$		0.023	0.000	0.006	0.000	0.000
$B_0(B_6(S, S), S)$		0.000	0.000	0.000	0.000	0.000
$B_0(B_0(S, S), S)$		0.000	0.000	0.000	0.000	0.000
$B_0(i_0, i_0)$		0.000	0.000	0.000	0.015	0.000

Fig. 4. The probability distribution at the beginning (top left), after 50 generations (center left) and upon convergence after 139 generations (bottom left) of an example run of the EDA on the Royal Tree problem. Also, the probability distribution is shown after 35 generations in an example run of the EDA on the binary-functions problem (right). For brevity, only the expansion trees E_i of each production rule are shown and the production rule index lists are dropped for the symbols S .

from the base grammar into each currently available production rule. Although this significantly reduces the number of candidate distributions in the greedy algorithm, it also significantly improves the running time. Moreover, since the greedy algorithm is iterative and the probability distribution is estimated anew each generation, the most important subfunctions are still expected to emerge.

Because our approach to estimating probability distributions over trees does not fix or bound the tree structure beforehand, our approach can be seen as a more principled way of identifying arbitrarily-sized important subfunctions than by constructing subfunctions randomly (e.g. GLiB [1]) or by evolving them (e.g. ADFs [7] and ARL [13]). As such, this paper may provide one of the first steps in a new and interesting direction for GP that allows to detect and exploit substructures in a more principled manner for enhanced optimization performance.

References

1. Peter J. Angeline and Jordan B. Pollack. The evolutionary induction of subroutines. In *Proceedings of the Fourteenth Annual Conference of the Cognitive Science Society*, pages 236–241, Hillsdale, NJ, 1992. Lawrence Erlbaum Associates.
2. Peter A. N. Bosman. *Design and Application of Iterated Density–Estimation Evolutionary Algorithms*. PhD thesis, Utrecht Univ., Utrecht, the Netherlands, 2003.
3. Wray Buntine. A guide to the literature on learning probabilistic networks from data. *IEEE Transactions On Knowledge And Data Engineering*, 8:195–210, 1996.
4. Michael L. Cramer. A representation for the adaptive generation of simple sequential programs. In John J. Grefenstette, editor, *Proceedings of the First International Conference on Genetic Algorithms and their Applications*, pages 183–187, Hillsdale, NJ, 1985. Carnegie-Mellon University, Lawrence Erlbaum Associates.
5. Emin E. Korkmaz and Göktürk Üçoluk. Design and usage of a new benchmark problem for genetic programming. In *Proceedings of the 18th International Symposium on Computer and Information Sciences ISCIS-2003*, pages 561–567, Berlin, 2003. Springer–Verlag.
6. John R. Koza. *Genetic Programming*. The MIT Press, Cambridge, MA, 1992.
7. John R. Koza. *Genetic Programming II: Automatic Discovery of Reusable Programs*. The MIT Press, Cambridge, MA, May 1994.
8. Pedro Larrañaga and José A. Lozano. *Estimation of Distribution Algorithms. A New Tool for Evolutionary Computation*. Kluwer Academic, London, 2001.
9. Martin Pelikan. *Bayesian optimization algorithm: From single level to hierarchy*. PhD thesis, University of Illinois at Urbana–Champaign, Urbana, Illinois, 2002.
10. Martin Pelikan, David E. Goldberg, and Fernando G. Lobo. A survey of optimization by building and using probabilistic models. *Computational Optimization and Applications*, 21(1):5–20, 2002.
11. William F. Punch, Douglas Zongker, and Erik D. Goodman. The royal tree problem, a benchmark for single and multiple population genetic programming. In P. J. Angeline and K. E. Kinnear, Jr., editors, *Advances in Genetic Programming 2*, pages 299–316. The MIT Press, Cambridge, MA, USA, 1996.
12. Jorma Rissanen. Hypothesis selection and testing by the MDL principle. *The Computer Journal*, 42(4):260–269, 1999.
13. Justinian P. Rosca and Dana H. Ballard. Discovery of subroutines in genetic programming. In P.J. Angeline and K. E. Kinnear, Jr., editors, *Advances in Genetic Programming 2*, chapter 9, pages 177–202. The MIT Press, Cambridge, MA, 1996.
14. Rafal P. Salustowicz and Jürgen Schmidhuber. Probabilistic incremental program evolution. *Evolutionary Computation*, 5(2):123–141, 1997.
15. Kumara Sastry and David E. Goldberg. Probabilistic model building and competent genetic programming. In Rick L. Riolo and Bill Worzel, editors, *Genetic Programming Theory and Practise*, chapter 13, pages 205–220. Kluwer, 2003.
16. Y. Shan, R.I. McKay, R. Baxter, H. Abbass, D. Essam, and H.X. Nguyen. Grammar model-based program evolution. In *Proceedings of the 2004 Congress on Evolutionary Computation – CEC2004*, Piscataway, New Jersey, 2004. IEEE Press.