

# Probabilistic Structured Grammatical Evolution

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**Abstract**—The grammars used in grammar-based Genetic Programming (GP) methods have a significant impact on the quality of the solutions generated since they define the search space by restricting the solutions to its syntax. In this work, we propose Probabilistic Structured Grammatical Evolution (PSGE), a new approach that combines the Structured Grammatical Evolution (SGE) and Probabilistic Grammatical Evolution (PGE) representation variants and mapping mechanisms. The genotype is a set of dynamic lists, one for each non-terminal in the grammar, with each element of the list representing a probability used to select the next Probabilistic Context-Free Grammar (PCFG) derivation rule. PSGE statistically outperformed Grammatical Evolution (GE) on all six benchmark problems studied. In comparison to PGE, PSGE outperformed 4 of the 6 problems analyzed.

**Index Terms**—Grammatical Evolution, Grammar-based Genetic Programming, Grammar Design, Probabilistic.

## I. INTRODUCTION

Evolutionary Algorithms (EAs) are metaheuristic algorithms driven by an objective function that follow a trial-and-error approach to problem-solving. Inspired by the principles of natural selection and genetics, these algorithms evolve a population of individuals towards better solutions, using an objective function, over several generations. The quality of solutions improves by selecting the most promising ones (taking into account the objective function), and applying stochastic variations using operators similar to mutations and recombinations that take place in biological systems, where individuals with higher fitness are more likely to survive and reproduce.

Genetic Programming (GP) [1] is a branch of EAs in which individuals are represented as computer programs that evolve to solve problems, without the need to program the solution explicitly. Grammatical Evolution (GE) [2]–[4] is a GP approach that uses a Context-Free Grammar (CFG) to constrain the search space of possible solutions. The individuals are represented by a list of integers (i.e., genotype), where each value (i.e., codon) is used to choose a production rule of the grammar until it forms a solution to the problem (i.e., phenotype).

Despite being one of the most widely used GP variants, GE is not exempt from having some issues [5], [6]. GE has low locality, which means that small changes in the genotype often cause large changes in the phenotype, causing exploitation to be replaced for exploration, which can lead to a behaviour

similar to random search [7]. GE also suffers from high redundancy, which means that often changes in the genotype do not cause changes in the phenotype [5]. To overcome these issues, numerous methods have been proposed in the literature. Most of these methods perform changes in grammars [8]–[11], representation of individuals [12]–[17] or population initialization [18]–[22].

In this paper we propose a new method called Probabilistic Structured Grammatical Evolution (PSGE) that results from the combination of the representation of Structured Grammatical Evolution (SGE) and the mapping mechanism of Probabilistic Grammatical Evolution (PGE). The main motivation for this work rises from the interest of creating a method that inherits the main advantages of the representation used by SGE, namely the high locality and low redundancy [23], [24], with the probabilistic mapping form PGE that is able to guide the evolutionary process towards better solutions by iteratively adjusting the biases of the grammar.

Identically to SGE, the genotype in PSGE is a set of dynamic lists of real values, with a list for each non-terminal of the grammar. Each element of the list (i.e., codon) represents the probability of choosing a production rule from the grammar, which are updated based on the phenotype of the best individual at the end of each generation, using the same mapping mechanism proposed by PGE. PSGE is compared with GE, PGE and SGE on six different benchmark problems and the results showed that PSGE version is better than GE and PGE.

The remainder of this work is structured as follows: Section II presents the background necessary to understand the work presented, introducing GE as well as related work. Section III present the proposed method, detailing the representation and mapping method used. Section IV details the experimentation framework used and Section V the experimental results regarding performance. Section VI gathers the main conclusions and provides some insights regarding future work.

## II. GRAMMATICAL EVOLUTION

GE [2]–[4] is a grammar-based GP approach used to evolve programs. Each individual in the population is represented by a list of integers, called genotype, and each value is randomly generated in the interval  $[0, 255]$ . The elements of the list are used in the mapping process to create the phenotype, that is

the solution of the problem, using the production rules defined by a CFG. A grammar is a tuple  $G = (NT, T, S, P)$  where  $NT$  and  $T$  represent the non-empty set of *Non-Terminal* ( $NT$ ) and *Terminal* ( $T$ ) symbols,  $S$  is an element of  $NT$  in which the derivation sequences start, called the axiom, and  $P$  is the set of production rules. The rules in  $P$  are in the form  $A ::= \alpha$ , with  $A \in NT$  and  $\alpha \in (NT \cup T)^+$ . The  $NT$  and  $T$  sets are disjoint. Each grammar defines a language  $L(G) = \{w : S \xrightarrow{*} w, w \in T^*\}$ , that is the set of all sequences of terminal symbols that can be derived from the axiom. The symbol  $*$  represents the unary operator Kleene star.

```

<expr> ::= <expr><op><expr>
          | <var>
<op> ::= +
          | -
          | *
          | /
<var> ::= x
          | y
          | 1.0

```

Fig. 1. Example of a CFG.

The mapping from genotype to phenotype is done starting from the axiom of the grammar and expanding the leftmost non-terminal. The codons of the genotype are used to choose which production rule to expand by applying the modulo operator ( $mod$ ) between the codon and the number of derivation rules of the respective non-terminal.

Genotype	
[34, 13, 9, 151, 95, 221, 23, 98, 145, 42, 153]	
<expr> → <expr><op><expr>	34mod2 = 0
<expr><op><expr> → <var><op><expr>	13mod2 = 1
<var><op><expr> → x<op><expr>	9mod3 = 0
x<op><expr> → x/<expr>	151mod4 = 3
x/<expr> → x/<var>	95mod2 = 1
x/<var> → x/1.0	221mod3 = 2
<b>Phenotype:</b> x/1.0	

Fig. 2. Example of the genotype-phenotype mapping of GE.

An example of the genotype-phenotype process is shown in Fig. 2, using the example of grammar presented in Fig. 1. The mapping begins with the axiom of the grammar,  $\langle \text{expr} \rangle$ , which has two expansion alternatives, and the first unused codon of the genotype, 34. By applying the modulo operator between the codon and the number of production rules,  $34 \bmod 2 = 0$ , we obtain the index of the rule to be expanded which is  $\langle \text{expr} \rangle \langle \text{op} \rangle \langle \text{expr} \rangle$ . This procedure is repeated until there are no more non-terminal symbols to expand or numbers from the genotype to read. In the last case, if we still have non-terminals to expand, we can employ a wrapping technique, in which the genotype is reused until it yields a valid individual or the predefined number of wraps is reached. If we haven't mapped all of the non-terminals after all of the wraps, the mapping procedure will stop and the individual will be considered invalid. The fitness function is

used to evaluate each individual's phenotype, and then the population is subjected to selection procedures.

#### A. Related Work

GE is one of the most popular GP variants, and it has undergone various modifications over the years to address some of its major criticisms, namely high redundancy and low locality. Low locality refers to small genotype changes that result in large phenotypic changes, whereas high redundancy refers to multiple genotypes corresponding to the same phenotype. The majority of these proposed solutions include changes to grammars [8]–[11], individual representation [12], [13], [15]–[17], [25], or population initialization [18]–[22].

SGE [25] addresses GE's locality and redundancy issues while achieving better performance results [14]. The genotype in SGE is a set of dynamic lists of ordered integers, one list for each non-terminal of the grammar. Each value in the list represents which production rule to select from the non-terminal. Different grammar-based GP approaches were compared in [26], and the authors demonstrated that SGE outperformed several grammar-based GP representations in some problems.

Position Independent Grammatical Evolution ( $\pi$ GE) [16] is a method that uses a new representation and mapping mechanism in which the genotype of the individual determines the order of expansion of the non-terminals, reducing the positional dependency that exists in GE. Individual genotypes are made of tuples of two values ( $nont$ ,  $rule$ ), with  $nont$  determining which non-terminal to expand next and  $rule$  determining the rule to derive from that non-terminal. On several problems, this technique outperformed GE, with statistical differences.

Chorus [17] is another method that allows for positional independence, with each gene encoding only one production of the grammar. This strategy, however, has not been proved to be superior than the GE standard.

The design of the grammars is another aspect that has had some attraction for researchers since they define the search space, and thus the choice of grammar can affect the speed of convergence to the best solution [9]. Some research has been done to study the performance of GE with various types of grammars, such as the use of recursively balanced grammars [8], [9] and the reduction of non-terminal symbols [9], [10].

Harper et al. [8] demonstrated that the grammar used at the start of the evolutionary process can have a significant impact on the solutions, such as generating a large number of invalid individuals when using recursive grammars. It has also been demonstrated that when a balanced grammar is used, there is more variety in the size of solutions.

Nicolau et al. [9] tested GE with different grammars, which included balanced grammars, grammars with corrected biases, and grammars with unlinked productions. The experimental tests using a recursively balanced grammar, in which there is a non-recursive production for every recursive one, yielded better results than the original grammar. However it resulted in a larger number of individuals consisting of a non-terminal

symbol. Nicolau [10] proposed a method for reducing the number of non-terminal symbols, replacing them with their productions, which, while showing a slight improvement in performance, has the disadvantage of producing complex grammars that are difficult to read.

Another area of research has been the evolution of the grammar throughout the evolutionary process [11]–[13], [15].

Grammatical Evolution by Grammatical Evolution ((GE)<sup>2</sup>) [11] is a method where the grammar and genetic code co-evolve. The method employs two distinct grammars: universal grammar and solution grammar. The structure of the solution grammar, which is used to map the individuals, is dictated by the universal grammar. This method has been shown to be effective in developing biases toward non-terminal symbols. Later, it was implemented into a new algorithm, meta-Grammar Genetic Algorithm (mGGA) [27], which resulted in improved performance.

PGE [15] is a recent variant of GE in which the individuals are mapped using a Probabilistic Context-Free Grammar (PCFG) and the genotype is a list of real numbers. A PCFG is a quintuple  $PG = (NT, T, S, P, Probs)$  where  $NT$  and  $T$  represent the non-empty set of *Non-Terminal* ( $NT$ ) and *Terminal* ( $T$ ) symbols,  $S$  is an element of  $NT$  called the axiom,  $P$  is the set of production rules, and  $Probs$  is a set of probabilities associated with each production rule. The mapping begins with the leftmost non-terminal, and the rule whose probability interval includes the codon is chosen for each non-terminal to be expanded. The PCFG probabilities are updated at the end of each generation based on the expansion rules used to create the best individual of the current generation alternating with the best individual overall. PGE proved to be superior than GE with statistical differences in the two problems studied.

Kim et al. [12] proposed Probabilistic Model Building Grammatical Evolution (PMBGE), in which the mapping is based on a PCFG and the probabilistic technique Estimation Distribution Algorithm (EDA), which also replaces the mutation and crossover operators. The probabilities of the grammar are changed every generation based on the frequency of the rules expanded by the best individuals. This technique generates a new population from the new grammar at each generation. When compared to GE, the proposed approach performed similarly. Later, Kim et al. [13] adapted Conditional Dependency Tree (CDT) to the mechanism of updating the grammar, creating cdPMBGE which takes into account the dependencies between production rules. The results revealed no statistical differences between GE and the proposed approach. This method outperformed GE with statistical differences in two of the four problems analysed.

### III. PROBABILISTIC STRUCTURED GRAMMATICAL EVOLUTION

In this work we propose PSGE<sup>1</sup> in which the representation of individuals and the mapping mechanism is a combination

<sup>1</sup>The implementation of PSGE is available at: <https://github.com/jessicamegane/psge>

of the approaches followed by SGE and PGE. The mapping resorts to a PCFG to choose the derivation rules. At the end of each generation the probabilities of the grammar are updated according to the production rules expanded by the best individual of the current generation or the best individual overall.

The individuals are represented by a set of dynamic lists, with each list being associated with a non-terminal of the grammar. The lists contain an ordered sequence of real numbers, with each codon corresponding to the probability of choosing a production rule.

The pseudo-code of the initialization of individuals in PSGE is presented in Alg. 1. The algorithm takes as parameters the genotype (which starts with an empty list for each non-terminal), the non-terminal symbol to expand (the axiom of the grammar in the first iteration), the current depth (which starts at 0), the maximum depth limit and the PCFG. The function is recursive and ends when the genotype belongs to a valid individual. At each iteration a random value between 0 and 1 is generated and added to the list of the non-terminal to be expanded (Alg. 1, lines 2-3). To determine which rule to expand next based on the new codon, the mapping process is simulated (Alg. 1, line 4).

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#### Algorithm 1 Random candidate solution of PSGE

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```

1: procedure CREATEINDIVIDUAL(genotype, symb, depth,
   max_depth, pcfg)
2:   codon = random(0,1)
3:   genotype[symb].append(codon)
4:   selected_rule = generate_expansion(symb, codon,
   pcfg, depth, max_depth)
5:   expansion_symbols = pcfg[symb][selected_rule]
6:   for sym in expansion_symbols do
7:     if not is_terminal(sym) then
8:       createIndividual(genotype, symb, depth + 1,
   max_depth, pcfg)
9:     end if
10:  end for
11: end procedure

```

---

The approach for genotype-phenotype mapping is described in Alg. 2. The genotype, a counter called *positions\_to\_map* (which is initially empty and is used to store the genotype position of each non-terminal list at the current iteration), the symbol to expand (which starts in the axiom), the current depth, the maximum depth limit, and the grammar are all passed as arguments to the algorithm. If more codons are required to construct a valid individual during mapping, they will be created at random and added to the genotype (Alg. 2, lines 3-6). One of the benefits of this representation is that with the depth limit, it is feasible to add productions as needed without the risk of bloat (a significant increase in the size of the solutions [28]), ensuring that valid individuals are always created.

To choose the derivation rule to expand, we use the function that is described in Algorithm 3. The function receives as

**Algorithm 2** Genotype-Phenotype mapping of PSGE

```

1: procedure MAPPING(genotype, positions_to_map, symb,
depth, max_depth, pcfg)
2:   phenotype = ""
3:   if positions_to_map[symb] >= len(genotype[symb])
then
4:     codon = random(0,1)
5:     genotype[symb].append(codon)
6:   end if
7:   codon = genotype[symb][positions_to_map[symb]]
8:   selected_rule = generate_expansion(symb, codon,
pcfg, current_depth, max_depth)
9:   expansion = pcfg[symb][selected_rule]
10:  positions_to_map[symb] += 1
11:  for sym in expansion do
12:    if is_terminal(sym) then
13:      phenotype += sym
14:    else
15:      phenotype += mapping(genotype,
positions_to_map, sym, depth + 1, max_depth, pcfg)
16:    end if
17:  end for
18:  return phenotype
19: end procedure

```

parameters the non-terminal symbol to be expanded, the codon, the grammar, the current depth and the maximum depth established. The mechanism for choosing the derivation rule is based on that of PGE [15], in which the rule whose probability interval incorporates the value of the codon is chosen (Alg. 3, lines 15-21), however for PSGE when the depth limit is reached, only non-recursive production rules are considered (Alg. 3, lines 4-13). In this case, the probabilities of the non-recursive rules are adjusted proportionally so that their sum is 1. The codon value is compared with the new probability values, and the rule whose probability range includes the codon value is chosen.

PCFG	Prob.
<expr> ::= <expr><op><expr>	[0.00; 0.37]
<var>	[0.37; 1.00]
<op> ::= +	[0.00; 0.22]
-	[0.22; 0.39]
*	[0.39; 0.68]
/	[0.68; 1.00]
<var> ::= x	[0.00; 0.41]
y	[0.41; 0.67]
1.0	[0.67; 1.00]

Fig. 3. PCFG example. Prob. represents the range of values covered by each production rule, and the size of the range corresponds to the probability of that production rule being chosen.

An example of an individual's mapping process is depicted in Fig. 4, using the grammar in Fig. 3. The process begins by expanding the axiom of the grammar, <expr>, using the first codon in the list of the respective non-terminal of the genotype,

**Algorithm 3** PSGE function to select an expansion rule

```

1: procedure GENERATE_EXPANSION(symb, codon, pcfg,
depth, max_depth)
2:   cum_prob = 0.0
3:   if depth ≥ max_depth then
4:     nr_prods = get_non_recursive_prods(pcfg[symb])
5:     total_nr_prods = sum(nr_prods.getProb())
6:     for prod in non_recursive_prods do
7:       new_prob = prod.getProb() / total_nr_prods
8:       cum_prob = cum_prob + new_prob
9:       if codon ≤ cum_prob then
10:        selected_rule = prod
11:       break
12:     end if
13:   end for
14:   else
15:     for prod in pcfg[symb] do
16:       cum_prob = cum_prob + prod.getProb()
17:       if codon ≤ cum_prob then
18:        selected_rule = prod
19:       break
20:     end if
21:   end for
22:   end if
23:   return selected_rule
24: end procedure

```

in this case 0.19. The non-terminal <expr> presents two derivation rules, with different probabilities of being chosen. The 0.19 codon is included in the range of probabilities of the first rule, <expr><op><exp>, therefore expansion is made for that rule. The derivation is always done from the leftmost non-terminal, so the next non-terminal to expand is <expr>. The next available codon in the list of the non-terminal <expr> is 0.46, which falls within the probability range of the second expansion rule, <var>. The <var> will be the next to expand and has three derivation rules. 0.32 is the first codon available in the list of <var> of the genotype, and falls within the range of probabilities covered by the first production rule, *x*, which is a terminal symbol, so <op> is the next symbol to expand. The procedure is repeated until a valid individual is formed.

Genotype		
<expr>	<op>	<var>
[0.19,0.46,0.87]	[0.27]	[0.32, 0.64]
<expr> → <expr><op><expr> (0.19)		
<expr><op><expr> → <var><op><expr> (0.46)		
<var><op><expr> → x <op><expr> (0.32)		
x <op><expr> → x - <expr> (0.27)		
x - <expr> → x - <var> (0.87)		
x - <var> → x - y (0.64)		
<b>Phenotype: x - y</b>		

Fig. 4. Example of the genotype-phenotype mapping of PSGE with a PCFG.

At the end of each generation the best individual overall and the best individual from the current generation are used alternately to update the PCFG probabilities, using the same mechanism proposed for PGE [15]. All individuals are re-mapped to update the phenotype according to the new updated grammar.

For each production  $i$  of each non-terminal  $j$  we have a *counter* with the number of times that each production was chosen, and the probability (*prob*) of the PCFG of choosing that production. If the counter is greater than zero, that is, the production rule was used to map the individual, we use (1). If the counter is zero, that is, the production rule has not been used by the individual, we use (2). The learning factor is represented by  $\lambda$ , with  $\lambda \in [0, 1]$ , and is used to make the transitions on the search space smoother.

$$prob_i = \min(prob_i + \lambda * \frac{counter_i}{\sum_{k=1}^j counter_k}, 1.0) \quad (1)$$

$$prob_i = prob_i - \lambda * prob_i \quad (2)$$

After updating the probabilities using the equations, these are adjusted until the sum of the probabilities of each production rule of each non-terminal is 1.

#### A. Variation Operators

Genetic operators are used to introduce genotype-level changes in individuals, such as mutation and crossover. The mutation operator changes randomly chosen codons, and in PSGE a Gaussian mutation is applied to these codons, keeping the new value in the interval  $[0, 1]$ . This type of mutation is widely used in the literature and has proven to be an effective method for making small changes in the search space [29], [30].

##### Genotype before mutation:

< expr >	< op >	< var >
[0.19, <b>0.46</b> , 0.87]	[0.27]	[0.32, 0.64]

##### Genotype after mutation:

< expr >	< op >	< var >
[0.19, <b>0.29</b> , 0.87]	[0.27]	[0.32, 0.28]

Fig. 5. Example of PSGE’s mutation on one codon of the genotype.

Fig. 5 is an example of Gaussian mutation in an individual. Assuming that the second codon of the non-terminal  $\langle expr \rangle$ , was randomly selected (0.46) and the value generated with a normal distribution of mean 0 and standard deviation 0.50 ( $N(0, 0.50)$ ) was  $-0.17$ , the codon will now assume a value of 0.29.

The crossover operator combines the genetic material of two individuals to generate an offspring, and is based on the crossover proposed by SGE [25]. The offspring inherits the list of each non-terminal from one of the parents, and this decision is made based on a randomly generated binary mask. The mask contains a binary value for each list of the genotype

#### Parents genotype:

##### Parent 1:

< expr >	< op >	< var >
[0.19, 0.46, 0.87]	[0.27]	[0.32, 0.64]

##### Parent 2:

< expr >	< op >	< var >
[0.02, 0.90, 0.13]	[0.48]	[0.75, 0.42, 0.56]

#### Mask and offspring after crossover:

##### Mask:

< expr >	< op >	< var >
1	1	0

##### Offspring:

< expr >	< op >	< var >
[0.02, 0.90, 0.13]	[0.48]	[0.32, 0.64]

Fig. 6. Example of PSGE’s crossover between two individuals, generating one offspring.

(i.e., one for each non-terminal of the grammar). In Fig. 6 are represented an example of crossover, showing the parents, the mask used and the offspring. In the example, the descendant inherited the lists of the non-terminals  $\langle expr \rangle$  and  $\langle op \rangle$  from Parent 2, and the list of the non-terminal  $\langle var \rangle$  from Parent 1. In case two descendants are generated, the other would get the opposite lists.

#### IV. EXPERIMENTAL SETUP

The performance of PSGE will be carried out following the framework proposed by Whigham et al. [7], examining the evolution of the mean best fitness of each generation over 100 independent runs in six problems of different scopes. The results will be compared with the standard GE, PGE, and SGE. Table I presents the parameters used by all the approaches.

TABLE I  
PARAMETERS USED IN THE EXPERIMENTAL ANALYSIS FOR GE, PGE, SGE AND PSGE.

Parameters	GE	PGE	SGE	PSGE
Population Size	1000			
Generations	50			
Elitism Count	100			
Mutation Rate	0.05			
Crossover Rate	0.90			
Tournament	3			
Size of Genotype	128		-	
Max Depth	-			10

In what concerns the variation operators, GE and PGE use a one point crossover. The mutation of GE replaces the selected codons by new ones randomly generated in the interval  $[0, 255]$  and in the case of PGE a float mutation is used, in which the codons are replaced by new ones generated in the interval  $[0, 1]$ . The wrapping mechanism was removed from GE and PGE. Regarding the genetic operators used by SGE and PSGE, these methods all use the same crossover, which is the one

presented in Section III-A. Regarding the mutation operator, in the case of SGE, the mutated codon is replaced with a different valid option, while in PSGE a Gaussian mutation with  $N(0, 0.50)$  in the codon value is performed.

A detailed description of the problems and the grammars used can be found in the work done by Lourenço et al. [26] and Whigham et al. [7], and were selected on the basis of the recommendations of McDermott et al. [31]. The problems considered were the quartic symbolic regression, pagie symbolic regression [32], the Boston Housing symbolic regression [33], 5-bit even parity, 1-bit Boolean multiplexer and the Santa Fe artificial ant problem [1]. The objective functions used to evaluate the individuals consider the minimization of the error. In the case of Symbolic Regression and classification problems the fitness is the Root Relative Squared Error (RRSE) between the individual's solution and the target on a data set. For the Boolean functions, the error is the number of incorrect predictions, and for the Path finding problem, the fitness is the number of pieces remaining after exceeding the step limit.

## V. RESULTS

A statistical analysis was done to be able to fairly compare the different methods and support our analysis. Since the populations were independently initialized and the results do not meet the criteria for parametric tests, the Kruskal-Wallis non-parametric test was used to check for meaningful differences between the different methods. When the methods show differences, we verify in which pairs the differences exist, using the Mann-Whitney *post-hoc* test with the Bonferroni correction. To determine how significant the differences are, the effect size  $r$  was calculated. The "~" sign was used when there were no significant differences between samples, the "+" sign was used when the effect size was small ( $r \leq 0.3$ ), "++" was used when the effect size was medium ( $0.3 < r \leq 0.5$ ), and "+++" was used when the effect size is large ( $r > 0.5$ ). For all the statistical tests we considered a significance level of  $\alpha = 0.05$ .

TABLE II

RESULTS OF THE MANN-WHITNEY POST-HOC STATISTICAL TESTS. THE BONFERRONI CORRECTION IS USED CONSIDERING A SIGNIFICANCE LEVEL OF  $\alpha = 0.05$ . VALUES IN BOLD MEAN THAT PSGE IS STATISTICALLY BETTER THAN GE, PGE OR SGE.

Problem	PSGE-GE	PSGE-PGE	PSGE-SGE
Quartic Polynomial	<b>0.000</b>	<b>0.003</b>	0.299
Pagie Polynomial	<b>0.033</b>	0.008	0.013
Boston Housing Train	<b>0.000</b>	1.000	0.001
Boston Housing Test	<b>0.000</b>	0.525	0.577
5-bit Parity	<b>0.000</b>	<b>0.000</b>	0.131
11-multiplexer	<b>0.000</b>	<b>0.000</b>	0.000
Santa Fe Ant Trail	<b>0.000</b>	<b>0.000</b>	0.317

Focusing on the results of Tables II and III, several observations about the approach proposed in this work can be drawn. In bold are the p-values of the comparisons where PSGE is statistically better than GE, PGE or SGE.

PSGE is statistically better than GE on all problems. Comparing the performance of PSGE with PGE, we see that PSGE

TABLE III  
EFFECT SIZE BETWEEN PSGE AND GE, PGE AND SGE.

Problem	PSGE-GE	PSGE-PGE	PSGE-SGE
Quartic Polynomial	++	+	~
Pagie Polynomial	+	-	-
Boston Housing Train	+	~	-
Boston Housing Test	++	~	~
5-bit Parity	+++	+++	~
11-multiplexer	++	+++	- - -
Santa Fe Ant Trail	+	+	~

outperforms PGE with significant differences on four of the problems. In relation to the SGE, PSGE never outperforms.

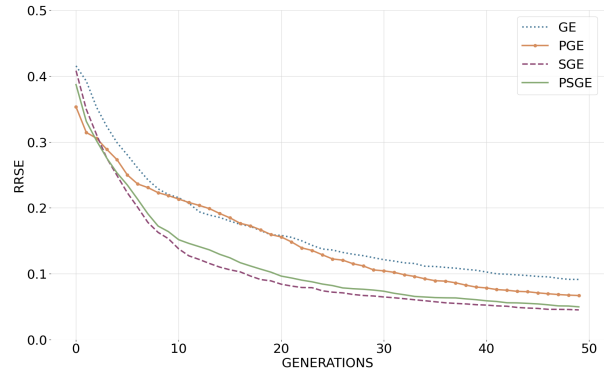


Fig. 7. Performance results for the Quartic Polynomial. Results are the mean best fitness of 100 runs.

Fig. 7 shows the evolution of the mean best fitness for the quartic polynomial. We can see that the decrease in SGE and PSGE is similar, with SGE ending up with slightly better average fitness, but with no statistical differences between the methods (Table II). Looking at the PGE curve, we notice that it starts with better fitness, being surpassed by SGE and PSGE around generation 3, decreasing more slowly in relation to the other methods. From generation 20 the fitness starts to move away from GE values, however these never reach the performance of SGE and PSGE during the 50 generations. PSGE presents statistical differences from PGE with a small effect size.

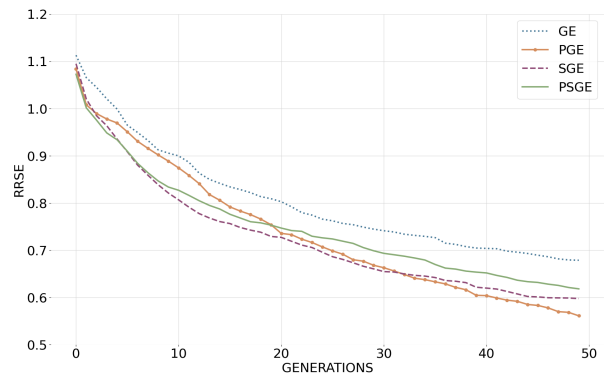


Fig. 8. Performance results for the Pagie Polynomial. Results are the mean best fitness of 100 runs.

The results for the pagie polynomial are shown in Fig. 8. By analysing the plot we see that all methods perform better than GE, with the curves decreasing faster, and looking at the statistical test results in Table II we see that PSGE is better than GE statistically with a small effect size. The method that ends up with the best average fitness is PGE, which is in line with the results presented in [15].

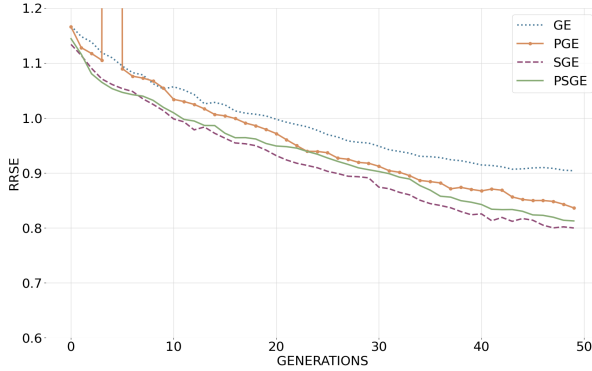


Fig. 9. Testing results for the Boston Housing. Results are the mean best fitness of 100 runs.

Regarding the results for the Boston Housing problem, these are divided in 90% for training and 10% for testing. The test results are the most relevant since they are the ones that evaluate the models with unseen data. The statistical tests show that in this problem PSGE only presents statistical differences relative to GE, having a small effect size in training and medium in testing. PSGE ends with better fitness than PGE, however these do not present significant differences. We also see that when comparing with SGE in the training, PSGE presents small statistical differences, being worse, however, in the test, these are not significant. The small improvement in the results of test PSGE over training when compared to GE and PSGE, may indicate that PSGE has a better generalisation ability to predict unknown data.

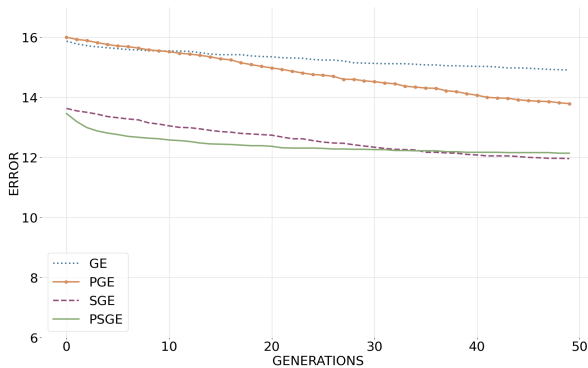


Fig. 10. Performance results for the 5-bit Even Parity problem. Results are the mean best fitness of 100 runs.

Looking at the results for the 5-bit Even Parity problem, we observe that the performance of SGE and PSGE is better than that of GE and PGE, starting with lower fitness values.

According to the statistical results, PSGE is statistically better than GE and PGE, with a large effect size. In comparison to SGE we see that the decrease of PSGE is slightly faster, maintaining better average fitness for 30 generations, and then it is reached by SGE, presenting no significant differences between the two methods.

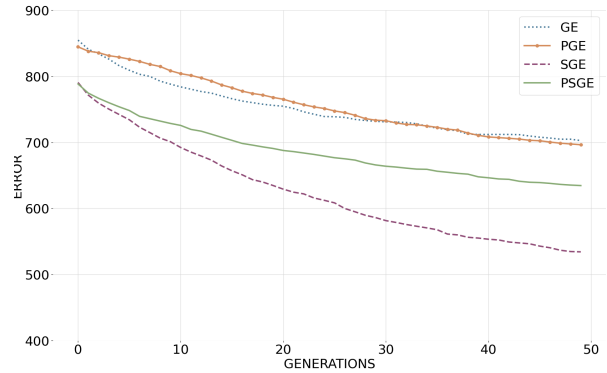


Fig. 11. Performance results for the 11-bit Boolean Multiplexer problem. Results are the mean best fitness of 100 runs.

Regarding the results of the tests done for the 11-bit Boolean Multiplexer (Fig. 11), we can see that the methods behave quite differently. As observed previously for the 5-bit parity problem (Fig. 10), the average fitness of SGE and PSGE individuals at the beginning of the evolutionary process is better, with significant differences between PSGE and GE, with a medium effect size, and also with PGE presenting a large effect size. In this problem we see that the decrease of SGE is much steeper, rapidly moving away from the average fitness of PSGE.

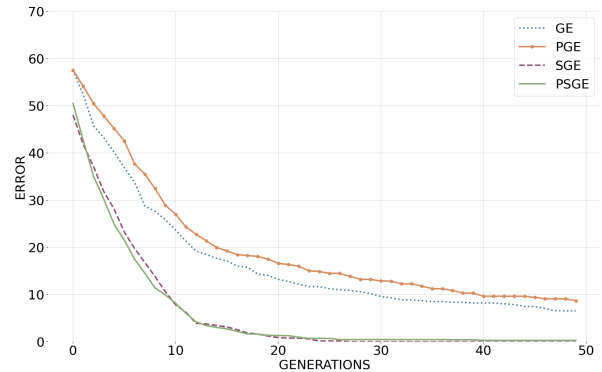


Fig. 12. Performance results for the Santa Fe Artificial Ant problem. Results are the mean best fitness of 100 runs.

The last analysis studies the performance on the Santa Fe Ant problem (Fig. 12). In contrast to the previous analyses, in this problem the method that performs worst over generations is PGE. On the other hand we observe that the fitness of the individuals of SGE and PSGE decreases rapidly, approaching the optimal solution after 20 generations. PSGE is statistically better than GE and PGE, not presenting statistical differences in relation to SGE.

## VI. CONCLUSION

GE is a grammar-based GP variant that has attracted the attention of many researchers and practitioners, since its proposal in the late 1990s and it has been applied with success to many problem domains. However, it has been shown that it suffers from some issues, such as low locality and high redundancy [5], [6].

In grammar-based GP, the choice of the grammar has a significant impact on the quality of the generated solutions as it is the grammar that defines the space of possible solutions. Our goal work was to create a variant of GE that could guide the search towards better solutions, inserting bias in the production rules that generate better individuals, in order to achieve a better overall performance, and at the same time overcome the problems of GE.

In this paper we present PSGE, a new variant of GE that introduces a new representation alternative to SGE, using PGE's mapping mechanism. The genotype is a set of dynamic lists, one for each non-terminal of the grammar. Each codon in the list represents the likelihood of selecting a production rule. At the end of each generation the PCFG is updated and individuals are remapped, same as in PGE.

The proposed method is compared to the standard versions of GE, PGE and SGE on different benchmark problems, analysing the evolution of the mean best fitness. PSGE outperformed GE with statistical differences in all problems, while it outperformed PGE in 4 of the 6 problems. Regarding the relative performance with SGE, we show that the methods obtain similar performances.

PSGE proved to be a good alternative to PGE, since it presents better performance, keeping the advantage of using a probabilistic grammar. At the end of the evolutionary process we get a specialised grammar for the problem at hand which can be used to obtain information about which production rules are more relevant to create the best individuals. The use of a PCFG can also be used by manually guide the search, for example, in the real-world problems where we have some information regarding some problems, we can alter the probabilities of the grammar by introducing some known biases. As future work it will be interesting to analyze the average fitness of sample populations created with a previously evolved grammar and also to analyze the fitness evolution over multiple generations. Another line of work that will be interesting to analyze is to test the algorithm behavior with the probabilities of grammars initialized randomly, or with different types of grammars, similar to the study done by Nicolau et al. [9].

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