Hierarchical Grammatical Evolution

Eric Medvet
DIA - Università di Trieste
Trieste, Italy
emedvet@units.it

ABSTRACT

We present Hierarchical Grammatical Evolution (HGE) and its variant Weighted HGE (WHGE), two novel genotype-phenotype mapping procedures to be used in the Grammatical Evolution (GE) framework. HGE/WHGE are designed to exhibit better variational inheritance than standard GE without imposing any constraint on the structure of the genotype nor on the genetic operators. Our proposal considers the phenotype as a hierarchy of non-terminal expansions and is based on two key ideas: (i) the closer the non-terminal to be expanded to the root of the hierarchy, the larger the genotype substring determining its expansion, and (ii) upon expansion, a non-terminal divides its genotype substring among the resulting non-terminals. We experimentally evaluate our proposals on a set of benchmark problems and show that for the majority of them WHGE outperforms GE (and its variant πGE).

CCS CONCEPTS

•**Computing methodologies → Genetic programming;**

KEYWORDS

Genotype-phenotype mapping, Representation, Locality, Redundancy

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1 INTRODUCTION

The distinctive feature of Grammatical Evolution (GE) [7] is its ability to evolve programs in any language, using a user-provided context-free grammar (CFG). In GE, each individual is represented as a string of bits (the *genotype*) which is then mapped to a program in the language defined by the grammar (the *phenotype*) by means of a genotype-phenotype mapping procedure. This mechanism relieves from the user the burden of adapting the internals of the evolutionary algorithm to his specific problem, hence favoring GE usage in a wide range of applications (e.g., [1, 6, 10]).

However, the mapping procedure of GE has been often deemed to weakly comply to the variational inheritance principle, stating that offspring should closely resemble, but not be identical to their parents [2]. In particular, many studies elaborate on GE locality and redundancy (e.g., [4, 8, 9]) and highlight its limitations in terms of these properties.

In this paper, we describe a novel genotype-phenotype mapping procedure, called Hierarchical Grammatical Evolution (HGE), and its variant Weighted HGE (WHGE), which we designed precisely with the aim of addressing GE shortcomings in terms of variational inheritance. We experimentally compare HGE/WHGE with GE showing that WHGE outperforms GE in most of the benchmark problems.

Since its original introduction, many variants of GE have been proposed (e.g., [3, 5]). The most relevant variant, w.r.t. our proposal, is Structured Grammatical Evolution (SGE) [3], which has been motivated by the same need of addressing GE poor locality and high redundancy. However, unlike our HGE/WHGE, SGE operates on an integer string genotype, whose length is a function of the grammar and the maximum depth of phenotypes (a parameter which has to be set by the user in advance), using specific genetic operators.

2 HGE/WHGE MAPPING

We consider the problem of mapping a genotype g (a bit string) to a phenotype $p \in \mathcal{L}(\mathcal{G})$, i.e., the language defined by the CFG $\mathcal{G} = (N, T, s_0, R)$, where N is the set of non-terminal symbols, T is the set of terminal symbols, $s_0 \in N$ is the starting symbol, and R is the set of production rules.

HGE mapping consists in iterating the following steps, starting with the association of the full genotype g with the only symbol $s' = s_0$ (i.e., the starting symbol) initially present in the phenotype p: (1) Let s' be a non-terminal s' in p, g' the genotype substring associated with s', and $r_{s'}$ the rule for s'. If the size of g' is greater of equal than the number of options in $r_{s'}$ (i.e., if $|g'| \geq |r_{s'}|$), then: (a) split g' in $|r_{s'}|$ substrings of equal length or, if not possible, in a way such that the variance of the lengths is the lowest; (b) find the index i for which the *relative cardinality* (i.e., count of bits set to 1 divided by the number of all bits) of the i-th substring of g' is the largest or, in case of tie, the lowest index among ties; (c) use the i-th option of $r_{s'}$ to expand s'. Otherwise, i.e., if $|g'| < |r_{s'}|$, use the option of $r_{s'}$ which leads to a sequence of terminals in the lowest number of expansions starting from s'. (2) After the expansion of s', split g' in a number $n_{s'}$ of substrings of equal length (or with lengths determined as above), with $n_{s'}$ being the number of non-terminals resulting from the expansion of s'. Then, associate with each resulting j-th non-terminal the j-th substring of g'. The procedure stops when no more non-terminals are present in the phenotype.

WHGE mapping differs from HGE in step 2, where the sizes of the substrings are proportional to the expressive powers of the

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corresponding non-terminals. We omit the details due to space constraints. An implementation of HGE/WHGE is publicly available at https://github.com/ericmedvet/evolved-ge.

Concerning locality and redundancy, some differences arise between HGE/WHGE and GE. W.r.t. locality, it can be noted that in HGE/WHGE the expansion option for a node close to the root is chosen by processing a large genotype substring, and hence it is unlikely that a single bit leads to a different choice; on the other hand, for a node far from the root, the single bit may impact on the choice. In GE a modification of a single bit could instead result in a very different phenotype. W.r.t. redundancy, it can be noted that in HGE/WHGE each bit of the genotype concurs in determining the mapping, whereas in GE, if the mapping procedure ends before the first wrapping, all the bits of the codons which were not used do not concur in the mapping.

3 EXPERIMENTAL EVALUATION

We experimentally assessed HGE/WHGE and compared them against GE and πGE [5] on 4 benchmark problems (Harmonic, Polynomial, Santa-Fe, and Text, fully described in [4]) with 3 different genotype sizes $|g|$. For each GE variant, problem, and genotype size, we performed 30 independent executions of the evolutionary search by varying the random seed and with the following evolution parameters: population of 500 individuals randomly initialized, 50 generations, one-point independent cut point crossover for GE/πGE or two-points same cut points crossover for HGE/WHGE with 0.8 rate, bit flip mutation with $p_{\text{mut}} = 0.01$ and 0.2 rate, tournament selection with size 5, $m + 1$ replacement strategy. Moreover, we set, for GE/πGE, the codon size to $n = 8$ and the maximum number of wrappings to $n_w = 5$.

Table 1 presents the results of the experimentation in terms of the fitness of the best individuals at the end of the evolution, averaged across the 30 repetitions, for different problems and mappers. For πGE, HGE, and WHGE, the table also shows the statistical significance of the Mann-Withney test performed on the best fitness values of the variant and those of GE.

It can be seen that WHGE outperforms the other variants in 11 on 16 problem/genotype size combinations. In particular, the performance gap is very large for the Harmonic problem, for which both HGE and WGHE greatly improve the best fitness at the end of the evolution with all the values for $|g|$, the differences being also statistical significant. WGHE is the best variant also in the Polynomial problem with all $|g|$ values, but the improvements are smaller.

Concerning the two other problems, our experiments do not allow to declare a clear winner among the variants: however, it can be noted that in both cases the gap between HGE and WHGE is large. Our explanation for this finding is that Santa-Fe and Text grammars exhibit a larger difference in expressive power among non-terminals than the symbolic regression grammars. This aspect likely highlights the HGE limitation concerning the splitting of the genotype among children, which is addressed in WHGE, hence justifying the performance gap.

4 CONCLUDING REMARKS

We presented HGE/WHGE, two variants of a novel genotype-phenotype mapping procedure for Grammatical Evolution. HGE/WHGE are designed to exhibit a better variational inheritance than standard GE and, in particular, to improve its locality and redundancy.

Table 1: Best fitness at the end of the evolution. In each row, the best figure is highlighted in bold. For each variant other than GE, the statistical significance of the Mann-Whitney test w.r.t. GE is shown: * means $p < 0.1$, ** means $p < 0.05$, *** means $p < 0.01$, no subscript means $p \geq 0.1$.

Problem	$\lvert g\rvert$	GE	πGE	HGE	WHGE
Harmonic	256	10.78	11.20	7.67	**6.24*****
	512	13.53	11.05	6.89***	**5.87*****
	1024	11.74	12.09	6.70	**5.83*****
Polynomial	256	2.50	2.70	2.31	**2.19**
	512	2.55	2.64	2.62	**2.36**
	1024	2.54	2.58	2.94	**1.80*****
Santa-Fe	256	44.13	**41.03****	68.00***	43.60
	512	42.30	**41.40**	62.30***	41.43
	1024	40.63	43.07	53.57***	**37.90****
Text	256	**4.70**	5.27**	6.40***	5.27**
	512	**4.87**	5.02	5.87***	4.93
	1024	5.17	5.20	5.40	**4.87**

We assessed experimentally our proposal and showed that WHGE is more effective than GE in the majority of the considered benchmark problems.

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