Semantic Operators for Evolutionary Art

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Semantic aware crossover and mutation operators [5] have become a hot topic of research within the Genetic Programming (GP) community. Inspired on the works of Sims [4] and Hart [1] concerning the generation of short animations through "genetic morphing" between individuals we propose semantic aware operators for evolutionary art.

The works of Sims [4] and Hart [1] rely on the use of a *lerp* function, which can be defined as follows: lerp(A,B) = A.t + B.(t-1), with $A, B : \mathbb{R}^n \to \mathbb{R}$ and $t \in [0, 1]$. The difference between *lerp* and the geometric semantic crossover defined by Moraglio et al. [3] is minimal: *lerp* uses the variable t to control the influence A and B on the outcome while the geometric semantic crossover uses a random function, T_R, for the same effect. Based on the work of Vanneschi et al. [6] we redefine *lerp* as follows: $lerp(T_1, T_2, T_R) = T_1.sig(T_R) + T_2.(1 - sig(T_R))$, with $T_1, T_2, T_R : \mathbb{R}^n \to \mathbb{R}$, and $sig(x) = \frac{1}{1+e^{-x}}$. Considering this redefinition of *lerp* we propose four semantic aware crossover operators based on different tree alignment algorithms [4, 1, 2].

Root Alignment: this is the simplest alignment algorithm, the roots of both parents, A and B are aligned and no further alignments are made. Considering this algorithm the result of the crossover operator between any pair of individuals A and B is $lerp(A, B, T_R)$, where T_R is a randomly generated tree. This operator is equivalent to the one presented by Moraglio et al. [3], and can, therefore, be classified as a geometric semantic operator.

First Differences Alignment: if the roots of the trees are equal recursively call the alignment algorithm for each of their arguments (unless they are leafs); if the roots are different align both roots. This approach was used by Sims [4] for creating his famous *genetic cross dissolves* between images. When the root nodes of the parents are different the outcome is equal to Root Alignment.

Constraint Alignment: considering two trees, A and B, we begin by establishing a top to bottom correspondence between the levels of both trees, discarding levels of the deepest tree when the trees have different depths; we then proceed in level by level fashion, randomly discarding nodes so that the number of nodes at each level coincides; the remaining nodes are aligned in left to right order. As noted by Hart [1] the rationale for this operator is to "continue matching nodes after encountering a difference between the trees,

since the result of the blend will often move rather than fade".

Optimal Alignment: this algorithm calculates all possible alignments between pairs of nodes and forests of children, that is every node of the first parent is compared against every node of the second parent and every forest of children of a node of the first parent is compared against every forest of children of every node of the second. The quality of each alignment between a pair of nodes, n_1, n_2 is determined by a predefined function, μ, which penalizes alignments between nodes of different types. The quality of an alignment between two trees is given by the sum of the μ values of all alignments between nodes, and the algorithm efficiently minimizes this sum.

The experimental results highlight the differences among the proposed operators and conventional crossover. They indicate that First Differences and Optimal Alignment are the most adequate for the recombination of structurally similar individuals. Optimal alignment was the operator that consistently produced interesting results when recombining structurally dissimilar ones. Although the exponential increase of program size limits the use of these operators, these semantic method are promising for the recombination of fit individuals. Future work will focus on the use of dynamic programming techniques, partial alignment and the combination of conventional and semantic methods.

References

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