

GENETIC PROGRAMMING WITH EMBEDDED FEATURES OF SYMBOLIC COMPUTATIONS

Yaroslav V. Borcheninov, Yuri S. Okulovsky

*Institute of Mathematics and Computer Sciences, Ural Federal University, Mira str. 56, Yekaterinburg, Russia
yaroslav.borcheninov@gmail.com, yuri.okulovsky@gmail.com*

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Abstract: Genetic programming is a methodology, widely used in data mining for obtaining the analytic form that describes a given experimental data set. Genetic programming is often complemented by symbolic computations that simplifies found expressions. We propose to unify the induction of genetic programming with the deduction of symbolic computations in one genetic algorithm. Our approach was implemented in the .NET library and successfully tested at various data mining problems: function approximation, invariants finding and classification.

1 INTRODUCTION

Genetic programming (Koza, 1992) is a methodology of using the genetic algorithms (Goldberg, 1986) to find a program that performs a user-specified task. We consider the particular case of genetic programming that operates not with arbitrary programs, but with expressions. Genetic programming (GP) is widely used to obtain the analytic form of the experimental data in natural sciences (Schmidt and Lipson, 2009), robotics (Robertson and Dumont, 2002), economics (Koza, 1994), medicine (Zhang and Wong, 2008), etc.

The classic GP approach can shortly be described as follows. The expressions are represented as operation trees. Initially, the *population* of expressions consists of the randomly generated expressions. On each algorithm's iteration, the following actions are performed:

- **Mutation.** The randomly chosen expression is changed by a replacement of a node.
- **Crossover.** Two randomly chosen expressions exchange subtrees.
- **After mutation and crossover,** the resulting expressions' set is subjected to selection, which evaluates how each expression fits the experimental data. The least valuable expressions are then removed from the population.

The well known problem of GP is excessive growing of expressions, or bloating. Various methods are proposed to resolve the issue: limitation of tree depth;

special mutations and crossovers that prevent bloating; selection that sort out bloated trees (Poli et al., 2008); removal of subtrees that have lesser analogs in the pool basing on evaluation on small control data sets (Mori et al., 2009).

The obvious way to reduce the expression size is algebraic or numerical simplification. If the algorithm has succeed in finding a correct expression, this expression can be simplified by some known simplification technique. However, aside from producing non-aesthetic solutions, bloating also reduces the algorithm's performance. Recent studies (Zhang et al., 2006; Kinzett et al., 2008) show the effectiveness of *online simplification*, when expressions are simplified during the evolution.

Simplifying of the expression inevitably leads to elimination of potential growing points. For example, while approximating the function $(x+2)y^2$, the intermediate solution $(2+2)y^{1+1}$ can be found. This solution will be simplified to $4y^2$, which requires at least two mutations to become a correct answer, e.g. $4y^2 \Rightarrow xy^2 \Rightarrow (x+2)y^2$. The initial solution $(2+2)y^{1+1}$ requires only one mutation $(2+2)y^{1+1} \Rightarrow (x+2)y^{1+1}$. We see, that simplification hampers the evolution in this case. On other hand, the partial simplification $(2+2)y^{1+1} \Rightarrow (2+2)y^2$ does not produce such effect for the function $(x+2)y^2$, but does so for $4y^{x+1}$. Therefore, the question of where to apply the simplification depends on the approximating function, on the particular solution, etc.

The main idea is to integrate online simplification with genetic programming on the most basic level.

To do so, we need to widen the view on the online simplification. Online simplification transforms the expression according to some rules and does not change the function, encoded by the expression. Let us call such transformations *deductive*. Transform $x + 2x \Rightarrow 3x$ is both deductive and simplifying, while $(x + y)z \Rightarrow xz + yz$ is only deductive, since it is not clear which form is more preferable. The *inductive* transforms change both the form of the expression and the encoded function. Classic mutations and crossovers above are inductive.

To combine inductive and deductive transforms, we introduce the following changes in the classic genetic programming algorithm. For mutation, a collection of rules is defined. Each rule transforms an expression in inductive or deductive way. When we need to perform the mutation operation, we randomly select a rule from the collection and apply it to a tree. Crossover operation is also defined by the set of rules. Crossover's rules have a slightly different format, they accept two trees and produce one.

Inductive and deductive tendencies can be opposing or independent. For example, while approximating $(x + 2)y^2$, the transition $2y^2 \Rightarrow (x + 2)y^2$ favors induction to the prejudice of deduction, when the transition $(2 + 2)y^2 \Rightarrow (x + 2)y^2$ is neutral for deduction. Correspondingly, the transition $(2 + 2)y^{1+1} \Rightarrow (2 + 2)y^2$ is neutral for induction, while $(2 + 2)y^{1+1} \Rightarrow 4y^{1+1}$ eliminates the future possibility for inductive transition. Therefore, we should measure fitness for both tendencies independently, to find the appropriate balance between them. In our variation of GP, the selection is performed based on various metrics. We calculate these metrics for each expression, obtain their weighted total, and then remove expressions that have the least weighted total in the population.

Our approach was implemented as a library for .NET framework in C# language (Drayton et al., 2002) and tested in various data mining problems. The project will be released under GPL v.3. license.

2 ALGORITHM'S ESSENTIALS

2.1 Trees

An expression is represented as a tree of *nodes*. The example of such tree that encodes the function $f(x) = |x|$ is shown in the Fig. 1. Three types of nodes are considered: *constants*, *variables* and *operators*. In Fig. 1, node \hat{x} is a variable node, $\textcircled{0}$ is a constant node. The remaining nodes are operators: addition \oplus , comparison $\textcircled{>}$ and ternary logical operator $\textcircled{?}$,

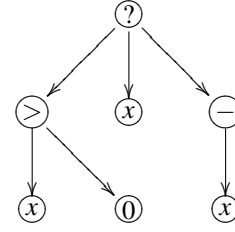


Figure 1: The tree representation of the function $f(x) = |x|$.

defined as follows

$$?(x, y, z) = \begin{cases} y, & \text{if } x \\ z, & \text{if } \neg x \end{cases}.$$

Each node has a *return type*, which is an arbitrary C# type. Different return types can be used in one expression. For example, in Fig. 1, all nodes have `double` return type, except for the node $\textcircled{>}$ that has the `bool` return type.

Each tree can be compiled into .NET lambda expression. Suppose $f(x_1, \dots, x_n)$ is a function encoded by a tree. Let a be an array of arguments $a = (x_1, \dots, x_n)$. A node for a constant c is compiled into lambda $a \mapsto c$. A node for i -th variable is compiled to $a \mapsto a[i]$. If a node encodes an operator $g(y_1, \dots, y_k)$, it is compiled into $a \mapsto g(c_1(a), \dots, c_k(a))$, where c_i is a compiled i -th child of the node. Compilation of nodes is possible due to abstract syntax trees, one of .NET features. It improves the performance of the evaluation.

2.2 Rules

Trees can be modified according to *rules*. A rule consists of the condition and the action. The first stage of a rule's application is finding all the tuples of nodes that satisfy the condition. The second stage is to apply the action to one of the selected tuples. Let us consider some examples of rules.

select ?A **where** A.Type=double **mod** A→Plus(A,c) (R1)

Here A is an identifier of selected node, c is a random constant. The rule R1 processes a tree and selects all its nodes of `double` type. It is possible to apply the rule to one of selected nodes, and replace the node with a new subtree, as shown in the Fig. 2.

The R1 rule allows us introducing an addition in a tree. Due to the type check `A.Type=double`, the `Plus` operation can only be applied to a `double` node, and therefore the tree remains correct. That shows how the rules assure correctness of mutations and crossover.

The following R2 rule shows, how the operation can be removed from a tree.

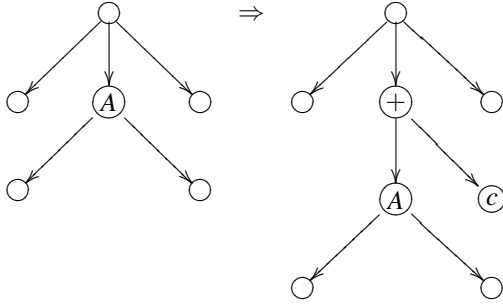


Figure 2: Application of rule R1 to a tree.

select ?A(B) **where** A.Type=B.Type (R2)
mod A→B

The rule R2 searches for a pairs (A, B) , where A is an arbitrary node, B is an arbitrary child of A , and types of A and B coincide. In each such pair, A can be replaced with B .

We also need rules for simplification of expressions. The following rules R3 and R4 are examples of such rules.

select ?A(B,C) **where** A is Plus &&
B is Const &&
C is Const (R3)
mod A→B.Val+C.Val

select ?A(B(C)) **where** A is Minus &&
B is Minus (R4)
mod A→C

Crossover operation can also be based on rules. The following rule R5 is the simplest crossover that exchanges subtrees.

select ?A,?B **where** A.Type=B.Type (R5)
produce A→B; ret A.Root

This rule accepts two trees, searches for a pair (A, B) where A is from the first tree, B is from the second tree, and their types coincide. Since the rule accepts two trees instead of one, it is not clear in which of them the crossover's result is stored. To resolve this, **mod** clause is replaced with **produce** clause, which modifies trees and returns some node as the result of the rule's application. More complex crossover schemata are available. For example, the following rule R5

select A,B **where** A.Type=double &&
B.Type=double (R6)
produce ret Div(Plus(A,B),2)

is applicable only to trees' roots A and B and returns their half-sum.

We have developed an elegant way to define rules in C#. Rules can be programmed in the almost natural way, by only defining its logic, without excessive

code to adopt this logic to C#. That was achieved with intensive use of lambda-expressions, generics and code generation. For example, rule R1 can be programmed with the code in List. 1.

Listing 1 Rule R1 definition in C#

```
var rule=Rule
.New("Intro +")
.Select("?A")
.Where<INode>(c=>c.A.Type
               ==typeof(double))
.Mod(c=>c.A.Replace(new Plus(c.A,0)))
```

2.3 Types, domains and tags

Rules are very numerous and their categorization is necessary. The first category is universal rules that are applicable to any expressions. Rules R2 and R5 are examples of such rules. The second category of rules describes data types. Following rules are required for each data type:

- T1 Introduction of a constant: replacement of a subtree with return type T to a constant of the same type;
- T2 Introduction of a variable: replacement of a subtree with return type T to a variable of the same type;
- T3 Adjustment of a constant: replacement of a constant with another constant. This action is not always reducible to the introduction of a constant. For better performance, we may replace a constant not uniformly. For example, floating point constant c may be replaced to a random number from an interval $[c(1 - \epsilon), c(1 + \epsilon)]$, where ϵ depends on the expression's valuation.

Rules of the third category describe domains of operations. Let us define a *domain* as a set of operations, which are often used in expressions together. For example, algebraic domain consists of addition, subtraction, multiplication, and so on. Trigonometric domain includes sinus, cosines and tangent operations, and relations' domain is composed of equality and inequality operators. In each domain, following types of rules can be developed:

- D1 Introduction of each operator (for example, R1);
- D2 Calculation rules for each operator (R3);
- D3 Deductive rules for operators (R4, distributivity laws, De Morgan's laws);
- D4 Special crossover rules, if they are available (R6).

In the programming implementation, an arbitrary amount of *tags* can be chosen for each rule. Tags indicate the category of the rule, the domain it belongs to, whether the rule is purposed for mutation or crossover, etc. During the work of the algorithm, each tag is associated with its weight. We also calculate the weight of each rule as a product of associated tags' weights. The weight of the rule determines how often it will be used. The probability of applying a rule with weight w is w/W , where W is a total sum of all rules' weights. Tags and weights allow us managing the algorithm. For example, on early stages, when the optimal solution is not found, inductive rules should be applied more often. When the optimal solution is found and we need to get its acceptable presentation, we should use calculation and deductive rules.

3 APPLICATION AREAS AND METRICS

3.1 Function approximation

In *function approximation* problem we are given a set of tuples $\{(x_{i,1}, x_{i,2}, \dots, x_{i,m}, y_i) : i = 1, \dots, n\}$, where $y_i = f(x_{i,1}, \dots, x_{i,m}) \cdot c_i$ and c_i is a random number from the interval $[1 - \alpha, 1 + \alpha]$. The goal is to find the analytic form of f . To do that, we use our algorithm with the following two metrics. *Fitness* metric for the function g , found by the algorithm, is calculated as

$$\rho(g) = \left(1 + \sum_{i=1}^n |g(x_{i,1}, \dots, x_{i,m}) - y_i|\right)^{-1}.$$

Taking the reciprocal value is important, because it allows bounding the value of ρ , and providing correspondence between a higher value of ρ and a better expression.

Length metric $\lambda(g)$ is a number, reciprocal to the count of operations in g . Valuation of expression is determined as a weighted total $e(g) = w_\rho \rho(g) + w_\lambda \lambda(g)$. Typically, $w_\rho = 1$ and $w_\lambda = 0.1$. In our implementation of the algorithm, we allow user adjusting metrics' weights during the algorithm's work. Such adjustment leads to interesting effects. For example, setting the weight of the length metric to negative value can drive the algorithm out of the local minimum. On the other hand, when the average ρ of the population is high, increasing the weight metric to 0.2–0.3 allows finding the most compact form of g .

In order to debug the algorithm, we may also use

perfect fitness metric

$$\rho'(g) = \left(1 + \sum_{i=1}^n |g(x_{i,1}, \dots, x_{i,m}) - f(x_{i,1}, \dots, x_{i,m})|\right)^{-1}.$$

Of course, we should not use this metric for the selection, i.e. $w_{\rho'} = 0$. However, it is interesting to compare $\rho(g)$ and $\rho'(g)$. When the noise level α is high, it is possible that for functions g_1 and g_2 holds $\rho(g_1) > \rho(g_2)$ and $\rho'(g_1) < \rho'(g_2)$. In this case, a good choice of w_λ is important: the expressions, well adjusted to noise, are often unreasonably long, and the length metric helps to sort them out.

3.2 Invariants finding

In *invariants finding* problem we are given the set $\{(x_{i,1}, x_{i,2}, \dots, x_{i,m}) : i = 1, \dots, n\}$ and need to find f such that $f(x_{i,1}, \dots, x_{i,m}) \approx 0$ (or equals to zero in the absence of noise). The algorithm requires three metric to solve the problem. The first metric is the length metric λ . The second metric is the *invariance* metric

$$\mathfrak{I}(f) = \left(1 + \sum_{i=1}^m f^2(x_{i,1}, \dots, x_{i,m})\right)^{-1}.$$

However, these two metrics are not enough. The expression $\frac{1}{2^{100+x}}$ is almost invariant on small x , however this expression is not acceptable. The solution is introducing the *tautology* metric

$$\tau(f) = 1 - \left(1 + \sum_{i=1}^k f^2(y_{i,1}, \dots, y_{i,m})\right)^{-1},$$

where $y_{i,j}$ are random numbers.

Typical weights of metrics are $w_\lambda = 1$, $w_\tau = 1$ and $w_\lambda = 0.1$.

3.3 Classification

In *classification* problem we are given the set $\{(x_{i,1}, x_{i,2}, \dots, x_{i,m}, c_i) : i = 1, \dots, n\}$, where c_i is a Boolean value indicating whether the corresponded tuple belongs to a class. It is easy to see, that our approach allows reducing the classification problem to a function classification problem by only changing the rules. We need to use the following sets of rules:

- rules for floating point type and associated operators' domains;
- rules to support Boolean type (defined by items T1–T3 in the section 2.3)
- rules to support relation operators $<$, $>$, $=$ (only D1 and D2, because these operators do not preserve the operands' types)

- rules for logical domain: operators \vee, \wedge, \neg (D1–D4).

The fitness metric is adjusted as follows

$$\sigma(g) = \left(1 + \frac{|\{i : g(x_{i,1}, \dots, x_{i,m}) = c_i\}|}{n} \right)^{-1}.$$

To debug the algorithm, we may also use control samples $\{(y_{i,1}, y_{i,2}, \dots, y_{i,m}, c_i)\}$ with the corresponded metric σ' and $w_{\sigma'} = 0$.

4 CONCLUSION AND FUTURE WORKS

We have proposed a methodology of genetic programming algorithm that combines inductive and deductive approaches. This approach was implemented in .NET library. We have supported algebraic, trigonometric and comparison operations with floating-points numbers, as well as logical operations with Boolean values. Using the library, we were able to solve the different data mining problems: function approximation, invariants finding and classification.

Our future research will be conducted in the following directions:

- Finding the parameters that provide the most efficient GP performance. By our observation, changing of rules' and metrics' intensity leads to significant changes in performance. Moreover, changing the parameters during the algorithm's work has different effect depending on the current state of the population. We believe that the thorough examination of such effects can lead to significant improvements in genetic programming.
- Using genetic programming in new domains: fuzzy numbers, fuzzy logic, temporal logic, etc.
- Exploring substitutions for length metric. Length metric does not seem to catch the intuitive meaning of "good" expression. We plan to introduce computation complexity and aesthetics metrics instead, and understand how it improves the work of the algorithm.

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