Automatic Generation of Benchmarks for Plagiarism Detection Tools using Grammatical Evolution

Manuel Cebrián, Manuel Alfonseca and Alfonso Ortega
Universidad Autónoma de Madrid
28049 Madrid, Spain
{manuel.cebrian, manuel.alfonseca, alfonso.ortega}@uam.es

Abstract

Student plagiarism is a major problem in universities worldwide. In this paper, we focus on plagiarism in answers to computer programming assignments, where students mix and/or modify one or more original solutions to obtain counterfeits. Although several software tools have been developed to help the tedious and time consuming task of detecting plagiarism, little has been done to assess their quality, because determining the real authorship of the whole submission corpus is practically impossible for graders. In this article we present a Grammatical Evolution technique which generates benchmarks for testing plagiarism detection tools. Given a programming language, our technique generates a set of original solutions to an assignment, together with a set of plagiarisms of the former set which mimic the basic plagiarism techniques performed by students. The authorship of the submission corpus is predefined by the user, providing a base for the assessment and further comparison of copy-catching tools. We give empirical evidence of the suitability of our approach by studying the behavior of one state-of-the-art detection tool (AC) on four benchmarks coded in APL2, generated with our technique.

Keywords: Education, Plagiarism detection, Computer programming assignment, Detection tools assessment, Automatic generation of benchmarks, Grammatical evolution.

1 Introduction

Undergraduate student plagiarism is becoming one of the biggest problems faced today by universities worldwide [5]. Two main types of documents are targets of plagiarism: essays and computer assignments, although cases in art degrees have also been reported [22, p. 4]. In this paper we focus on computer assignments.
Every computer science lecturer knows that plagiarism detection (copy-catch) is tedious, and extremely time consuming. Several plagiarism detection tools have been implemented since the 1960s: MOSS [3], SIM [11], YAP [13], JPlag [18], SID [7] and recently the integrative AC [15], to name the most widespread in the academic community.

The problem we are interested in occurs when facing the assessment of such tools. Quoting Whale [21, p. 145]: “Assessing different techniques for similarity detection is possible only on a relative scale”. The reason is very simple: it is almost impossible to determine whether an assignment solution is a plagiarism of another. What is more, in some cultures, a student will deny a plagiarism even in the most blatant cases. The decision of whether a solution is original or not is a matter of judgment and generally depends on the sensibility of the grader to find abnormally similar works. This subjectivity contaminates all benchmarks constructed in this way, thus little accuracy can be expected in the assessment.

Two main attempts to ameliorate this issue have been carried on. The first [10] consists of edit operations on a solution to obtain a plagiarized one: variable and function name renaming, comment removal, inversion of adjacent statements, permutation of functions, etc. The problem with this approach is that these modifications are usually done by researchers, who have a deep understanding of the assignment solution, while students have a very poor understanding of it. Another problem is due to the artisanal nature of this task, generally resulting in benchmarks of very small size. The second attempt (less ambitious) [7] builds plagiarized assignment solutions by means of random insertion of irrelevant statements into the original code in hopes that such insertions will confuse the detection mechanism.

We feel that a more principled approach is necessary in order to perform a fair comparison of detection tools. In this article we present a technique which, fed with some realistic specifications and the grammar of a programming language, is able to generate benchmarks of the desired size. Each benchmark is made of a subset containing independent solutions to the specifications, coded from scratch, and another subset - the plagiarized solutions - built from one or two solutions taken from the original subset. Both the authentic and the plagiarized sets are built by means of evolutionary techniques adapted from Grammatical Evolution [16], whose suitability for automatic programming is well established.

In this paper we try to show that having an arbitrary number of large solutions to an assignment, with a priori knowledge of their phylogeny, is the first step towards a benchmark for plagiarism.

The remainder of the paper is organized as follows: in Sect. 2 we detail the benchmark generation technique; in Sect. 3 we give experimental evidence of the suitability of this technique through several examples. Sect. 4 discusses the propriety of our approach for the generation of benchmarks. Sect. 5 proposes some conclusions and possibilities for improvement.
2 Automatic generation of benchmarks

Our benchmarks simulate the answers of different students to a practical assignment. In this paper, each benchmark consists of APL2 functions which fit a set of points generated by applying one particular function to the set of inputs (values of \( x \)) \( 1, 2, 3, 4, 5 \). Four benchmarks have been generated, corresponding to the following toy problem functions: \( x^2, 1 + x + x^2 + x^3, \cos(\log x) \) and \( \log(x^3) \).

To mimic the solutions of the students to this assignment, two sets of programs are generated for each benchmark: the first is considered original, the second contains plagiarisms. Both sets are built by means of a genetic engine in two phases: in the first, 30 original programs are generated using grammatical evolution (GE)[16]. Then 14 solutions are generated by applying several selected genetic operators, trying to reproduce the basic plagiarizing techniques performed by students.

Figure 1: Context free grammar to generate and modify the original APL2 functions. The repetition of a symbol affects the probability of its choice.

\[
E ::= O \mid \circ O \mid O O O \\
O ::= 0 1 2 3 4 5 6 7 8 9 \|
\]

\[
X | X | X | Z | Z | Z | Z | Z | Z | Z | Z | Z |
\]

\[
( E ) | ( E ) | ( E ) | ( E ) | ( E ) | ( E ) | ( E ) | ( E ) | ( E ) | ( E )
\]

\[
o ::= + | - | \times | \div | | | | | \star | O | \Theta | !
\]

Figure 1: Context free grammar to generate and modify the original APL2 functions. The repetition of a symbol affects the probability of its choice.

All the solutions consist of an APL2 function with the same header: the name of the function is \( F \), their input is argument \( X \), and their return value is variable \( Z \). The first instruction assigns the value of \( X \) to \( Z \) to guarantee that \( F \) always returns a proper value. In the ‘original’ solutions, \( F \) contains a number of additional instructions between 0 and 255. Every one assigns the value of an expression to variable \( Z \). These expressions are generated by means of GE. Figure 1 shows the context free grammar used to generate the expressions. \( E \) is the axiom. A genotype consists of a number (between 100 and 200) of integers (codons) in the \([0,255]\) interval. The first codon indicates the number of instructions to be added to the function. The genotype is mapped in the usual way, deriving the number of expressions indicated by the first codon from the initial word \( E \). The alternate execution mechanism provided by APL2 has been used to intercept semantic errors in the generated expressions, thus avoiding program failures and unexpected end conditions. Each instruction is executed in the same way and occupies a single line, therefore the size of the generated APL2 function is equal to the value of the first codon plus one.

The fitness function is the mean quadratic error of the generated APL2 function applied to the set of control points, as compared with the set of control results, scaled by a factor to punish long genotypes (size(genotype)/100), to favor parsimonial answers. The fitness optimal value is 0. The experiment stops
when the solution found has a fitness value less than 1 or when the number of
generations equals 1000. The genetic operators used are taken from mutation
with elision, mutation with elongation, genotypic recombination and phenotypic
recombination. [16].

In the generation of the 30 original solutions we have used 30 different pop-
ulations with one independently generated genotype each (corresponding to 30
different random seeds), which is equivalent to performing a hill-climbing local
search. The genotype of the next population is obtained by applying mutation
with elision to the previous individual, which is either mutated or shortened
with the same probability (0.5). Elision deletes a codon in an arbitrary location
of the genotype. The new genotype replaces the old one only if its fitness is
better.

Mutation with elongation is similar to mutation with elision: an arbitrary
codon is added in a random location of the genotype, rather than being deleted.
Each time the operator is applied on the genotype, the process is repeated 5
times.

One single point recombination is used in genotypic and phenotypic recom-
combination. In our approach, only the child that begins like its first parent is taken
into account. If we want to obtain two children, the same parents may be used
in the opposite order, although in the second case the recombination point will
be usually different. The procedure is performed 5 times and the child with the
best fitness is selected as the result of the recombination.

Phenotypic recombination acts directly on the APL2 functions, so each child
will contain the first lines of one parent and the remaining instructions of the
other parent. We have included this approach to compensate the well-known
tendency to phenotypic disruption caused by the ripple crossover operator used
in GE program generation [17].

We have applied three different techniques to plagiarize one or two origi-
nal functions. First the 5th, 10th, 15th, 20th, 25th and 30th original solutions
are plagiarized using mutation with elongation to generate 6 new APL2 solu-
tions. This technique mimics plagiarism from a single source, where the source
is changed by adding and replacing a few fragments. The second and third tech-
niques simulate plagiarisms from two sources (two different originals are mixed
to produce a new solution) by means of recombination. The second technique
generates 4 new APL2 functions through the genotypic recombination of the
following couples of originals: 5th and 10th, 10th and 5th, 15th and 20th and
20th and 15th. The third technique mixes the 20-15, 7-14, 5-22, and 30-1 cou-
pies using phenotypic recombination. Figure 2 shows a graphic scheme of the
whole process.

Figure 3 shows the existing plagiarism relations in the benchmarks. Round
vertices stand for original submissions, squares for plagiarism using a single
source, rhomboids and octagons for the two different types of plagiarism using
two sources. A black solid line between vertices A and B denotes that A has
used B as the unique source of plagiarism; a red dashed lines between A and
B denotes that A has used B as one of the two sources of plagiarism; a green
dotted line denotes that they are indirect copies, i.e. they share a common
2.1 The APL2 choice

The APL2 language has been selected as the language in which the benchmarks are coded for the following reasons:

- APL2 is a very powerful language, especially for the generation of expressions, with a large number of primitive functions and operators available.

- The APL2 expression grammar is very simple and can be implemented with just three non-terminal symbols, which simplifies the grammatical evolution process.

- APL2 instructions can be protected to prevent semantic and execution errors from giving rise to program failures. In this way, we can rest assured that all the programs in the benchmark will execute (although their results may not be a good answer to the assignment). Grammatical evolution is also simplified, because we don’t need to include any semantic information, such as attribute grammars or Christiansen’s grammars [9, 2].

- APL2 makes it possible to define new programming functions in execution time, thus providing the feasibility of integrating the fitness computation
Figure 3: Plagiarism relations of the benchmarks. Round vertices stand for original submissions, squares for plagiarism using a single source, rhomboids and octagons for the two different types of plagiarism using two sources. A black solid line between vertices A and B denotes that A has used B as the unique source of plagiarism; a red dashed line between A and B denotes that A has used B as one of the two sources of plagiarism; a green dotted line denotes that they are indirect copies, i.e. they share a common source of plagiarism.

with the genetic algorithms which generate the benchmark. With a compilable language, such as C, this would be very difficult. For a short introduction of the APL2 language see [4].

3 Experimental results

Summarizing: we have generated 4 benchmarks, each consisting of 44 submissions coded in APL2. Each benchmark is divided in the same manner:

- 30 original solutions, named P1 to P30.
- 6 mutational plagiarized results, named MPx, where x stands for the original source of plagiarism (5, 10, 15, 20, 25 and 30).
• 4 genotypic recombination plagiarized results, named P\(_x\)RGP\(_y\), where \(x\) and \(y\) represent the two source genotypes used as parents in genotypic recombination; \(y\) is considered to be the first parent.

• 4 phenotypic recombination plagiarized results, named P\(_x\)RFP\(_y\), where \(x\) and \(y\) represent the two source genotypes used as parents in phenotypic recombination; \(y\) is considered to be the first parent.

As indicated in the previous Section, the specifications of the 4 benchmarks were the functions \(x^2\), \(x^3 + x^2 + x + 1\), \(\cos(\log x)\) and \(\log x^3\). Some statistic of the generation process are shown in Table 1. Executions took about one hour per benchmark on a 2.5 GHz computer with 512 MBytes memory.

<table>
<thead>
<tr>
<th>Function</th>
<th>Ave. program size</th>
<th>Ave. instructions</th>
</tr>
</thead>
<tbody>
<tr>
<td>(x^2)</td>
<td>1889</td>
<td>120.25</td>
</tr>
<tr>
<td>(x^3 + x^2 + x + 1)</td>
<td>1954</td>
<td>126</td>
</tr>
<tr>
<td>(\cos(\log x))</td>
<td>2349</td>
<td>140</td>
</tr>
<tr>
<td>(\log x^3)</td>
<td>1735</td>
<td>108</td>
</tr>
</tbody>
</table>

Table 1: Statistics of the generation of the four benchmarks (the average program size is measured in bytes).

Now we want to check whether the sets generated with this process match our idea of typical plagiarism. To do this, we are going to feed our 4 benchmarks into the plagiarism detection tool AC [15], which works in two steps: firstly, one of the similarity metrics available is selected\(^1\), then, once pairwise distances between all submissions have been obtained, several graphical interfaces are displayed to point abnormal low distances which could imply a plagiarism.

In Fig. 4 we display a similarity graph obtained by computing a novel similarity distance on the benchmark \(x^2\). This distance looks for the longest-most infrequent string which two submissions have in common; the longer and the more infrequent the string, the lower the distance between solutions. A graph is provided by the tool, whose vertices stand for each submission solution and whose edges represent the distance between each solutions. Only distances smaller than the value chosen with the slider are shown. The bigger and hotter (more red) the edge, the smaller is the value (or the more similar are the sources). This graph constructs and displays minimum spanning trees (MSTs) built only with those distances below the threshold, 0.01 in this Figure. It can be seen that the obtained MSTs are exactly what one would desire: plagiarized versions clustered with their sources, in all but submission P17, which is a paradigmatic case of an accidental coincidence. In Fig 5, where the threshold has been increased to 0.02, the overwhelming majority of the plagiarized versions have been detected (13 out of 14), against only one additional non-plagiarized MST (P3-P28), i.e. plagiarized versions tend to appear long before non-plagiarized ones.

\(^1\)All ranging between 0 (complete similarity) to 1 (complete dissimilarity)
Figure 4: The vertices of the graph stand for each submission of the benchmark $x^2$ and the edges represent values of pairwise distances calculated using the longest-most infrequent similarity distance. Only the submissions whose pairwise distance is lower that the distance chosen by the slider (below) are shown. In this figure, the slider is set to 0.01. The bigger and hotter (more red) is the edge between two vertices (submissions), the smaller is the distance (or the more similar are the sources).

Fig. 6 shows results for a different benchmark, function $\cos(\log x)$. The distance used is the normalized compression distance (NCD, see [8]) which, in simple terms, gives a low distance to sources which compress well together, i.e. which share a large amount of literal coincidence. Finally, the visualization is based on individual temperature histograms, meaning that the hotter the color, the more elements are in this range. Each row displays the histogram of NCD distances between the submission in the leftmost part of the row and the rest of the benchmark. It can be seen that plagiarized versions are nearer to their sources than to others at distances usually outlying from the rest of the sample.

Another option available in AC provides a raw list of pairs sorted by their increasing chosen distance. In Tables 2 and 3 we display the 15 lowest distances for benchmarks $\log x^3$ and $x^3 + x^2 + x + 1$, where the NCD and the longest-most infrequent distances are used respectively. In both, authentic-plagiarized or plagiarized-plagiarized-from-the-samesubmission sources are gen-
4 Relating plagiarism to function optimization

In Sections 2 and 3 we have tried, first conceptually and then empirically, to show that copies generated by our procedure match the intuitive idea of plagiarism: an improbable high similarity between works done by different authors. If we consider this definition in depth, we find that a philosophical problem shows up:

Assume that students have some specifications for an assignment and there exists only an optimal way to code the solution. This is what we consider as optimal:

- Perfect functionality: for every input, the computer program must produce the specified output.
- Maximal parsimony: the program must be as simple as possible. During the generation process, solutions with a high number of lines are penalized, although other measures of parsimony can be used [19, 14, 6, 20].
Figure 6: We explain the first row, the next are analogue. We calculate the pairwise distances between MP10 (leftmost part of the row) and the rest of submissions of the \( \cos(\log x) \) corpora. We then depict a ‘hue histogram’ of the distances, i.e. the more red (hotter) is the color at some point (distance), the higher is the number of submissions lying at that distance from MP10. The horizontal axis of the hue histogram ranges from 0 (leftmost part, complete similarity) to 1 (rightmost part, complete dissimilarity).

In this way, there may exist only one solution with perfect functionality and maximal parsimony. These conditions are not very restrictive if, for example, we consider the way in which programming challenges are qualified (see for example [1]).

In this situation, two students delivering the optimal solution to the grader could incur in the already mentioned definition of plagiarism: absolute coincidence. What could the grader do in this situation? It could be argued that it is highly improbable that two students end up with the same code and consider them plagiarisms, but the students can reject this argument with the easy explanation that they have optimized the program independently until no further improvement was possible. If the programmers are good enough, the probability of reaching the same optimal or quasi-optimal solution is very high.

The solution to this problem is provided by the experience of the grader at copy-catching: plagiarism is usually detected much more by observing abnormal
Table 2: Lowest 15 pairwise distances obtained using the longest-most frequent distance on the benchmark $x^3 + x^2 + x + 1$.

<table>
<thead>
<tr>
<th>Distance</th>
<th>P10</th>
<th>MP10</th>
</tr>
</thead>
<tbody>
<tr>
<td>9.881421E-4</td>
<td>P15RFP20</td>
<td>P15</td>
</tr>
<tr>
<td>0.0014822131</td>
<td>P20RGP15</td>
<td>P15</td>
</tr>
<tr>
<td>0.0014822131</td>
<td>P20RGP15</td>
<td>P15RFP20</td>
</tr>
<tr>
<td>0.0019762842</td>
<td>P30</td>
<td>P1RFP30</td>
</tr>
<tr>
<td>0.0019762842</td>
<td>MP20</td>
<td>P20RGP15</td>
</tr>
<tr>
<td>0.0024703552</td>
<td>P15RGP20</td>
<td>P20RGP15</td>
</tr>
<tr>
<td>0.0029644263</td>
<td>MP30</td>
<td>P1RFP30</td>
</tr>
<tr>
<td>0.0029644263</td>
<td>MP30</td>
<td>P30</td>
</tr>
<tr>
<td>0.0039525684</td>
<td>P10RGP5</td>
<td>MP10</td>
</tr>
<tr>
<td>0.004446639</td>
<td>P18</td>
<td>P7</td>
</tr>
<tr>
<td>0.004446639</td>
<td>P18</td>
<td>P14RFP7</td>
</tr>
<tr>
<td>0.0049407105</td>
<td>P26</td>
<td>P4</td>
</tr>
<tr>
<td>0.0049407105</td>
<td>P26</td>
<td>P12</td>
</tr>
<tr>
<td>0.0049407105</td>
<td>P26</td>
<td>P18</td>
</tr>
</tbody>
</table>

coincidences in trash code, i.e. erroneous or spurious code, than for finding coincidences like similar variable or function names in correct portions of the code. The underlying idea is that there are few ways of doing things correctly, but many of doing it inaccurately, so why should two students have chosen the same way of making mistakes? Reported cases of copy-catching talk about shared lines of code that simply do nothing or two compiled codes which produce the same errors when executed. This happens because plagiarists have a poor understanding of the code and tend to incorporate trash code from the source into their code. Even those most daring who try to change some fragments of code usually fail to do it usually worsening that code.

To simulate the plagiarism process, one has to take this into account. It turns out that there is a strong correspondence of these ideas with search and optimization: perfect solutions are equivalent to global optima, while approximate solutions, those which include trash code, are equivalent to local optima.

Our proposed generation process can be seen in this light. We perform a light optimization, i.e., we try to maximize functionality and parsimony, without seeking the global optimum. This is done by limiting the number of optimization steps. In a second step the counterfeits are created. Using genotypical mutation with elongation, a new solution is created which will share a big percentage of code with the original. The shared code will consist of both useful and trash code. On the other hand, the new code generated by the mutation/elongation will probably worsen the fitness of the submission.

Figure 7 shows code fragments of submissions P5 and MP5 from benchmark cos(log $x$). Shared code and trash code are annotated to the right. Detection is possible precisely due to the shared trash code, not the useful code, because
Table 3: Lowest 15 pairwise distances obtained using NCD on the benchmark \( \log x^3 \).

<table>
<thead>
<tr>
<th>( \log x^3 )</th>
<th>( x = 3 )</th>
<th>( P1 )</th>
<th>( P1RFP30 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.01538462</td>
<td>P1</td>
<td>P15</td>
<td>P1RFP30</td>
</tr>
<tr>
<td>0.02339181</td>
<td>P15RFP20</td>
<td>P15</td>
<td></td>
</tr>
<tr>
<td>0.02339181</td>
<td>MP15</td>
<td>P15</td>
<td></td>
</tr>
<tr>
<td>0.02339181</td>
<td>MP15</td>
<td>P15RFP20</td>
<td></td>
</tr>
<tr>
<td>0.02469136</td>
<td>MP25</td>
<td>P25</td>
<td></td>
</tr>
<tr>
<td>0.13580246</td>
<td>P25</td>
<td>P20RGP15</td>
<td></td>
</tr>
<tr>
<td>0.13580246</td>
<td>MP25</td>
<td>P20RGP15</td>
<td></td>
</tr>
<tr>
<td>0.15789473</td>
<td>P20RGP15</td>
<td>P15</td>
<td></td>
</tr>
<tr>
<td>0.15789473</td>
<td>P20RGP15</td>
<td>P15RFP20</td>
<td></td>
</tr>
<tr>
<td>0.16374269</td>
<td>MP15</td>
<td>P25</td>
<td></td>
</tr>
<tr>
<td>0.16428572</td>
<td>P10RGP5</td>
<td>P5</td>
<td></td>
</tr>
<tr>
<td>0.16959064</td>
<td>P25</td>
<td>P15</td>
<td></td>
</tr>
<tr>
<td>0.16959064</td>
<td>P25</td>
<td>P15RFP20</td>
<td></td>
</tr>
<tr>
<td>0.16959064</td>
<td>MP15</td>
<td>P20RGP15</td>
<td></td>
</tr>
<tr>
<td>0.16959064</td>
<td>MP25</td>
<td>P15</td>
<td></td>
</tr>
</tbody>
</table>

the latter can be the same in both cases with a high probability. The same happens if we consider genotypical (Fig. 8) or phenotypical (Fig. not shown) recombination. The obtained codes are mixtures of the sources where trash code has been inherited from both. As it can be seen in all examples, the trash code is the fingerprint for plagiarism detection.

5 Conclusions and future work

Copy-catching computer tools are difficult to evaluate, because actual work by real students is always subject to uncertainty. To help in their evaluation for the field of computer programming assignment plagiarism, we offer a procedure which automatically generates different benchmarks which may be useful for this purpose. A benchmark for a given assignment is made of a number of original solutions, together with another set of plagiarized solutions, generated in a way so to mimic the way in which students act. We have used these benchmarks to assess the performance of one state-of-the-art detection tool (AC) with satisfactory results. The APL2 programming language has been selected for the implementation of the benchmarks because of certain properties which make it very applicable as a first instance of this process.

Benchmarks for programming in other programming languages, such as C or Java, will be attempted in the next step of our research. We will also improve the generational mechanism, so that it can code bigger and more complex submissions, not just toy problems: for instance, submissions with several functions or source files. This can be achieved by using smarter genetic operators and/or
other different automatic programming techniques (classic GP trees [12], etc).

We also intend to perform direct comparisons between the tools by using benchmarks generated with our procedure. This could be done by making some statistical analysis of the number of plagiarized sources correctly detected by each tool. It would be also possible to weight the different types of plagiarism for that analysis because, in real docent environments, the detection of single source plagiarism is usually less challenging that when several sources are mixed.

Additionally, We think it is worth to dedicate some effort to further study the role of trash code in plagiarism identification.

The APL2 program used to generate the benchmarks and the four benchmarks themselves can be found at

http://www.eps.uam.es/~mcebrian/plagiarism-benchmark

Acknowledgements

This work has been supported by grant TSI 2005-08255-C07-06 of the Spanish Ministry of Education and Science. We would also like to thank Manuel Freire for his implementation of AC, and Emilio del Rosal for his support with AC and many useful suggestions for the manuscript.
References


