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Better Similarity Coefficients to Identify Refactoring Opportunities

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Abstract Similarity coefficients are used by several techniques to identify refactoring opportunities. As an example, it is expected that a method is located in a class that is structurally similar to it. However, the existing coefficients in Literature have not been designed for the structural analysis of software systems, which may not guarantee satisfactory accuracy. This article, therefore, proposes new coefficients—based on genetic algorithms over a training set of 10 systems—to improve the accuracy of the identification of Move Class, Move Method, and Extract Method refactoring opportunities. We conducted an empirical study comparing these proposed coefficients with other 18 coefficients in other 101 systems. The results indicate, in relation to the best analyzed coefficient, an improvement from 5.23% to 6.81% for the identification of Move Method refactoring opportunities, 12.33% to 14.79% for Move Class, and 0.25% to 0.40% for Extract Method. Moreover, we implemented a tool that relies on the proposed coefficients to recommend refactoring opportunities.

Keywords Software Architecture · Structural Similarity · Code Refactoring · Move Class · Move Method · Extract Method

1 Introduction

During software development, the software architecture is subjected to several problems. Code Smells (also called Bad Smells) are defined as any symptoms

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in the code that might indicate one of these problems (Fowler et al 1999). Frequently, such Code Smells imply in the establishment of unnecessary dependencies. However, considering that ensuring architectural design is extremely important for maintainability, reusability, scalability and portability of software systems (Passos et al 2010), it is expected that the code elements of a software project be located in structurally similar entities.

It should be noted that this article takes into consideration structural dependencies among the code elements of a system for similarity calculation among packages, classes, methods and blocks. Structural dependencies occur when a compilation unit depends on another in relation to compile time or link time (Fowler 2004). Among the several types of dependency that exist in an object-oriented programming, it can be mentioned as more relevant: method and attribute access (*access*), variable declaration (*declare*), object creation (*create*), class extension (*extend*), interface implementation (*implement*), exception activation (*throw*) and use of annotations (*useannotation*).

A code structure with good similarity indexes directly influences software quality, since it evidences the high cohesion degree and low coupling, positively affecting the software architecture and maintenance characteristics.

In order to ensure the structural similarity among code entities and to avoid the occurrence of Code Smells, it must be verified the similarity of dependencies among its elements (whether in the level of package, class, method or block), besides performing refactorings when necessary. This implies moving methods and classes, and in the extraction of a code block from a method (generating a new method), through refactorings like *Move Class*, *Move Method* and *Extract Method* (Fowler et al 1999).

Figure 1 shows an example of a system that executes an MVC architecture, consisting of three layers: $Model$, $View$ and $Controller$. It is possible to note that C_2 is badly located in the $Controller$ layer, since it depends on graphical elements while other classes of the layer have dependencies to manipulation elements of request and answers (e.g., `HttpRequest` e `HttpResponse`). Therefore, it is possible to suggest moving such class (*Move Class*) to a structurally similar layer that, in this scenario, would be the $View$ layer. Such structural similarity occurs because C_2 and classes from the $View$ layer ($V_1, \ldots, V_n$) have dependencies on common graphical elements (e.g., `JPanel` e `JLabel`). Thus, refactoring would not only guarantee an architecture with properly located entities, but would also respect a MVC architecture.

Several coefficients were proposed for the calculation of similarity among code entities. However, the use of such coefficients often does not actually guarantee satisfactory accuracy. Moreover, the main current coefficients in the literature were not designed for the structural analysis of a software system. For instance, the *Jaccard* coefficient, one of the most used in Software Engineering, was initially designed to compare the similarity among flower species in different districts (Jaccard 1912).

Therefore, this article aims primarily to propose new similarity coefficients for a more precise identification of *Move Class*, *Move Method* and *Extract Method* refactoring opportunities . This makes it possible to (i) locate more ac-

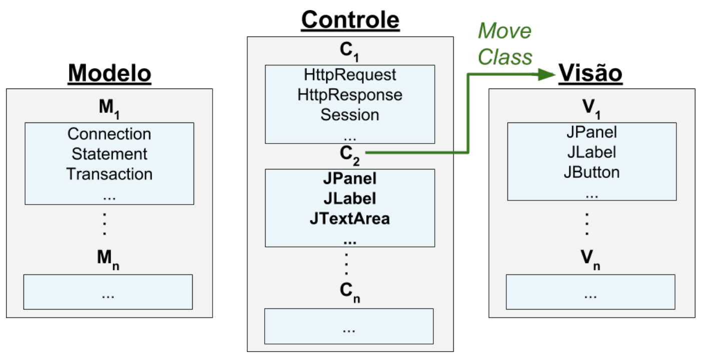


Fig. 1: Move Class Refactoring Example

curately entities improperly positioned on a system architecture and (ii) leverage the accuracy of tools for identification of refactoring opportunities based on structural similarity. It is important to emphasize, however, that the new coefficients are specific to these three refactorings, since they are the most widely used by developers (Silva et al 2016).

Firstly, the accuracy of 18 similarity coefficients in 10 systems (training set) of *Qualitas.class Corpus* (Tempero et al 2010) is analyzed. Secondly, the *Simple Matching* coefficient is adapted through genetic algorithms in order to generate three new coefficients ($PTMC$, $PTMM$ e $PTEM$) with greater precision in the identification of *Move Class*, *Move Method* e *Extract Method* refactoring opportunities, respectively. Thirdly, the proposed coefficients are compared with those existent in other 101 systems. The results indicate, in relation to the best analyzed coefficient, a statistically significant improvement from 5.23% to 6.81% for identification of *Move Method* opportunities , 12.33% to 14.79% for *Move Class* and 0.25% to 0.40% for *Extract Method*. Finally, a tool that identifies refactoring opportunities is implemented based on the proposed coefficients.

This article is an extended version of our first work on our first work on proposing such coefficients (Pinto and Terra 2017) where we highlight the following improvements: (i) an adaptation in the proposal of the coefficients, where exponents weights and more concise numbers are applied in their formulas; (ii) the introduction of a new experiment in the methodology to ensure better results of the adapted coefficients; (iii) an improved analysis of the results, addressing the problem that some data do not follow a normal distribution; (iv) new results, with higher precision of the proposed coefficients, thus more efficient; and (v) a more complete and detailed tool section.

The remainder of this article is organized as described below. Section 2 introduces fundamental concepts to the study. Section 3 describes the used methodology. Section 4 presents an analysis of existing coefficients, with the objective of selecting the coefficient to be adapted. Section 5 proposes three new coefficients for identifying refactoring opportunities. Section 6 shows an evaluation of the proposed coefficients in 101 systems. Section 7 describes the implementation of a tool to identify refactoring opportunities based on the proposed coefficients. Section 8 discusses related studies. Finally, Section 9 presents the final considerations and future research.

2 Background

In order to provide the necessary knowledge for the conception and understanding of this article, its fundamental concepts are presented. Section 2.1 deals with the refactoring process, which involves methods for source code restructuring. Section 2.2 deals with structural similarity, in besides presenting the current main coefficients in the literature. Section 2.3 introduces optimization algorithms, focusing on genetic algorithms, besides presenting an illustrative example of optimization.

2.1 Refactoring

Code refactoring is the process of moving a software system in a way that preserves the external code behavior while improves its internal structure (Fowler et al 1999). Through the refactoring, it becomes possible to treat the occurrence of different Code Smells. Although some refactoring processes take into consideration other aspects (e.g., semantics), the present study focuses exclusively on Code Smells structurally manifested in the source code.

Several techniques can be used for code refactoring. Considering that this article focuses its analysis exclusively on classes, methods and blocks of a system, the *Move Class*, *Move Method* and *Extract Method* refactorings will be used in order to address the occurrence of Code Smells. Whereas the application of *Move Class* and *Move Method* consists, respectively, in the simple movement from a class to another package and in the movement from a method to another class, *Extract Method* is accomplished through the extraction from a code block to a new method that will be generated by replacing the extracted fragment with a call to the new referred method.

Although the application of *Move Class* for repositioning a class in its due package does not address any specific Code Smell, it is fundamental to avoid the occurrence of any Code Smell, since the undue location of a class will contribute to its inadequate internal structure, i.e., it will result in inappropriately positioned methods and blocks.

However, the *Move Method* makes possible treating the following Code Smells: *Large Class*, in which the repositioning of undue methods will reduce the size of the referred class; *Divergent Change* and *Shotgun Surgery*, in which it will be possible to position methods that need changes in a specific class that does not cause the need for changes; *Feature Envy*, in which methods that overuse internal properties from another class can be moved to the other referred class; and *Refused Bequest*, where superclass methods, which do not have properties in common with all subclasses, can be moved to the subclasses that use them.

The *Extract Method* refactoring, in turn, provides means of dealing with *Long Method*, in which extracting code blocks into new methods will reduce the size of the referred method. Furthermore, although *Extract Method* deals only directly with *Long Method*, it can indirectly be used to treat other Code Smells (e.g., *Large Class*, *Divergent Change*, *Shotgun Surgery*, *Feature Envy* and *Refused Bequest*), since after extracting the code block in a new method, this one can be moved to another class through *Move Method*. In this way, the referred Code Smells can be handled in situations where they occur in only certain code blocks.

2.2 Structural Similarity

In order to identify the occurrence of Code Smells and hence code refactoring opportunities, it is primordial to analyze the structural similarity of the code entities present in a software design. Similarity, in the context of software architecture, deals with the relationship between shared properties between two or more entities present in the code structure.

For the calculation of similarity indices, several coefficients were proposed. Table 1 represents the main similarity coefficients proposed in the literature (Terra et al 2013).

Table 1: Similarity Coefficients

Coefficient	**Definition**	**Range**
Baroni-Urbani and Buser	$[a + (ad)^{\frac{1}{2}}]/[a + b + c + (ad)^{\frac{1}{2}}]$	[0-1*]
Dot-product	$a/(b + c + 2a)$	[0-1*]
Hamann	$[(a + d) - (b + c)]/[(a + d) + (b + c)]$	[-1-1*]
Jaccard	$a/(a + b + c)$	[0-1*]
Kulczynski	$\frac{1}{2}[a/(a + b) + a/(a + c)]$	[0-1*]
Ochiai	$a/[(a + b)(a + c)]^{\frac{1}{2}}$	[0-1*]
Phi	$(ad - bc)/[(a + b)(a + c)(b + d)(c + d)]^{\frac{1}{2}}$	[-1-1*]
PSC	$a^2/[(b + a)(c + a)]$	[0-1*]
Relative Matching	$[a + (ad)^{\frac{1}{2}}]/[a + b + c + d + (ad)^{\frac{1}{2}}]$	[0-1*]
Rogers and Tanimoto	$(a + d)/[a + 2(b + c) + d]$	[0-1*]
Russell and Rao	$a/(a + b + c + d)$	[0-1*]
Simple Matching	$(a + d)/(a + b + c + d)$	[0-1*]
Sokal and Sneath	$2(a + d)/[2(a + d) + b + c]$	[0-1*]
Sokal and Sneath 2	$a/[a + 2(b + c)]$	[0-1*]
Sokal and Sneath 4	$\frac{1}{4}[a/(a + b) + a/(a + c) + d/(b + d) + d/(c + d)]$	[0-1*]
Sokal binary distance	$[(b + c)/(a + b + c + d)]^{\frac{1}{2}}$	[0*-1]
Sorenson	$2a/(2a + b + c)$	[0-1*]
Yule	$(ad - bc)/(ad + bc)$	[0-1*]

The * symbol indicates the maximum similarity

For the understanding of each similarity coefficient, consider two code entities A and B. Taking into consideration that this article analyzes structural dependencies among code entities, it has the following variables:

a = number of dependencies in both entities,
b = number of exclusive dependencies of entity A,

c = number of exclusive dependencies of entity B, and
d = number of the remainder from the total dependencies considered.

In order to illustrate the calculation of structural similarity between two code entities, the *Jaccard* and *Simple Matching* coefficients were applied in two methods of the system MyAppointments, a system of control and management of commitments (Passos et al 2010). In this way, there were selected the methods `loadAppointments`, responsible for loading appointments of the system, and `getAppointmentRowAsDate`, responsible for returning the appointment date of a specific row in the data set. Both methods are present in the same control class. Code 1 shows the implementation of both methods `loadAppointments` and `getAppointmentRowAsDate`.

Based on the analysis of both methods and the structural dependencies present in their structures, it has:

- $a = 2$, since both methods access `AgendaView` and `DateUtils` methods (highlighted by red color);

- $b = 4$, since the method `loadAppointments` has the following exclusive dependencies: launching an exception of type `Exception`, declaration of `List`, declaration of type `Appointment` and access to `AgendaDAO` methods (highlighted by blue color);

```
public class AgendaController
   ...

   public void loadAppointments() throws Exception {
      List<Appointment> apps = agendaDAO.getAppointments
         (DateUtils.getCurrentDay(),
               DateUtils.getCurrentMonth(),
                      DateUtils.getCurrentYear());

      int i = 0 ;
      for(Appointment app : apps) {
         agendaView.insertAppointRow
            (i, DateUtils.toString(
               app.getDate(),
               DateUtils.HOUR_FMT),
               app.getTitle());
         i++ ;
      }
   }

   private Date getAppointmentRowAsDate(int row) {
      String[] appHour =
        agendaView.getAppointmentRow(row)[0].split(":");
      return DateUtils.newDate
         (DateUtils.getCurrentDay(),
            DateUtils.getCurrentMonth(),
            DateUtils.getCurrentYear(),
            Integer.parseInt(appHour[0]),
            Integer.parseInt(appHour[1]));
   }
}
```

Code 1: **AgendaController** Fragment

– $c = 1$, since the exclusive dependency of the method `getAppointmentRowAsDate` is the declaration of type `Date` as return (highlighted by green color);

– $d = 32$, since when considering the system as a whole, another 32 different types of dependencies are used.

It should be noted that dependencies to primitive types (e.g., `int`, `char`, `byte`, etc.), to wrappers classes (e.g., `Integer`, `Long`, `Character`, etc.) and `String` type are disregarded during the analysis, since almost all classes establish dependencies with these types, not contributing to the similarity calculation.

Therefore, when applying, as example, the *Jaccard* and *Simple Matching* coefficient, the following similarity indexes are found:

$$\textit{Jaccard} = \frac{a}{a + b + c} = \frac{2}{2 + 4 + 1} = 0.28 \tag{1}$$

$$\textit{Simple Matching} = \frac{a + d}{a + b + c + d} = \frac{2 + 32}{2 + 4 + 1 + 32} = 0.87 \tag{2}$$

Thus, it is important to mention that only the gross value does not indicate the similarity level with accuracy, since it is necessary to observe and compare the other similarity values of the system altogether. For instance, 0.28 (*Jaccard*) can be considered a high similarity value if the mean similarity of the system is 0.12. Similarly, 0.87 (*Simple Matching*) can be considered as a low value.

2.3 Optimization Algorithms

Optimization refers to the process of finding and comparing solutions to a given problem, maximizing and/or minimizing the values of the variables that compose the objective function until the best possible solution is found (Chis 2010). However, in many cases, a problem does not have an optimal solution, which results in the search for solutions that meet the desired objective satisfactorily. This concept, in turn, can be applied to adapt and improve the similarity coefficients discussed in the previous section.

When searching solution of optimization problems, several approaches can be applied, involving different types of algorithms. Among the several approaches, the application of a simple genetic algorithm has shown to be able to find satisfactory solutions effectively. Therefore, it has become the chosen approach for application in this article.

2.3.1 Genetic Algorithms

A genetic algorithm defines a set of candidates for the proposed solution and, at each iteration (each generation of the genetic algorithm), selects and combines the most suitable candidates, which may undergo slight changes. Thus, at the end of all execution, the solution set will consist of candidates with relative great potential to optimize the objective function (Sivanandam and Deepa 2007).

Considering the problem of optimizing similarity coefficients, the algorithm defines weights and exponents for each variable of the coefficient formula chosen and each iteration seeks to adapt each weight and exponent in order to optimize the result of the objective function, finally selecting the set of best results. For instance, considering the *Jaccard* coefficient (presented in Table 1), and the weights $P_{a'}$, $P_{a''}$, P_b and P_c, as also the exponents $E_{a'}$, $E_{a''}$, E_b and E_c, corresponding, respectively, to the variables a of the numerator and a, b and c of the denominator. Thus, it has as a result:

$$\textit{Resulting Coefficient} = \frac{P_{a'} * \texttt{a'}^{E_{a'}}}{P_{a''} * \texttt{a''}^{E_{a''}} + P_b * \texttt{b}^{E_b} + P_c * \texttt{c}^{E_c}} \tag{3}$$

During the execution of a genetic algorithm, the parameters are defined, such as objective function (or fitness function), initial population, number of generations, selection operator, crossover operator and mutation operator. The objective function represents the data or function to be optimized. The initial population stipulates the initial number of possible candidates for the desired weights and exponents in order to optimize the objective function. Number of generations refers to the number of times the genetic algorithm will be repeated, i.e., iterate by adapting the desired values. The selection operator will choose candidates that are more likely to cross-check between them, thus generating one or more candidates who may show more suitability to the solution set. Finally, the generated candidate(s) may undergo a slight mutation, i.e., a slight change in its value, which prevents its stagnation, besides allowing it arriving at any point of the search space.

Among the different operators of selection, crossing and mutation, this article uses, respectively, *Binary Tournament*, *Simulated Binary Crossover* e *Polynomial Mutation*. The *Binary Tournament* method selects, among all the possible generated candidates until then, two individuals that present higher results in relation to the objective function so that they are crossed. The *Simulated Binary Crossover* occurs through the crossing of two individuals, combining their binary representations, in order to generate two new individuals. Such a combination considers a defined probability, analyzing whether each binary index should be combined or not. Finally, the *Polynomial Mutation* also considers a defined probability in order to change one or more binary indexes of the individuals resulting from the crossover. In both crossover and mutation operators, a distribution index must be established in order to evaluate the diversity of the selected solutions in search space, which guarantees the selection of more heterogeneous individuals.

2.3.2 Illustrative Example

For a better understanding of the approach of optimization algorithms and concepts of genetic algorithms, this section presents the application of a genetic algorithm to optimize the *Jaccard* similarity coefficient in a little example of *Move Class* refactoring.

For instance, take as assumption a system with two packages $pkg1$ and $pkg2$ with a set of classes and their dependencies, respectively, as $pkg1 = \{A=\{X,Y,W,Z\}, B=\{X,Y,Z,L\}, C=\{X,Y,W,K\}\}$ and $pkg2 = \{D=\{X,W,R,T\}, E=\{R,T,Z\}, F=\{X,Z,R,T,M\}\}$, according to Figure 2.

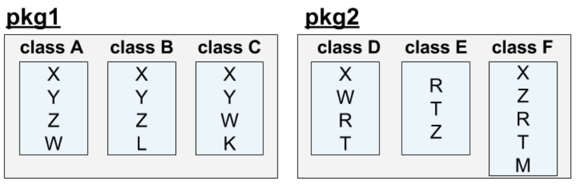


Fig. 2: Illustrative Example

Assume it is known that the current system architecture is the ideal one and we intend to use a similarity coefficient in which does not result in suggestions of *Move Class* refactoring, i.e., maintain the current architecture and guarantee good similarity indexes among classes from the same package. To this end, it is intended to adapt a coefficient in order to maximize the similarity of $sim(A,B)$, $sim(A,C)$, $sim(B,C)$, $sim(D,E)$, $sim(D,F)$ and $sim(E,F)$. Simultaneously, it is expected to minimize the similarity $sim(A,D)$, $sim(A,E)$, $sim(A,F)$, $sim(B,D)$, $sim(B,E)$, $sim(B,F)$, $sim(C,D)$, $sim(C,E)$ e $sim(C,F)$. However, only the gross value does not indicate the similarity level with accuracy, since it is necessary to observe and compare the other similarity values of the system altogether. In this way, it is intended obtaining the largest possible difference between the arithmetic mean of similarities aimed to maximize and to minimize.

Taking into consideration the *Jaccard* coefficient as an example, it is decided to apply the genetic algorithm defining weights and exponents for each coefficient variable, as previously described in Equation 3. In this way, the configurations presented in Table 2 were used, which was obtained after a series of attempts aimed to improve the coefficients, considering the computational resource disposition and execution time.

In this scenario, it was found as a possible solution set, the weights 1.34 ($P_{a'}$), 0.33 ($P_{a''}$), 1.0 (P_b) and 0.34 (P_c), as also 0.5 ($E_{a'}$), 1.0 ($E_{a''}$), 2.0 (E_b) and 2.0 (E_c), respectively to the variables a of the numerator and a, b and c of the denominator. The Comparison of similarity between *Jaccard* and the resulting coefficient is shown in Table 3.

Table 2: Genetic Algorithms Configuration

Objective function:	Number of optimized similarities	**Crossover operator:**	Simulated Binary Crossover
Population size:	1200	**Probability of mutation:**	0.6
Representation of the population:	$\{x \in \mathbb{R} \mid -2 \leq x \leq 2\}$	**Probability of crossover:**	0.9
Number of generations:	150	**Mutation distribution index:**	20.0
Selection operator:	Binary Tournament	**Crossover distribution index:**	20.0
Mutation operator:	Polynomial Mutation		

Table 3: Comparison between *Jaccard* and the Resulting Coefficient

Maximize				
Objective	***Jaccard***	**Similarity**	**Resulting Coefficient**	**Similarity**
sim(A,B) $=$	$\frac{3}{3+1+1} =$	0.6	$\frac{1.34*\sqrt{3}}{0.33*3^1+1.0*1^2+0.34*1^2} =$	0.9961
sim(A,C) $=$	$\frac{3}{3+1+1} =$	0.6	$\frac{1.34*\sqrt{3}}{0.33*3^1+1.0*1^2+0.34*1^2} =$	0.9961
sim(B,C) $=$	$\frac{2}{2+2+2} =$	0.3333	$\frac{1.34*\sqrt{2}}{0.33*2^1+1.0*2^2+0.34*2^2} =$	0.3148
sim(D,E) $=$	$\frac{2}{2+2+1} =$	0.4	$\frac{1.34*\sqrt{2}}{0.33*2^1+1.0*2^2+0.34*1^2} =$	0.3790
sim(D,F) $=$	$\frac{3}{3+1+2} =$	0.5	$\frac{1.34*\sqrt{3}}{0.33*3^1+1.0*1^2+0.34*2^2} =$	0.6928
sim(E,F) $=$	$\frac{3}{3+0+2} =$	0.6	$\frac{1.34*\sqrt{3}}{0.33*3^1+1.0*0^2+0.34*2^2} =$	0.9876
Mean		**0.5055**	Mean	**0.7277**

Minimize				
Objective	***Jaccard***	**Similarity**	**Resulting Coefficient**	**Similarity**
sim(A,D) $=$	$\frac{2}{2+2+2} =$	0.3333	$\frac{1.34*\sqrt{2}}{0.33*2^1+1.0*2^2+0.34*2^2} =$	0.3148
sim(A,E) $=$	$\frac{1}{1+3+2} =$	0.1667	$\frac{1.34*\sqrt{1}}{0.33*1^1+1.0*3^2+0.34*2^2} =$	0.1253
sim(A,F) $=$	$\frac{2}{2+2+3} =$	0.2857	$\frac{1.34*\sqrt{2}}{0.33*2^1+1.0*2^2+0.34*3^2} =$	0.2455
sim(B,D) $=$	$\frac{2}{2+2+2} =$	0.3333	$\frac{1.34*\sqrt{2}}{0.33*2^1+1.0*2^2+0.34*2^2} =$	0.3148
sim(B,E) $=$	$\frac{0}{0+4+3} =$	0.0	$\frac{1.34*\sqrt{0}}{0.33*0^1+1.0*4^2+0.34*3^2} =$	0.0
sim(B,F) $=$	$\frac{1}{1+3+4} =$	0.125	$\frac{1.34*\sqrt{1}}{0.33*1^1+1.0*3^2+0.34*4^2} =$	0.0907
sim(C,D) $=$	$\frac{1}{1+3+3} =$	0.1429	$\frac{1.34*\sqrt{1}}{0.33*1^1+1.0*3^2+0.34*3^2} =$	0.1081
sim(C,E) $=$	$\frac{1}{1+3+2} =$	0.1667	$\frac{1.34*\sqrt{1}}{0.33*1^1+1.0*3^2+.0.34*2^2} =$	0.1253
sim(C,F) $=$	$\frac{2}{2+2+3} =$	0.2857	$\frac{1.34*\sqrt{2}}{0.33*2^1+1.0*2^2+0.34*3^2} =$	0.2455
Mean		**0.2044**	Mean	**0.1744**

It is possible to observe that the coefficient resulting from the optimization showed to be much more efficient than the *Jaccard*, coefficient, since it obtained a difference between the mean of similarities that should be maximized and the mean of the similarities that should be minimized of 0.55, in contrast to *Jaccard* which obtained a difference of only 0.30. Therefore, the resulting coefficient proved to be the most adequate and accurate for the similarity analysis in the presented example.

3 Methodology

In order to create three new similarity coefficients that are more efficient in identifying, respectively *Move Class*, *Move Method* and *Extract Method*refactoring opportunities this article adopts a methodology based on the selection of a coefficient to be adapted through the analysis of the main existing similarity coefficients (Section 4), in the proposal of the three new coefficients after adaptation of the respective selected coefficient (Section 5) and in the evaluation of the same coefficients (Section 6). Finally, the proposed coefficients are applied through a plug-in implementation for the Eclipse IDE (Section 7).

In this respect, the similarity calculation, used in each methodology step, is performed by comparing a given class to a given package, besides comparing a certain method to a particular class, as well as analyzing the resulting similarity of a given class after the extraction of a particular block for generation of a new method. Such process is detailed below.

3.1 Similarity Calculation

Class-Package: The similarity of a class with a package is given through the arithmetic mean of the similarity between the respective class and the other classes present in the package. This is because whether only the class similarity to the package were calculated in general, the set of dependencies of the package could result in a high similarity even though the classes were not similar, presenting low indices. Consequently, it is possible to suggest *Move Class* refactorings for packages that actually have similar classes.

Method-Class: The same approach used to identify *Move Class* refactoring opportunities is applied to the similarity analysis between methods and classes, in which it is considered the similarity mean between one method and the other methods in the class.

Block-Method: Initially, the similarity of each method of a class is calculated with the other methods of the same class, thus obtaining the internal similarities of the class. Then, for each method, all the extraction possibilities of its blocks will be analyzed in order to generate a new method (*Extract Method*), i.e., for each extracted block, the similarities of the class after extraction will be recalculated, including the new generated method. Finally, the arithmetic means of both sets of values are compared in order to verify whether or not the *Extract Method* refactoring should be suggested.

In this way, the coefficients are analyzed and evaluated using the systems from *Qualitas.class Corpus* (Tempero et al 2010), database with 111 object-oriented systems, more than 18 million LOC (*Lines Of Code*), 200 thousand compiled classes and 1.5 million compiled methods. Based on the fact that the *Qualitas.class Corpus* is composed of more mature and stable systems, it is assumed that the current structure of systems has the highest similarity index in relation to possible code refactorings. To briefly summarize, it is intended that the structure be maintained and no refactoring be performed. Thus, it is possible to evaluate the accuracy of each similarity coefficient in view of each analyzed system.

Execution Instructions: To avoid the occurrence of false positives in the resulting refactoring recommendations, after a series of experimental tests and executions, nine execution instructions were defined for the implementation of the proposed solution:

1. *The entity under review is disregarded whereas the system searches for refactoring opportunities.* When the similarity between a class A and its respective package Pkg is calculated, the system considers Pkg to be Pkg - $\{A\}$. In this case, individually located entities are totally discarded;
2. *Packages and test classes are not considered*, since most systems organize their test classes into a single package. Therefore, this package contains classes related to different parts of the system, i.e., they are not structurally related. For this purpose, an approach that disregards packages and classes containing the text "`test`" (uppercase or lowercase) anywhere in its name is used. Although neither all test package or class containing the text "`test`" and not every package or class that contains it is in fact a test package or class, the gain in precision is greater than the loss when test packages or classes are erroneously detected;
3. *Trivial dependencies are ignored.* Dependencies such as those established with primitive types and wrappers (e.g., `int` and `java.lang.Integer`), dependencies of `java.lang.String` and `Java.lang.Object`, etc are filtered. Since the vast majority of code elements establish dependencies with these types, they do not actually contribute to the similarity calculation;
4. *Class, method, or block entities that establish dependencies with fewer than three types are not analyzed.* Although there may be entities with few dependencies that should be refactored, these entities contain little information for calculating similarity or for making any inference based on their structural dependencies. However, it should be noted that although these entities are not analyzed whether they should be refactored, they are still considered as a possible refactoring destination, whether they have at least some dependency;
5. *Entities that are not colocated with at least two other parsable entities are not analyzed.* For instance, a package with only two classes does not provide enough structural information to recommend whether or not to move its classes. Again, this criterion disregards only the analysis of such entities, but can still be considered as a refactoring destination;
6. *It is not possible to extract the first block of a method.* The extraction of the first block of a method will not change a similarity. Since the extraction of a block will result in the extraction of its internal blocks, this operation will only recreate the respective method. In this situation, the ideal would be to move the method;
7. *Any dependency present on an internal entity class, method or block will be assigned to its external entities.* Given that an internal code entity

(e.g., nested classes, internal methods and blocks, etc.) is present within the scope of the external entity(ies), any established dependency must be assigned to external entities;

8. *Methods and blocks belonging to an* `Interface` *type will be disregarded.* Due to the very nature of interfaces being composed of abstract members, they should not be moved or extracted, since this would lead to a series of conflicts in the project structure; and
9. *Constructor methods and their respective blocks will be disregarded.* Considering the requirement of constructors in a class, the movement of this method type is disregarded, although it is intended to evaluate the possible extraction of its internal blocks.

4 Analysis and Comparison of Coefficients

This section analyzes and compares the existing similarity coefficients in order to find the most adequate coefficient to be adapted. Thus, new similarity coefficients are proposed in order to obtain higher precision rates. Thus, 18 similarity coefficients (Table 1) are analyzed in 10 completely randomized systems (training set) of *Qualitas.class Corpus*, as can be observed in Table 4.

Table 4: Target-Systems

System	Version	System	Version
Ant	1.8.2	JFreeChart	1.0.13
ArgoUML	0.34	JHotDraw	7.5.1
Collections	3.2.1	JMeter	2.5.1
Hibernate	4.2.0	JUnit	4.1
JEdit	4.3.2	Tomcat	7.0.2

All analyzed similarity coefficients were applied to each entity of the selected target systems, analyzing whether an entity has the highest similarity degree found with the entity to which it should be positioned. For instance, for a class A, each coefficient is applied by comparing A with each package in the system, seeking to verify whether the highest found similarity rate (*Top #1*) corresponds to the package in which A is actually positioned. This evaluation also analyzes the second (*Top #2*) and the third (*Top #3*) higher rate in order to verify whether the applied coefficient has at least results close to the desired one. Finally, the arithmetic mean is calculated on each system of training set considering *Top #1*, *Top #2* and *Top #3*. Considering that some sets of means do not follow a normal distribution, the analysis is performed over the median of these sets of means, since median represents a better estimate of central tendency than the overall mean for a system.

Each coefficient was evaluated separately in relation to the types of code refactoring *Move Class*, *Move Method* and *Extract Method*. Table 5 presents the similarity accuracy of the addressed coefficients in relation to the identification of the *Move Class*, *Move Method* and *Extract Method* refactoring opportunities. *Extract Method* refactorings take into consideration only a single success rate, since for *Extract Method* refactorings it is only analyzed whether the method should be extracted or not, therefore, the possibility of success in the second or third attempt is discarded (*Top #2* ou *Top #3*). For space constraints, the detailed table with the results of each system is publicly available from (Pinto and Terra 2018).

For a complementary analysis between the data, Figure 3 presents a violin plot regarding *Top #1* of each refactoring, where it is illustrated the density of each coefficient (i.e, probability of a variable assume a certain value), as well as its quartiles, including its median. The dashed line indicate the highest coefficient median.

After analyzing and comparing the main existing coefficients, *Simple Matching* was selected to be adapted in order to generate a new coefficient. This choice was because the *Simple Matching* coefficient has an easy structure to be adapted, defining weights for the variables, thus contributing to obtain good results in the proposal of new coefficients. In contrast, a large part of the analyzed coefficients already had defined weights. Although it was not the best-performing coefficient, the possible weight definition of *Simple Matching* allows simulating coefficients as *Sokal and Sneath 2*, which was the best coefficient in *Move Method* and second best in *Move Class*[1], as well as *Russell and Rao*, which obtained greater accuracy in *Extract Method*. Additionally, the coefficient considers the universe of dependencies, in contrast to the coefficients *Jaccard*, *Sorenson*, *Ochiai*, *PSC*, *Dot-product* and *Sokal and Sneath 2*.

5 Proposal of New Coefficients

Given the fact that genetic algorithms have nondeterministic execution and results, it becomes a problem to know if their results are satisfactory or even adequate for the expected purpose. In order to address this problem, it was designed an experiment for the proposal of the new coefficients. The experiment consists in a treatment combination with replication, i.e. the repetition of multiple executions in different groups of factor levels. This design is composed by two factors, the initial population size and the number of generations for the genetic algorithm.

After selecting the *Simple Matching* coefficient to be adapted, several executions of a genetic algorithm is applied to the referred coefficient, having 10 systems of the *Qualitas.class Corpus* as training set.

The conducted experiment aimed to find which candidates resulted in a better value for the objective function. For this purpose, the configuration used by the genetic algorithm was the same as that used in the illustrative example

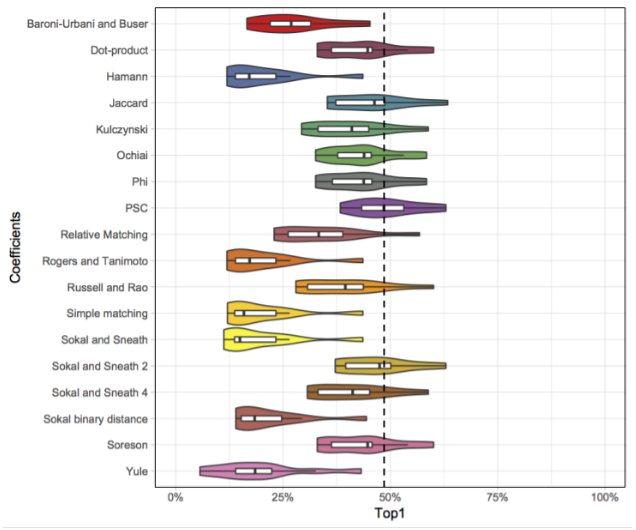
[1] *PSC* was the best coefficient for *Move Class*, however, it was not selected because it englobes elementary arithmetic operations among the variables a, b, and c. Such mathematical relation is out of the scope of this study.

Table 5: Similarity precision of the 18 similarity coefficients (training set)

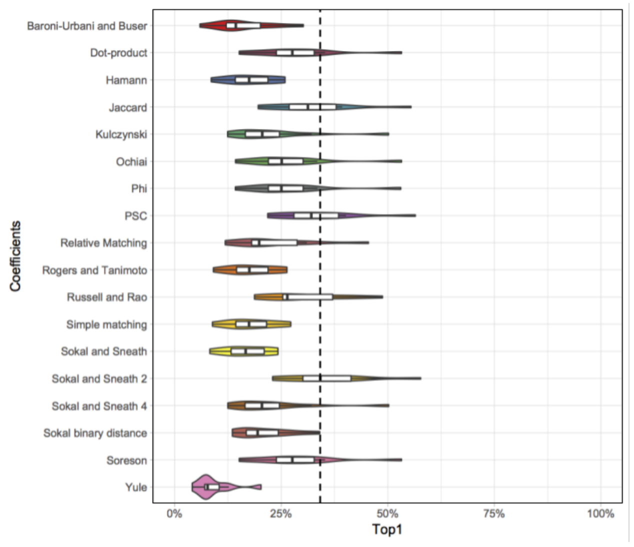
MOVE CLASS			
Coefficient		**Median**	
	Top1	**Top2**	**Top3**
Baroni-Urbani and Buser	26.91%	40.39%	47.10%
Dot-product	44.73%	55.69%	62.34%
Hamann	17.14%	22.94%	25.15%
Jaccard	46.30%	59.24%	64.25%
Kulczynski	41.03%	55.41%	63.02%
Ochiai	43.89%	56.72%	63.55%
Phi	43.80%	56.84%	63.00%
PSC	48.49%	62.33%	71.32%
Relative Matching	33.33%	45.95%	52.75%
Rogers and Tanimoto	17.23%	23.17%	25.35%
Russell and Rao	39.52%	53.14%	61.12%
Simple matching	15.90%	22.94%	25.20%
Sokal and Sneath	14.96%	22.61%	24.80%
Sokal and Sneath 2	47.50%	60.10%	66.08%
Sokal and Sneath 4	41.23%	55.52%	63.12%
Sokal binary distance	18.40%	24.57%	27.06%
Sorenson	44.73%	55.69%	62.34%
Yule	18.51%	29.42%	34.62%

MOVE METHOD			
Coefficient		**Median**	
	Top1	**Top2**	**Top3**
Baroni-Urbani and Buser	14.34%	19.03%	23.66%
Dot-product	27.61%	37.43%	44.09%
Hamann	17.47%	23.78%	28.48%
Jaccard	31.25%	41.54%	48.59%
Kulczynski	20.54%	28.38%	35.27%
Ochiai	25.11%	33.88%	40.41%
Phi	25.03%	33.88%	40.41%
PSC	32.05%	43.75%	51.06%
Relative Matching	19.82%	27.90%	33.41%
Rogers and Tanimoto	17.52%	23.95%	28.84%
Russell and Rao	26.43%	36.13%	43.52%
Simple matching	17.45%	23.78%	28.32%
Sokal and Sneath	16.65%	23.06%	27.58%
Sokal and Sneath 2	34.17%	45.26%	52.27%
Sokal and Sneath 4	20.46%	28.33%	35.27%
Sokal binary distance	19.46%	26.73%	33.12%
Sorenson	27.61%	37.43%	44.09%
Yule	7.72%	12.81%	17.28%

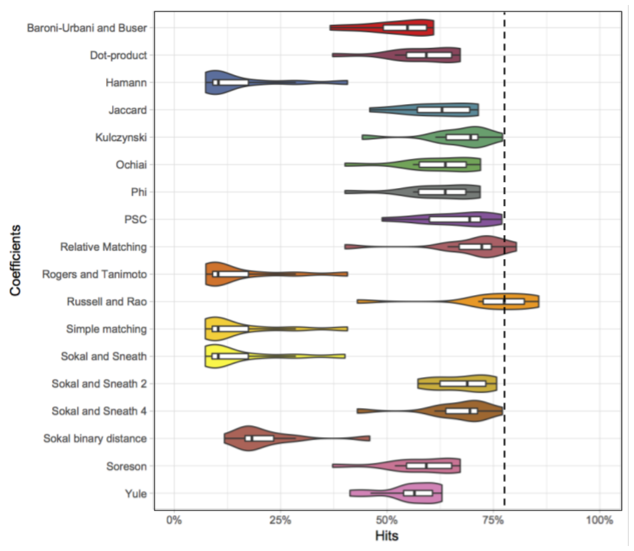
EXTRACT METHOD	
Coefficient	**Median**
	Hits
Baroni-Urbani and Buser	54.80%
Dot-product	59.23%
Hamann	10.37%
Jaccard	62.92%
Kulczynski	69.65%
Ochiai	63.71%
Phi	63.69%
PSC	69.42%
Relative Matching	72.27%
Rogers and Tanimoto	10.29%
Russell and Rao	77.55%
Simple matching	10.31%
Sokal and Sneath	10.34%
Sokal and Sneath 2	68.85%
Sokal and Sneath 4	69.48%
Sokal binary distance	18.24%
Sorenson	59.23%
Yule	56.45%



(a) Move Class



(b) Move Method



(c) Extract Method

Fig. 3: Refactorings Plots

of Section 2.3.2 (see Table 2). However, in order to find better results and lower the degree of uncertainty, it was defined five configuration groups, with the combination of different factor levels, and replicated five times each, totaling 25 executions. More precisely, each group maintains the original genetic algorithm configuration, changing only the initial population size and the number of generations (the experiment factors), as shown in Table 6.

Table 6: Experiment Groups of Factor Level

	Population Size	**№ of Generations**
Group 1	2000	1000
Group 2	1500	1500
Group 3	500	2000
Group 4	300	2500
Group 5	100	3000

It is important to clarify that each new proposed coefficient is resulting from a different set of executions of the genetic algorithm (25 executions for each coefficient). Since a single iteration of the genetic algorithm performs thousands of comparisons between code entities to improve results, this number of executions is relatively satisfactory.

After generating the set of solutions, in most cases are presented several possibilities that result in the same highest accuracy rate. Therefore, a single solution is selected that shows a greater distance between the mean of similarity indexes that it seeks to maximize with the mean of indexes that it seeks to minimize, since a greater distance indicates that the coefficient will tend to maximize and to minimize the similarities correctly in other systems.

Thus, considering the possibility of defining weights to the *Simple Matching* coefficient variables, it was initially simulated as genetic algorithm candidates the weights of *Sokal and Sneath 2* coefficient for *Move Class* and *Move Method* refactorings, as well as *Russell and Rao* weights for *Extract Method* refactorings, which facilitates the selection of new candidates, since they were among the best results in their respective refactorings. Subsequently, it was performed the executions of the genetic algorithm on the 10 systems (training set) in order to obtain more adequate weights for each coefficient variable and to create the new coefficients to be evaluated in the other 101 systems (test set).

Finally, each execution of the experiment was carried out in order to find a higher value for the objective function. Table 7 shows the values of each execution.

In this way, the following coefficients were proposed, where each one corresponds to a type of refactoring code: $PTMC$ for *Move Class* operations, $PTMM$ for *Move Method* operations and $PTEM$ for *Extract Method* operations. The implementation of the genetic algorithm on *Simple Matching* in the defined training set resulted in the first version of the three sought coefficients. The resulting weights $P_{a'}$, $P_{d'}$, $P_{a''}$, P_b, P_c and $P_{d''}$, as also the resulting exponents $E_{a'}$, $E_{d'}$, $E_{a''}$, E_b, E_c and and $E_{d''}$, corresponding to the variables a

Table 7: Experiment's Objective Function Results

MOVE CLASS					
	Execution #1	Execution #2	Execution #3	Execution #4	Execution #5
Group 1	3268	3176	3282	3112	3198
Group 2	3288	3061	3241	3281	3186
Group 3	3273	3044	3273	3171	3098
Group 4	3211	2989	3065	3163	3177
Group 5	3138	3250	3151	**3382**	3281

MOVE METHOD					
	Execution #1	Execution #2	Execution #3	Execution #4	Execution #5
Group 1	9794	9736	10142	9256	9915
Group 2	9376	10058	9794	9736	10129
Group 3	9060	9126	9051	**10189**	10075
Group 4	9944	9370	9995	9611	9922
Group 5	9890	9446	9164	9892	10091

EXTRACT METHOD					
	Execution #1	Execution #2	Execution #3	Execution #4	Execution #5
Group 1	21128	21165	21217	21192	21110
Group 2	21173	21235	21141	21229	21261
Group 3	**21291**	21207	21135	21112	21175
Group 4	21285	21156	21262	21287	21262
Group 5	21145	21234	21235	21290	21270

and d of the numerator and a, b, c and d of the denominator, are reported in Table 8.

Table 8: Proposed coefficients weights

Coefficient	$P_{a'}$	$E_{a'}$	$P_{d'}$	$E_{d'}$	$P_{a''}$	$E_{a''}$	P_b	E_b	P_c	E_c	$P_{d''}$	$E_{d''}$
PTMC	2.0	3.0	0.1	0.5	1.71	2.0	1.98	2.0	1.78	2.0	0.1	1.0
PTMM	2.0	3.0	0.85	1.0	1.64	1.0	1.95	0.5	0.1	1.0	0.9	1.0
PTEM	0.48	0.5	1.56	2.0	1.82	1.0	0.89	1.0	1.87	2.0	0.47	2.0

Thereby, when assigning each weight to the corresponding variable of *Simple Matching*, we have the following proposed coefficients:

$$PTMC = \frac{2a^3 + 0.1\sqrt{d}}{1.71a^2 + 1.98b^2 + 1.78c^2 + 0.1d} \tag{4}$$

$$PTMM = \frac{2a^3 + 0.85d}{1.64a + 1.95\sqrt{b} + 0.1c + 0.9d} \tag{5}$$

$$PTEM = \frac{0.48\sqrt{a} + 1.56d^2}{1.82a + 1.89b + 1.87c^2 + 0.47d^2} \tag{6}$$

6 Evaluation of the Proposed Coefficients

In order to evaluate the efficiency of the proposed coefficients, the accuracy of the respective coefficients was compared with other 18 coefficients in the literature (Table 1), involving the other 101 systems of the *Qualitas.class Corpus* (test set). Each proposed coefficient is analyzed and compared according to its respective code refactoring, i.e., this section presents a different comparison for *Move Class*, *Move Method* and *Extract Method*.

For the evaluation of the results, the same analysis approach described in Section 4 was adopted. Thus, Table 9 presents the results of the accuracy rates of coefficients analyzed for *Move Class* (including *PTMC*), *Move Method* (including *PTMM*) and *Extract Method* (including *PTEM*) refactorings. Again, the analysis considers the median of the sets of means, since some data do not follow a normal distribution. For space constraints, the detailed table comprehending the results of each of the 101 systems is publicly available from (Pinto and Terra 2018). Table 9 reports the results.

Move Class: It can be noticed that the proposed coefficient reached higher values compared to the others, having an approximate median of 62.20%, 71.52% e 79.45% in relation to the similarity rates *Top #1*, *Top #2* and *Top #3*. *PSC* presented the second best median among the coefficients analyzed. For *Top #1*, *Top #2* and *Top #3*, *PSC* reached, respectively, the accuracy values of 55.98%, 71.26% e 77.31%.

More importantly, In addition, when comparing the *Top #1* of both coefficients, *PTMC* presented a statistically significant improvement from 5.23% to 6.81%, according to the Wilcoxon Test (Verzani 2014) with a 95% confidence ($p\text{-}value = 2.2^{-16}$). As presented in section 4, Figure fig:graph2 presents a violin plot regarding Top #1 of each *Move Class* refactoring, in order to provide a complementary analysis between the data.

Move Method: It can be noticed that *PTMM* surpassed the other coefficients data in the three cases of similarity rate (*Top #1*, *Top #2* and *Top #3*), reaching, respectively, a median of approximately 52.89%, 61.09% and 64.66%. The second highest rate was from *Sokal and Sneath 2* where, considering the three cases of similarity rate (*Top #1*, *Top #2* and *Top #3*), the coefficient reached, respectively, the median values of 38.02%, 49.35% and 56.04%. Moreover, *PTMM* presented a statistically significant improvement from 12.33% to 14.74%, when comparing *Top #1* of both coefficients, according to the Wilcoxon Test with a 95% confidence ($p\text{-}value = 2.2^{-16}$). Again, Figure fig:graph3 presents a violin plot regarding Top #1 of each *Move Method* refactoring.

Extract Method: It can be noticed that *PTEM* presented a median of approximately 88.32%, surpassing the second best coefficient (*Russell and Rao*), which had a median of 87.93%. In addition, *PTEM* presented a statistically significant improvement from 0.24% to 0.40% over *Russell and Rao*, according to the Wilcoxon Test with a 95% confidence ($p\text{-}value =$

Table 9: Similarity precision of the 19 similarity coefficients (test set)

MOVE CLASS			
Coefficient	**Top1**	**Top2 Median**	**Top3**
Baroni-Urbani and Buser	36.31%	48.65%	57.17%
Dot-product	49.93%	65.22%	72.87%
Hamann	22.62%	32.18%	38.77%
Jaccard	51.60%	67.52%	75.48%
Kulczynski	46.86%	64.15%	72.61%
Ochiai	49.66%	64.94%	72.47%
Phi	49.39%	65.22%	72.35%
PSC	55.98%	71.26%	77.31%
Relative Matching	36.86%	54.35%	63.71%
Rogers and Tanimoto	22.88%	32.18%	38.88%
Russell and Rao	45.59%	61.90%	71.31%
Simple matching	23.05%	33.18%	39.23%
Sokal and Sneath	22.56%	32.25%	38.64%
Sokal and Sneath 2	53.35%	69.05%	76.59%
Sokal and Sneath 4	46.95%	63.99%	72.54%
Sokal binary distance	26.09%	35.69%	44.36%
Sorenson	49.93%	65.22%	72.87%
Yule	26.88%	38.64%	47.79%
PTMC	62.20%	71.52%	79.45%

MOVE METHOD			
Coefficient	**Top1**	**Top2 Median**	**Top3**
Baroni-Urbani and Buser	17.09%	25.08%	29.97%
Dot-product	31.25%	41.45%	49.23%
Hamann	20.21%	27.18%	31.61%
Jaccard	35.43%	46.60%	53.09%
Kulczynski	25.33%	36.09%	42.79%
Ochiai	29.30%	41.45%	47.49%
Phi	29.46%	41.29%	47.41%
PSC	36.71%	48.45%	55.98%
Relative Matching	23.23%	34.41%	40.39%
Rogers and Tanimoto	20.36%	27.47%	31.81%
Russell and Rao	30.70%	43.51%	49.86%
Simple matching	20.25%	27.04%	31.59%
Sokal and Sneath	19.56%	26.37%	30.46%
Sokal and Sneath 2	38.02%	49.35%	56.04%
Sokal and Sneath 4	24.35%	35.54%	42.94%
Sokal binary distance	23.75%	30.91%	35.49%
Sorenson	31.25%	41.45%	49.23%
Yule	9.45%	17.38%	22.25%
PTMM	52.89%	61.09%	64.66%

EXTRACT METHOD	
Coefficient	**Hits Median**
Baroni-Urbani and Buser	61.94%
Dot-product	69.62%
Hamann	10.48%
Jaccard	71.73%
Kulczynski	78,36%
Ochiai	72.95%
Phi	72.68%
PSC	76.11%
Relative Matching	82.46%
Rogers and Tanimoto	10.52%
Russell and Rao	87.93%
Simple matching	10.48%
Sokal and Sneath	10.32%
Sokal and Sneath 2	74.67%
Sokal and Sneath 4	77.27%
Sokal binary distance	16.52%
Sorenson	69.62%
Yule	65.90%
PTEM	88.32%

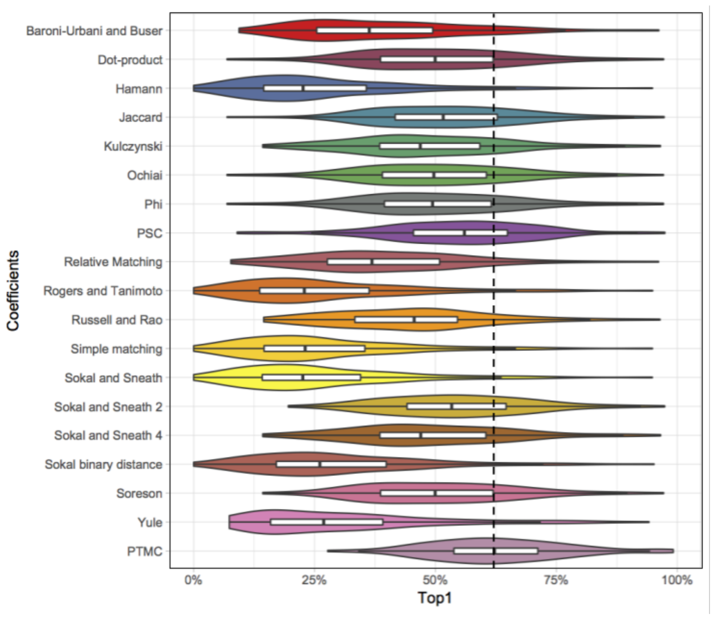


Fig. 4: Move Class Plot

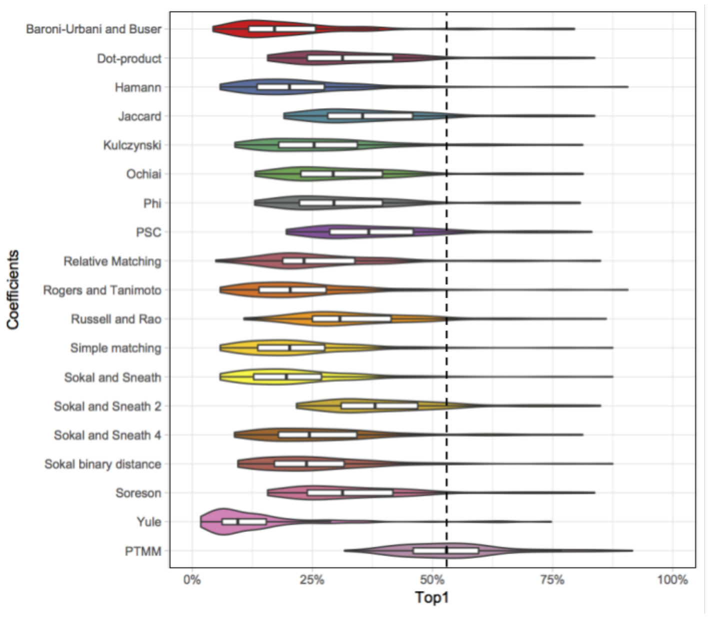


Fig. 5: Move Method Plot

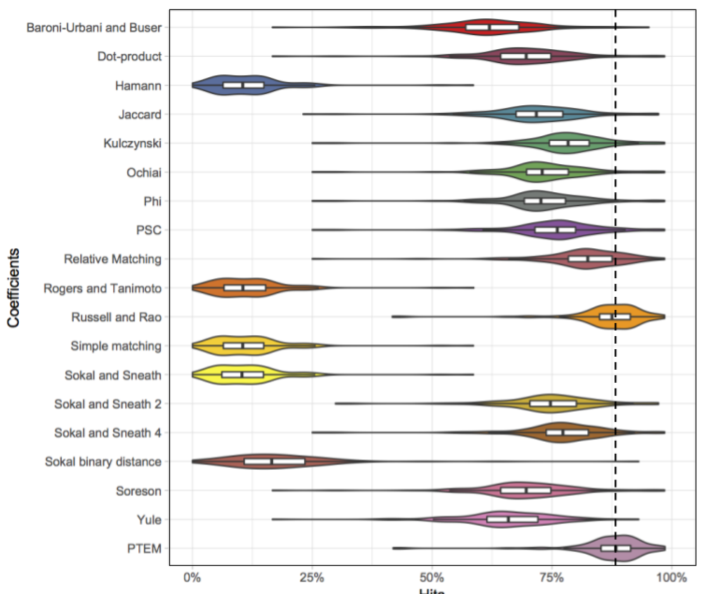


Fig. 6: Extract Method Plot

2.2^{-16}). Finally, Figure fig:grap4 presents a violin plot regarding each *Extract Method* refactoring.

Threats to validity: Although the execution instructions have been proposed after a series of experimental tests and runs, it cannot be said that the execution instructions described in Section 3.1 are complete, since false positives (internal validity) are still possible. Moreover, as it is common in empirical studies in Software Engineering, the results cannot be extrapolated (external validity). Although the test set has a reasonable number of 101 systems, it is important to evaluate the new coefficients in real development scenarios.

7 Recommendation System

Aiming to apply the new coefficients proposed in this article to identify refactoring opportunities, a plug-in prototype for the IDE Eclipse was developed. The tool, named $AIRP^2$, is composed of an architecture based on four main modules::

– ***Dependency Extraction Module***: Responsible for identifying and storing all dependencies of a class, method, or block. In other words, it identifies the set of types at which a code entity establishes structural dependency. This includes method calling, attribute access, instantiation,

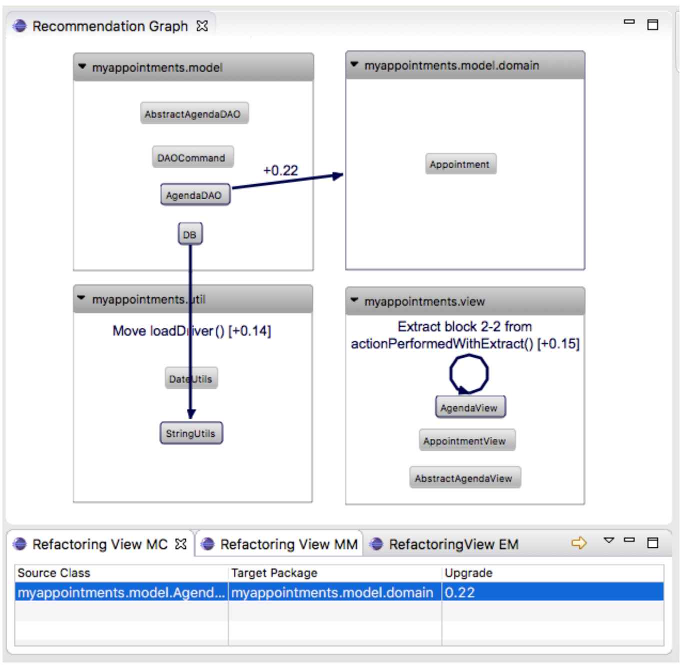
[2] Publicly available from: `https://github.com/rterrabh/AIRP`

variable declaration, annotation, etc. In order to perform such extraction, it is used a syntactic analysis through an AST (*Abstract Syntax Tree*) that checks each element in the source code and, if it refers to a dependency to other entities, stores it according to its package, class, method and/or block.;

- ***Similarity Calculation Module***: It calculates the structural similarity of a given code entity in the target system. This calculation is performed using the formula of the chosen similarity coefficient, making a comparison between the previously stored dependencies of a given class, method or block with its respective entity (package, class or method), as described in the methodology of this article (See Section 3.1). By default, the $PTMC$, $PTMM$ and $PTEM$ coefficients are used, although it is possible to select any of the other 18 coefficients presentes in Table 1;
- ***Recommendation Module***: This module calls the previous one to calculate the resulting similarity of every possible *Move Class*, *Move Method* and *Extract Method* refactorings in the code. After calculating similarity, its results are compared with a minimum acceptance index of improvement specified by the user. If the result is higher than this user-defined *threshold* , a list of suggestions is presented with possible refactoring opportunities. Afterwards, the recommendations are reported for the user analysis, being ordered by their similarity index improvement. If the user does not specify a minimum acceptance index, all refactorings that leads to an improvement are displayed. ; and
- ***Visualization Module***: In order to provide more details on the structural organization of the target system, a graph of the implemented architecture is generated using the Zest[3] library. This graph will report all refactorings in the list of suggestions from previous module. The module also highlights the selected refactoring by the user, showing more details about it, and its respective resulting similarity upgrade. In this way, it makes possible a greater understanding by the user regarding the process performed by the tool, being able to observe the repositioning of involved entities and the architecture resulting from each recommendation. Figure 7 illustrates shows an example of the refactoring opportunity graph.

Figure 7 illustrates three examples of suggestions for refactoring. For the respective system, class $AngendaDAO$ has a similarity mean value 0.22 higher with the classes of package $myappointments.model.domain$ (*Move Class*), method $loadDriver()$ from class DB has a similarity mean value 0.14 higher with methods from $StringUtils$ (*Move Method*), and finally, method $actionPerformed$ will result in a similarity mean value 0.15 higher with methods from class $AgendaView$ if its second inner block from the second block is extracted to a new method (*Extract Method*).

[3] https://www.eclipse.org/gef/zest/



Source Class	Target Package	Upgrade
myappointments.model.Agend...	myappointments.model.domain	0.22

Fig. 7: Refactoring opportunity graph

8 Related Work

Although only one study regarding the proposal of new similarity coefficients was found, some studies present methodologies and techniques for the identification of refactoring opportunities, adaptations of existing metrics or empirical studies regarding the concepts discussed in the present article. Considering that the objective of this article is to improve the identification of refactoring opportunities through similarity coefficients, studies that do not use such coefficients are not considered. The most relevant studies to this article are presented below, according to their categories.

Proposal of structural similarity coefficients: (Naseem et al 2010) propose a new similarity coefficient aimed at its application in clustering algorithms. In turn, the new proposed coefficient is an adaptation of the *Jaccard* coefficient, called *Jaccard-NM*, whose main difference is the addition of a new variable that considers the universe of analyzed factors, i.e., all the existing factors in the set in which analyzed entities are present. It is important to emphasize that the proposed new similarity coefficient is compared only to the *Jaccard*, coefficient, from which it was adapted and for only three systems. On the other hand, this article has an in-depth analysis of the proposed coefficients for a more precise identification in relation to the other existing coefficients.

Empirical studies: Terra et al (2013) perform a robust evaluation in 111 systems of the base *Qualitas.class Corpus*, involving 18 of the main similarity coefficients. Considering the study purpose, it is fundamental to the accomplishment of this article, considering that the used coefficients and their analyses, besides the approach involving structural dependencies, acted as the main basis for the proposal of new coefficients, as well as their evaluations.

Szőke et al (2015) present a case study where it is discussed whether automatic code refactorings actually improve maintainability of software systems. Although the study reports that refactorings usually have a positive impact on maintainability, their execution without proper analysis can negatively impact the system. Although it is extremely important to investigate the actual use of automatic refactorings, this article proposes coefficients that allow identifying more precisely refactoring opportunities that may or *may not* be amenable to automatic refactoring.

Systematic reviews of literature: Dallal (2015) presents a systematic review of the literature regarding code refactoring. The study addresses 47 studies on the types of refactoring activities, the different approaches to identify refactoring opportunities, as well as the data sets and the means used to evaluate them. This review was highly relevant in this article, since the performed analyses allow detecting the most appropriate approaches to be used, as well as to better understand the process of identifying code refactoring opportunities, as well as their accomplishment and evaluation.

Tools for identifying refactoring opportunities: Sales et al (2013) described the proposal of JMove tool, an Eclipse IDE plug-in indicating *Move Method* refactoring opportunities based on the structural similarity coefficient *Sokal and Sneath 2*. The tool, however, involves analysis only of *Move Method*. More importantly, the use of the $PTMM$, coefficient, proposed in this article, could improve accuracy of JMove by 13.39%.

Silva et al (2014) proposed JExtract tool, an Eclipse IDE plug-in aimed at identifying *Extract Method* refactoring opportunities based on *Kulczynski* similarity coefficient. JExtract, in turn, focuses only on the *Extract Method* refactoring. Similarly, the use of the $PTEM$ coefficient, proposed in this article, could improve accuracy of JExtract by 9.38%.

Fokaefs et al (2011) present the JDeodorant tool, which identifies Code Smells and applies different code refactoring techniques in order to treat them. JDeodorant does not use the similarity comparison between the dependencies of a project. On the other hand, it uses the *Jaccard* coefficient to calculate only the similarity between attributes and methods of the analyzed classes, which can affect its efficiency, since *Jaccard*—although it is one of the most used coefficients in Software Engineering—does not present good accuracy in relation to the other existing coefficients.

Although the analyzed studies show a focus on the identification of code refactoring opportunities or approaches involving structural similarity coefficients, no studies that proposed new coefficients were found aiming at greater accuracy in the identification of such opportunities. Thus, the proposal of new coefficients, based on statistics, robust analyses and comparisons between the main existing similarity coefficients focused on three different types of refactoring, emphasizes the originality of this study.

9 Conclusion

This article presents the proposal of three new structural similarity coefficients in order to provide more precise ways to identification of code refactoring opportunities: $PTMC$, for identification of *Move Class* refactoring opportunities; $PTMM$, for *Move Method*; and $PTEM$, for *Extract Method*. The proposed coefficients are more accurate than the hitherto accurate coefficients used to identify refactoring opportunities. In numerical terms, $PTMC$, $PTMM$ and $PTEM$ showed a statistically significant improvement from 5.23% to 6.81%, 12.33% to 14.79% and 0.25% to 0.40%, respectively, in relation to the second best coefficients.

As future studies, it is intended to: (i) to use more coefficients in the analysis stage; (ii) apply cross-validation techniques; (iii) perform a comparative study among techniques in order to identify refactoring opportunities that use or not similarity coefficients; (iv) propose a single coefficient that meets other types of refactoring; and (v) measure the acceptance degree of new coefficients in real scenarios.

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