# An Improved Approach for Class Test Ordering Optimization using Genetic Algorithms

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Abstract: Identifying the order in which the application classes have to be tested during the integration testing of objectoriented software systems is essential for reducing the testing effort. The Class Integration Test Order (CITO) problem refers to determining the test class order that minimizes stub creation cost, and subsequently testing effort. The goal of this paper is to propose an efficient approach for *class integration test order* optimization using a genetic algorithm with stochastic acceptance. The main goal of the *class integration test order* problem is to minimize the *stubbing effort* needed during the class-based integration testing. In our proposal, the complexity of creating a stub is estimated by assigning weights to different types of dependencies in the software system's Object Relation Diagram. The experimental evaluation is performed on two synthetic examples and five software systems often used in the literature for the *class integration test ordering*. The results obtained using our approach are better than the results of the existing related work which provide experimental results on the case studies considered in this paper.

## **1 INTRODUCTION**

*Class-based integration testing* is a systematic testing technique applied when the application classes of a software are integrated in the final software system. The classes are integrated sequentially and after adding each class the obtained system is tested. If no errors have been found during testing at some point in the integration, then the next application class will be integrated. An important problem during integration testing of object-oriented software systems is the one of deciding the order in which the application classes should be integrated in the final software, called the *class integration test order* (CITO) problem (Briand et al., 2002b).

In most situations, there is a dependency relation between the application classes, namely a class may require another class to be available before it can be tested. In cases when dependency cycles exist among the application classes from a software system, the dependency has to be broken and a *stub* for emulating the behavior of the required class has to be created (Assunção et al., 2011). If, at a particular step during class-based integration testing, one adds a class which depends on another application class that has not been integrated yet, a simulation of that class is necessary. This is done by creating a *stub* for the required class, more precisely a dummy class that replaces the required one and simulates its behavior. Stubs are those parts of a software system that are built for simulating components of the software which are not developed or unit tested yet, but are needed to test classes that depend on them (Briand et al., 2002b). There is a difference between specific and generic stubs. A spe*cific* stub replicates only the class functionalities for a specific client class, while the generic (realistic) stubs reproduce all functionalities that the original class can provide. Therefore when a class is used by many client classes we will need only one generic stub, but as many specific stubs as the number of client classes. Since stub creation increases the cost of the integration testing process, it is essential to reduce stubbing cost by determining a class order for integration testing that minimizes the overall stubbing effort.

The CITO problem does not cover aspects related to the actual creation of stubs nor does it approach the problem of *test case effectiveness*. The main objective of the CITO problem is to reduce the number of stubs needed, not to increase early bug detection. Software developers are still responsible for creating stub classes that closely model the effective class to be stubbed.

There are numerous strategies proposed in the literature for solving the CITO problem with the aim of minimizing the *stubbing effort* required during the integration process. The *stubbing effort* estimates the

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cost for creating the stubs needed during the integration testing. It can be computed either as the number of needed stubs or considering measures related to *coupling*, number of attributes and methods or the complexity of the methods that need to be replicated. Most of the solutions existing in the literature for the CITO problem can be divided in two categories: graph based approaches and genetic algorithm based approaches (Bansal et al., 2009). The graph-based approaches consider the Object Relation Diagram which represents the classes and the relationship between them in object-oriented software systems.

In this paper we are approaching the CITO problem as a combinatorial optimization problem, with the goal of determining the order in which the application classes should be tested for minimizing the total cost of *stubbing*. We consider the *stubbing* cost as the effort for creating the specific stubs needed during the class-based integration testing. The complexity of creating a stub is estimated by assigning weights to different types of dependencies (i.e., aggregation, association, inheritance) in the software system's Object Relation Diagram (ORD).

The main contributions of this paper can be summarized as follows.

- We propose an efficient approach for *class integration test order* optimization using a genetic algorithm with stochastic acceptance based on a static analysis of object-oriented software systems. Our proposal improves the existing strategies based on genetic algorithms for finding a solution for the CITO problem and provides a more general theoretical model that can be applied for generic stubs and specific stubs with different weighting strategies.
- We experimentally evaluate our approach on 7 case studies often used in the literature for the *class integration test ordering*. The obtained results outperform existing related work which provide experimental results on the case studies considered in this paper.

The paper is organized as follows. We start by reviewing in Section 2 existing approaches which provide solutions for the CITO problem considering weighted stubs and give experimental results on the case studies that are considered in this paper. Our approach based on a genetic algorithm with stochastic acceptance for solving the CITO problem is introduced in the Section 3. Section 4 describes the case studies used for evaluation and also provides the experimental settings and results. In Section 5 we compare the results obtained by our proposal with some state-of-the-art techniques. Our conclusions as well as several future research directions are presented in Section 6.

#### 2 RELATED WORK

In this section we will present a short overview of existing approaches for the CITO problem, focusing mainly on the ones that, like our approach, consider that not every stub has the same complexity. Most of these approaches build a graph, called Object Relation Diagram (ORD), where nodes represent the application classes and directed edges represent the relationships between these classes. Edges often have labels that represent the type of the relationship between the two classes. The number of relationships can be different from one approach to another, but the most frequently used relations are inheritance, aggregation and association.

If the ORD contains no cycles then a simple topological sorting can give the integration order. For such systems, a bottom-up integration strategy can be used, and no stubs are needed. But in most software systems there are cyclic dependencies between the classes in the ORD as shown by Melton and Tempero in (Melton and Tempero, 2007) where a study was conducted on 78 Java software systems with different sizes (from 17 to 11644 classes). The authors concluded that almost all systems contained cycles, moreover, about 85% of them contained strongly connected components of at least 10 classes.

The first paper that considered the CITO problem was written by Kung et al. (Kung et al., 1995). They consider an ORD with inheritance, aggregation and association relations. The first step of their approach is to transform it into an acyclic one, by first replacing clusters of mutually reachable nodes with one single node. A topological sorting of this acyclic graph will give the *major level* of nodes. For finding the *minor level* of nodes, the order inside the clusters, association relations are removed, since every cycle has to contain at least one association edge.

Major and minor level numbers are used by Tai and Daniels as well (Tai and Daniels, 1997), but they are computed differently. For assigning major level numbers, only the inheritance and aggregation relations of the ORD are considered and a Depth First Search (DFS) is performed. Minor levels are assigned to nodes that have the same major level. Strongly Connected Components (SCC) are identified for the nodes belonging to the same major level, and to each association edge e a weight is assigned as the sum of the number of incoming edges to the source node of e and the number of outgoing edges from the target node of *e*. The edge with the highest weight is removed, because it has a higher chance of breaking many cycles. This process is repeated until no cycles are left.

Hanh et al. use Test Dependency Graph (TDG), which is more detailed than an ORD, because it can contain method-to-class and method-to-method relations as well. They present in (Hanh et al., 2001) two integration strategies, a graph-based one and a genetic algorithm (GA) based one. For the graph-based approach, called Triskell, they find the node that participates in the maximum number of cycles and remove it (consider that it will be stubbed). This produces one generic stub, and a specific stub for each incoming edge into the node. Relation types are considered only if two nodes participate in the same number of cycles, in this case the node with more association relations participating in cycles is removed. They repeat the process until no cycles are left. The GA approach considers only the number of stubs, no relations are considered.

In (Briand et al., 2002b) Briand et al. propose a graph-based approach, which identifies SCC in the graph, and for each association edge in each SCC computes a weight which is similar to the weight computed by Tai and Daniels, but instead of taking the sum, for an edge they take the product of the number of incoming edges to the source node and the number of outgoing edges from the target node. They remove the edge with the highest weight and continue until no cycles are left. In (Briand et al., 2002a) Briand et al. proposed a Genetic Algorithm based approach as well. They use constraints to make sure that inheritance and aggregation relations will not be broken (they specify partial ordering of nodes based on these relations) and compute weights for association edges. The weight of an association relation depends on the complexity of the class represented by the target node, and this complexity depends on the number of methods and/or number of attributes of the class.

While previous approaches considered weights mainly just for association edges (since inheritance and aggregation edges are never removed), the approach presented by Malloy et al. in (Malloy et al., 2003) considers weights for 6 different relations: association, composition, dependency, inheritance, ownedElement, polymorphic. They use the ORD and find SCC in it. For each SCC they compute the weight of the edges and remove the edge with the minimum weight. For the experimental evaluation they use 7 case studies of different sizes and two different sets of weights. The only difference between the two sets of weights was the weight assigned to inheritance edges. In the first set of weights, inheritance has weight 2, which is a low value, making it probable that inheritance edges will be removed. In the second set, inheritance has a weight of 100 which makes removal of inheritance edges very unlikely. They conclude that in the situations when no inheritance edges are removed, approximately twice as much stubs are needed.

Another graph-based approach is the one presented by Abdurazik and Offutt (Abdurazik and Offutt, 2009). The novelty in their approach is that they consider weights for both edges and nodes in the ORD (though the weights for the nodes are computed considering the weights for the edges). They consider 9 different relations between classes and compute the weight of an edge based on several measures of coupling. Their algorithm computes for each edge a Cycle to Weight Ratio, which considers both the number of cycles that include that edge and the weight of the edge. The edge with the maximum CWR is removed, and the process is repeated until no cycles are left.

Bansal et al. present an approach which is based on the approach presented by Malloy, but they introduce two new relation types specific for C++ applications: friend coupling and exception coupling and define weights to them: 25 and 5 (Bansal et al., 2009). They also present an overview of existing graph-based and genetic algorithm-based approaches.

### **3 METHODOLOGY**

In this section we introduce our proposal for optimizing *class integration test order* using a genetic algorithm (GA) with stochastic acceptance. GAs are used due to their flexibility and applicability in successful solving of a large variety of optimization problems.

Our approach is based on a static analysis of object-oriented software systems and on computing the *stubbing effort* as the cost of creating the specific stubs needed during the integration testing. Depending on the type of dependency between classes, creating a stub requires different cost (effort). We are considering *weighted stubs*, thus the complexity of creating a stub is computed by assigning weights to different types of dependencies between the application classes.

We start by describing in Section 3.1 how the class relationships are considered in the literature for stubbing, followed by the dependencies and weighting scheme considered in our approach. We present in Section 3.2 the main characteristics of genetic algorithms. Section 3.3 introduces the genetic algorithm model proposed for the CITO problem.

#### 3.1 Stubbing Relationships

Kung et al. (Kung et al., 1995) show that if there are no dependency cycles among classes in the ORD of a software system, the integration order can be simply obtained by performing a reverse topological ordering of classes based on their dependencies (Briand et al., 2002b). But if cyclic dependencies among classes can be found, most existing strategies propose to broke some dependencies for obtaining an acyclic graph and then to apply a topological sorting on it. Breaking a dependency requires that the target class needs to be stubbed when integrating and testing the source class (Briand et al., 2002b).

Three types of dependencies between application classes in the ORD are considered by Kung et al. (Kung et al., 1995): Association/Usage (As), Aggregation (Ag) and Inheritance (I). In order to obtain an acyclic graph, the authors propose the removal of association relationships. They consider that an association relationship exists in each directed cycle of an ORD and this type of relation is the weakest one between related classes.

A literature review (Kung et al., 1995), (Tai and Daniels, 1997), (Abdurazik and Offutt, 2006) reveals that by removing association relationships simpler stubs are created compared to those obtained by selecting aggregation or inheritance relationships. Traon et al. (Traon et al., 2000) proposes a strategy allowing to break aggregation or inheritance relations, which may conduct to complex stubs. The results obtained by Malloy et al. (Malloy et al., 2003) revealed that the removal of inheritance relationships is more effective for cycles breaking.

In our proposal we are considering a Weighted ORD, in which each relationship (As, Ag and I) has an associated weight. We consider the *inheritance* (I) relationship as the strongest relationship between the application classes, followed by the *aggregation* (Ag) and then by the *association* (As) relationship which is viewed as the weakest relation between the classes. A stub class is a controllable replacement for an existing dependency in the system, the main factor that influences the effort needed for creating a stub is the type of the dependency.

Based on the existing results in the literature we assign the largest weight to the *inheritance* relation, the smallest weight to the *association* relation and an intermediate weight to the *aggregation* relation. This weighting scheme reflects the relative effort needed to implement a stub class for a particular client class that has a dependency on the stubbed class.

#### **3.2** Genetic Algorithms

*Genetic Algorithms* (GAs) represent a *machine learning* model which is inspired from the processes of evolution in nature. They are specific type of metaheuristic optimization techniques from the *computational intelligence* domain used for solving search and optimization problems. Even if there is no guarantee that the GAs will converge to the global minimum, since they are based on heuristics, they are able to prevent the search from falling into local minima (Whitley, 2001).

GAs are population based approaches and artificial models for the biological processes of natural selection and evolution. The main idea behind GAs is that a population of individuals adapts to environmental changes over multiple generations, and the fittest individuals of the population are those who survive longer (Melanie, 1999).

GAs start with a population of noInd candidate solutions, also called individuals or chromosomes, usually randomly generated. Each individual from the population is characterized by a numerical value called its fitness, which indicates how "good" is that individual for solving the considered problem. Over a number of iterations (generations) or until acceptable solutions are found, the population is evolved using genetic operators as follows. A pair of chromosomes is selected (using a *selection* strategy), then we cross**over** (with probability  $p_c$ ) the selected pair and form two offspring and lastly we **mutate** the two offsprings (with probability  $p_m$ ) and add the obtained individuals in the new population. At the end of the iterative process, the individual with the maximum fitness from the current population is reported as a solution.

Figure 1 describes the skeleton of a simple GA.

#### 3.3 The Proposed GA Model

Let us consider that the analyzed software system S is composed by a set of classes  $C_1, C_2, \ldots, C_n$ . Starting from the ORD graph built for the software system and based on a static analysis of it, we aim to identify an appropriate order in which the application classes should be integrated (and tested) in the final software. The solution is viewed as a permutation of the classes representing the integration order that needs the minimum *stubbing effort*. Consequently, the optimal solution  $\tau$  of  $\{1, 2, \ldots, n\}$  which minimizes the total *cost* for creating the stubs needed when the classes are integrated and tested in the order  $\tau$ :  $C_{\tau} = (C_{\tau_1}, C_{\tau_2}, \ldots, C_{\tau_n})$  (n > 1). The *stubbing effort* required for the integration testing of a sequence of

Algorithm GA is: Input: noInd - the number of individuals from the population  $p_{m}$ - the probability for mutation  $p_{c}$ - the probability for crossover Output: best - the best individual (solution) Begin (//a population of noInd individuals is initialized (usual

//a population of noInd individuals is initialized (usually randomly)  $P \leftarrow initializePopulation();$ //repeat until a termination criterion is met (number of generations, fitness, etc) While not TERMINATION do //the fitness of the individuals from the current population is computed computeFitness(P); //the new population is initialized  $P' \leftarrow \emptyset;$ //repeat until noInd individuals are created While |P'| < noInd do //the survivors from the current population are preserved  $P' \leftarrow survive(P);$ @ Select from P a pair  $(c_1, c_2)$  of chromosomes for crossover @ With probability  $p_c$  cross-over the pair  $(c_1, c_2)$  and form two offsprings 0 With probability  $p_m$  mutate the offsprings and add the new individuals in  $P^\prime$ EndWhile; //the current population is replaced with the new population  $P \leftarrow P';$ EndWhile

//the individual with the maximum fitness from the current population is reported  $best \leftarrow maxFitness(P);$ 

End GA

Figure 1: The skeleton of a GA.

classes  $C_{\tau} = (C_{\tau_1}, C_{\tau_2}, \dots, C_{\tau_n})$  is denoted by  $Cost_{C_{\tau}}$ and is defined as in Formula (1):

$$Cost(C_{\tau}) = \sum_{i=1}^{n} stub(C_{\tau_i}, C_{\tau_{i-1}}, \dots, C_{\tau_1})$$
(1)

where  $stub(C_{\tau_i}, C_{\tau_{i-1}}, \dots, C_{\tau_1})$  represents the cost for creating the weighted stubs for integrating the class  $C_{\tau_i}$  to the system formed by the classes  $\{C_{\tau_{i-1}}, C_{\tau_{i-2}}, \dots, C_{\tau_1}\}$ . This cost is computed by summing the weights associated with the relationships between class  $C_{\tau_i}$  and all its neighboring classes from the Weighted ORD which were not already integrated.

An individual from the GA population is an integer-valued vector whose length is equal to the number of application classes from the analyzed software system and represents a possible order for integrating the classes during the integration testing. Thus, a candidate solution to the CITO problem is encoded in an individual (chromosome)  $ind = (ind_1, ind_2 \dots ind_n)$  representing a permutation of  $\{1, 2, \dots, n\}$  ( $1 \le ind_i \le n \quad \forall i \in \{1, 2 \dots n\}$  and  $ind_i \ne ind_j \quad \forall 1 \le i, j \le n, i \ne j$ ).

We define the value of the *fitness function* for a given individual *ind* as in Formula (2).

$$fitness(ind) = Max - Cost(C_{ind})$$
 (2)

where *Max* represents a large positive constant. Considering the definition of the fitness given in Formula (2), maximizing the fitness of a chromosome *ind* will be equivalent with minimizing the stubbing cost required when the classes are integrated and tested in the order  $C_{ind}$ . Accordingly, the components of the fittest individual reported by the GA will give us the class integration test order.

The improvements we propose to the classical GA model are described in the following. In order to assure a proper exploration of the search space the initial population is generated using the following heuristic. Given the fact that every chromosome represents a permutation, the dimension of the search space is *n*! where *n* is the number of classes in the system. In order to evenly divide the search space we will generate the k-combinations for the set of classes, where k is chosen based on the size of the initial population. For example if we have the set of classes  $\{A, B, C, D, E, F, G, H\}$  we can generate 2combinations:  $\{A, B\}, \{A, C\}, \dots$  in total 28 different sets with 2 elements. We use the k-sets when generating the initial population by creating chromosomes that start with genes according to the generated kcombinations followed by randomly generated genes.

The GA model we propose for solving the CITO problem also considers a selection operator based on the stochastic acceptance technique (Lipowski and Lipowska, 2012). In this algorithm, the widely used roulette-wheel selection operator used in the population for reproduction is replaced with the following one: an individual ind is randomly selected and this selection is accepted with probability fitness(ind)/fitness(M), where M is the fittest individual (has the highest fitness value). Through the stochastic acceptance based selection operator, the fittest individual will always be accepted if selected. Several studies in the literature indicate that the selection based on stochastic acceptance performs considerably better than versions based on linear or binary search (Lipowski and Lipowska, 2012).

In our proposed GA we used a variant of the *Order Crossover 1* operator, known as *C1*, which is specific for using GAs for permutation problems (Whitley and wook Yoo, 1995). Basically, a sequence of consecutive genes is removed from the first parent and is directly copied to the child. The remaining genes are placed in the offspring in the order in which they appear in the second parent. From the time performance viewpoint, *C1* is the fastest crossover operator that generates valid chromosomes (preserves the ordering constrains).

The mutation operator is a variant of the *swap mutation*, but we swap a randomly generated gene with its adjacent gene.

We have also used *elitism* in our GA, which means that the next generation will always contain a small proportion ( $P_{elitism}$ ) of the fittest individuals from the current population.

### 4 COMPUTATIONAL EXPERIMENTS

We provide in this section an experimental evaluation of our GA approach presented in Section 3.3 for solving the CITO problem on seven case studies often used in the literature: two synthetic examples and five real-life case studies.

For the GA model proposed in Section 3.3 we used our own implementation, without any third party libraries. The following parameter setting will be used for all experiments: the constant *Max* used in the fitness computation was set to 10000; the number of individuals from the GA population *noInd* is  $2 \cdot C_n^2$ ; the mutation and crossover probabilities are  $p_m = 0.3$  and  $p_c = 0.3$ ; the proportion  $P_{elitism}$  used for the *elitism* parameter was considered 0.1 (10% of the population survives from one generation to another).

As a termination condition for our GA we used a predefined number of trials depending on the number of application classes,  $50 \cdot n$ . Regarding the parameters, we tried different values, but no significant difference was observed in the obtained results.

The experiments are conducted in two directions, considering different weighting schemes for the stubs in computing the *stubbing effort*.

- Differential Weighting. We used the following weights for the relationships between the application classes: 30 for an *Inheritance* relation, 5 for an *Association* relation and 20 for an *Aggregation* relation. These values for the weights were selected after analyzing the similar literature which assigns weights for the stubs (Malloy et al., 2003), as well as our software development experience. The proposed weighting scheme reflects the effort needed to implement a stub class for a particular client class that has a dependency on the stubbed class (see Section 3.1).
- 2. Equal Weighting. In this scheme, equal weights (e.g. 1) are assigned for all stubs, independent of the type of relationship between a client class and the application class to be stubbed. Such a weighting method allows us to determine non-weighted *specific* stubs.

#### 4.1 Case Studies

For our experiments, we have selected two synthetic case studies and five software systems often used in the CITO literature.

A description of the case studies is given in Table 1, where the second column depicts the number of classes and the third column presents the number of dependencies between the application classes. For each case study, the existing number of cycles between the application classes is given in the fourth column. The number of cycles indicates the complexity of the stubbing process, since a larger number of cycles leads to a larger number of stubs needed in the integration process.

In order to mitigate some threats to external validity issues, in our experiments we chose software systems of various size, complexity and domain (as shown in Table 1). Even if an industrial software system would probably have more classes, for those systems integration testing would be performed on component-level, instead of class-level. Integration of classes from one component should be done on the class-level (Briand et al., 2002b).

The first synthetic example consists of 8 classes, and is presented in Figure 2. This case study was

considered for evaluation in several papers approaching the CITO problem (Hewett and Kijsanayothin, 2009), (Briand et al., 2002b), (Abdurazik and Offutt, 2009), (Borner and Paech, 2009), (Bansal et al., 2009). Our second synthetic example consists of 8classes as well, and its Object Relation Diagram is depicted in Figure 3. This example was previously used in the CITO literature for weighted stubs (Hanh et al., 2001).



Figure 2: ORD for the first simple 8-class example.



Figure 3: ORD for the second simple 8-class example.

The other five case studies used in our experiments are taken from the Briand benchmark (Briand et al., 2002a) and used in different papers from the CITO literature (Briand et al., 2002b), (Cabral et al., 2012). The systems from this benchmark are the following: ATM (automated teller machine simulation), Ant (a Java-based build tool for maintaining, updating and regenerating related programs and files according to their dependencies), SPM (Security Patrol Monitoring, a project developed by a graduate student at Carleton University), BCEL (Byte Code Engineering Library, a tool for analyzing, creating and manipulating binary Java files) and DNS (a Java implementation of the Domain Naming System). For all these systems, we have used the Object Relation Diagram from the Appendix provided by Briand et al. (Briand et al., 2002a).

We have applied our GA-based approach for the case studies presented in Table 1. Due to some randomness in the execution, the GA was ran 20 times. We found that, in every case, the solution reported is the same, except for the Ant case study with equal weighting. For this case study we have run our GA 100 times out of which in 85 cases it reported 9 stubs, while in the other 15 cases it reported 10 stubs. In Table 2 we give the most frequent number of stubs, which is 9. Thus, under the considered parameter setting, our GA with stochastic acceptance has a deterministic behavior for differential weighting for all case studies. The number of specific weighted stubs obtained by the proposed GA is shown in Table 2.

## 5 DISCUSSION AND COMPARISON TO RELATED WORK

Considering the results from Table 2 we can observe that for the Ant and BCEL case studies there is a difference between the number of stubs needed in case of differential and equal weighting. For both systems we need less stubs if we do not take into consideration the relation between the classes (i.e., we use equal weighting). If we differentiate between the types of relationships we need slightly more stubs but, for our case studies, only association relations will be broken (this can be seen by the fitness of the best individual, which is not reported in Table 2). This shows that differential weighting can improve the total complexity of the stubs needed to be created. Unfortunately, for the other case studies this difference is not visible, but this might be related to their size or to the distribution of relations between classes (generally more than half of the relations are associations). In the future we intend to test our approach on larger systems as well to further analyze the difference between the number of stubs for the two weighting schemes.

For Table 2 we can observe that for each case study, for the differential weighting scheme, the GA provided the same number of stubs for all the 20 runs of the algorithm. For the equal weighting scheme for the Ant case study we had two different solutions (but the solution with the less number of stubs is the most frequently reported one). This suggests that using different weights might contribute to making the GA deterministic. In order to test this assumption we will extend the experimental evaluation.

Regarding the selection of the weights for different relations between classes, in the literature there are different perspectives: it is commonly accepted that *association* relations are the easiest to stub, but there is no clear agreement regarding the difficulty for stubbing *aggregations* and *inheritance*. There are approaches which consider that only associations can be broken (for ex. (Briand et al., 2002a)). Malloy et al.

Case study	# of classes	# of dependencies	# of cycles
8-class first example	8	17	11
(Hewett and Kijsanayothin, 2009)			
8-class second example	8	15	7
(Hanh et al., 2001)			
ATM (Briand et al., 2002b)	21	67	30
Ant (Briand et al., 2002b)	25	83	654
SPM (Briand et al., 2002b)	19	72	1178
BCEL (Briand et al., 2002b)	45	294	416091
DNS (Briand et al., 2002b)	61	276	16

Table 1: Description of the case studies.

in (Malloy et al., 2003) show through an example why inheritance relations are complicated to be stubbed. However, there might be situations, when stubbing a base class is easier than breaking other relations (e.g. if the base class is not abstract). Moreover, it is possible that by breaking inheritance relationships a lower number of total stubs is required (Malloy et al., 2003). This is why, a different approach for the CITO problem assigns weights for the classes from the ORD instead of the relationships. Weights assigned for classes can be determined based on the complexity of the class: number of attributes, number of methods, etc. In the future we intend to investigate this direction as well.

In the following we provide a comparison of the results obtained by the proposed GA approach to the results reported in the literature for the case studies considered for evaluation. The comparison is depicted in Table 3. For the simple case studies we have also computed the optimal number of stubs using a brute force approach. For the larger software systems, the brute force method is not feasible, due to its exponential time complexity. The best result obtained using a non-brute force approach (i.e., the one which reports the minimum number of weighted stubs) is highlighted. For each result we indicate the paper where the result was taken from.

For the brute force approach we implemented a parallel algorithm based on Heap's algorithm for generating permutations and we run the experiment on a server machine with 16 cores. The running times for the larger systems are over 48h while the proposed GA approach finds the optimal ordering in less than 3 minutes/run for every system (the genetic algorithm is not parallel, it uses only a single core). For the two smaller systems the required time is less than 30 seconds.

For the 8-class examples, we found in the literature results reported considering the *differential weighting* scheme and the same weights as considered in our experiments (Bansal et al., 2009). Unlike

	Case study	Weighting scheme	# of stubs
Ī	8-class first example	Differential	4
		Equal	4
ľ	9 alaca assand	Differential	2
	example	Equal	2
	ATM	Differential	7
		Equal	7
1	Ant	Differential	10
		Equal	9
CDM	Differential	16	
	SPM	Equal	16
	DCEI	Differential	60
	DUEL	Equal	58
đ	DNC	Differential	6
DINS	Equal	6	

Table 2: Number of stubs obtained by our GA approach for

for the simple 8-class case studies, for the case studies from the Briand benchmark there are no results reported in the literature considering weighted stubs as in our approach (i.e. assigning different weights for specific types of relationships between the application classes). For these systems, only the results obtained for *generic* and *specific* stubs are available. That is why, for the case studies from the Briand benchmark we applied our GA with stochastic acceptance under the *equal weighting* scheme which is equivalent to obtaining the *specific* stubs.

The first line from Table 3 shows the results for the first 8-class example from Figure 2. Bansal et al. (Bansal et al., 2009) report the results obtained by several approaches from the literature on this case study. The approach from Le Traon et al. provides multiple solutions with different number of stubs and we included all of them in the table. The second line of Table 3 contains the comparison of the results for the second 8-class example from Figure 3. This case study was previously used by Hanh et al. (Hanh et al.,

#	Case study	Weighting	Approach	
		scheme		stubs
	9 alage first avample	Differential	Our GA solution	
1	o-class first example		Brute force	4
		weighting	Tai et al. (Bansal et al., 2009)	5
			Le Traon et al. (Bansal et al., 2009)	5
			Le Traon et al. (Bansal et al., 2009)	6
			Le Traon et al. (Bansal et al., 2009)	4
			Briand et al. (Bansal et al., 2009)	4
			Malloy et al. (Bansal et al., 2009)	6
			Abdurazik et al. (Bansal et al., 2009)	4
	8-class second example	Differential	Our GA solution	2
2	o cluss second example	Differential	Brute force	2
		weighting	Kung et al. (Hanh et al., 2001)	4
			Tai and Daniels (Hanh et al., 2001)	2
			Hanh et al Triskell strategy(Hanh et al., 2001)	2
			Hanh et al Genetic algorithm (Hanh et al., 2001)	3
3		Equal	Our GA solution	9 or 10
	Ant		Briand et al. (Briand et al., 2002b)	11
	Ant			
	Ant	weighting	Tai and Daniels (Briand et al., 2002b)	28
	Ant	weighting	Tai and Daniels (Briand et al., 2002b) Le Traon et al. (Briand et al., 2002b)	28 19
4	Ant	weighting	Tai and Daniels (Briand et al., 2002b) Le Traon et al. (Briand et al., 2002b) <b>Our GA solution</b>	28 19 7
4	Ant	weighting Equal	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)	28 19 <b>7</b> 7
4	Ant	weighting Equal weighting	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)	28 19 7 7 8
4	Ant	weighting Equal weighting	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)	28 19 7 7 8 7
4	Ant	weighting Equal weighting	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solution	28 19 7 8 7 16
4	Ant	weighting Equal weighting Equal	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Briand et al. (Briand et al., 2002b)	28 19 7 7 8 7 <b>16</b> 17
4	ATM	weighting Equal weighting Equal weighting	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)	28 19 7 7 8 7 <b>16</b> 17 20
4	Ant ATM SPM	weighting Equal weighting Equal weighting	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)	28 19 7 7 8 7 <b>16</b> 17 20 27
4 5 6	ATM SPM	weighting Equal weighting Equal weighting	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Cur GA solution	28 19 7 8 7 <b>16</b> 17 20 27 <b>58</b>
4 5 6	ATM	weighting Equal weighting Equal weighting Equal	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Briand et al. (Briand et al., 2002b)	28 19 7 8 7 <b>16</b> 17 20 27 <b>58</b> 70
4	Ant ATM SPM BCEL	weighting Equal weighting Equal weighting Equal weighting	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Cour GA solutionBriand et al. (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)	28 19 7 8 7 <b>16</b> 17 20 27 <b>58</b> 70 128
4	Ant ATM SPM BCEL	weighting Equal weighting Equal weighting Equal weighting	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)	28 19 7 8 7 <b>16</b> 17 20 27 <b>58</b> 70 128 67
4 5 6 7	Ant ATM SPM BCEL	weighting Equal weighting Equal weighting Equal weighting	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Dur GA solutionOur GA solutionOur GA solutionOur GA solution	28 19 7 8 7 <b>16</b> 17 20 27 <b>58</b> 70 128 67 <b>6</b>
4 5 6 7	Ant ATM SPM BCEL	weighting Equal weighting Equal weighting Equal weighting	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Cur GA solutionBriand et al. (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Briand et al. (Briand et al., 2002b)	28 19 7 7 8 7 <b>16</b> 17 20 27 <b>58</b> 70 128 67 <b>6</b> 6
4 5 6 7	Ant ATM SPM BCEL DNS	weighting Equal weighting Equal weighting Equal weighting Equal weighting	Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Our GA solutionBriand et al. (Briand et al., 2002b)Tai and Daniels (Briand et al., 2002b)Le Traon et al. (Briand et al., 2002b)Dur GA solutionBriand et al. (Briand et al., 2002b)Dar GA solutionBriand et al. (Briand et al., 2002b)	28 19 7 7 8 7 <b>16</b> 17 20 27 <b>58</b> 70 128 67 <b>6</b> 6 27

Table 3: Comparison to related work considering weighted and specific stubs.

2001), where the result of several approaches are reported for it. The next lines from Table 3 depicts the comparison of the results obtained using our GA with those provided by Briand et al. (Briand et al., 2002b) on Ant, ATM, SPM, BCEL and DNS systems.

Table 3 show that the results provided by our GA approach are better than or at least equal to the approaches existing in the literature considering the case studies we used in our experiments. In **8** cases, the number of weighted stubs obtained is the same as the one from the related work, while in **18** situations a smaller number of weighted stubs was obtained by our approach. The comparison to the related work

is graphically illustrated in Figure 4. For each case study we represent the average number of weighted stubs reported in the literature and through the dashed bars the number of weighted stubs reported by our GA solution.

## 6 CONCLUSIONS AND FUTURE WORK

We have approached in this paper the problem of *class integration test ordering* and we proposed a genetic



Figure 4: GA performance compared to the average performance of the related work on the considered data sets.

algorithm with stochastic acceptance for defining an integration test order strategy for object-oriented systems. The goal is to identify, based on a static analysis of object-oriented software systems, the test order requiring a minimum stubbing effort. We considered a weighted cost for creating the specific stubs needed for testing. Seven case studies were considered in our experimental evaluation, both synthetic examples and systems used in the literature for the CITO problem. The results obtained using our approach outperformed those of existing similar work.

We plan to extend the experimental evaluation of the proposed GA technique for real software systems and to consider a parallel implementation of the GA, in order to test its scalability to larger systems. We will also investigate new dependencies between application classes for computing the *stubbing effort*. Another possible direction to improve our proposal would be to identify (possibly through machine learning) appropriate values for the weights associated with the dependencies between the classes from the software systems.

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