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An empirical evaluation of evolutionary algorithms for unit test suite generation

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ABSTRACT

Context: Evolutionary algorithms have been shown to be effective at generating unit test suites optimised for code coverage. While many specific aspects of these algorithms have been evaluated in detail (e.g., test length and different kinds of techniques aimed at improving performance, like seeding), the influence of the choice of evolutionary algorithm has to date seen less attention in the literature.
Objective: Since it is theoretically impossible to design an algorithm that is the best on all possible problems, a common approach in software engineering problems is to first try the most common algorithm, a genetic algorithm, and only afterwards try to refine it or compare it with other algorithms to see if any of them is more suited for the addressed problem. The objective of this paper is to perform this analysis, in order to shed light on the influence of the search algorithm applied for unit test generation.
Method: We empirically evaluate thirteen different evolutionary algorithms and two random approaches on a selection of non-trivial open source classes. All algorithms are implemented in the EvoSuite test generation tool, which includes recent optimisations such as the use of an archive during the search and optimisation for multiple coverage criteria.
Results: Our study shows that the use of a test archive makes evolutionary algorithms clearly better than random testing, and it confirms that the DynaMOSA many-objective search algorithm is the most effective algorithm for unit test generation.
Conclusion: Our results show that the choice of algorithm can have a substantial influence on the performance of whole test suite optimisation. Although we can make a recommendation on which algorithm to use in practice, no algorithm is clearly superior in all cases, suggesting future work on improved search algorithms for unit test generation.

1. Introduction

Search-based testing has been successfully applied to generating unit test suites optimised for code coverage on object-oriented classes. A popular approach is to use evolutionary algorithms where the individuals of the search population are whole test suites, and the optimisation goal is to find a test suite that achieves maximum code coverage [1]. Tools like EvoSuite [2] have been shown to be effective in achieving code coverage on different types of software [3].

Since the original introduction of whole test suite generation [4], many different optimisations have been introduced to improve performance even further, and to get a better understanding of the current limitations. For example, the insufficient guidance provided by basic coverage-based fitness functions has been shown to cause random search to often be equally effective as evolutionary algorithms [5]. Optimisation now no longer focuses on individual coverage criteria, but combinations of multiple different coverage criteria [6,7]. To cope with the resulting larger number of coverage goals, evolutionary search can be supported with archives [8] that keep track of useful solutions encountered throughout the search. To improve effectiveness, whole test suite optimisation has been re-formulated as a many-objective optimisation problem [9]. In the context of these developments, one aspect of

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whole test suite generation remains largely unexplored: What is the influence of the specific flavour of evolutionary algorithms applied to evolve test suites?

In this paper, we aim to shed light on the influence of the different evolutionary algorithms in whole test suite generation, to find out whether the choice of algorithm is important, and which one should be used. By using a large set of complex Java classes as case study, and the EVOSUITE [2] search-based test generation tool, we investigate specifically:

RQ1: Which archive-based single-objective evolutionary algorithm performs best?
RQ2: How does evolutionary search compare to random search and random testing?
RQ3: Which archive-based many-objective evolutionary algorithm performs best?
RQ4: How does evolution of whole test suites compare to many-objective optimisation of test cases?

We investigate each of these questions in the light of individual and multiple coverage criteria as optimisation objectives. This paper extends an earlier study [10], where we compared seven evolutionary algorithms and two random approaches. Our experiments now cover five additional algorithms, for a total of 13 different evolutionary algorithms, and corroborate the original findings: In most cases a simple (μ, λ) Evolutionary Algorithm (EA) is better than other, more complex algorithms. In most cases, the variants of EAs and GAs are also clearly better than random search and random testing, when a test archive is used. This study also extends the previous study with experiments using many-objective search algorithms using multiple criteria, and our experiments confirm that many-objective search, in particular the DynaMOSA algorithm [11], achieves higher branch coverage, even in the case of optimisation for multiple criteria, than all the other evaluated single/many-objective evolutionary algorithms.

2. Evolutionary algorithms for test suite generation

Evolutionary Algorithms (EAs) are inspired by natural evolution, and have been successfully used to address many kinds of optimisation problems. In the context of EAs, a solution is encoded "genetically" as an individual ("chromosome"), and a set of individuals is called a population. The population is gradually optimised using genetics-inspired operations such as *crossover*, which merges genetic material from at least two individuals to yield new offspring, *mutation*, which independently changes the elements of an individual with a low probability, and *selection* which chooses individuals for reproduction, preferring better, fitter individuals. While it is impossible to comprehensively cover all existing algorithms, in the following we discuss common variants of EAs for test suite optimisation. Expansion of the evaluation to less common algorithms (e.g., Differential Evolution [12], PAES [13], Coral Reef Optimisation [14], etc.) will be future work.

2.1. Representation

For test suite generation, the individuals of a population are sets of test cases (test suites); each test case is a sequence of calls. The length of a sequence of calls is variable, and there can be dependencies between statements. For example, one statement may define a variable used as a parameter for a call later in the call sequence. Standard types of statements in such sequences are definitions of primitive variables (e.g., integers or strings), calls to constructors to instantiate objects, and method calls on these objects.

Crossover on test suites is based on exchanging test cases between sets [1]. Mutation adds/modifies tests to suites, and adds/removes/changes statements within tests. The mutations applied at test case level need to ensure that test cases remain valid (e.g., when adding a new call there need to be suitable parameter objects defined earlier in the sequence).

Although standard selection techniques are largely used (e.g., rank or tournament selection), the variable size representation (the number of statements in a test and number of test cases in a suite can vary) requires modification to avoid bloat [15]; this is typically achieved by ranking individuals with identical fitness based on their length, and then using rank selection.

Standard whole test suite optimisation algorithms use test suites as individuals, since they are targeting coverage of all goals at the same time. Existing many-objective algorithms, on the other hand, aim to optimise an individual test for each distinct coverage goal, and so the search representation in this case is test cases. In this case, the test case mutation operators used when test suites are mutated are still used and bloat control is also active during selection. Crossover, however, needs to ensure that sequences of calls remain valid (i.e., all dependency variables need to exist). This is typically achieved by using repair actions when attaching to subsequences.

2.2. Optimisation goals and archives

The selection of individuals is guided by fitness functions, such that individuals with good fitness values are more likely to survive and be involved in reproduction. In the context of test suite generation, the fitness functions are based on code coverage criteria such as statement or branch coverage.

To provide a gradient to the search, most common fitness functions rely on the approach level and branch distance metrics [16,17]. The approach level $\mathcal{A}(t, x)$ for a given test t on a coverage goal $x \in X$ (for any given set of coverage goals X) is the minimal number of control dependent edges in the control dependency graph between the target goal x and the control flow path represented by the test case t. That is, it estimates the approximation between the execution path of a given test input and the target. The branch distance $d(t, x)$ heuristically quantifies how far a branch (i.e., the control flow edge resulting from a true/false evaluation of an if-condition) is from being evaluated to true or to false. When optimising for individual coverage goals, the fitness function is usually a combination of approach level and branch distance. For example, for branch coverage the fitness function to minimise the approach level and branch distance between a test t and a branch coverage goal x is defined as:

$$f(t, x) = \mathcal{A}(t, x) + \nu(d(t, x)) \tag{1}$$

where ν is any normalizing function in the range [0,1] [18]. When evolving test suites, however, one does not target individual goals but *all* coverage goals. For example, for branch coverage the resulting fitness function aims to minimise the branch distance of *all* branches B in the program under test. Thus, the fitness function for a test suite T and a set of branches B is:

$$f_{BC}(T, B) = \sum_{b \in B} d(T, b) \tag{2}$$

where $d(T, b)$ is defined as:

$$d(T, b) = \begin{cases} 0 & \text{if branch } b \text{ has been covered,} \\ \nu(d_{min}(t \in T, b)) & \text{if the predicate has been executed at least twice,} \\ 1 & \text{otherwise.} \end{cases} \tag{3}$$

More recently, there is a trend to optimise for multiple coverage criteria at the same time. Since coverage criteria usually do not represent conflicting goals, it is possible to combine fitness functions with a weighted linear combination [6]. However, the increased number of coverage goals may affect the performance of the EA. To counter these effects, it is possible to store tests for covered goals in an archive [8], and then to dynamically adapt the fitness function to optimise only for

the remaining uncovered goals. That is, during fitness evaluation, if a test case is found that newly covers a non-covered goal (e.g., branch, line, etc.), the covering test case and the covered goal are added to an archive. The fitness function is then optimised to only take into account the remaining goals. Note that this optimisation is only performed at the end of an iteration, i.e., only after evaluating all individuals, and not during the evaluation of one test suite or during the creation of a new population, as it would make fitness values between individuals inconsistent. Once the search ends, the best individual of the EA is no longer the best individual of the search population, but a test suite composed by all the tests in the archive. Besides optimising fitness functions to make use of the archive, search operators can also be adapted to make use of the test archive; for example, new tests may be created by mutating tests in the archive rather than randomly generating completely new tests.

2.3. Random search & random testing

Random search is a baseline search strategy which does not use crossover, mutation, or selection, but a simple replacement strategy [19]. Random search consists of repeatedly sampling candidates from the search space; the previous candidate is replaced if the fitness of the new sampled individual is better. Random search can make use of a test archive by changing the sampling procedure as indicated above. It has been shown that in unit test generation, due to the flat fitness landscapes and often simple search problems, random search is often as effective as EAs, and sometimes even better [5].

Random testing is a variant of random search in test generation which builds a test suite incrementally. Test cases (rather than test suites) are sampled individually, and if a test case improves the coverage of the test suite, it is retained in the test suite, otherwise it is discarded. This incremental process does not benefit from using an archive, because every sampled test case that covers a goal that has not been covered is added to the test suite.

2.4. Genetic algorithms

The genetic algorithm (GA) is one of the most widely-used EAs in many domains because it is well understood, it can be easily implemented, and it tends to obtain good results on average. Algorithm 1 illustrates a Standard GA. It starts by creating an initial random population of size p_s (Line 1). Then, a pair of individuals is selected from the population using a strategy s_f, such as rank-based, elitism or tournament selection (Line 6). Next, both selected individuals are recombined using crossover c_f (e.g., single point, multiple-point) with a probability of c_p to produce two new offspring o_1, o_2 (Line 7). Afterwards, mutation is applied on both offspring (Lines 8–9), independently changing the genes with a probability of m_p, which usually is equal to $\frac{1}{n}$, where n is the number of genes in a chromosome. The two mutated offspring are then included in the next population (Line 10). At the end of each iteration the fitness value of all individuals is computed (Line 13).

Many variants of the Standard GA have been proposed to improve effectiveness. Specifically, we consider a *monotonic* version of the Standard GA (Algorithm 2) which, after mutating and evaluating each offspring, only includes either the best offspring or the best parent in the next population (whereas the Standard GA includes both offspring in the next population regardless of their fitness value). Another variation of the Standard GA is a *Steady State* GA (Algorithm 3), which uses the same replacement strategy as the Monotonic GA, but instead of creating a new population of offspring, the offspring replace the parents from the current population immediately after the mutation phase.

A Breeder GA [20] (Algorithm 4) is a GA variant that does not aim to mimic Darwinian evolutionary, but instead tries to mimic breeding mechanism, as used for example in livestock. This is done by selecting a fixed percentage (e.g., 50%) of the best individuals of the total

Input: Stopping condition C, Fitness function δ, Population size p_s, Selection function s_f, Crossover function c_f, Crossover probability c_p, Mutation function m_f, Mutation probability m_p
Output: Population of optimised individuals P

1: $P \leftarrow$ GenerateRandomPopulation(p_s)
2: PerformFitnessEvaluation(δ, P)
3: **while** $\neg C$ **do**
4: $\quad N_P \leftarrow \{\} \cup$ Elitism(P)
5: $\quad$ **while** $|N_P| < p_s$ **do**
6: $\quad\quad p_1, p_2 \leftarrow$ Selection(s_f, P)
7: $\quad\quad o_1, o_2 \leftarrow$ Crossover(c_f, c_p, p_1, p_2)
8: $\quad\quad$ Mutation(m_f, m_p, o_1)
9: $\quad\quad$ Mutation(m_f, m_p, o_2)
10: $\quad\quad N_P \leftarrow N_P \cup \{o_1, o_2\}$
11: $\quad$ **end while**
12: $\quad P \leftarrow N_P$
13: $\quad$ PerformFitnessEvaluation(δ, P)
14: **end while**
15: **return** P

Algorithm 1. Standard genetic algorithm.

Input: Stopping condition C, Fitness function δ, Population size p_s, Selection function s_f, Crossover function c_f, Crossover probability c_p, Mutation function m_f, Mutation probability m_p
Output: Population of optimised individuals P

```
1:  P ← GenerateRandomPopulation(p_s)
2:  PerformFitnessEvaluation(δ, P)
3:  while ¬C do
4:      N_P ← {} ∪ Elitism(P)
5:      while |N_P| < p_s do
6:          p_1, p_2 ← Selection(s_f, P)
7:          o_1, o_2 ← Crossover(c_f, c_p, p_1, p_2)
8:          Mutation(m_f, m_p, o_1)
9:          Mutation(m_f, m_p, o_2)
10:         PerformFitnessEvaluation(δ, o_1)
11:         PerformFitnessEvaluation(δ, o_2)
12:         if Best(o_1, o_2) is better than Best(p_1, p_2) then
13:             N_P ← N_P ∪ {o_1, o_2}
14:         else
15:             N_P ← N_P ∪ {p_1, p_2}
16:         end if
17:     end while
18:     P ← N_P
19: end while
20: return P
```

Algorithm 2. Monotonic genetic algorithm.

Input: Stopping condition C, Fitness function δ, Population size p_s, Selection function s_f, Crossover function c_f, Crossover probability c_p, Mutation function m_f, Mutation probability m_p
Output: Population of optimised individuals P

$P \leftarrow$ GenerateRandomPopulation(p_s)
PerformFitnessEvaluation(δ, P)
while $\neg C$ **do**
  $p_1, p_2 \leftarrow$ Selection(s_f, P)
  $o_1, o_2 \leftarrow$ Crossover(c_f, c_p, p_1, p_2)
  Mutation(m_f, m_p, o_1)
  Mutation(m_f, m_p, o_2)
  PerformFitnessEvaluation(δ, o_1)
  PerformFitnessEvaluation(δ, o_2)
  if Best(o_1, o_2) is better than Best(p_1, p_2) **then**
    $P \leftarrow P \setminus \{p_1, p_2\} \cup \{o_1, o_2\}$
  else
    $P \leftarrow P \setminus \{o_1, o_2\} \cup \{p_1, p_2\}$
  end if
end while
return P

Algorithm 3. Steady-state genetic algorithm.

population as gene pool, and then uniformly sampling from this pool for reproduction (using standard crossover and mutation) when generating a new population. In addition, the best q individuals (e.g., 1) survive in terms of elitism.

The Cellular GA [21] differs from the Standard GA by considering a structured population which influences selection. For example, individuals can be set in a toroidal d-dimensional grid where each individual takes a place per a grid (i.e., cell) and belongs to an overlapped neighbourhood. The grid of individuals can have different number of dimensions; common values are one-dimensional (i.e., ring) or two-dimensional grids. In the case of a bi-dimensional grid, different shapes (i.e., models) of a neighbourhood can be defined. For example, the linear 5 model considers the individual itself and the individuals in its north, south, east, and west positions as neighbours of the current one.

Each individual is only allowed to interact with its neighbours and therefore the search operators are only applied on the individuals of one neighbourhood. First, two parents p_1, p_2 are selected among the neighbours of one individual p according to a selection criterion. Then, crossover is performed to create two new individuals o_1, o_2, which are then evaluated. The best individual (o) among the two new generated individuals is mutated and evaluated. Finally, if fitness value of p is better than the fitness value of o, the former is included in the next population, otherwise the later is included in the next population. Due to the neighbourhood overlapping, the Cellular GA motivates slow diffusion of solutions through the population and thus the exploration of the search space and the exploitation inside each neighbourhood are promoted during the search.

The $1 + (\lambda, \lambda)$ GA (Algorithm 6), introduced by Doerr et al. [22], starts by generating a random population of size 1. Then, mutation is used to create λ different mutated versions of the current individual. Mutation is applied with a high mutation probability, defined as $m_p = \frac{k}{n}$, where k is typically greater than one, which allows, on average, more than one gene to be mutated per chromosome. Then, uniform crossover is applied to the parent and best generated mutant to create λ offspring. While a high mutation probability is intended to support faster exploration of the search space, a uniform crossover between the best individual among the λ mutants and the parent was suggested to repair the defects caused by the aggressive mutation. Then all offspring are evaluated and the best one is selected. If the best offspring is better than the parent, the population of size one is replaced by the best offspring. $1 + (\lambda, \lambda)$ GA could be very expensive for large values of λ, as fitness has to be evaluated after mutation and after crossover.

2.5. Evolution strategies

Evolution strategies, dating back to Rechenberg [23], primarily use mutation and selection as search operators. Algorithm 7 shows a basic $(\mu + \lambda)$ Evolutionary Algorithm (EA), where a population of μ individuals is evolved by generating λ individuals in each generation through mutation of the μ individuals in the population. Among the different $(\mu + \lambda)$ EA versions, two common settings are $(1+\lambda)$ EA and $(1+1)$ EA, where the population size is 1, and the number of offspring is also limited to 1 for the $(1+1)$ EA. In the $(\mu + \lambda)$ EA, after the mutation step the best μ individuals out of the previous generation and the offspring are selected and kept as the new population. A variant of this is a (μ, λ) EA (Algorithm 8), where the μ new individuals are only selected from the offspring, and the parents are discarded.

2.6. Chemical Reaction Optimisation (CRO)

The Chemical Reaction Optimisation (CRO) [24] (Algorithm 9) is a metaheuristic algorithm which incorporates the best of a population-based algorithm (e.g., as genetic algorithms) and the simulated annealing [25] local search. CRO is inspired by the nature of chemical reactions, i.e., the process of transforming a set of unstable molecules in

Input: Stopping condition C, Fitness function δ, Population size p_s, Selection function s_f, Crossover function c_f, Crossover probability c_p, Mutation function m_f, Mutation probability m_p
Output: Population of optimised individuals P

1: $P \leftarrow$ GenerateRandomPopulation(p_s)
2: PerformFitnessEvaluation(δ, P)
3: **while** $\neg C$ **do**
4: $N_P \leftarrow \{\} \cup$ Elitism(P)
5: $P' \leftarrow$ Truncate(P)
6: **while** $|N_P| < p_s$ **do**
7: $p_1 \leftarrow$ SelectRandom(P')
8: $p_2 \leftarrow$ SelectRandom(P')
9: $o_1, o_2 \leftarrow$ Crossover(c_f, c_p, p_1, p_2)
10: Mutation(m_f, m_p, o_1)
11: Mutation(m_f, m_p, o_2)
12: $o \leftarrow$ SelectRandom(o_1, o_2)
13: $N_P \leftarrow N_P \cup \{o\}$
14: **end while**
15: $P \leftarrow N_P$
16: PerformFitnessEvaluation(δ, P)
17: **end while**
18: **return** P

Algorithm 4. Breeder genetic algorithm.

Input: Stopping condition C, Fitness function δ, Population size p_s, Selection function s_f, Crossover function c_f, Crossover probability c_p, Mutation function m_f, Mutation probability m_p, Neighbourhood model n_m
Output: Population of optimised individuals P

1: $P \leftarrow$ GenerateRandomPopulation(p_s)
2: PerformFitnessEvaluation(δ, P)
3: **while** $\neg C$ **do**
4: $N_P \leftarrow \{\}$
5: **for all** $p \in P$ **do**
6: $N_B \leftarrow$ GetNeighbourhood(p, P, n_m)
7: $p_1, p_2 \leftarrow$ Selection(s_f, N_B)
8: $o_1, o_2 \leftarrow$ Crossover(c_f, c_p, p_1, p_2)
9: PerformFitnessEvaluation(δ, o_1)
10: PerformFitnessEvaluation(δ, o_2)
11: $o \leftarrow$ Best(o_1, o_2)
12: Mutation(m_f, m_p, o)
13: PerformFitnessEvaluation(δ, o)
14: $N_P \leftarrow N_P \cup$ Best(o, p)
15: **end for**
16: $P \leftarrow N_P$
17: **end while**
18: **return** P

Algorithm 5. Cellular genetic algorithm.

Input: Stopping condition C, Fitness function δ, Offspring size λ, Crossover function c_f, Crossover probability c_p, Mutation function m_f, Mutation probability m_p
Output: Best individual p

1: $p \leftarrow$ GenerateRandomIndividual()
2: PerformFitnessEvaluation(δ, p)
3: **while** $\neg C$ **do**
4: $M \leftarrow \{\}$
5: **for** $i \leftarrow 1, \lambda$ **do**
6: $o \leftarrow$ Mutation(m_f, m_p, p)
7: PerformFitnessEvaluation(δ, o)
8: $M \leftarrow M \cup \{o\}$
9: **end for**
10: $p' \leftarrow$ Best(M)
11: $O \leftarrow \{\}$
12: **for** $i \leftarrow 1, \frac{\lambda}{2}$ **do**
13: $o_1, o_2 \leftarrow$ Crossover(c_f, c_p, p, p')
14: PerformFitnessEvaluation(δ, o_1)
15: PerformFitnessEvaluation(δ, o_2)
16: $O \leftarrow O \cup \{o_1, o_2\}$
17: **end for**
18: $p' \leftarrow$ Best(O)
19: **if** p' is better than p **then**
20: $p \leftarrow p'$
21: **end if**
22: **end while**
23: **return** p

Algorithm 6. 1 + (λ, λ) Genetic algorithm.

Input: Stopping condition C, Fitness function δ, Population size μ, Offspring size λ, Mutation function m_f, Mutation probability m_p
Output: Population of optimised individuals P

```
1:  P ← GenerateRandomPopulation(μ)
2:  PerformFitnessEvaluation(δ, P)
3:  while ¬C do
4:      O ← {}
5:      for all p ∈ P do
6:          for i ← 1, λ/μ do
7:              o ← Mutation(m_f, m_p, p)
8:              O ← O ∪ {o}
9:          end for
10:     end for
11:     PerformFitnessEvaluation(δ, O)
12:     P ← select best μ individuals from P ∪ O
13: end while
14: return P
```

Algorithm 7. $(\mu + \lambda)$ Evolutionary algorithm.

Input: Stopping condition C, Fitness function δ, Population size μ, Offspring size λ, Mutation function m_f, Mutation probability m_p
Output: Population of optimised individuals P

```
1:  P ← GenerateRandomPopulation(μ)
2:  PerformFitnessEvaluation(δ, P)
3:  while ¬C do
4:      O ← {}
5:      for all p ∈ P do
6:          for i ← 1, λ/μ do
7:              o ← Mutation(m_f, m_p, p)
8:              O ← O ∪ {o}
9:          end for
10:     end for
11:     PerformFitnessEvaluation(δ, O)
12:     P ← select best μ individuals from O
13: end while
14: return P
```

Algorithm 8. (μ, λ) Evolutionary algorithm.

Input: Stopping condition C, Fitness function δ, Population size p_s (i.e., number of molecules), Crossover function c_f, Crossover probability c_p, Mutation function m_f, Mutation probability m_p, Collision rate c_r, Decomposition threshold d_t, Synthesis threshold s_t, Initial kinetic energy k_e, Kinetic energy loss rate k_r,
Output: Population of optimised molecules P

```
1:  P ← GenerateRandomPopulation(p_s, k_e)
2:  PerformFitnessEvaluation(δ, P)
3:  while ¬C do
4:      r ← Random(0,1)
5:      if r > c_r then
6:          m ← Random(P)
7:          if NumberCollisions(m) > d_t then
8:              Decomposition(δ, m_f, m_p, P, m)
9:          else
10:             OnwallIneffectiveCollision(δ, m_f, m_p, k_r, P, m)
11:         end if
12:     else
13:         m_1, m_2 ← Random(P)
14:         if SynthesisThreshold(m_1) ≤ s_t and
15: SynthesisThreshold(m_2) ≤ s_t then
16:             Synthesis(δ, c_f, c_p, P, m_1, m_2)
17:         else
18:             IntermolecularIneffectiveCollision(δ, m_f, m_p, P, m_1, m_2)
19:         end if
20:     end if
21: end while
22: return P
```

Algorithm 9. Chemical Reaction Optimisation (CRO).

a container (similar to a population in GAs) to a set of stable molecules. The basic unit in CRO is a molecule (similar to a chromosome in GAs) and it is characterised by its potential energy (corresponding to the fitness value in GAs), its kinetic energy, and the number of collisions that is has been involved in. To manipulate individuals and explore the search space, CRO iteratively applies chemical reactions, which are similar to the search operations in a GA.

There are four types of reactions, each occurring in each iteration of CRO: *on-wall ineffective collision* and *inter-molecular ineffective collision* are used as local search operators, and on the other hand *decomposition* and *synthesis* are used as global search operators. An on-wall ineffective collision occurs when a molecule hits a wall of the container and stays as a single molecule. In the process some of molecule's kinetic energy is transferred to the container. An inter-molecular ineffective collision occurs when multiple molecules (typically two) collide with each other. Although this collision could be modelled as two independent on-wall ineffective collisions, the energy is handled in a different way, as molecules could exchange energy. A decomposition occurs when a molecule hits a wall of a container, but rather than bouncing away as a single molecule as in an inter-molecular ineffective collision, it breaks into several molecules (typically two). If the kinetic energy of the molecule is not enough to create two new molecules, some energy from the container is added to the newly generated molecules. On the other hand, a synthesis occurs when multiple molecules (typically two) collide with each other and form a single molecule. The kinetic energy of both molecules is joined and added to the new molecule.

CRO has more parameters to control than a common GA, in particular: the rate at which molecules lose kinetic energy after a collision (*kinetic energy loss rate*, a lower value would allow molecules to explore their local search space for longer), the rate of molecular collisions (*molecular collision rate*, a higher value would allow molecules to exchange information, i.e., energy more often), and the *initial kinetic energy* of each molecule (a higher value would allow molecules to explore their local search space for longer). There are two other parameters to control the degree of diversity of the container (i.e., population of molecules): a *decomposition threshold* to control whether a decomposition can be applied to a molecule (only molecules that have not been involved in *n* collisions can be decomposed), and a *synthesis threshold* to control whether a molecules can be synthesised (a molecule can synthesised if its kinetic energy is lower than a threshold). In this paper we used the values suggested by Lam and Li [26], i.e., *kinetic energy loss rate* and *molecular collision rate* of 0.2, an *initial kinetic energy* of 1000, a *decomposition threshold* of 500, and a *synthesis threshold* equal to 10.

2.7. Linearly Independent Path based Search (LIPS) algorithm

The Linearly Independent Path based Search (LIPS) algorithm [27] uses a single-objective genetic algorithm to optimise one coverage target (i.e., a branch) at a time. Algorithm 10 illustrates how LIPS works. As neither the pseudo-code nor the source code of the original LIPS implementation are available, we refer to the implementation proposed by Panichella et al. [28] and implemented on EvoSuite.

Briefly, it starts by generating and evaluating a random test case *i*. If *i* covers any branch goal, it is added to a pool of test cases (which keeps the best test cases found by the search, similar to an archive). Then, the list of branches not covered by test *i* is computed. For the next iteration of the algorithm, a target goal is chosen from the list of uncovered goals (i.e., the last uncovered goal of the path traversed by the last test case added to the pool of test cases), and a population (which includes *i*) is randomly generated. In LIPS, every target goal has an initial time limit to be covered equal to the total search budget divided by the total number of targets. However, as the search evolves, the time limit to satisfy each target is dynamically updated as branches are covered during the search (as some branches could be easier/quicker to cover than others). Within this time limit new offspring are generated based on traditional selection, crossover, and mutation operators. Once the offspring is generated it is then evaluated to assess whether it covers the target goal or any other goal. If any offspring (i.e., test cases) cover the current target goal: 1) the target goal is removed from the list of uncovered goals, 2) the new test case is added to the final pool of test cases, and 3) a new uncovered target goal is selected. If no offspring is able to cover the target goal within the allocated time budget, no test case is added to the pool and a new uncovered target goal is selected. Note that whether a new offspring covers the target goal or not, it may by chance cover other goals ("collateral coverage"). In this case, all goals covered by the new offspring are removed from the list of uncovered goals and the test is added to the final pool of test cases. At the end of each iteration the current population seeds the next iteration of the algorithm as it may include individuals covering alternative branches of the uncovered target branch. The algorithm stops when all targets are covered or a stopping condition is met.

2.8. Many-objective sorting algorithm

Unlike the single-objective optimisation on the test suite level described above, the Many-Objective Sorting Algorithm (MOSA) [9] regards each coverage goal as an independent optimisation objective. MOSA is a variant of NSGA-II [29], and uses a preference sorting criterion to reward the best tests for each non-covered target, regardless of their dominance relation with other tests in the population. MOSA also uses an archive to store the tests that cover new targets, which aiming to keep record on current best cases after each iteration.

Algorithm 11 illustrates how MOSA works. It starts with a random population of test cases. Then, and similar to typical EAs, the offspring are created by applying crossover and mutation (Line 6). Selection is based on the combined set of parents and offspring. This set is sorted (Line 9) based on a non-dominance relation and preference criterion. MOSA selects non-dominated individuals based on the resulting rank, starting from the lowest rank (F_0), until the population size is reached (Lines 11–14). In fewer than p_s individuals are selected, the individuals of the current rank (F_r) are sorted by crowding distance (Lines 16 and 17), and the individuals with the largest distance are added. Finally, the archive that stores previously uncovered branches is updated in order to yield the final test suite (Line 18). In order to cope with the large numbers of goals resulting from the combination of multiple coverage criteria, the DynaMOSA [11] extension dynamically selects targets based on the dependencies between the uncovered targets and the newly covered targets. Both, MOSA and DynaMOSA, have been shown to result in higher coverage of some selected criteria than traditional GAs for whole test suite optimisation.

2.9. Many Independent Objective (MIO) algorithm

The Many Independent Objective (MIO) Algorithm [30] is a search algorithm that is tailored for test suite generation. Its main motivation is to tackle cases when there is a large number of testing targets, and comparatively little available search budget. This is mainly the case for system testing, but could also happen for unit testing of large classes with test criteria like mutation testing (which typically results in many test targets).

A high level pseudo-code of how MIO works is listed in Algorithm 12. MIO evolves individual test cases, which are stored in an archive. At the end of search, a test suite is composed of the tests in the archive. In MIO, testing targets are sought independently, and a population of test cases is kept for each testing target. Once a target is covered, its best solution is saved in the archive, and the population is deleted. To avoid memory problems, the number of populations is dynamic: MIO only holds populations for targets that are reached and not fully covered yet.

At the beginning of the search, all populations are empty, and a random test case is generated. This test is added to all the populations of the targets reached by its execution. At each iteration, like in a (1 + 1) EA, a test case is sampled and mutated. The resulting offspring is copied

Input: Stopping condition C, Branch fitness function δ, Branch coverage goals B, Population size p_s, Selection function s_f, Crossover function c_f, Crossover probability c_p, Mutation function m_f, Mutation probability m_p
Output: Population of optimised individuals A

```
1:  A ← {}
2:  i ← GenerateRandomIndividual()
3:  PerformFitnessEvaluation(δ, i)
4:  U_B ← GetUncoveredBranches(B, i)
5:  b ← PopLast(U_B)
6:  UpdateOptimisedPopulation(A, i)
7:  P ← GenerateRandomPopulation(p_s − 1) ∪{i}
8:  while ¬C and U_B ≠ Ø do
9:      N_P ← {} ∪ Elitism(P)
10:     while |N_P| < p_s do
11:         p_1, p_2 ← Selection(s_f, P)
12:         o_1, o_2 ← Crossover(c_f, c_p, p_1, p_2)
13:         Mutation(m_f, m_p, o_1)
14:         Mutation(m_f, m_p, o_2)
15:         N_P ← N_P ∪ {o_1, o_2}
16:     end while
17:     PerformFitnessEvaluation(δ, N_P)
18:     CollateralCoverage(U_B, N_P)
19:     UpdateUncoveredBranches(U_B, N_P)
20:     UpdateOptimisedPopulation(A, N_P)
21:     if b ∉ U_B or ¬HasBudgetLeftForBranchB(U_B, b) then
22:         b ← PopLast(U_B)
23:     end if
24:     P ← N_P
25: end while
26: return A
```

Algorithm 10. Linearly Independent Path based Search (LIPS) algorithm.

Input: Stopping condition C, Fitness function δ, Population size p_s, Crossover function c_f, Crossover probability c_p, Mutation probability m_p
Output: Archive of optimised individuals A

1: $p \leftarrow 0$
2: $N_p \leftarrow$ GenerateRandomPopulation(p_s)
3: PerformFitnessEvaluation(δ, N_p)
4: $A \leftarrow \{\}$
5: **while** $\neg C$ **do**
6: $\quad N_o \leftarrow$ GenerateOffspring(c_f, c_p, m_p, N_p)
7: $\quad R_t \leftarrow N_p \cup N_o$
8: $\quad r \leftarrow 0$
9: $\quad F_r \leftarrow$ PreferenceSorting(R_t)
10: $\quad N_{p+1} \leftarrow \{\}$
11: $\quad$ **while** $|N_{p+1}| + |F_r| \leq p_s$ **do**
12: $\quad\quad$ CalculateCrowdingDistance(F_r)
13: $\quad\quad N_{p+1} \leftarrow N_{p+1} \cup F_r$
14: $\quad\quad r \leftarrow r + 1$
15: $\quad$ **end while**
16: $\quad$ DistanceCrowdingSort(F_r)
17: $\quad N_{p+1} \leftarrow N_{p+1} \cup F_r$ with size $p_s - |N_{p+1}|$
18: $\quad$ UpdateArchive(A, N_{p+1})
19: $\quad p \leftarrow p + 1$
20: **end while**
21: **return** A

Algorithm 11. Many-Objective Sorting Algorithm (MOSA).

Input: Stopping condition C, Fitness function δ, Population size N, Mutation function m_f, Mutation probability m_p, Probability of random sampling R, Start of focused search F
Output: Archive of optimised individuals A

```
1:  Z ← SetOfEmptyPopulations()
2:  A ← {}
3:  while ¬C do
4:      if R > Random(0,1) then
5:          p ← GenerateRandomIndividual()
6:      else
7:          p ← SampleIndividual(Z)
8:          p ← Mutation(m_f, m_p, p)
9:      end if
10:     for all t ∈ ReachedTargets(p) do
11:         if IsTargetCovered(t) then
12:             UpdateArchive(A, p)
13:             Z ← Z \ {Z_t}
14:         else
15:             Z_t ← Z_t ∪ {p}
16:             if |Z_t| > N then
17:                 RemoveWorstTest(Z_t, δ)
18:             end if
19:         end if
20:     end for
21:     UpdateParameters(F, R, N)
22: end while
23: return A
```

Algorithm 12. Many Independent Objective (MIO) algorithm.

and added to all the populations of targets reached by the offspring execution. When a population size reaches a certain threshold N, adding a new offspring will be followed by removing the worst test case in that population, where the fitness value is only based on that single target the population is for. In other words, a population will not increase in size more than N.

The sampling of which offspring to generate is done in two ways: with probability P, it is created at random, whereas with $1 - P$ it is sampled from one of the populations. When a population to sample from is chosen, the actual test in the population to copy and mutate is chosen randomly with uniform probability.

To handle the tradeoff between exploration and exploitation of the search landscape, MIO employs a dynamic parameter control. For example, give a starting value for R (e.g., $R = 0.5$), this value is decreased linearly over time until it reaches $R = 0$, when a more focused search starts. Similarly, N decreases down to $N = 1$. In other words, at the beginning of the search, MIO is similar to random search, but, with the passing of iterations, it becomes closer and closer to a focused $(1+1)$ EA. When the focused search starts is controlled by a parameter F, which represents the amount of search budget consumed before starting the focused search.

To handle possible issues with infeasible targets, the choice of which population to sample from is not at random. MIO keeps track of how often there are improvements in fitness value for the different testing targets that are not yet covered. Populations for testing targets with recent fitness improvements are more likely to be sampled from compared to populations for targets whose best fitness value has been stagnating (which would happen for infeasible targets).

3. Empirical study

In order to evaluate the influence of the evolutionary algorithm on test suite generation, we conducted an empirical study. In this section, we describe the experimental setup.

3.1. Experimental setup

3.1.1. Selection of classes under test

A key factor of studying evolutionary algorithms on automatic test generation is the selection of classes under test. As many open source classes, for example contained in the SF110 [3] corpus, are trivially simple [5] and would not reveal differences between algorithms, we used the selection of non-trivial classes from the DynaMOSA study [11]. This is a corpus of 117 open-source Java projects and 346 classes, selected from four different benchmarks. The complexity of classes ranges from 14 statements and 2 branches to 16,624 statements and 7938 branches. The average number of statements is 1109, and the average number of branches is 259.

3.1.2. Unit test generation tool

We used EvoSuite [2], which provides search algorithms to evolve coverage-optimised test suites, and allows an unbiased comparison of the algorithms as the underlying implementation of the tool is the same across all algorithms. By default, EvoSuite uses a Monotonic GA described in Section 2.4. It also provides a Standard and Steady State GA, Random search, Random testing and, more recently, MOSA, DynaMOSA, and LIPS. For this study, we extended EvoSuite with seven algorithms: the $1+(\lambda, \lambda)$ GA, $(\mu + \lambda)$ EA, (μ, λ) EA, Breeder GA, Cellular GA, CRO, and MIO. All evolutionary algorithms use a test archive.

3.1.3. Experiment procedure

We performed two experiments to assess the performance of the 13 selected evolutionary algorithms (described in Section 2). First, we conducted a tuning study to select the best population size (μ) of nine algorithms, number of mutations (λ) of $1 + (\lambda, \lambda)$ GA, population size (μ) and number of mutations (λ) of $(\mu + \lambda)$ EA and (μ, λ) EA, and the amount of search budget consumed before starting MIO's focused search, as the performance of each EA can be influenced by the parameters used [31]. Random-based approaches do not require any tuning. Then, we conducted a larger study to perform the comparison.

For both experiments we have two configurations: 1) single-criterion optimisation (i.e., branch coverage optimisation), and 2) multiple-criteria optimisation[1] (i.e., line, branch, exception, weak-mutation, output, method, method-no-exception, and context-dependent branch coverage) [6] to study the effect of the number of coverage criteria on the coverage of resulting test suites. For both configurations we used EvoSuite's default search budget of 1 min. Due to the randomness of EAs, we repeated the experiments 30 times.

For the tuning study, we randomly selected 10% (i.e., 34) of DynaMOSA's study classes [11] (with 15 to 1707 branches, 227 on average) from 30 Java projects. This resulted in a total of 25,500 (13,260 single-criterion configurations, and 12,240 multiple-criteria configurations; the number of multiple-criteria configurations is lower because LIPS only supports single criteria) calls to EvoSuite and more than 17 days of CPU-time overall. For the second experiment, we used the remaining 308 classes (346 total - 34 used to tune each EA - 4 discarded due to crashes of EvoSuite) from the DynaMOSA study [11]. Besides the tuned μ, λ parameters, and MIO's exploitation starting point, we used EvoSuite's default parameters [31].

3.1.4. Experiment analysis

For each test suite generated by EvoSuite on any experimental configuration we measure the coverage achieved on eight criteria, alongside other metrics, such as the number of generated test cases, the length of generated test suites in terms of statements, number of iterations of each EA, number of fitness evaluations, mutation score of the generated test suites, etc. As described by Arcuri and Fraser [31] "easy" branches are always covered independently of the parameter settings used, and several others are just infeasible. Therefore, rather than using raw coverage values, we use relative coverage [31]: Given the coverage of a class c in a run r, $cov(c, r)$, the best and worst coverage of c in any run, $max(cov(c))$ and $min(cov(c))$ respectively, a *relative coverage*, $\delta(c, r)$, can be defined as

$$\delta(c, r) = \frac{cov(c, r) - min(cov(c))}{max(cov(c)) - min(cov(c))}$$

If the best and worst coverage of c is equal, i.e., $max(cov(c)) = = \min(cov(c))$, then $\delta(c, r)$ is 1 (if range of $cov(c, r)$ is between 0 and 1) or 100 (if range of $cov(c, r)$ is between 0 and 100). Given a set of runs R, the average relative coverage of a class c is defined as

$$\Delta(c) = \frac{1}{|R|} \sum_{r \in R} \delta(c, r)$$

Thus, the coverage achieved by an algorithm A can be defined as

$$cov_A = \frac{1}{|C|} \sum_{c \in C} \Delta(c)$$

where C represents the set of classes. This way, the coverage of a trivial small class would be as important as the coverage of a large (perhaps more complex) class. For each averaged coverage value we compute common statistics such as standard deviation (σ), and confidence intervals ("CI") using bootstrapping at 95% confidence level. In order to statistically compare the performance of each EA we use the Vargha–Delaney $\widehat{A}_{12}$ effect size, the Wilcoxon–Mann–Whitney U-test with a 95% confidence level, and the Friedman test. Note that we do not perform any p-value adjustments in this study, e.g., Bonferroni, as the

[1] At the time of writing this paper, LIPS did not support all the criteria used by EvoSuite.

use of such adjustments has been discouraged [32] due to substantial reduction in the statistical power of rejecting an incorrect null hypothesis [33], and therefore increasing the likelihood of Type II errors.

3.1.5. Threats to validity

Threats to *internal validity* might result from how the empirical study was carried out. We thoroughly tested the experiment framework and test generation tool in order to reduce the chances of having faults, but it is well-known that testing alone cannot prove the absence of defects. Since the randomised algorithms underlying our study are affected by chance, we ran each experiment 30 times and followed rigorous statistical procedures to evaluate the results. To avoid possible confounding factors when comparing different algorithms, they were all implemented in the same tool. Furthermore, we used the same default values for all relevant parameters, and tuned the algorithm-specific ones. It is nevertheless possible that different parameter values might influence the performance of each EA.

We measured the success of different EAs using code coverage. While higher coverage is a desirable goal for test generation, there is an ongoing debate on how code coverage correlates to fault finding potential, and so there is a threat to *construct validity* resulting from how we measure test suite quality. However, code coverage is nevertheless sufficient to compare the effectiveness of different optimisation algorithms at achieving their optimisation goal.

As with any empirical study, there are threats to *external validity* regarding the generalisation to other types of software. The results reported in this paper are limited to the number and type of EAs used in the experiments. However, we believe these are representative of state-of-art algorithms, and are sufficient in order to demonstrate the influence of each algorithm on the problem, and of the choice of algorithm on the problem in general. We used 346 complex classes from 117 open-source Java projects in our experiments. While this resulted in a substantial computational effort, our results may not generalise to other classes. However, we specifically chose classes that are complex, as also used in previous studies [11] on test generation.

3.2. Parameter tuning

The execution of an EA requires a number of parameters to be set. As there is not a single best configuration setting to solve all problems [34] in which an EA could be applied, a possible alternative is to tune EA's parameters for a specific problem at hand to find the "best" ones. Our experimental setup largely relies on two previous tuning studies: 1) Arcuri and Fraser [31] determined the best values for most parameters of EvoSuite, such as crossover rate, elitism rate, selection function, etc.; and 2) Shamshiri et al. [35] determined the best values for CRO in the context of search-based test generation, for instance, the best potential energy value, or the best number of collisions allowed, etc. Both studies performed a similar tuning study as the one defined and reported in this paper to identify the best parameters. Note that, although neither Breeder GA, Cellular GA, $1 + (\lambda, \lambda)$ GA, $(\mu + \lambda)$ EA, and (μ, λ) EA have been evaluated in the context of unit test generation, none of the algorithms except Cellular GA require any new parameters. For the Cellular GA we use the best parameter (i.e., neighbourhood model) that has been reported by previous work [21]. The main distinguishing factors between the algorithms we are considering in this study are μ (i.e., the population size) and λ (i.e., the number of mutations), or F which represents the amount of search budget consumed before starting the focused search in MIO. In particular, we selected common values used in previous studies and reported to be the best for each EA:

- Population size of 10, 25, 50, and 100 for Standard GA, Monotonic GA, SteadyState GA, Breeder GA, Cellular GA, CRO, MOSA, DynaMOSA, and LIPS.
- λ size of 1, 8 [22], 25, and 50 for $1 + (\lambda, \lambda)$ GA.
- μ size of 1, 7 [36], 25, and 50, and λ size of 1, 7, 25, and 50 for $(\mu + \lambda)$ EA and (μ, λ) EA.
- F of 0.00, 0.25, 0.50, 0.75, 1.00 for MIO.

Thus, for Standard GA, Monotonic GA, SteadyState GA, Breeder GA, Cellular GA, CRO, MOSA, DynaMOSA, LIPS, and $1 + (\lambda, \lambda)$ GA there are 4 different configurations; for $(\mu + \lambda)$ EA and (μ, λ) EA, and as λ must be divisible by μ, there are 8 different configurations (i.e., $1 + 1, 1 + 7, 1 + 25, 1 + 50, 7 + 7, 25 + 25, 25 + 50, 50 + 50$); for MIO there are 5 different configurations, i.e., a total of 61 different configurations.

To identify the best parameter of each EA, we performed a pairwise comparison of the coverage achieved by using any μ (population size), $\mu + \lambda$, or F. The parameter for which an EA achieved a significantly higher coverage more often was selected as the best. Table 1 shows the best parameter per EA. For single and multiple-criteria the best population size is shared by several EAs, for instance, Standard GA, Steady-State GA, Breeder GA, and CRO share the same value (10 for single-criteria, and 100 for multiple-criteria). The best population size for MOSA and DynaMOSA is the same for single-criteria (i.e., 10), but different for multiple-criteria (25 for MOSA, and 10 for DynaMOSA). The best F value for MIO is 1.0 for single-criteria, and 0.25 for multiple-criteria, i.e., for a smaller number of coverage goals MIO works best without focusing the search, and for a larger number of coverage goals (multiple-criteria scenario) MIO works best if the focus search is enabled once 25% of the search budget has been consumed. Table 1 also reports the average effect size of the best parameter value when compared to all possible parameter values; and the effect size of pairwise comparisons in which the best parameter was significantly better/worse.

Table 1
Best parameter (X, i.e., μ, $\mu + \lambda$, or F) of each EA for single and multiple criteria optimisation. "Branch Coverage" column reports the branch coverage per EA, and column "Overall Coverage", the overall coverage of a multiple-criteria optimisation, "Avg. $\widehat{A}_{12}$" represents the average effect size of the best parameter value when compared to all possible parameter values, "Better $\widehat{A}_{12}$" the effect size of all pairwise comparisons in which the best parameter was significantly better, and "Worse $\widehat{A}_{12}$" the effect size of pairwise all comparisons in which the best parameter was significantly worse.

Algorithm	X	Branch cov.	Overall cov.	Avg. $\widehat{A}_{12}$	Better $\widehat{A}_{12}$	Worse $\widehat{A}_{12}$
Search budget of 60 s – Single-criteria						
Standard GA	10	0.74	–	0.53	0.76	0.31
Monotonic GA	25	0.75	–	0.54	0.73	0.32
Steady-State GA	10	0.70	–	0.54	0.73	0.32
$1 + (\lambda, \lambda)$ GA	8	0.61	–	0.53	0.69	0.30
$(\mu + \lambda)$ EA	7+7	0.74	–	0.52	0.78	0.26
(μ, λ) EA	1,7	0.76	–	0.65	0.83	0.28
Breeder GA	10	0.67	–	0.51	0.73	0.23
Cellular GA	100	0.60	–	0.52	0.77	0.26
CRO	10	0.70	–	0.51	0.73	0.26
MOSA	10	0.74	–	0.53	0.72	0.24
DynaMOSA	10	0.75	–	0.55	0.73	0.16
LIPS	100	0.58	–	0.54	0.72	0.31
MIO	1.00	0.68	–	0.52	0.72	0.34
Search budget of 60 s – Multiple-criteria						
Standard GA	100	0.64	0.66	0.52	0.74	0.23
Monotonic GA	100	0.63	0.65	0.53	0.76	0.22
Steady-State GA	100	0.58	0.61	0.53	0.77	0.23
$1 + (\lambda, \lambda)$ GA	50	0.49	0.51	0.60	0.77	0.31
$(\mu + \lambda)$ EA	50+50	0.67	0.69	0.55	0.77	0.21
(μ, λ) EA	25,50	0.68	0.70	0.61	0.81	0.25
Breeder GA	100	0.61	0.63	0.57	0.75	0.23
Cellular GA	100	0.57	0.60	0.62	0.79	0.25
CRO	100	0.62	0.64	0.49	0.73	0.23
MOSA	25	0.73	0.73	0.58	0.77	0.29
DynaMOSA	10	0.77	0.73	0.55	0.72	0.20
LIPS	–	–	–	–	–	–
MIO	0.25	0.67	0.66	0.54	0.71	0.28

Table 2
For each algorithm, we report several statistics on the obtained results, such as branch and overall coverage, standard deviation (σ), mutation score, number of generated test cases (#T), and the rank of each algorithm based on their average performance (R), which is statistically significant for both single and multiple criteria according to the Friedman test (p-value is < 0.0001 for both single and multiple criteria, full data is available on the accompanying website [37]). For averaged coverage values we also report confidence intervals (CI) using bootstrapping at 95% significance level.

Algorithm	Branch Cov.	σ	CI	Overall Cov.	σ	CI	Mut. Score	#T	R	σ
Search budget of 60 seconds – Single-criteria										
Random Search	0.73	0.07	[0.70, 0.76]	—	—	—	0.44	28	8.3	3.9
Random Testing	0.69	0.08	[0.66, 0.72]	—	—	—	0.43	25	10.5	3.3
Standard GA	0.79	0.09	[0.77, 0.82]	—	—	—	0.46	27	6.3	3.0
Monotonic GA	0.79	0.08	[0.76, 0.81]	—	—	—	0.45	27	6.2	2.7
Steady-State GA	0.76	0.08	[0.73, 0.79]	—	—	—	0.44	27	8.1	3.1
$1 + (\lambda, \lambda)$ GA	0.61	0.13	[0.58, 0.65]	—	—	—	0.41	18	11.0	3.8
$(\mu + \lambda)$ EA	0.79	0.08	[0.77, 0.82]	—	—	—	0.46	28	5.9	2.7
(μ, λ) EA	0.81	0.09	[0.79, 0.83]	—	—	—	0.46	28	5.1	2.9
Breeder GA	0.72	0.10	[0.70, 0.76]	—	—	—	0.44	25	9.5	3.0
Cellular GA	0.67	0.09	[0.64, 0.71]	—	—	—	0.43	26	10.8	3.2
CRO	0.74	0.10	[0.71, 0.77]	—	—	—	0.44	26	8.6	2.8
MOSA	0.82	0.08	[0.79, 0.84]	—	—	—	0.47	29	5.1	3.3
DynaMOSA	0.82	0.08	[0.80, 0.85]	—	—	—	0.47	30	4.8	3.5
LIPS	0.62	0.11	[0.59, 0.66]	—	—	—	0.42	23	11.9	3.5
MIO	0.75	0.09	[0.72, 0.78]	—	—	—	0.44	27	7.9	3.4
Search budget of 60 seconds – Multiple-criteria										
Random Search	0.65	0.10	[0.62, 0.67]	0.64	0.10	[0.62, 0.66]	0.44	31	9.1	4.3
Random Testing	0.55	0.09	[0.52, 0.59]	0.45	0.12	[0.42, 0.48]	0.41	28	12.3	2.5
Standard GA	0.71	0.08	[0.68, 0.74]	0.76	0.07	[0.73, 0.78]	0.46	42	5.6	2.5
Monotonic GA	0.71	0.08	[0.68, 0.74]	0.75	0.08	[0.73, 0.78]	0.46	41	6.1	2.4
Steady-State GA	0.65	0.08	[0.61, 0.68]	0.70	0.07	[0.67, 0.73]	0.45	39	8.9	2.7
$1 + (\lambda, \lambda)$ GA	0.48	0.13	[0.45, 0.52]	0.54	0.12	[0.51, 0.57]	0.40	26	11.3	3.2
$(\mu + \lambda)$ EA	0.72	0.08	[0.69, 0.75]	0.77	0.08	[0.75, 0.79]	0.46	42	5.3	2.5
(μ, λ) EA	0.72	0.09	[0.69, 0.75]	0.77	0.08	[0.75, 0.79]	0.47	40	5.6	2.7
Breeder GA	0.66	0.09	[0.63, 0.69]	0.71	0.08	[0.69, 0.74]	0.45	39	8.2	2.3
Cellular GA	0.61	0.09	[0.58, 0.64]	0.66	0.08	[0.63, 0.69]	0.44	39	10.2	2.4
CRO	0.69	0.09	[0.65, 0.72]	0.73	0.08	[0.71, 0.75]	0.46	40	7.1	2.7
MOSA	0.79	0.09	[0.76, 0.81]	0.81	0.08	[0.79, 0.83]	0.49	44	4.3	3.2
DynaMOSA	0.84	0.08	[0.82, 0.86]	0.86	0.07	[0.84, 0.87]	0.51	48	3.2	3.0
LIPS	—	—	—	—	—	—	—	—	—	—
MIO	0.68	0.10	[0.65, 0.71]	0.71	0.09	[0.69, 0.74]	0.45	37	7.9	3.7

4. Experiment results

Table 2 summarises the results of the main experiment described in the previous section. For each algorithm we report the branch coverage achieved for single and multiple criteria, the overall coverage for multiple criteria, the mutation score, the number of generated test cases, and the rank of each algorithm based on their average performance. Table 2 also reports the standard deviation and confidence intervals (CI) using bootstrapping at 95% significance level of the coverage achieved (either branch or overall coverage).

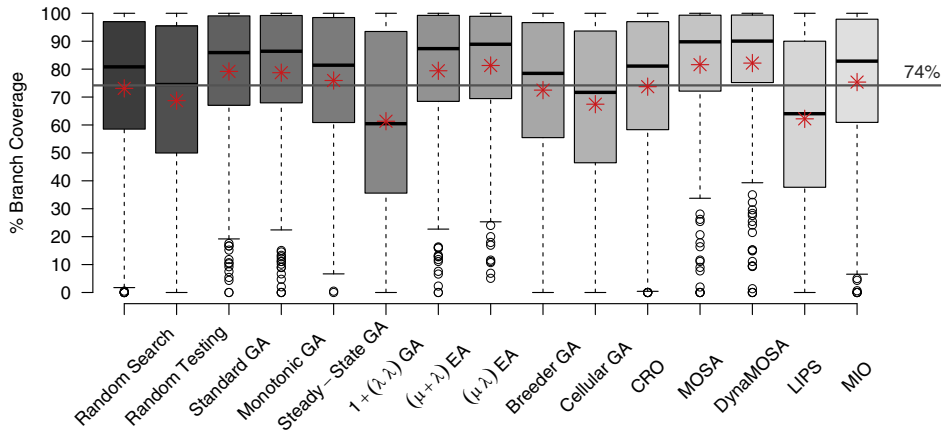
On one hand, MOSA and DynaMOSA achieve the highest coverage on average (82%) for single criteria. Although the CI of both algorithms overlap ([80%, 85%] vs. [79%, 84%]), DynaMOSA is ranked first. The results of the Friedman test are statistically significant, i.e., p-values are < 0.0001 for both single and multiple criteria (full data is available on the accompanying website [37]). This means that, for both single and multiple criteria, the rankings reported in Table 2 are statistically different (i.e., there is at least one algorithm that has performance different from the others). For multiple criteria, DynaMOSA achieves the highest overall coverage (86%) and CI among all algorithms. On the other hand, the $1 + (\lambda, \lambda)$ EA achieves the lowest branch coverage (61%) for single criteria, and Random testing achieves the lowest overall coverage (45%) for multiple criteria, thus it is ranked as the worst algorithm. There are a few algorithms that perform similarly, for instance, Standard GA, Monotonic GA, and $(\mu + \lambda)$ EA achieve the same branch coverage for single criteria (79%); and $(\mu + \lambda)$ EA, and (μ, λ) EA achieve the same overall coverage for multiple criteria (77%). To make these quantitative results more accessible, Fig. 1 shows the coverage distribution achieved by each algorithm. It also shows the median and the mean per algorithm, and the mean of all algorithms. For single criteria the average coverage among all algorithms is 74%, which means 7 algorithms (i.e., Random search and Random testing, $1 + (\lambda, \lambda)$ EA, Breeder GA, Cellular GA, and LIPS) out of 15 perform below the average. On the other hand, for multiple criteria only 4 algorithms perform below the average (i.e., Random search and testing, $1 + (\lambda, \lambda)$ EA, and Cellular GA).

In terms of mutation score and number of generated test cases, all algorithms performed similarly. For instance, MOSA and DynaMOSA generated 29 and 30 test cases for single criteria, respectively, and both sets of test cases achieve the same mutation score (47%). The algorithm that generated the lowest number of test cases (18) and achieved the lowest mutation score (41%) is the $1 + (\lambda, \lambda)$ EA. Besides these three EAs, the range of mutation scores for single criteria is only [42%, 46%], and the number of test cases is in the range of [23, 28]. Note that for both, single and multiple criteria, the EA that generated more test cases is the one that achieved the highest coverage (either branch or overall coverage) and mutation score.

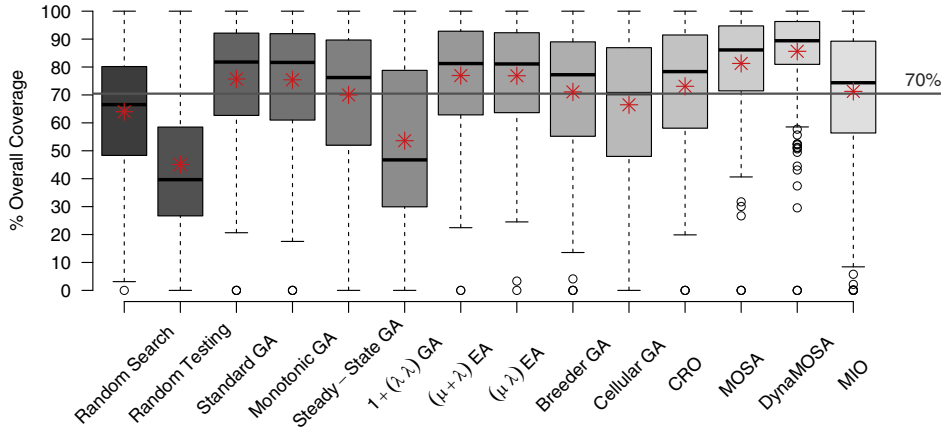
Although DynaMOSA achieved the highest coverage and mutation score among all algorithms, and is ranked first for both single and multiple criteria, it is not clear whether it performs consistently better than any other algorithm across all classes under test. In the following sections we perform further analyses to address this issue and answer our research questions.

4.1. RQ1 – Which archive-based single-objective evolutionary algorithm performs best?

Table 3 summarises the results of a pairwise tournament of all EAs. An EA X is considered to be better than an EA Y if it performs significantly better on a higher number of comparisons. For example, the



(a) Single criteria.

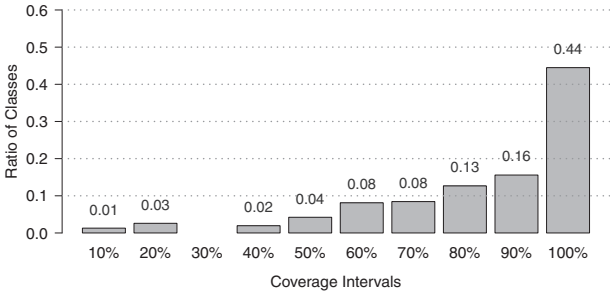


(b) Multiple criteria.

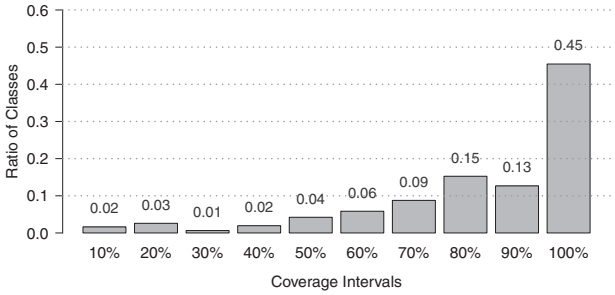
Fig. 1. Coverage achieved by each algorithm. Middle line of each boxplot marks the median, white circles represent outliers, * symbol signifies the mean, and the grey line represents the mean of all coverages.

Table 3
X Pairwise comparison of all evolutionary algorithms. "Better than" and "Worse than" give the number of comparisons for which the best EA is statistically significantly (i.e., *p-value* < 0.05) better and worse, respectively. Columns $\widehat{A}_{12}$ give the average effect size.

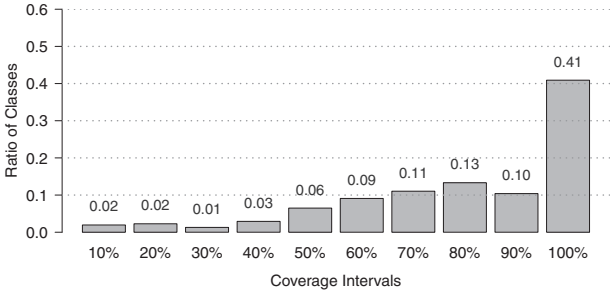
	Tourn.	Branch	Overall	Better			Worse	
Algorithm	position	cov.	cov.	$\widehat{A}_{12}$	than	$\widehat{A}_{12}$	than	$\widehat{A}_{12}$
Search budget of 60 s – Single-criteria								
Standard GA	4	0.79	–	0.58	741 / 2464	0.82	210 / 2464	0.26
Monotonic GA	3	0.79	–	0.58	733 / 2464	0.81	189 / 2464	0.26
Steady-State GA	5	0.76	–	0.50	536 / 2464	0.82	599 / 2464	0.21
1 + (λ, λ) GA	8	0.61	–	0.33	189 / 2464	0.76	1218 / 2464	0.12
(μ + λ) EA	2	0.79	–	0.60	815 / 2464	0.81	128 / 2464	0.28
(μ, λ) EA	1	0.81	–	0.63	1028 / 2464	0.81	60 / 2464	0.30
Breeder GA	7	0.72	–	0.44	322 / 2464	0.82	846 / 2464	0.21
Cellular GA	9	0.67	–	0.35	210 / 2464	0.82	1256 / 2464	0.17
CRO	6	0.74	–	0.50	460 / 2464	0.82	528 / 2464	0.23
Search budget of 60 s – Multiple-criteria								
Standard GA	2	0.71	0.76	0.62	961 / 2464	0.82	130 / 2464	0.26
Monotonic GA	4	0.71	0.75	0.60	892 / 2464	0.81	188 / 2464	0.26
Steady-State GA	7	0.65	0.70	0.44	371 / 2464	0.85	893 / 2464	0.21
1 + (λ, λ) GA	9	0.48	0.54	0.22	120 / 2464	0.76	1724 / 2464	0.08
(μ + λ) EA	1	0.72	0.77	0.64	1066 / 2464	0.83	106 / 2464	0.27
(μ, λ) EA	3	0.72	0.77	0.62	1012 / 2464	0.83	216 / 2464	0.24
Breeder GA	6	0.66	0.71	0.47	411 / 2464	0.84	733 / 2464	0.23
Cellular GA	8	0.61	0.66	0.37	223 / 2464	0.88	1207 / 2464	0.18
CRO	5	0.69	0.73	0.53	601 / 2464	0.82	460 / 2464	0.22



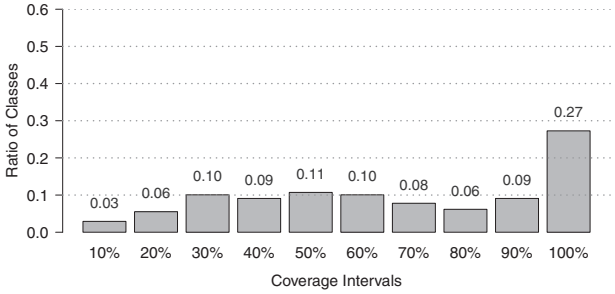
(a) Standard GA.



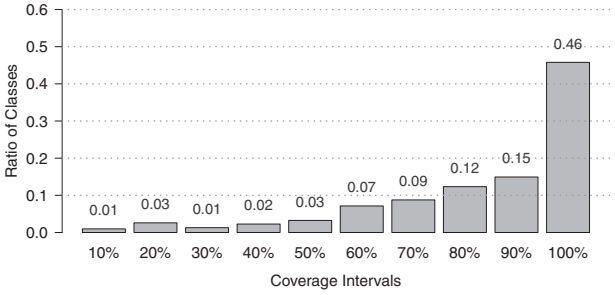
(b) Monotonic GA.



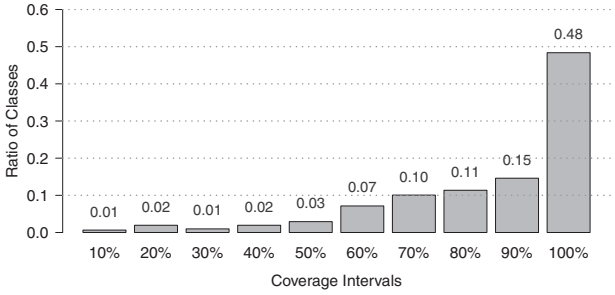
(c) Steady-State GA.



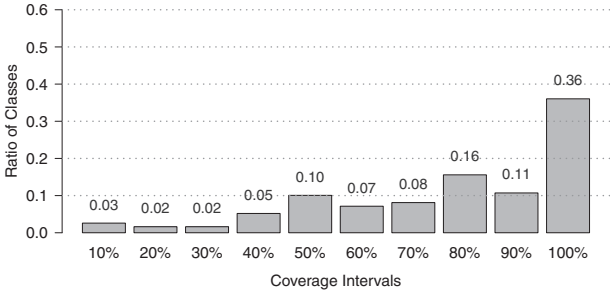
(d) $1 + (\lambda, \lambda)$ GA.



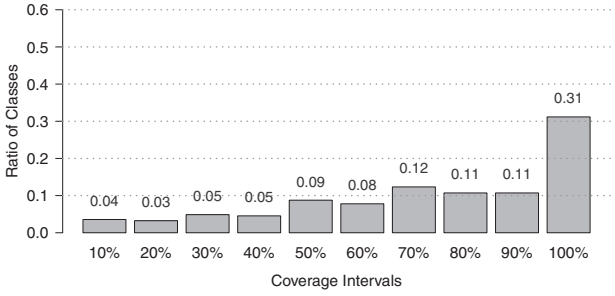
(e) $(\mu + \lambda)$ EA.



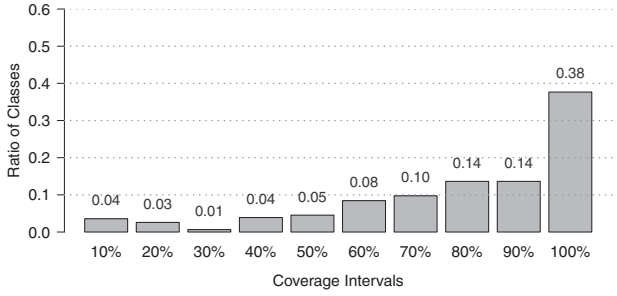
(f) (μ, λ) EA (**best**).



(g) Breeder GA.

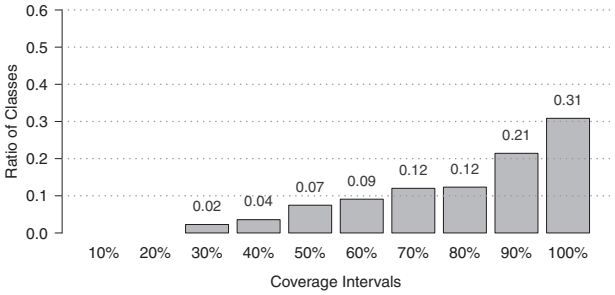


(h) Cellular GA.

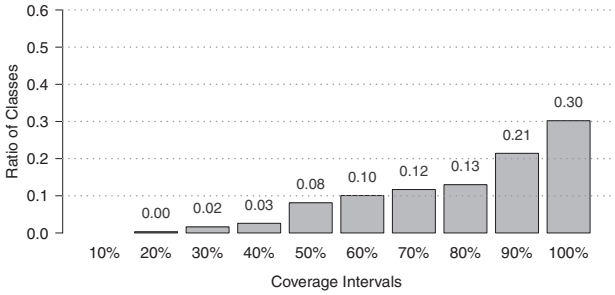


(i) CRO.

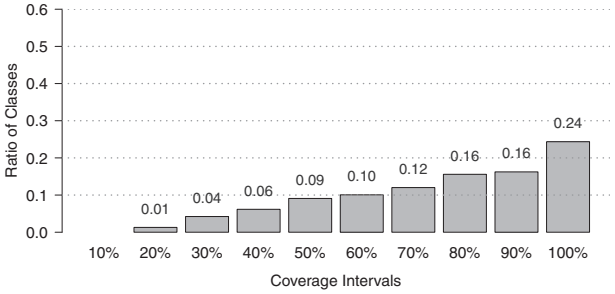
Fig. 2. Proportion of classes that have an average branch coverage (averaged out of 30 runs on all their classes) within each 10% branch coverage interval. X-labels show the upper limit (inclusive). For example, the group 30% represents all the classes with an average branch coverage greater than 20% and lower than or equal to 30%.



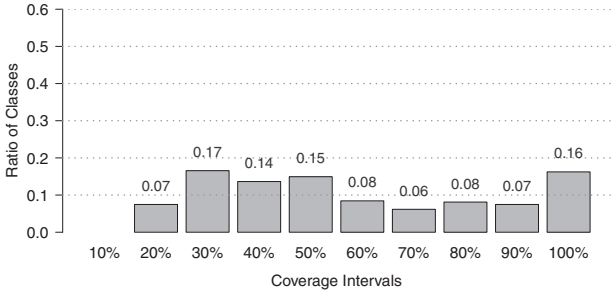
(a) Standard GA.



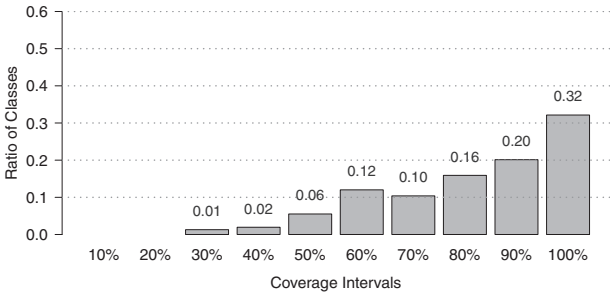
(b) Monotonic GA.



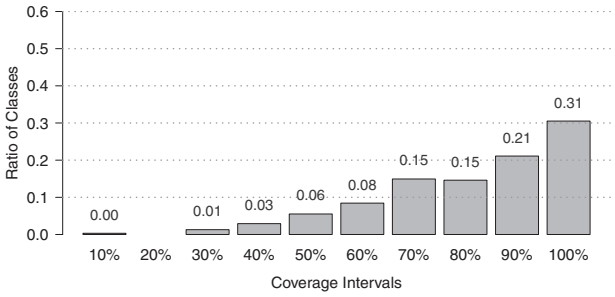
(c) Steady-State GA.



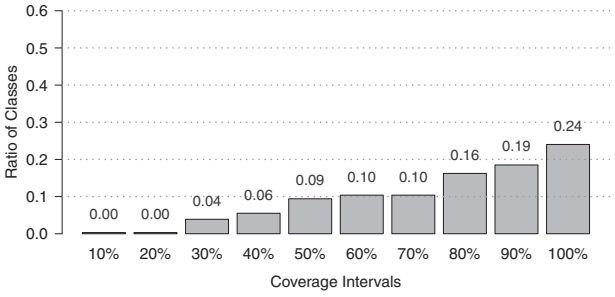
(d) $1 + (\lambda, \lambda)$ GA.



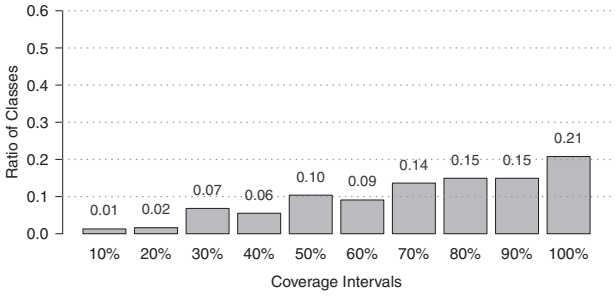
(e) $(\mu + \lambda)$ EA (**best**).



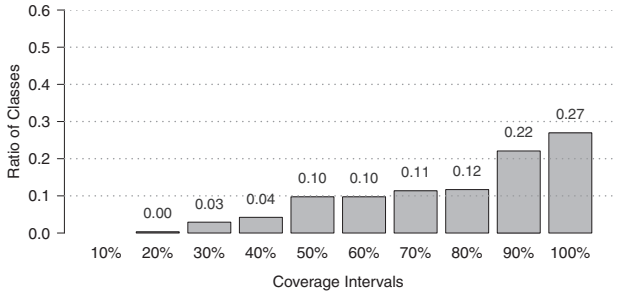
(f) (μ, λ) EA.



(g) Breeder GA.



(h) Cellular GA.



(i) CRO.

Fig. 3. Proportion of classes that have an average overall coverage (averaged out of 30 runs on all their classes) within each 10% overall coverage interval. X-labels show the upper limit (inclusive). For example, the group 30% represents all the classes with an average overall coverage greater than 20% and lower than or equal to 30%.

(μ, λ) EA was the one with more positive comparisons (1028) and the least negative comparisons (just 60) – thus, being the best EA for single criteria. While it is ranked third for multiple criteria, it achieved the same branch and overall coverage (72% and 77%, respectively) as the first ranked EA, i.e., ($\mu + \lambda$) EA, with an $\widehat{A}_{12}$ effect size of 62% averaged over all comparisons.

Figs. 2 and 3 illustrate these results visually by showing the proportion of classes per coverage interval for single and multiple criterion respectively. For example, (μ, λ) EA achieved a branch coverage between 91% and 100% for 63% of all classes under test (see Fig. 2f), and an overall coverage between 91% and 100% for 52% of all classes under test (see Fig. 3f). As expected, the best EA for single and multiple criteria is the one with the highest ratio of classes within the coverage interval]90%, 100%].

Surprisingly, despite its reported good performance [22] the $1 + (\lambda, \lambda)$ EA was statistically significantly better only on 120 comparisons for multiple criteria, while it was statistically significantly worse on 1724 comparisons out of 2464 – which make it the worst EA in our comparison. A recent study has shown that due to the presence of many plateaus in the landscape of a test generation problem (and not the number of local optima), crossover has little or no impact on the search [38]. Thus, our conjecture is that the worst performance of the $1 + (\lambda, \lambda)$ EA in our evaluation is due to the fact the only individual in the population heavily relies on the outcome of λ crossover operations, which may or may not perform successfully (i.e., generate an individual that is better than the single one in the population). Another EA that performed poorly is the Cellular GA. To the best of our knowledge, this is the first time a Cellular GA has been applied to automatic software test generation and therefore it has not been studied in detail, for instance, the question which neighbourhood model works best for this particular problem still remains.

> RQ1: For a small number of coverage goals a (μ, λ) EA is better than the other considered evolutionary algorithms, for a large number of coverage goals a ($\mu + \lambda$) EA performed better.

Table 4
Comparison of evolutionary algorithms and two random-based approaches: Random search and Random testing. Statistically significant effect sizes are shown in bold.

	Branch	Overall	vs. Random search		vs. Random testing	
Algorithm	cov.	cov.	$\widehat{A}_{12}$	p	$\widehat{A}_{12}$	p
Search budget of 60 s – Single-criteria						
Random search	0.73	–	–	–	0.64	0.16
Random testing	0.69	–	0.36	0.16	–	–
Standard GA	0.79	–	0.58	0.12	0.70	0.09
Monotonic GA	0.79	–	0.58	0.13	0.70	0.07
Steady-State GA	0.76	–	0.50	0.16	0.63	0.12
$1 + (\lambda, \lambda)$ GA	0.61	–	0.38	0.11	0.42	0.11
$(\mu + \lambda)$ EA	0.79	–	0.59	0.12	0.71	0.08
(μ, λ) EA	0.81	–	0.63	0.11	0.73	0.07
Breeder GA	0.72	–	0.47	0.12	0.56	0.14
Cellular GA	0.67	–	0.37	0.11	0.48	0.11
CRO	0.74	–	0.51	0.13	0.63	0.11
Search budget of 60 s – Multiple-criteria						
Random search	0.65	0.64	–	–	0.75	0.05
Random testing	0.55	0.45	0.25	0.05	–	–
Standard GA	0.71	0.76	0.67	0.07	**0.87**	**0.02**
Monotonic GA	0.71	0.75	0.66	0.07	**0.87**	**0.02**
Steady-State GA	0.65	0.70	0.58	0.06	**0.81**	**0.03**
$1 + (\lambda, \lambda)$ GA	0.48	0.54	**0.39**	**0.05**	0.56	0.15
$(\mu + \lambda)$ EA	0.72	0.77	0.69	0.06	**0.89**	**0.03**
(μ, λ) EA	0.72	0.77	0.68	0.06	**0.89**	**0.03**
Breeder GA	0.66	0.71	0.60	0.07	**0.83**	**0.03**
Cellular GA	0.61	0.66	0.53	0.07	**0.78**	**0.05**
CRO	0.69	0.73	0.63	0.07	**0.84**	**0.03**

4.2. RQ2 – How does evolutionary search compare to random search and random testing?

Table 4 compares the results of each EA with the two random-based techniques considered in this study: Random search and Random testing. Both random approaches are hardly affected by the number of coverage goals. For instance, Random testing covers 69% of all branch goals for single criteria, where for multiple criteria it only covers 45% of all goals (55% of all branch goals). The % of goals covered by Random search decreases from 73% (single criteria) to 64% (multiple criteria).

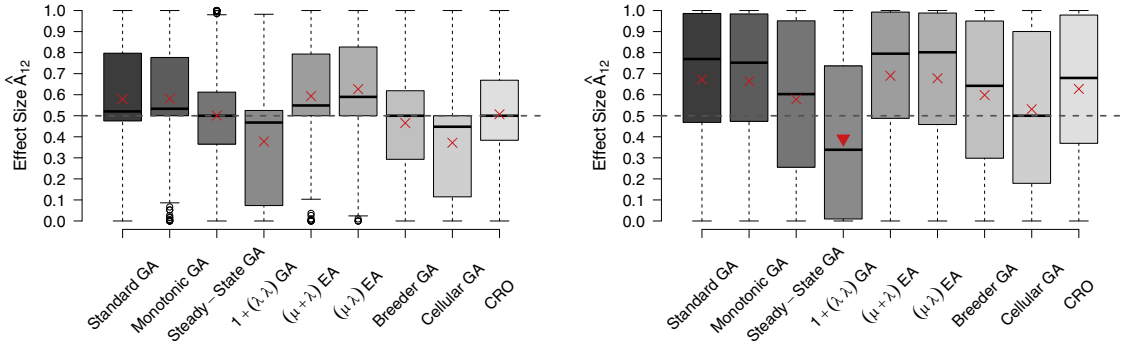
As we can see in Fig. 5, for single criteria all EAs but $1 + (\lambda, \lambda)$ EA and Cellular GA achieve higher branch coverage than Random testing. For multiple criteria, all EAs achieve higher overall coverage than Random testing, most of them significantly higher overall coverage. For example, Random testing covers 45% of all coverage goals for multiple criteria where $\mu + \lambda$ EA covers 77% (an effect size $\widehat{A}_{12}$ of 0.89 and a p-value of 0.03). When compared to Random search (see Fig. 4), six out of nine EAs performed better for single criteria (i.e., Standard GA, Monotonic GA, Steady-State GA, ($\mu + \lambda$) EA, (μ, λ) EA), and CRO; and all EAs but $1 + (\lambda, \lambda)$ EA performed better than Random search for multiple criteria. This result is different to the earlier study by Shamshiri et al. [5], where random achieved similar, and sometimes higher coverage than a genetic algorithm. Our conjecture is that the better performance of some EAs in our evaluation is due to (1) the use of the test archive, and (2) the use of more complex classes in the experiment.

> RQ2: Evolutionary algorithms (in particular (μ, λ) EA) perform better than random search and statistically better than random testing.

4.3. RQ3 – Which archive-based many-objective evolutionary algorithm performs best?

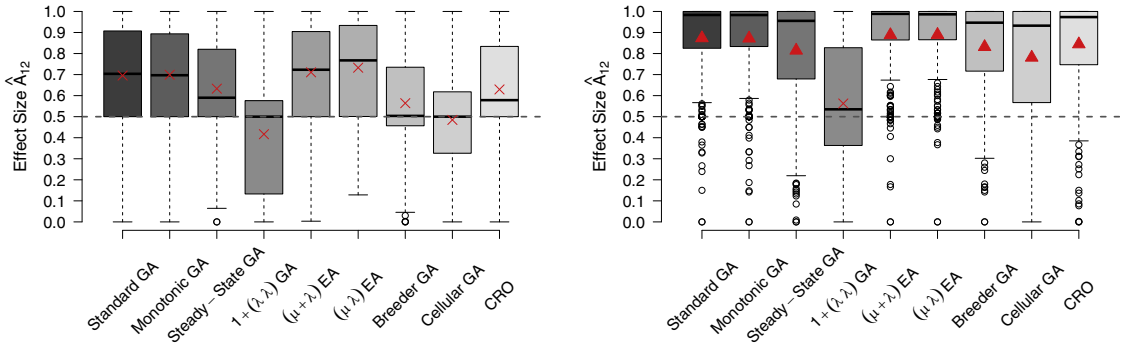
Table 5 summarises the results of a pairwise tournament of all many objective algorithms, i.e., MOSA, DynaMOSA, LIPS, and MIO. For both single and multiple criteria configurations, DynaMOSA is ranked first (e.g., it was statistically significantly better on 391 comparisons and significantly worse on only 31 out of 924 comparisons), MOSA is second, followed by MIO and then LIPS. As we discussed in RQ1, the most effective algorithm (i.e., the one with more positive comparisons) is the one with the highest ratio of classes with a coverage between]90%, 100%]. For DynaMOSA, 70% of all classes fall into the]90%, 100%] interval, while for MOSA this number is lower at 67%, for MIO at 54%, and LIPS only managed to achieve coverage in this interval for 35% of classes (see Fig. 6). For the multiple criteria configuration, for DynaMOSA 77% of all classes under test fall into the]90%, 100%] interval, for MOSA it is 62%, and for MIO 42% (see Fig. 7).

The ranking of many-objective algorithms for single criteria (i.e., branch coverage) is in line with previous studies in which DynaMOSA outperformed its predecessor MOSA [11], and MOSA in turn was more effective than LIPS [28] at generating test cases for Java static methods with purely procedural behaviour. Note that although MOSA and DynaMOSA achieve the same branch coverage for single criteria on average, DynaMOSA is statistically significantly better on more comparisons (391 vs 370) and significantly worse on less comparison (31 vs 51) than MOSA. Thus, DynaMOSA is statistically better than MOSA. MIO achieves a branch coverage of 75% for single criteria, and 71% overall coverage for multiple criteria (see Table 6); therefore it is ranked third. This result is different to two studies conducted by Arcuri [30,39], where MIO performed better than MOSA. Our conjecture is that the testing level influences this difference: Arcuri [30,39] performed an empirical evaluation on the automatic generation of *system tests*, and we performed an empirical evaluation on the automatic generation of *unit tests*. Besides the larger number of coverage goals in system testing, a main difference is that system tests are usually



(a) Single criteria. (b) Multiple criteria.

Fig. 4. Effect size $\widehat{A}_{12}$ of EA X vs. Random search. Middle line of each boxplot marks the median, white circles represent the outliers, ▲ represents the mean of a significant effect size greater than 0.5 (i.e., EA X performs significantly better than Random search), ▼ the mean of a significant effect size lower than 0.5 (i.e., EA X performs significantly worse than Random search), × the mean of a no significant effect size.



(a) Single criteria. (b) Multiple criteria.

Fig. 5. Effect size $\widehat{A}_{12}$ of EA X vs. Random testing. Please refer to Fig. 4 for an explanation of each symbol.

Table 5
Pairwise comparison of all many objective algorithms. "Better than" and "Worse than" give the number of comparisons for which the best EA is statistically significantly (i.e., *p-value* < 0.05) better and worse, respectively. Columns $\widehat{A}_{12}$ give the average effect size.

	Tourn.	Branch	Overall	Better			Worse	
Algorithm	position	cov.	cov.	$\widehat{A}_{12}$	than	$\widehat{A}_{12}$	than	$\widehat{A}_{12}$
Search budget of 60 s – Single-criteria								
MOSA	2	0.82	–	0.63	370 / 924	0.86	51 / 924	0.23
DynaMOSA	1	0.82	–	0.66	391 / 924	0.87	31 / 924	0.26
LIPS	4	0.62	–	0.24	40 / 924	0.83	614 / 924	0.09
MIO	3	0.75	–	0.48	196 / 924	0.89	301 / 924	0.18
Search budget of 60 s – Multiple-criteria								
MOSA	2	0.79	0.81	0.55	212 / 616	0.85	140 / 616	0.21
DynaMOSA	1	0.84	0.86	0.71	352 / 616	0.85	15 / 616	0.20
LIPS	–	–	–	–	–	–	–	–
MIO	3	0.68	0.71	0.25	16 / 616	0.80	425 / 616	0.13

computationally more expensive to execute than unit test, which would benefit algorithms with small populations, such as MIO. On the other hand, algorithms with large populations (e.g., Standard GA) would take longer for evaluating the fitness of its individuals, and therefore fewer solutions would be explored.

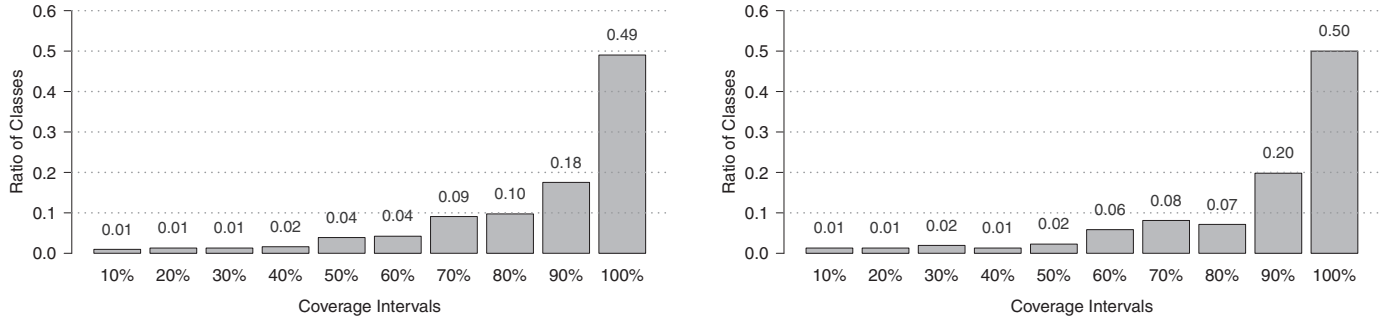
RQ3: DynaMOSA outperforms the other many-objective algorithms for individual and multiple criteria.

4.4. RQ4 – How does evolution of whole test suites compare to many-objective optimisation of test cases?

Table 6 compares each EA with the many-objective optimisation algorithms MOSA, DynaMOSA, LIPS, and MIO.

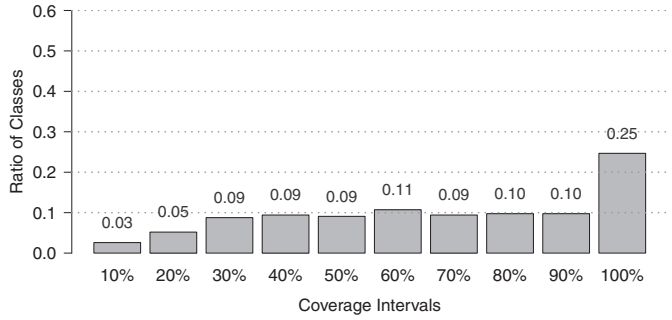
Our results confirm and enhance previous studies [9,11] by evaluating eight different EAs (i.e., Standard GA, Steady-State GA, 1 + (λ, λ) GA, (μ + λ) EA, (μ, λ) EA, Breeder GA, Cellular GA, CRO) in addition to Monotonic GA, and show that MOSA and DynaMOSA perform better at optimising test cases than any EA at optimising test suites for single and multiple criteria (see Figs. 8 and 9). Interestingly, and unlike any other algorithm, DynaMOSA achieves higher branch coverage on multiple criteria than on single criteria. This shows that DynaMOSA is suitable for optimising a large number of coverage goals (which is to be expected in a multiple criteria configuration) without negative effects on the final coverage.

We can only include LIPS in the single criterion scenario; here, all EAs performed better than LIPS (see Fig. 10). When compared to MIO, only four EAs performed better than MIO for both single and multiple

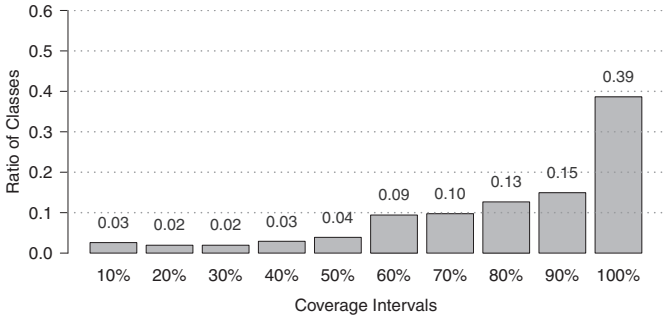


(a) MOSA.

(b) DynaMOSA.

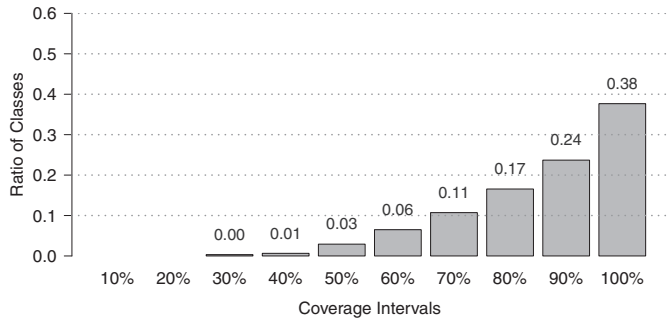


(c) LIPS.

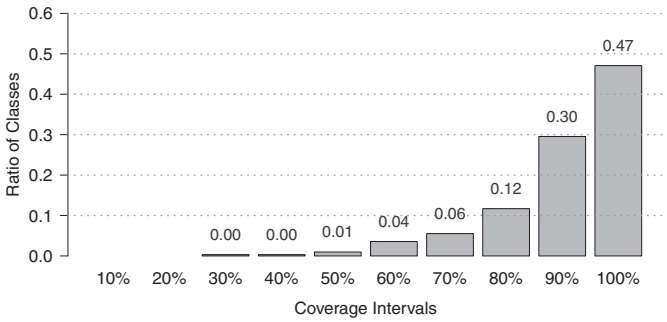


(d) MIO.

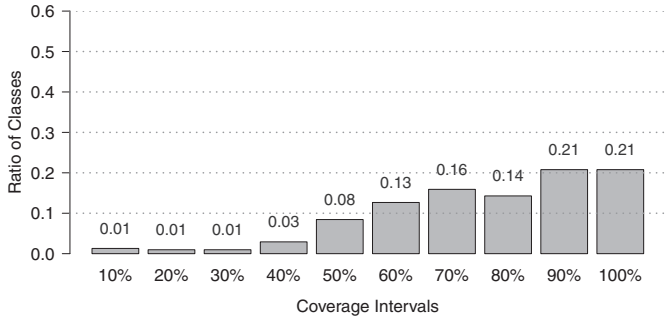
Fig. 6. Proportion of classes that have an average branch coverage (averaged out of 30 runs on all their classes) within each 10% branch coverage interval. X-labels show the upper limit (inclusive). For example, the group 30% represents all the classes with an average branch coverage greater than 20% and lower than or equal to 30%.



(a) MOSA.



(b) DynaMOSA.



(c) MIO.

Fig. 7. Proportion of classes that have an average overall coverage (averaged out of 30 runs on all their classes) within each 10% overall coverage interval. X-labels show the upper limit (inclusive). For example, the group 30% represents all the classes with an average overall coverage greater than 20% and lower than or equal to 30%.

Table 6
Comparison of evolutionary algorithms on whole test suites optimisation and many-objective optimisation algorithms of test cases. Statistically significant effect sizes are shown in bold.

Algorithm	Branch cov.	Overall cov.	vs. MOSA		vs. DynaMOSA		vs. LIPS		vs. MIO	
			$\widehat{A}_{12}$	p	$\widehat{A}_{12}$	p	$\widehat{A}_{12}$	p	$\widehat{A}_{12}$	p
Search budget of 60 s – Single-criteria										
MOSA	0.82	–	–	–	0.47	0.31	0.78	0.05	0.64	0.15
DynaMOSA	0.82	–	0.53	0.31	–	–	0.78	0.05	0.65	0.12
LIPS	0.62	–	0.22	0.05	0.22	0.05	–	–	0.28	0.08
MIO	0.75	–	0.36	0.15	0.35	0.12	0.72	0.08	–	–
Standard GA	0.79	–	0.43	0.16	0.41	0.15	0.77	0.05	0.56	0.17
Monotonic GA	0.79	–	0.42	0.15	0.40	0.15	0.76	0.06	0.56	0.15
Steady-State GA	0.76	–	0.36	0.10	0.35	0.11	0.74	0.09	0.47	0.13
$1 + (\lambda, \lambda)$ GA	0.61	–	0.28	0.10	0.28	0.09	0.50	0.10	0.35	0.14
$(\mu + \lambda)$ EA	0.79	–	0.44	0.15	0.42	0.15	0.77	0.05	0.58	0.15
(μ, λ) EA	0.81	–	0.47	0.17	0.45	0.15	0.79	0.05	0.61	0.17
Breeder GA	0.72	–	0.32	0.10	0.31	0.10	0.68	0.08	0.43	0.14
Cellular GA	0.67	–	0.25	0.06	0.24	0.05	0.63	0.09	0.34	0.09
CRO	0.74	–	0.36	0.11	0.34	0.11	0.71	0.07	0.48	0.16
Search budget of 60 s – Multiple-criteria										
MOSA	0.79	0.81	–	–	0.37	0.17	–	–	0.72	0.10
DynaMOSA	0.84	0.86	0.63	0.17	–	–	–	–	0.78	0.09
LIPS	–	–	–	–	–	–	–	–	–	–
MIO	0.68	0.71	0.28	0.10	0.22	0.09	–	–	–	–
Standard GA	0.71	0.76	0.35	0.10	0.29	0.08	–	–	0.60	0.14
Monotonic GA	0.71	0.75	0.35	0.10	0.28	0.09	–	–	0.58	0.13
Steady-State GA	0.65	0.70	0.27	0.09	0.22	0.05	–	–	0.47	0.11
$1 + (\lambda, \lambda)$ GA	0.48	0.54	**0.17**	**0.05**	**0.14**	**0.04**	–	–	0.24	0.08
$(\mu + \lambda)$ EA	0.72	0.77	0.37	0.12	0.30	0.09	–	–	0.63	0.11
(μ, λ) EA	0.72	0.77	0.37	0.14	0.30	0.09	–	–	0.62	0.13
Breeder GA	0.66	0.71	0.28	0.10	0.23	0.07	–	–	0.48	0.13
Cellular GA	0.61	0.66	0.22	0.07	**0.18**	**0.04**	–	–	0.40	0.13
CRO	0.69	0.73	0.32	0.11	0.26	0.09	–	–	0.53	0.12

criteria: Standard GA, Monotonic GA, $(\mu + \lambda)$ EA, and (μ, λ) EA (see Fig. 11).

RQ4: DynaMOSA outperforms any EA at optimising test suites for individual and multiple criteria.

4.5. Discussion

Given the results of our study, we now discuss some of the implications and insights.

4.5.1. Does the choice of evolutionary algorithm matter?

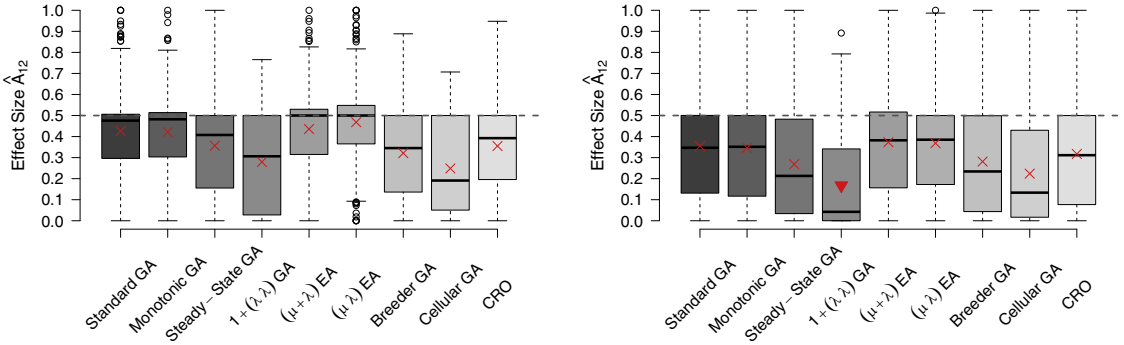
In line with common wisdom on evolutionary algorithms, there is not a single EA that works best in all scenarios. Our experiments do, however, provide evidence that the choice of algorithm has a substantial impact in the coverage achieved in test generation. For instance, the range of branch coverage achieved by each EA for single criteria goes from 61% ($1 + (\lambda, \lambda)$ EA) up to 82% (DynaMOSA), and the overall coverage for multiple criteria from 54% up to 86% (see Fig. 2). Thus, clearly the choice of evolutionary algorithm matters.

4.5.2. Does the representation of individuals in an evolutionary algorithm matter?

All EAs except MOSA, DynaMOSA, LIPS, and MIO represent the individuals of a population as test suites (i.e., a sets of test cases). On the other hand, algorithms such as MOSA, DynaMOSA, LIPS, and MIO represent individuals as test cases. An interesting question for future work therefore is to study the influence of the representation on the effectiveness of the search.

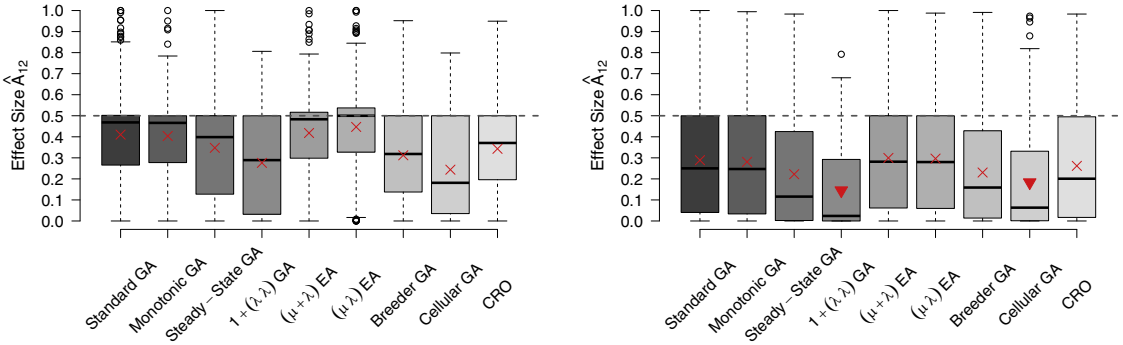
4.5.3. Is there room for improvements?

Table 7 reports the number of classes under test to which an EA X performed significantly better than all the other evaluated EAs. For instance, for single criteria DynaMOSA performed significantly better



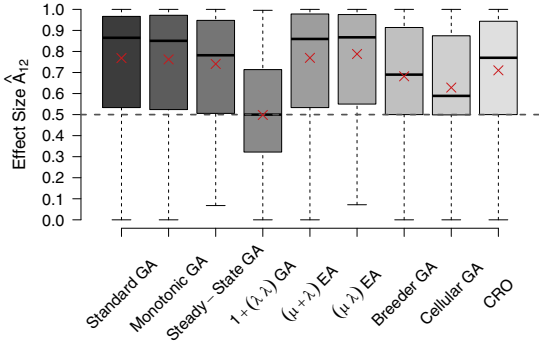
(a) Single criteria. (b) Multiple criteria.

Fig. 8. Effect size $\widehat{A}_{12}$ of EA X vs. MOSA. Please refer to Fig. 4 for an explanation of each symbol.



(a) Single criteria. (b) Multiple criteria.

Fig. 9. Effect size $\hat{A}_{12}$ of EA X vs. DynaMOSA. Please refer to Fig. 4 for an explanation of each symbol.



(a) Single criteria.

Fig. 10. Effect size $\hat{A}_{12}$ of EA X vs. LIPS. Please refer to Fig. 4 for an explanation of each symbol.

than all the other EAs for 21 classes, (μ, λ) EA for 5 classes, MIO for 3 classes, MOSA performed significantly better for 2 classes, and Standard GA, Monotonic GA, and Steady-State GA for only 1 class. Considering that there are classes on which other EAs (e.g., MIO) performed better than DynaMOSA, there might be potential to improve DynaMOSA by incorporating some of MIO's features into DynaMOSA. For example, rather than generating an offspring based on the population, in each iteration DynaMOSA could (given a certain probability) sample individuals, that still do not satisfy some coverage goals, from the archive as MIO does. There may also be potential to develop entirely new search algorithms tailored for test generation.

4.5.4. Technical limitations

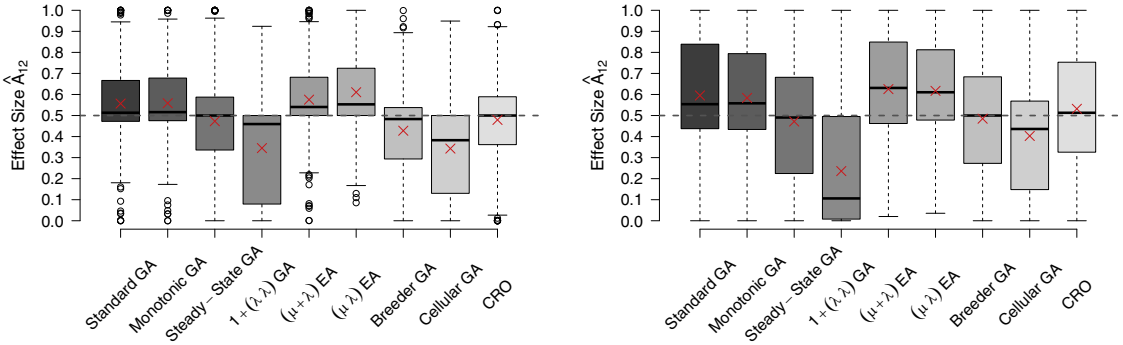
Overall, there is a large number of classes under test for which EAs were able to achieve high coverage. For example, DynaMOSA covered

Table 7
Number of classes on which an EA X performed significantly better than all the other evaluated EAs. Note: for multiple criteria, no EA performed significantly better than all the other evaluated EAs for any class under test (CUT).

	Branch			Overall				
Algorithm	cov.	σ	CI	cov.	σ	CI	$\hat{A}_{12}$	#CUT
Search budget of 60 s – Single-criteria								
Standard GA	1.00	0.01	[1.00, 1.00]	–	–	–	0.94	1
Monotonic GA	0.93	0.08	[0.90, 0.96]	–	–	–	0.76	1
Steady-State GA	0.65	0.05	[0.63, 0.67]	–	–	–	0.84	1
(μ, λ) EA	0.67	0.23	[0.59, 0.75]	–	–	–	0.85	5
MOSA	0.85	0.08	[0.82, 0.88]	–	–	–	0.89	2
DynaMOSA	0.89	0.06	[0.88, 0.92]	–	–	–	0.93	21
MIO	0.69	0.12	[0.65, 0.74]	–	–	–	0.92	3

half of all classes under test with a branch coverage between 90% and 100%. However, there are some classes for which all EAs and random approaches evaluated in our empirical study failed to achieve any substantial coverage due to limitations of the test generation tool. Fig. 12 shows the 28 classes on which all EAs and all random approaches failed to achieve more than 25% branch coverage. We looked closer at three problematic classes that stand out particularly:

1. `Battle` class from project `feudalismgame`, which represents the largest area in the figure. It consists of 786 branch goals, however only 1% of all goals have been covered. Despite the fact the class `Battle` is composed by eight public methods, all of them are invoked with Java reflection as described in the following snippet of code:
   Thus, in order to cover the methods of the class under test and therefore their branches, EVOSUITE would have to generate a string parameter exactly as the name of one of the methods. When a string



(a) Single criteria. (b) Multiple criteria.

Fig. 11. Effect size $\hat{A}_{12}$ of EA X vs. MIO. Please refer to Fig. 4 for an explanation of each symbol.

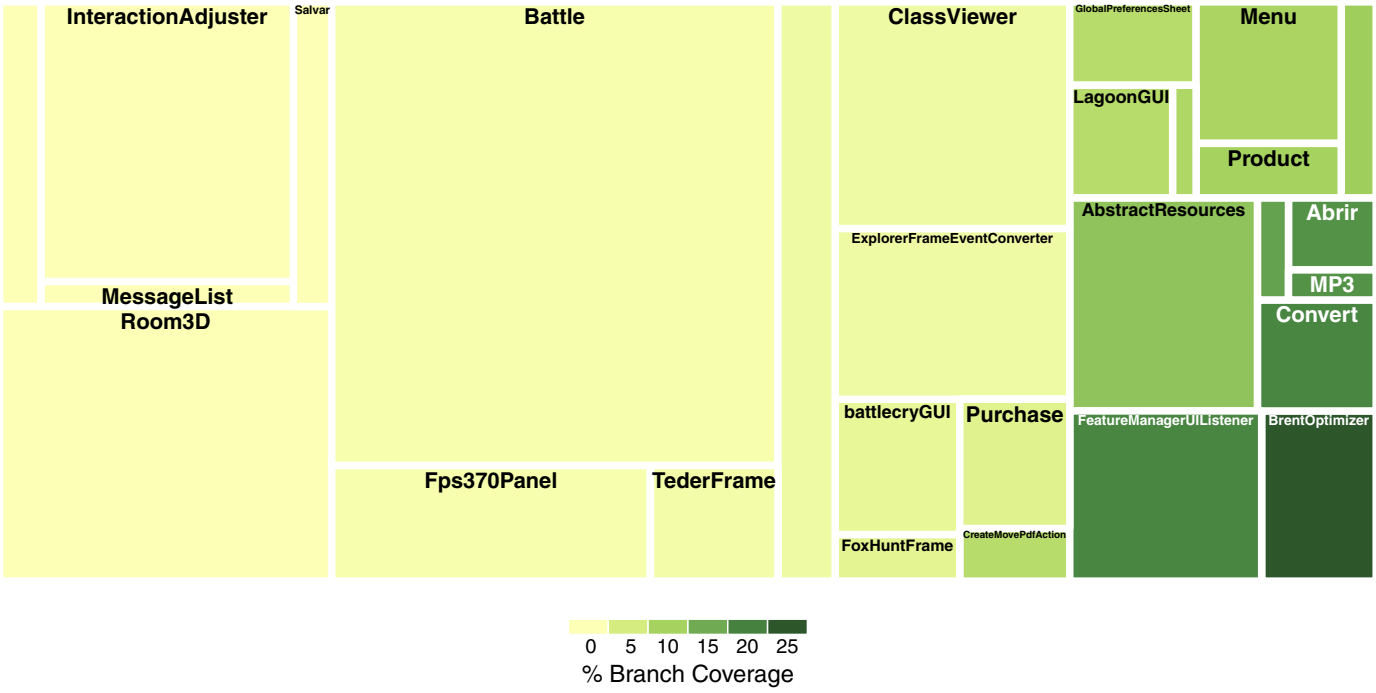


Fig. 12. Classes on which all evaluated EAs and random approaches achieved less than 25% branch coverage. The area of each box is proportional to the number of branches in each class, and the colour represents the coverage achieved averaged over 30 repetitions.

```
public class ArrayByteList_ESTest {
  @Test
  public void test0() throws Throwable {
    ArrayByteList arrayByteList0 = new ArrayByteList();
    arrayByteList0.ensureCapacity(550);
    assertEquals(0, arrayByteList0.size());
  }

  @Test
  public void test1() throws Throwable {
    ArrayByteList arrayByteList0 = new ArrayByteList();
    arrayByteList0.add((byte) (-113));
    arrayByteList0.add(0, (byte)0);
    byte byte0 = arrayByteList0.removeElementAt(0);
    assertEquals(1, arrayByteList0.size());
    assertEquals((byte)0, byte0);
  }
}
```

Listing 1. Example of a test suite (with only a subset of test cases) automatically generated by EvoSuite [2] for `ArrayByteList` class of project `Apache Commons Collections`.

is required, EvoSuite either randomly generates one (with a certain probability) or uses static / dynamic seeds from the class under test [40]. Static seeds are all string constants in the bytecode of the class under test, and dynamic seeds are strings observed at runtime, for example, a call to the `equals` method of `String` class. It would be of interest to extend EvoSuite to also seed the name of methods or class fields for cases such as this particular one that uses Java reflection to invoke methods of the class under test.

2. `MP3` class from project `celwars2009`, which represents the smallest area in the figure (i.e., the smallest class represented in Fig. 12). Although it only consists of 10 branch goals, EAs only managed to achieve a branch coverage of 18%. Although EvoSuite has been extended to support environment requirements such as interactions with the file system, console inputs, and many non-deterministic functions of the Java Virtual Machine (JVM) such as date and time [41], this particular class under test requires an MP3 file to successfully exercise the code under test, as described in the following snippet of code:
Without guidance, EvoSuite is unlikely to produce data that represents valid MP3 files. To increase the adoption of EvoSuite, it would be of interest to extend it to generate not only music files, but also other types of files, e.g., image files that could be required to test a graphics editor software.
3. `MessageList` class from project `bpmail`. Despite the fact that it only consists of 24 branch goals, no EA or random approach was able to cover any goal at all. `MessageList` is an abstract class for which there is no concrete class, i.e., a non-abstract class that extends it, in the project. Therefore, no new objects of type `MessageList`could have been created. Although EvoSuite has been extended to mock certain type of classes, e.g., interfaces [42], it will have to be further extended to handle cases such as this one, i.e., an abstract class without a concrete class to instantiate.

These examples suggest that there are fundamental *technical* challenges sometimes prohibiting high code coverage in practice; the choice of search algorithm in such cases is minor. Consequently, it will be important to drive research not only on algorithmic improvements, but to also accompany these improvements with advances in the engineering of test generation tools.

5. Related work

Although a common approach in search-based testing is to use genetic algorithms, numerous other algorithms have been proposed in the domain of nature-inspired algorithms, as no algorithm can be best on all domains [34]. Many researchers compared evolutionary algorithms to solve problems in domains outside software engineering

```
// Arguments for battle follows the following order: 1) Method name (attack
// target), e.g., vassal; 2) Attacker's Name
public void perform(Collection args) {
  try {
    Iterator argsIter = args.iterator();
    // The following will call a method dinamically according to the item
    // the player wants to buy
    Class aMethod = this.getClass().forName("feudalism.Battle");
    Class[] argType = {String.class};
    Method methodObj = aMethod.getMethod((String)argsIter.next(), new
        Class[]{Collection.class});
    methodObj.invoke(this, args);
    GameAutoActions.saveAll();
  } catch (Exception e) {
    e.printStackTrace();
} }
```

Listing 2. Piece of code from class `Battle` of project `feudalismgame`.

[43–45]. Within search-based software engineering, comparative studies have been conducted in several domains such as discovery of software architectures [46], pairwise testing of software product lines [47], test case selection [48], or finding subtle higher order mutants [49].

In the context of test data generation, Harman and McMinn [50] empirically compared GA, Random testing and Hill Climbing for structural test data generation. While their results indicate that sophisticated evolutionary algorithms can often be outperformed by simpler search techniques, there are more complex scenarios (e.g., test data generation for Matlab Simulink models [51]), for which evolutionary algorithms are better suited. Ghani et al. [51] compared Simulated Annealing (SA) and GA for the test data generation for Matlab Simulink models, and their results show that GA performed slightly

```
public class MP3 extends Thread {
  AudioInputStream in = null;
  AudioInputStream din = null;
  String filename = "";

  public MP3(String filename) {
    this.filename = filename; this.start();
  }

  public void run() {
    AudioInputStream din = null;
    try {
      File file = new File(filename);
      AudioInputStream in = AudioSystem.getAudioInputStream(file);
      AudioFormat baseFormat = in.getFormat();
      // +18 lines of code that are never executed because 'file' does not
      // point to a valid mp3 file
    } catch (Exception e) {
      e.printStackTrace();
    } finally {
      if (din != null) {
        try { din.close(); } catch(IOException e) { }
      }
} } }
```

Listing 3. Piece of code from class `MP3` of project `celwars2009`.

better than SA. Sahin and Akay [52] evaluated Particle Swarm Optimisation (PSO), Differential Evolution (DE), Artificial Bee Colony, Firefly Algorithm and Random search algorithms on software test data generation benchmark problems, and concluded that some algorithms performs better than others depending on the characteristics of the problem. Varshney and Mehrotra [53] proposed a DE-based approach to generate test data that cover data-flow coverage criteria, and compared the proposed approach to Random search, GA and PSO with respect to number of generations and average percentage coverage. Their results show that the proposed DE-based approach is comparable to PSO and has better performance than Random search and GA. In contrast to these studies, we consider unit test generation, which arguably is a more complex scenario than test data generation, and in particular local search algorithms are rarely applied.

Although often newly proposed algorithms are compared to random search as a baseline (usually showing clear improvements), there are some studies that show that random search can actually be very efficient for test generation. In particular, Shamshiri et al. [5] compared GA against Random search for generating test suites, and found almost no difference between the coverage achieved by evolutionary search compared to random search. They observed that GAs cover more branches when standard fitness functions provide guidance, but most branches of the analyzed projects provided no such guidance. Similarly, Sahin and Akay [52] showed that Random search is effective on simple problems.

Recently, Scalabrino et al. [27] compared LIPS (Linearly Independent Path-Based Search) and MOSA (Many-Objective Sorting Algorithm) [9] with respect to generating test data for C programs. They used 35 simple C functions extracted from different open-source C libraries on their evaluation. Results show that there are no major differences between LIPS and MOSA when it comes to branch coverage. However, authors found that LIPS outperforms MOSA with respect to running time, but MOSA produces shorter test suites. Motivated by the several threats to the validity of such empirical evaluation (e.g., most subjects are trivial and can be fully covered in a few seconds), Panichella et al. [28] replicated this empirical study by comparing LIPS and MOSA in different settings: LIPS were implemented within EvoSuite [2] and 33 functions from the original benchmark were implemented as Java static methods. Additionally, 37 static methods were randomly selected from open source libraries, which means the evaluation was performed over 70 subjects. Results show that the new LIPS implementation is superior than the original implementation given the flexibilities provided by EvoSuite. They noticed that the new LIPS implementation reached higher branch coverage using less time budget. Despite these improvements, results show that MOSA is more effective and efficient than LIPS when new and more complex subjects are considered.

To the best of our knowledge, no study has been conducted to evaluate several different evolutionary algorithms in a whole test suite generation context and considering a large number of complex classes. As can be seen from this overview of comparative studies, it is far from obvious what the best algorithm is, since there are large variations between different search problems.

6. Conclusions

Although evolutionary algorithms are commonly applied for whole test suite generation, there is a lack of evidence on the influence of different algorithms. Our study yielded the following key results:

- The choice of algorithm can have a substantial influence on the performance of whole test suite optimisation, hence tuning is important. While EvoSuite provides tuned default values, these values may not be optimal for different flavours of evolutionary algorithms.
- Although previous studies showed little benefit of using a GA over random testing, our study shows that on complex classes and with a test archive, evolutionary algorithms are on average superior to random testing and random search.
- The Dynamic Many Objective Sorting Algorithm (DynaMOSA) is superior to whole test suite optimisation and other many objective search algorithms.

It would be of interest to extend our experiments to further search algorithms. In particular, the use of other non-functional attributes such as readability [54] suggests the exploration of multi-objective algorithms. Considering the variation of results with respect to different configurations and classes under test, it would also be of interest to use these insights to develop hyper-heuristics that select and adapt the optimal algorithm to the specific problem at hand.

Acknowledgements

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