

# GASSER

# USER MANUAL

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## 1. Introduction

GASSER (Genetic Algorithm for Test Suite Reduction) implements a Genetic Algorithm (GA) Based approach for Test Suite Reduction and a number of instances of the process underlying this approach. The goal of GASSER is to reduce the original Test Suites by identify reduced Test Suites which maximize both statement coverage and test-case-statement-coverage diversity, while minimize the number of test cases. To pursue such a three-fold objective GASSER, starting from initial randomly created reduced Test Suites, improves them by the use of GA (namely NSGAI). In particular, at each iteration a fitness function is computed for each Test Suite based on three objectives: (i) statement coverage, (ii) test-case-statement-coverage diversity (or simply test-case diversity), and (iii) test suite size. To estimate the test-case diversity, GASSER considers a number of measure (e.g., Hamming Distance), each of them represents a GASSER instance. Then the fittest reduced Test Suites are selected to define new better reduced Test Suites by the use of genetic operators (i.e., mutation and crossover). A screencast of GASSER in action is available at <https://youtu.be/20Uf1ugEvAQ>.

## 2. Environment

GASSER is a Java console program which works on each machine on which a Java 8 is installed. You can download it from <https://www.java.com/it/download/>. To use the String Kernels-Based Dissimilarity you must install R from <https://cran.r-project.org/bin/windows/base/old/3.3.1/> and the kernlab and rjava packages. Packages can be installed with the `install.packages('package_name')` function in R.

## 3. Running CUTER

- ❖ To run GASSER you have to open a Console in the GASSER folder and type: `java -jar it.unibas.baselab.gasser_xxxx.jar` (see Figure 1).
- ❖ Now follow the instructions provided by the tool that will allow you to complete the GASSER configuration (e.g., coverage file path, dissimilarity measure, maxEvaluations value and maxPopulationSize value). In particular:
  1. **Dissimilarity file path:** If you have a file with the test cases dissimilarity matrix, GASSER will ask you for its complete path (.csv file);

2. **Dissimilarity measure:** if you do not have the test cases dissimilarity matrix, GASSER will ask you which one (among all of those possible) you want to use (see Figure 2). GASSER will compute this information on the fly during its execution;
  3. **Coverage file path:** the complete path of the test cases statement coverage XML file;
  4. **SUT name:** The name of your System Under Test;
  5. **maxPopulationSize** and **maxEvaluations:** The possibility to change the value for maxPopulationSize (100 is the default value) and **maxEvaluations** (1000 is the default value).
- ❖ Wait the GASSER execution end and enjoy your result files: **POPULATION\_SUT name.tsv** and **COMPLETE\_SOLUTION\_SUT name.tsv**

```
-----GASSER-----
Type the full path of your coverage information file:
D:\...\cov.xml
Type the name of you System Under Test:
SUT
Do you have a dissimilarity matrix? [Y/N]
N
Choose the dissimilarity measure you want to use:
C = Cosine Dissimilarity
E = Euclidean Distance
J = Jaccard-Based Dissimilarity
K = K-Based Dissimilarity
H = Hamming Distance
L = Levenshtein Distance
SK = String Kernel Dissimilarity
H
The default value for maxEvaluations is equal to 1000, do you want to change it? [Y/N]
N
The default value for populationSize is equal to 100, do you want to change it? [Y/N]
N
```

Figure 1. How to run GASSER