

Package ‘SimilaR’

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Title R Source Code Similarity Evaluation

Description An implementation of a novel method to quantify the similarity of the code-base of R functions by means of program dependence graphs. Possible use cases include detection of code clones for improving software quality and of plagiarism amongst students' assignments.

URL <https://github.com/bartoszukm/SimilaR>

BugReports <https://github.com/bartoszukm/SimilaR/issues>

Type Package

Depends R (>= 3.1.0)

License GPL (>= 3)

Encoding UTF-8

Imports Rcpp (>= 0.12.0), stringi

Suggests testthat

LinkingTo Rcpp (>= 0.12.0), BH

SystemRequirements C++11

RoxygenNote 7.1.0

NeedsCompilation yes

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SimilaR-package

The SimilaR Package

Description

See [SimilaR_fromDirectory\(\)](#) for details.

Author(s)

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SimilaR_fromDirectory *Quantify the Similarity of Pairs of R Functions*

Description

An implementation of the SimilaR algorithm - a method to quantify the similarity of R functions based on Program Dependence Graphs. Possible use cases include detection of code clones for improving software quality and of plagiarism among students' homework assignments.

`SimilaR_fromDirectory` scans for function definitions in all *.R source files in a given directory and performs pairwise comparisons.

`SimilaR_fromTwoFunctions` compares the code-base of two function objects.

Usage

```
SimilaR_fromDirectory(  
  dirname,  
  returnType = c("data.frame", "matrix"),  
  fileType = c("function", "file"),  
  aggregation = c("tnorm", "sym", "both")  
)
```

```
SimilaR_fromTwoFunctions(  
  function1,  
  function2,  
  functionNames,  
  returnType = c("data.frame", "matrix"),  
  aggregation = c("tnorm", "sym", "both")  
)
```

Arguments

dirname	path to a directory with source files named *.R
returnType	"data.frame" or "matrix"; indicates the output object type
fileTypes	"function" or "file"; indicates which pairs of functions extracted from the source files in dirname should be compared; "function" compares each function against every other function; "file" compares only the functions defined in different source files
aggregation	"sym", "tnorm", or "both"; specifies which model of similarity asymmetry should be used; "sym" means that one (overall) similarity degree is computed; "both" evaluates and returns the degree to which the first function in a function pair is similar ("contained in", "is subset of") to the second one, and, separately, the extent to which the second function is similar to the first one; "tnorm" computes two similarity values and aggregates them to a single number
function1	a first function object to compare
function2	a second function object to compare
functionNames	optional functions' names to be included in the output

Details

Note that, depending on the "aggregation" argument, the method may either return a single value, representing the overall (symmetric) similarity between a pair of functions, or or two different values, measuring the (non-symmetric) degrees of "subthood". The user might possibly wish to aggregate these two values by means of some custom aggregation function.

Value

If returnType is equal to "data.frame", a data frame that gives the information about the similarity of the inspected pairs of functions, row by row, is returned. The data frame has the following columns:

- name1 - the name of the first function in a pair
- name2 - the name of the second function in a pair
- SimilaR - values in the [0,1] interval as returned by the SimilaR algorithm; 1 denotes that the functions are equivalent, while 0 means that they are totally dissimilar; if aggregation is equal to "both", two similarity values are given: the one with suffix "12" quantifies the degree to which the first function is a subset of the second, and the another one with suffix "21" measures the extent to which the second function is a subset of the first one
- decision - 0 or 1; 1 means that two functions are classified as similar and 0 otherwise.

Rows in the data frame are sorted with respect to the SimilaR column (descending). Of course, SimilaR_fromTwoFunctions gives a data frame with only one row.

If returnType is equal to "matrix", a square matrix is returned. The element at index (i,j) equals to the similarity degree between the i-th and the j-th function. When aggregation is equal to "sym" or "tnorm", the matrix is symmetric. Column names and row names of the matrix are generated from the names of the functions being compared.

References

Bartozuk M., A source code similarity assessment system for functional programming languages based on machine learning and data aggregation methods, Ph.D. thesis, Warsaw University of Technology, Warsaw, Poland, 2018.

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Bartozuk M., Gagolewski M., *Detecting similarity of R functions via a fusion of multiple heuristic methods*, In: Alonso J.M., Bustince H., Reformat M. (Eds.), *Proc. IFSA/EUSFLAT 2015*, Atlantis Press, 2015, pp. 419-426.

Bartozuk M., Gagolewski M., *A fuzzy R code similarity detection algorithm*, In: Laurent A. et al. (Eds.), *Information Processing and Management of Uncertainty in Knowledge-Based Systems, Part III (CCIS 444)*, Springer-Verlag, Heidelberg, 2014, pp. 21-30.

Examples

```
f1 <- function(x) {x*x}
f2 <- function(x,y) {x+y}

## A data frame is returned: 1 row, 4 columns
SimilaR_fromTwoFunctions(f1,
  f2,
  returnType = "data.frame",
  aggregation = "tnorm")

## Custom names in the returned data frame
SimilaR_fromTwoFunctions(f1,
  f2,
  functionNames = c("first", "second"),
  returnType = "data.frame",
  aggregation = "tnorm")

## A data frame is returned: 1 row, 5 columns
SimilaR_fromTwoFunctions(f1,
  f2,
  returnType = "data.frame",
  aggregation = "both")

## A non-symmetric square matrix is returned,
## with 2 rows and 2 columns
SimilaR_fromTwoFunctions(f1,
  f2,
```

```
        returnType = "matrix",
        aggregation = "both")

## Typical example, where we wish to compare the functions from different files,
## but we do not want to compare the functions from the same file.
## There will be one value describing the overall similarity level.
SimilaR_fromDirectory(system.file("testdata", "data", package="SimilaR"),
                      returnType = "data.frame",
                      fileType="file",
                      aggregation = "sym")

## In this example we want to compare every pair of functions: even those
## defined in the same file. Two (non-symmetric) similarity degrees
## are reported.
SimilaR_fromDirectory(system.file("testdata", "data2", package="SimilaR"),
                      returnType = "data.frame",
                      fileType="function",
                      aggregation = "both")
```

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