## 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 Author Maciej Bartoszuk [aut, cre] (<https://orcid.org/0000-0001-6088-8273>), Marek Gagolewski [aut] (<https://orcid.org/0000-0003-0637-6028>) Maintainer Maciej Bartoszuk <bartoszuk@rexamine.com> Repository CRAN

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### **R** topics documented:

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SimilaR-package

#### Description

See SimilaR\_fromDirectory() for details.

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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"),
   fileTypes = 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 func- tion 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" com- putes 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 "subsethood". 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

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#### Examples

```
f1 <- function(x) {x*x}
f2 \leq 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")
```

fileTypes="function",
aggregation = "both")

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