

# Package ‘goSorensen’

December 10, 2024

**Type** Package

**Title** Statistical inference based on the Sorensen-Dice dissimilarity and the Gene Ontology (GO)

**Version** 1.8.0

**Description** This package implements inferential methods to compare gene lists in terms of their biological meaning as expressed in the GO. The compared gene lists are characterized by cross-tabulation frequency tables of enriched GO items. Dissimilarity between gene lists is evaluated using the Sorensen-Dice index.

The fundamental guiding principle is that two gene lists are taken as similar if they share a great proportion of common enriched GO items.

**Depends** R (>= 4.3)

**Imports** clusterProfiler, goProfiles, org.Hs.eg.db, parallel, stats, stringr

**Suggests** BiocManager, BiocStyle, knitr, rmarkdown, org.At.tair.db, org.Ag.eg.db, org.Bt.eg.db, org.Ce.eg.db, org.Cf.eg.db, org.Dm.eg.db, org.Dr.eg.db, org.EcSakai.eg.db, org.EcK12.eg.db, org.Gg.eg.db, org.Mm.eg.db, org.Mmu.eg.db, org.Rn.eg.db, org.Sc.sgd.db, org.Ss.eg.db, org.Pt.eg.db, org.Xl.eg.db

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**License** GPL-3

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|                     |   |
|---------------------|---|
| allBuildEnrichTable | <i>Iterate buildEnrichTable along the specified GO ontologies and GO levels</i> |
|---------------------|---|

---

### Description

Iterate buildEnrichTable along the specified GO ontologies and GO levels

### Usage

```
allBuildEnrichTable(
  x,
  check.table = TRUE,
  ontos = c("BP", "CC", "MF"),
  GOLevels = seq.int(3, 10),
  trace = TRUE,
  ...
)
```

### Arguments

|             |   |
|-------------|---|
| x           | object of class "list". Each of its elements must be a "character" vector of gene identifiers (e.g., ENTREZ). Then all pairwise contingency tables of joint enrichment are built between these gene lists, iterating the process for all specified GO ontologies and GO levels. |
| check.table | Boolean. If TRUE (default), all resulting tables are checked by means of function nice2x2Table.   |
| ontos       | "character", GO ontologies to analyse. Defaults to c("BP", "CC", "MF").   |
| GOLevels    | "integer", GO levels to analyse inside each of these GO ontologies.   |
| trace       | Logical. If TRUE (default), the (usually very time consuming) process of function allbuildEnrichTable is traced along the specified GO ontologies and levels.   |
| ...         | extra parameters for function buildEnrichTable.   |

### Value

An object of class "allTableList". It is a list with as many components as GO ontologies have been analysed. Each of these elements is itself a list with as many components as GO levels have been analysed. Finally, the elements of these lists are objects as generated by buildEnrichTable.list, i.e., objects of class "tableList" containing all pairwise contingency tables of mutual enrichment between the gene lists in argument x.

### Examples

```
# This example is highly time-consuming. It scans two GO ontologies and three
# GO levels inside them to obtain the contingency tables of joint enrichment.

# Obtaining ENTREZ identifiers for the gene universe of humans:
# library(org.Hs.eg.db)
# humanEntrezIDs <- keys(org.Hs.eg.db, keytype = "ENTREZID")
```

```

# Gene lists to be explored for enrichment:
# data(allOncoGeneLists)

# Computing Contingency Tables for all the possible pairwise comparisons for
# the ontologies MF, BP, and the GO levels from 4 to 6:
# allBuildEnrichTable(allOncoGeneLists,
#                       geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#                       ontos = c("MF", "BP"), GOLevels = seq.int(4,6))
# When the "ontos" and "GOLevels" arguments are not supplied, the function computes
# by default every possible contingency table between the lists being compared for
# the three ontologies (BP, CC, MF) and GO levels from 3 to 10.

```

---

```

allEquivTestSorensen  Iterate equivTestSorensen along the specified GO ontologies and
                       GO levels

```

---

## Description

Iterate equivTestSorensen along the specified GO ontologies and GO levels

## Usage

```

allEquivTestSorensen(x, ...)

## S3 method for class 'list'
allEquivTestSorensen(
  x,
  d0 = 1/(1 + 1.25),
  conf.level = 0.95,
  boot = FALSE,
  nboot = 10000,
  check.table = TRUE,
  ontos = c("BP", "CC", "MF"),
  GOLevels = seq.int(3, 10),
  trace = TRUE,
  ...
)

## S3 method for class 'allTableList'
allEquivTestSorensen(
  x,
  d0 = 1/(1 + 1.25),
  conf.level = 0.95,
  boot = FALSE,
  nboot = 10000,
  check.table = TRUE,
  ontos,
  GOLevels,
  trace = TRUE,
  ...
)

```

**Arguments**

|             |  |
|-------------|--|
| x           | either an object of class "list" or an object of class "allTableList". In the first case, each of its elements must be a "character" vector of gene identifiers (e.g., ENTREZ).  |
| ...         | extra parameters for function buildEnrichTable.  |
| d0          | equivalence threshold for the Sorensen-Dice dissimilarity, d. The null hypothesis states that $d \geq d_0$ , i.e., inequivalence between the compared gene lists and the alternative that $d < d_0$ , i.e., equivalence or dissimilarity irrelevance (up to a level $d_0$ ). |
| conf.level  | confidence level of the one-sided confidence interval, a value between 0 and 1.  |
| boot        | boolean. If TRUE, the confidence interval and the test p-value are computed by means of a bootstrap approach instead of the asymptotic normal approach. Defaults to FALSE.   |
| nboot       | numeric, number of initially planned bootstrap replicates. Ignored if boot == FALSE. Defaults to 10000.  |
| check.table | Boolean. If TRUE (default), argument x is checked to adequately represent a 2x2 contingency table (or an aggregate of them) or gene lists producing a correct table. This checking is performed by means of function nice2x2Table.   |
| ontos       | "character", GO ontologies to analyse. Defaults to c("BP", "CC", "MF").  |
| GOLevels    | "integer", GO levels to analyse inside each one of the GO ontologies.  |
| trace       | Logical. If TRUE (default), the (usually very time consuming) process of function allEquivTestSorensen is traced along the specified GO ontologies and levels.   |

**Value**

An object of class "AllEquivSDhtest". It is a list with as many components as GO ontologies have been analysed. Each of these elements is itself a list with as many components as GO levels have been analyzed. Finally, the elements of these lists are objects as generated by equivTestSorensen.list, i.e., objects of class "equivSDhtestList" containing pairwise comparisons between gene lists.

**Methods (by class)**

- allEquivTestSorensen(list): S3 method for class "list"
- allEquivTestSorensen(allTableList): S3 method for class "allTableList"

**Examples**

```
# Gene lists to be explored for enrichment:
data(allOncoGeneLists)

# Obtaining ENTREZ identifiers for the gene universe of humans:
library(org.Hs.eg.db)
humanEntrezIDs <- keys(org.Hs.eg.db, keytype = "ENTREZID")

# This example is highly time-consuming. It scans two GO ontologies and three
# GO levels inside them to perform the equivalence test.
# allEquivTestSorensen(allOncoGeneLists,
#                       geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#                       ontos = c("MF", "BP"), GOLevels = seq.int(4,6))
# When the "ontos" and "GOLevels" arguments are not supplied, the function computes
```

```
# by default every possible contingency table between the lists being compared for
# the three ontologies (BP, CC, MF) and GO levels from 3 to 10.
#
# Much faster:
# Object \code{allTabs} of class "allTableList" contains all the pairwise contingency tables of
# joint enrichment for the gene lists in \code{allOncoGeneLists}, obtained along all three GO
# ontologies and along GO levels 3 to 10:
data(allTabs)
tests <- allEquivTestSorensen(allTabs, ontos = c("MF", "BP"), GOLevels = seq.int(4,6))
tests$BP$`level 5`
getPvalue(tests)
```

---

|                    |  |
|--------------------|--|
| allHclustThreshold | <i>Iterate hclustThreshold along the specified GO ontologies and GO levels</i> |
|--------------------|--|

---

## Description

Iterate hclustThreshold along the specified GO ontologies and GO levels

## Usage

```
allHclustThreshold(x, ontos, GOLevels, trace = TRUE, ...)
```

## Arguments

|          |   |
|----------|---|
| x        | an object of class "distList".  |
| ontos    | "character", GO ontologies to iterate. Defaults to the ontologies in 'x'.                       |
| GOLevels | "integer", GO levels to iterate inside each one of these GO ontologies.                         |
| trace    | Logical. If TRUE (default), the process is traced along the specified GO ontologies and levels. |
| ...      | extra parameters for function hclustThreshold.  |

## Value

An object of class "equivClustSorensenList" descending from "iterEquivClust" which itself descends from class "list". It is a list with as many components as GO ontologies have been specified. Each of these elements is itself a list with as many components as GO levels have been specified. Finally, the elements of these lists are objects of class "equivClustSorensen", descending from "equivClust" which itself descends from "hclust".

## Examples

```
# Object \code{allTabs} of class "allTableList" contains all the pairwise contingency tables of
# joint enrichment for the gene lists in \code{allOncoGeneLists}, obtained along all three GO
# ontologies and along GO levels 3 to 10:
data(allTabs)
# Compute the Sorensen-Dice equivalence threshold dissimilarity (only for the MF and CC
# ontologies and from levels 4 to 6):
dists <- allSorenThreshold(allTabs, ontos = c("MF", "CC"), GOLevels = seq.int(4,6))
hclusts <- allHclustThreshold(dists)
```

```
hclusts$MF$`level 6`  
plot(hclusts$MF$`level 6`)
```

---

|                  |  |
|------------------|--|
| allOncoGeneLists | <i>7 gene lists possibly related with cancer</i> |
|------------------|--|

---

**Description**

An object of class "list" of length 7. Each one of its elements is a "character" vector of gene identifiers (e.g., ENTREZ). Only gene lists of length almost 100 were taken from their source web. Take these lists just as an illustrative example, they are not automatically updated.

**Usage**

```
data(allOncoGeneLists)
```

**Format**

An object of class "list" of length 7. Each one of its elements is a "character" vector of ENTREZ gene identifiers .

**Source**

<http://www.bushmanlab.org/links/genelists>

---

|                   |   |
|-------------------|---|
| allSorenThreshold | <i>Iterate sorenThreshold along the specified GO ontologies and GO levels</i> |
|-------------------|---|

---

**Description**

Iterate sorenThreshold along the specified GO ontologies and GO levels

**Usage**

```
allSorenThreshold(x, ...)  
  
## S3 method for class 'list'  
allSorenThreshold(  
  x,  
  geneUniverse,  
  orgPackg,  
  boot = FALSE,  
  nboot = 10000,  
  boot.seed = 6551,  
  ontos = c("BP", "CC", "MF"),  
  GOLevels = seq.int(3, 10),  
  trace = TRUE,  
  alpha = 0.05,
```

```

    precis = 0.001,
    ...
)

## S3 method for class 'allTableList'
allSorenThreshold(
  x,
  boot = FALSE,
  nboot = 10000,
  boot.seed = 6551,
  ontos,
  GOlevels,
  trace = TRUE,
  alpha = 0.05,
  precis = 0.001,
  ...
)

```

### Arguments

|              |   |
|--------------|---|
| x            | either an object of class "list" or an object of class "allTableList". In the first case, each of its elements must be a "character" vector of gene identifiers (e.g., ENTREZ). In the second case, the object corresponds to all contingency tables of joint enrichment along one or more GO ontologies and one or more GO levels. |
| ...          | extra parameters for function buildEnrichTable.   |
| geneUniverse | character vector containing the universe of genes from where gene lists have been extracted. This vector must be obtained from the annotation package declared in orgPackg. For more details see <a href="#">README File</a> .  |
| orgPackg     | A string with the name of the genomic annotation package corresponding to a specific species to be analyzed, which must be previously installed and activated. For more details see <a href="#">README File</a> .   |
| boot         | boolean. If TRUE, the confidence intervals and the test p-values are computed by means of a bootstrap approach instead of the asymptotic normal approach. Defaults to FALSE.  |
| nboot        | numeric, number of initially planned bootstrap replicates. Ignored if boot == FALSE. Defaults to 10000.   |
| boot.seed    | starting random seed for all bootstrap iterations. Defaults to 6551. see the details section  |
| ontos        | "character", GO ontologies to analyse.  |
| GOlevels     | "integer", GO levels to analyse inside each one of these GO ontologies.   |
| trace        | Logical. If TRUE (default), the (usually very time consuming) process is traced along the specified GO ontologies and levels.   |
| alpha        | simultaneous nominal significance level for the equivalence tests to be repeatedly performed, defaults to 0.05  |
| precis       | numerical precision in the iterative search of the equivalence threshold dissimilarities,   |



**Value**

An object of class "distList". It is a list with as many components as GO ontologies have been analysed. Each of these elements is itself a list with as many components as GO levels have been analysed. Finally, the elements of these lists are objects of class "dist" with the Sorensen-Dice equivalence threshold dissimilarity.

**Methods (by class)**

- allSorenThreshold(list): S3 method for class "list"
- allSorenThreshold(allTableList): S3 method for class "allTableList"

**Examples**

```
# # This example is highly time-consuming. It scans two GO ontologies and three
# # GO levels inside them to perform the equivalence test.

# Obtaining ENTREZ identifiers for the gene universe of humans:
# library(org.Hs.eg.db)
# humanEntrezIDs <- keys(org.Hs.eg.db, keytype = "ENTREZID")

# # Gene lists to be explored for enrichment:
# data("allOncoGeneLists")
# allSorenThreshold(allOncoGeneLists,
#                   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#                   #
# # Much faster:
# # Object allTabs of class "allTableList" contains all the pairwise contingency tables of
# # joint enrichment for the gene lists in \code{allOncoGeneLists}, obtained along all three GO
# # ontologies and along GO levels 3 to 10:
data(allTabs)
dSors <- allSorenThreshold(allTabs, ontos = c("MF", "BP"), GOLevels = seq.int(4,6))
dSors$BP$`level 5`
```

---

allTabs

*An example of an object of class "allTableList" resulting from a call to 'buildEnrichTable'*

---

**Description**

The result of generating all contingency tables of mutual enrichment, in a pairwise fashion, between the gene lists in data [allOncoGeneLists](#) along GO levels 3 to 10 for all three GO ontologies, BP, MF and CC. Object 'allTabs' is a list of length 3 with one element for each GO ontology: allTabs\$BP, allTabs\$MF and allTabs\$CC. Each one of these lists is itself a list of length 11, e.g., allTabs\$BP\$`level 3`, allTabs\$BP\$`level 4`, etc. to allTabs\$BP\$`level 10`. Finally, each one of these lists contains all contingency tables of mutual enrichment, in a pairwise fashion, for the gene lists in data [allOncoGeneLists](#). These results are based on gene lists which are not automatically updated, take them just as an illustrative example because the gene lists, and the GO, may change along time. The present version of these data was generated under Bioconductor version 3.17.

**Usage**

```
data(allTabs)
```

**Format**

An object of class "allTableList" inheriting from class "list".

---

allTabsBP.4

*An example of an object of class "tableList" resulting from a call to 'buildEnrichTable'*

---

**Description**

The result of generating all contingency tables of mutual enrichment, in a pairwise fashion, between the gene lists in data [allOncoGeneLists](#). The information in these data was summarized as 2x2 contingency tables of GO terms enrichment, at level 4 of the BP ontology. These results are based on gene lists which are not automatically updated, take them just as an illustrative example because the gene lists, the GO and Bioconductor, may change along time. The present version of these data was generated under Bioconductor version 3.17.

**Usage**

```
data(allTabsBP.4)
```

**Format**

An object of class "tableList" inheriting from class "list". It is a list of class "table" objects.

---

boot.cancerEquivSorensen

*An example of object of class "AllEquivSDhtest" resulting from a call to 'allEquivTestSorensen'*

---

**Description**

The bootstrap Sorensen-Dice test performed on the cancer gene lists in data [allOncoGeneLists](#) which is may be charged from this package. The test is iterated for all GO ontologies and for GO levels 3 to 10. These results are not automatically updated for changes in these gene lists, take them just as an illustrative example. The present version was obtained under Bioconductor 3.17.

**Usage**

```
data(boot.cancerEquivSorensen)
```

**Format**

An object of class "AllEquivSDhtest" inheriting from class "list". Each one of its elements, named BP, CC and MF respectively, corresponds to a GO ontology. It is itself a list of length 8 whose elements are named as "Level 3" to "Level 10". For each combination of ontology and level, there is an object of class "equivSDhtestList" codifying the result of all pairwise tests between these cancer gene lists.

**Details**

For each ontology and GO level, the result contains the result of all pairwise tests of equivalence between the cancer gene lists.

**Source**

<http://www.bushmanlab.org/links/genelists>

---

 boot.tStat

*Studentized Sorensen-Dice dissimilarity statistic*


---

**Description**

Efficient computation of the studentized statistic  $(\hat{dis} - dis) / \hat{se}$  where 'dis' stands for the "population" value of the Sorensen-Dice dissimilarity, ' $\hat{dis}$ ' for its estimated value and ' $\hat{se}$ ' for the estimate of the standard error of ' $\hat{dis}$ '. Internally used in bootstrap computations.

**Usage**

```
boot.tStat(xBoot, dis)
```

**Arguments**

xBoot            either an object of class "table", "matrix" or "numeric" representing a 2x2 contingency table of joint enrichment.

dis                the "known" value of the population dissimilarity.

**Details**

This function is repeatedly evaluated during bootstrap iterations. Given a contingency table 'x' of mutual enrichment (the "true" dataset):

$$\begin{array}{cc} n_{11} & n_{10} \\ n_{01} & n_{00}, \end{array}$$

summarizing the status of mutual presence of enrichment in two gene lists, where the subindex '11' corresponds to those GO terms enriched in both lists, '01' to terms enriched in the second list but not in the first one, '10' to terms enriched in the first list but not enriched in the second one and '00' to those GO terms non enriched in both gene lists, i.e., to the double negatives.

A typical bootstrap iteration consists in repeatedly generating four frequencies from a multinomial of parameters size = sum( $n_{ij}$ ),  $i, j = 1, 0$  and probabilities ( $n_{11}/size$ ,  $n_{10}/size$ ,  $n_{01}/size$ ,  $n_{00}/size$ ). The argument 'xBoot' corresponds to each one of these bootstrap resamples (indiferently represented in form of a 2x2 "table" or "matrix" or as a numeric vector) In each bootstrap iteration, the value of the "true" known 'dis' is the dissimilarity which was computed from 'x' (a constant, known value in the full iteration) and the values of ' $\hat{dis}$ ' and ' $\hat{se}$ ' are internally computed from the bootstrap data 'xBoot'.

**Value**

A numeric value, the result of computing  $(\hat{dis} - dis) / \hat{se}$ .

---

BP.4 *An example of an object of class "equivSDhctestList" resulting from a call to 'equivSorensenTest'*

---

### Description

The result of all pairwise Sorensen-Dice equivalence tests between the gene lists in data [allOncoGeneLists](#) which may be charged from this package. To perform the tests, the information in these data was summarized as 2x2 contingency tables of GO terms enrichment, at level 4 of the BP ontology, and the tests were performed for an equivalence limit  $d0 = 0.4444$  and a confidence level  $conf.int = 0.95$ . These results are based on gene lists which are non automatically updated, take them just as an illustrative example.

### Usage

```
data(BP.4)
```

### Format

An object of class "equivSDhctestList" inheriting from class "list". It is a list of class "equivSDhctest" objects.

### Source

<http://www.bushmanlab.org/links/genelists>

---

buildEnrichTable *Creates a 2x2 enrichment contingency table from two gene lists, or all pairwise contingency tables for a "list" of gene lists.*

---

### Description

Creates a 2x2 enrichment contingency table from two gene lists, or all pairwise contingency tables for a "list" of gene lists.

### Usage

```
buildEnrichTable(x, ...)

## Default S3 method:
buildEnrichTable(
  x,
  y,
  listNames = c("gene.list1", "gene.list2"),
  check.table = TRUE,
  geneUniverse,
  orgPackg,
  onto,
  GOLevel,
  showEnrichedIn = TRUE,
```

```

    pAdjustMeth = "BH",
    pvalCutoff = 0.01,
    qvalCutoff = 0.05,
    parallel = FALSE,
    nOfCores = 1,
    ...
)

## S3 method for class 'character'
buildEnrichTable(
  x,
  y,
  listNames = c("gene.list1", "gene.list2"),
  geneUniverse,
  orgPackg,
  onto,
  GOLevel,
  showEnrichedIn = TRUE,
  check.table = TRUE,
  pAdjustMeth = "BH",
  pvalCutoff = 0.01,
  qvalCutoff = 0.05,
  parallel = FALSE,
  nOfCores = 1,
  ...
)

## S3 method for class 'list'
buildEnrichTable(
  x,
  check.table = TRUE,
  geneUniverse,
  orgPackg,
  onto,
  GOLevel,
  showEnrichedIn = TRUE,
  pAdjustMeth = "BH",
  pvalCutoff = 0.01,
  qvalCutoff = 0.05,
  parallel = FALSE,
  nOfCores = min(detectCores() - 1, length(x) - 1),
  ...
)

```

### Arguments

- x            either an object of class "character" (or coerzable to "character") representing a vector of gene identifiers (e.g., ENTREZ) or an object of class "list". In this second case, each element of the list must be a "character" vector of gene identifiers (e.g., ENTREZ). Then, all pairwise contingency tables between these gene lists are built.
- ...           Additional parameters for internal use (not used for the moment)

|                |  |
|----------------|--|
| y              | an object of class "character" (or coerzable to "character") representing a vector of gene identifiers (e.g., ENTREZ).   |
| listNames      | a character(2) with the gene lists names originating the cross-tabulated enrichment frequencies. Only in the "character" or default interface.   |
| check.table    | Logical The resulting table must be checked. Defaults to TRUE.   |
| geneUniverse   | character vector containing the universe of genes from where gene lists have been extracted. This vector must be obtained from the annotation package declared in orgPackg. For more details see <a href="#">README File</a> . |
| orgPackg       | A string with the name of the genomic annotation package corresponding to a specific species to be analyzed, which must be previously installed and activated. For more details see <a href="#">README File</a> .              |
| onto           | string describing the ontology. Either "BP", "MF" or "CC".   |
| GOLevel        | An integer, the GO ontology level.   |
| showEnrichedIn | Boolean. If TRUE (default), the cross-table of enriched and non-enriched GO terms vs Gene Lists names (obtained from the enrichedIn function) is automatically saved in the Global Environment.                                |
| pAdjustMeth    | string describing the adjust method, either "BH", "BY" or "Bonf", defaults to 'BH'.  |
| pvalCutoff     | adjusted pvalue cutoff on enrichment tests to report   |
| qvalCutoff     | qvalue cutoff on enrichment tests to report as significant. Tests must pass i) pvalueCutoff on unadjusted pvalues, ii) pvalueCutoff on adjusted pvalues and iii) qvalueCutoff on qvalues to be reported                        |
| parallel       | Logical. Defaults to FALSE but put it at TRUE for parallel computation.  |
| nOfCores       | Number of cores for parallel computations. Only in "list" interface.   |

### Details

The arguments 'parallel' and 'nOfCores' are ignored in the 'default' and "character" interfaces, but included for possible future developments; they only apply to the "list" interface. In the "list" interface, 'parallel' defaults to FALSE but there is the possibility of some time saving when the number of gene lists (the length of 'x' in the "list" interface) is high. The trade off between the time spent initializing parallel computing and the possible time gain due to parallelization must be considered in each application and computer.

### Value

in the "character" interface, an object of class "table". It represents a 2x2 contingency table, the cross-tabulation of the enriched GO terms in two gene lists: "Number of enriched GO terms in list 1 (TRUE, FALSE)" x "Number of enriched Go terms in list 2 (TRUE, FALSE)". In the "list" interface, the result is an object of class "tableList" with all pairwise tables. Class "tableList" corresponds to objects representing all mutual enrichment contingency tables generated in a pairwise fashion: Given gene lists (i.e. "character" vectors of gene identifiers) l1, l2, ..., lk, an object of class "tableList" is a list of lists of contingency tables t(i,j) generated from each pair of gene lists i and j, with the following structure:

\$l2

\$l2\$l1\$t(2,1)

\$l3

\$l3\$l1\$t(3,1), \$l3\$l2\$t(3,2)

```
...
$lk
$lk$1$t(k,1), $lk$2$t(k,2), ..., $lk$l(k-1)t(K,k-1)
```

### Methods (by class)

- buildEnrichTable(default): S3 default method
- buildEnrichTable(character): S3 method for class "character"
- buildEnrichTable(list): S3 method for class "list"

### Examples

```
# Obtaining ENTREZ identifiers for the gene universe of humans:
library(org.Hs.eg.db)
humanEntrezIDs <- keys(org.Hs.eg.db, keytype = "ENTREZID")

# Gene lists to be explored for enrichment:
data(allOncoGeneLists)
?allOncoGeneLists

# Table of joint GO term enrichment between gene lists Vogelstein and sanger,
# for ontology MF at GO level 6.
vog.VS.sang <- buildEnrichTable(allOncoGeneLists[["Vogelstein"]],
                                allOncoGeneLists[["sanger"]],
                                geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
                                onto = "MF", GOLevel = 6, listNames = c("Vogelstein", "sanger"))

vog.VS.sang
# All tables of mutual enrichment:
all.tabs <- buildEnrichTable(allOncoGeneLists,
                             geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
                             onto = "MF", GOLevel = 6)

all.tabs$waldman
```

---

cancerEquivSorensen     *An example of an object of class "AllEquivSDhtest" resulting from a call to 'allEquivTestSorensen'*

---

### Description

The Sorensen-Dice test (normal asymptotic version) performed on the cancer gene lists in data [allOncoGeneLists](#) which may be charged from this package. The test is iterated for all GO ontologies and for GO levels 3 to 10. These results are not automatically updated for changes in these gene lists and Bioconductor or Go updates, take them just as an illustrative example. The present version was obtained under Bioconductor 3.17.

### Usage

```
data(cancerEquivSorensen)
```

**Format**

An object of class "AllEquivSDhtest" inheriting from class "list". Each one of its elements, named BP, CC and MF respectively, corresponds to a GO ontology. It is itself a list of length 8 whose elements are named as "Level 3" to "Level 10". For each combination of ontology and level, there is an object of class "equivSDhtestList" codifying the result of all pairwise tests between these cancer gene lists.

**Details**

For each ontology and GO level, the result contains the result of all pairwise tests of equivalence between the cancer gene lists.

**Source**

<http://www.bushmanlab.org/links/genelists>

---

|               |  |
|---------------|--|
| completeTable | <i>Reformats and completes (if necessary) a 2x2 enrichment contingency table for its appropriate use in package goSorensen. It is internally used by function 'buildEnrichTable'..</i> |
|---------------|--|

---

**Description**

Reformats and completes (if necessary) a 2x2 enrichment contingency table for its appropriate use in package goSorensen. It is internally used by function 'buildEnrichTable'..

**Usage**

```
completeTable(x, listNames)
```

**Arguments**

|           |   |
|-----------|---|
| x         | an object of class "table".                                       |
| listNames | a character(2) with the gene lists names. enrichment frequencies. |

**Value**

a complete contingency table to use in package goSorensen.



dSorensen

*Computation of the Sorensen-Dice dissimilarity***Description**

Computation of the Sorensen-Dice dissimilarity

**Usage**

```
dSorensen(x, ...)

## S3 method for class 'table'
dSorensen(x, check.table = TRUE, ...)

## S3 method for class 'matrix'
dSorensen(x, check.table = TRUE, ...)

## S3 method for class 'numeric'
dSorensen(x, check.table = TRUE, ...)

## S3 method for class 'character'
dSorensen(x, y, check.table = TRUE, ...)

## S3 method for class 'list'
dSorensen(x, check.table = TRUE, ...)

## S3 method for class 'tableList'
dSorensen(x, check.table = TRUE, ...)
```

**Arguments**

|             |   |
|-------------|---|
| x           | either an object of class "table", "matrix" or "numeric" representing a 2x2 contingency table, or a "character" vector (a set of gene identifiers) or "list" or "tableList" object. See the details section for more information. |
| ...         | extra parameters for function buildEnrichTable.   |
| check.table | Boolean. If TRUE (default), argument x is checked to adequately represent a 2x2 contingency table, by means of function nice2x2Table.   |
| y           | an object of class "character" representing a vector of valid gene identifiers (e.g., ENTREZ).  |

**Details**

Given a 2x2 arrangement of frequencies (either implemented as a "table", a "matrix" or a "numeric" object):

$$\begin{array}{cc} n_{11} & n_{10} \\ n_{01} & n_{00}, \end{array}$$

this function computes the Sorensen-Dice dissimilarity

$$\frac{n_{10} + n_{01}}{2n_{11} + n_{10} + n_{01}}.$$

The subindex '11' corresponds to those GO terms enriched in both lists, '01' to terms enriched in the second list but not in the first one, '10' to terms enriched in the first list but not enriched in the second one and '00' corresponds to those GO terms non enriched in both gene lists, i.e., to the double negatives, a value which is ignored in the computations.

In the "numeric" interface, if  $\text{length}(x) \geq 3$ , the values are interpreted as  $(n_{11}, n_{01}, n_{10}, n_{00})$ , always in this order and discarding extra values if necessary. The result is correct, regardless the frequencies being absolute or relative.

If  $x$  is an object of class "character", then  $x$  (and  $y$ ) must represent two "character" vectors of valid gene identifiers (e.g., ENTREZ). Then the dissimilarity between lists  $x$  and  $y$  is computed, after internally summarizing them as a 2x2 contingency table of joint enrichment. This last operation is performed by function `buildEnrichTable` and "valid gene identifiers (e.g., ENTREZ)" stands for the coherency of these gene identifiers with the arguments `geneUniverse` and `orgPackg` of `buildEnrichTable`, passed by the ellipsis argument `...` in `dSorensen`.

If  $x$  is an object of class "list", the argument must be a list of "character" vectors, each one representing a gene list (character identifiers). Then, all pairwise dissimilarities between these gene lists are computed.

If  $x$  is an object of class "tableList", the Sorensen-Dice dissimilarity is computed over each one of these tables. Given  $k$  gene lists (i.e. "character" vectors of gene identifiers)  $l_1, l_2, \dots, l_k$ , an object of class "tableList" (typically constructed by a call to function `buildEnrichTable`) is a list of lists of contingency tables  $t(i,j)$  generated from each pair of gene lists  $i$  and  $j$ , with the following structure:

```
$l2
$l2$l1$t(2,1)
$l3
$l3$l1$t(3,1), $l3$l2$t(3,2)
...
$lk
$lk$l1$t(k,1), $lk$l2$t(k,2), ..., $lk$l(k-1)t(k,k-1)
```

### Value

In the "table", "matrix", "numeric" and "character" interfaces, the value of the Sorensen-Dice dissimilarity. In the "list" and "tableList" interfaces, the symmetric matrix of all pairwise Sorensen-Dice dissimilarities.

### Methods (by class)

- `dSorensen(table)`: S3 method for class "table"
- `dSorensen(matrix)`: S3 method for class "matrix"
- `dSorensen(numeric)`: S3 method for class "numeric"
- `dSorensen(character)`: S3 method for class "character"
- `dSorensen(list)`: S3 method for class "list"
- `dSorensen(tableList)`: S3 method for class "tableList"

### See Also

`buildEnrichTable` for constructing contingency tables of mutual enrichment, `nice2x2Table` for checking contingency tables validity, `seSorensen` for computing the standard error of the dissimilarity, `duppSorensen` for the upper limit of a one-sided confidence interval of the dissimilarity, `equivTestSorensen` for an equivalence test.

**Examples**

```

# Gene lists 'atlas' and 'sanger' in 'allOncoGeneLists' dataset. Table of joint enrichment
# of GO terms in ontology BP at level 3.
data(tab_atlas.sanger_BP3)
tab_atlas.sanger_BP3
?tab_atlas.sanger_BP3
dSorensen(tab_atlas.sanger_BP3)

# Table represented as a vector:
conti4 <- c(56, 1, 30, 471)
dSorensen(conti4)
# or as a plain matrix:
dSorensen(matrix(conti4, nrow = 2))

# This function is also appropriate for proportions:
dSorensen(conti4 / sum(conti4))

conti3 <- c(56, 1, 30)
dSorensen(conti3)

# Sorensen-Dice dissimilarity from scratch, directly from two gene lists:
# (These examples may be considerably time consuming due to many enrichment
# tests to build the contingency tables of joint enrichment)
# data(allOncoGeneLists)
# ?allOncoGeneLists

# Obtaining ENTREZ identifiers for the gene universe of humans:
# library(org.Hs.eg.db)
# humanEntrezIDs <- keys(org.Hs.eg.db, keytype = "ENTREZID")

# (Time consuming, building the table requires many enrichment tests:)
# dSorensen(allOncoGeneLists$atlas, allOncoGeneLists$sanger,
#           onto = "BP", GOLevel = 3,
#           geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db")

# Essentially, the above code makes the same as:
# tab_atlas.sanger_BP3 <- buildEnrichTable(allOncoGeneLists$atlas, allOncoGeneLists$sanger,
#                                       onto = "BP", GOLevel = 3,
#                                       geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db")
# dSorensen(tab_atlas.sanger_BP3)
# (Quite time consuming, all pairwise dissimilarities:)
# dSorensen(allOncoGeneLists,
#           onto = "BP", GOLevel = 3,
#           geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db")

```

---

duppSorensen

*Upper limit of a one-sided confidence interval (0, dUpp] for the Sorensen-Dice dissimilarity*


---

**Description**

Upper limit of a one-sided confidence interval (0, dUpp] for the Sorensen-Dice dissimilarity

**Usage**

```
duppSorensen(x, ...)  
  
## S3 method for class 'table'  
duppSorensen(  
  x,  
  dis = dSorensen.table(x, check.table = FALSE),  
  se = seSorensen.table(x, check.table = FALSE),  
  conf.level = 0.95,  
  z.conf.level = qnorm(1 - conf.level),  
  boot = FALSE,  
  nboot = 10000,  
  check.table = TRUE,  
  ...  
)  
  
## S3 method for class 'matrix'  
duppSorensen(  
  x,  
  dis = dSorensen.matrix(x, check.table = FALSE),  
  se = seSorensen.matrix(x, check.table = FALSE),  
  conf.level = 0.95,  
  z.conf.level = qnorm(1 - conf.level),  
  boot = FALSE,  
  nboot = 10000,  
  check.table = TRUE,  
  ...  
)  
  
## S3 method for class 'numeric'  
duppSorensen(  
  x,  
  dis = dSorensen.numeric(x, check.table = FALSE),  
  se = seSorensen.numeric(x, check.table = FALSE),  
  conf.level = 0.95,  
  z.conf.level = qnorm(1 - conf.level),  
  boot = FALSE,  
  nboot = 10000,  
  check.table = TRUE,  
  ...  
)  
  
## S3 method for class 'character'  
duppSorensen(  
  x,  
  y,  
  conf.level = 0.95,  
  boot = FALSE,  
  nboot = 10000,  
  check.table = TRUE,  
  ...  
)
```

```

## S3 method for class 'list'
duppSorensen(
  x,
  conf.level = 0.95,
  boot = FALSE,
  nboot = 10000,
  check.table = TRUE,
  ...
)

## S3 method for class 'tableList'
duppSorensen(
  x,
  conf.level = 0.95,
  boot = FALSE,
  nboot = 10000,
  check.table = TRUE,
  ...
)

```

### Arguments

|              |  |
|--------------|--|
| x            | either an object of class "table", "matrix" or "numeric" representing a 2x2 contingency table, or a "character" (a set of gene identifiers) or "list" or "tableList" object. See the details section for more information. |
| ...          | additional arguments for function buildEnrichTable.  |
| dis          | Sorensen-Dice dissimilarity value. Only required to speed computations if this value is known in advance.  |
| se           | standard error estimate of the sample dissimilarity. Only required to speed computations if this value is known in advance.  |
| conf.level   | confidence level of the one-sided confidence interval, a numeric value between 0 and 1.  |
| z.conf.level | standard normal (or bootstrap, see arguments below) distribution quantile at the 1 - conf.level value. Only required to speed computations if this value is known in advance. Then, the argument conf.level is ignored.    |
| boot         | boolean. If TRUE, z.conf.level is computed by means of a bootstrap approach instead of the asymptotic normal approach. Defaults to FALSE.  |
| nboot        | numeric, number of initially planned bootstrap replicates. Ignored if boot == FALSE. Defaults to 10000.  |
| check.table  | Boolean. If TRUE (default), argument x is checked to adequately represent a 2x2 contingency table. This checking is performed by means of function nice2x2Table.   |
| y            | an object of class "character" representing a vector of gene identifiers (e.g., ENTREZ).   |

### Details

This function computes the upper limit of a one-sided confidence interval for the Sorensen-Dice dissimilarity, given a 2x2 arrangement of frequencies (either implemented as a "table", a "matrix" or a "numeric" object):

$$\begin{array}{cc} n_{11} & n_{10} \\ n_{01} & n_{00}, \end{array}$$

The subindex '11' corresponds to those GO terms enriched in both lists, '01' to terms enriched in the second list but not in the first one, '10' to terms enriched in the first list but not enriched in the second one and '00' corresponds to those GO terms non enriched in both gene lists, i.e., to the double negatives, a value which is ignored in the computations, except if `boot == TRUE`.

In the "numeric" interface, if `length(x) >= 4`, the values are interpreted as  $(n_{11}, n_{01}, n_{10}, n_{00})$ , always in this order and discarding extra values if necessary.

Arguments `dis`, `se` and `z.conf.level` are not required. If known in advance (e.g., as a consequence of previous computations with the same data), providing its value may speed the computations.

By default, `z.conf.level` corresponds to the  $1 - \text{conf.level}$  quantile of a standard normal  $N(0,1)$  distribution, as the studentized statistic  $(\hat{d} - d) / \hat{se}$  is asymptotically  $N(0,1)$ . In the studentized statistic,  $d$  stands for the "true" Sorensen-Dice dissimilarity,  $\hat{d}$  to its sample estimate and  $\hat{se}$  for the estimate of its standard error. In fact, the normal is its limiting distribution but, for finite samples, the true sampling distribution may present departures from normality (mainly with some inflation in the left tail). The bootstrap method provides a better approximation to the true sampling distribution. In the bootstrap approach, `nboot` new bootstrap contingency tables are generated from a multinomial distribution with parameters `size = n = n11 + n01 + n10 + n00` and probabilities  $(n_{11}/n, n_{01}/n, n_{10}/n, n_{00}/n)$ . Sometimes, some of these generated tables may present so low frequencies of enrichment that make them unable for Sorensen-Dice computations. As a consequence, the number of effective bootstrap samples may be lower than the number of initially planned bootstrap samples `nboot`. Computing in advance the value of argument `z.conf.level` may be a way to cope with these departures from normality, by means of a more adequate quantile function. Alternatively, if `boot == TRUE`, a bootstrap quantile is internally computed.

If `x` is an object of class "character", then `x` (and `y`) must represent two "character" vectors of valid gene identifiers (e.g., ENTREZ). Then the confidence interval for the dissimilarity between lists `x` and `y` is computed, after internally summarizing them as a 2x2 contingency table of joint enrichment. This last operation is performed by function `buildEnrichTable` and "valid gene identifiers (e.g., ENTREZ)" stands for the coherency of these gene identifiers with the arguments `geneUniverse` and `orgPackg` of `buildEnrichTable`, passed by the ellipsis argument `...` in `dUppSorensen`.

In the "list" interface, the argument must be a list of "character" vectors, each one representing a gene list (character identifiers). Then, all pairwise upper limits of the dissimilarity between these gene lists are computed.

In the "tableList" interface, the upper limits are computed over each one of these tables. Given gene lists (i.e. "character" vectors of gene identifiers) `l1`, `l2`, ..., `lk`, an object of class "tableList" (typically constructed by a call to function `buildEnrichTable`) is a list of lists of contingency tables  $t(i,j)$  generated from each pair of gene lists `i` and `j`, with the following structure:

```
$l2
$l2$l1$t(2,1)
$l3
$l3$l1$t(3,1), $l3$l2$t(3,2)
...
$lk
$lk$l1$t(k,1), $lk$l2$t(k,2), ..., $lk$l(k-1)t(k,k-1)
```

**Value**

In the "table", "matrix", "numeric" and "character" interfaces, the value of the Upper limit of the confidence interval for the Sorensen-Dice dissimilarity. When `boot == TRUE`, this result also has an extra attribute: "eff.nboot" which corresponds to the number of effective bootstrap replicats, see the details section. In the "list" and "tableList" interfaces, the result is the symmetric matrix of all pairwise upper limits.

**Methods (by class)**

- `duppSorensen(table)`: S3 method for class "table"
- `duppSorensen(matrix)`: S3 method for class "matrix"
- `duppSorensen(numeric)`: S3 method for class "numeric"
- `duppSorensen(character)`: S3 method for class "character"
- `duppSorensen(list)`: S3 method for class "list"
- `duppSorensen(tableList)`: S3 method for class "tableList"

**See Also**

[buildEnrichTable](#) for constructing contingency tables of mutual enrichment, [nice2x2Table](#) for checking contingency tables validity, [dSorensen](#) for computing the Sorensen-Dice dissimilarity, [seSorensen](#) for computing the standard error of the dissimilarity, [equivTestSorensen](#) for an equivalence test.

**Examples**

```
# Gene lists 'atlas' and 'sanger' in 'Cangenes' dataset. Table of joint enrichment
# of GO terms in ontology BP at level 3.
data(tab_atlas.sanger_BP3)
?tab_atlas.sanger_BP3
duppSorensen(tab_atlas.sanger_BP3)
dSorensen(tab_atlas.sanger_BP3) + qnorm(0.95) * seSorensen(tab_atlas.sanger_BP3)
# Using the bootstrap approximation instead of the normal approximation to
# the sampling distribution of  $(\hat{d} - d) / se(\hat{d})$ :
duppSorensen(tab_atlas.sanger_BP3, boot = TRUE)

# Contingency table as a numeric vector:
duppSorensen(c(56, 1, 30, 47))
duppSorensen(c(56, 1, 30))

# Upper confidence limit for the Sorensen-Dice dissimilarity, from scratch,
# directly from two gene lists:
# (These examples may be considerably time consuming due to many enrichment
# tests to build the contingency tables of mutual enrichment)
# data(allOncoGeneLists)
# ?allOncoGeneLists

# Obtaining ENTREZ identifiers for the gene universe of humans:
# library(org.Hs.eg.db)
# humanEntrezIDs <- keys(org.Hs.eg.db, keytype = "ENTREZID")

# Computing the Upper confidence limit:
# duppSorensen(allOncoGeneLists$atlas, allOncoGeneLists$sanger,
#             onto = "CC", GOLevel = 5,
```

```
#           geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db")
# Even more time consuming (all pairwise values):
# duppSorensen(allOncoGeneLists,
#           onto = "CC", GOLevel = 5,
#           geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db")
```

---

|            |  |
|------------|--|
| enrichedIn | <i>This function builds a cross-tabulation of enriched (TRUE) and non-enriched (FALSE) GO terms vs. gene lists</i> |
|------------|--|

---

## Description

This function builds a cross-tabulation of enriched (TRUE) and non-enriched (FALSE) GO terms vs. gene lists

## Usage

```
enrichedIn(x, ...)
```

## Default S3 method:

```
enrichedIn(
  x,
  geneUniverse,
  orgPackg,
  onto,
  GOLevel,
  pAdjustMeth = "BH",
  pvalCutoff = 0.01,
  qvalCutoff = 0.05,
  parallel = FALSE,
  nOfCores = 1,
  ...
)
```

## S3 method for class 'character'

```
enrichedIn(
  x,
  geneUniverse,
  orgPackg,
  onto,
  GOLevel,
  pAdjustMeth = "BH",
  pvalCutoff = 0.01,
  qvalCutoff = 0.05,
  parallel = FALSE,
  nOfCores = 1,
  ...
)
```

## S3 method for class 'list'

```
enrichedIn(
```



```

    x,
    geneUniverse,
    orgPackg,
    onto,
    GOLevel,
    pAdjustMeth = "BH",
    pvalCutoff = 0.01,
    qvalCutoff = 0.05,
    parallel = FALSE,
    nOfCores = min(detectCores() - 1, length(x)),
    ...
)

```

### Arguments

|              |  |
|--------------|--|
| x            | either an object of class "character" (or coerzable to "character") or "list". In the "character" interface, these values should represent Entrez gene (or, in general, feature) identifiers. In the "list" interface, each element of the list must be a "character" vector of Entrez identifiers |
| ...          | Additional parameters  |
| geneUniverse | character vector containing the universe of genes from where gene lists have been extracted. This vector must be obtained from the annotation package declared in orgPackg. For more details see <a href="#">README File</a> .   |
| orgPackg     | A string with the name of the genomic annotation package corresponding to a specific species to be analyzed, which must be previously installed and activated. For more details see <a href="#">README File</a> .  |
| onto         | string describing the ontology. Belongs to c('BP', 'MF', 'CC')   |
| GOLevel      | GO level, an integer   |
| pAdjustMeth  | string describing the adjust method. Belongs to c('BH', 'BY', 'Bonf')  |
| pvalCutoff   | adjusted pvalue cutoff on enrichment tests to report   |
| qvalCutoff   | qvalue cutoff on enrichment tests to report as significant. Tests must pass i) pvalueCutoff on unadjusted pvalues, ii) pvalueCutoff on adjusted pvalues and iii) qvalueCutoff on qvalues to be reported  |
| parallel     | Logical. Only in "list" interface. Defaults to FALSE but put it at TRUE for parallel computation   |
| nOfCores     | Number of cores for parallel computations. Only in "list" interface  |

### Details

The arguments 'parallel' and 'nOfCores' are ignored in the 'default' and "character" interfaces because (in the present implementation) parallelisation is only applied to repeated calls to function 'clusterProfiler::enrichGO' which, in turn, does not provide for the possibility of parallelisation. They only apply to the "list" interface.

### Value

In the "character" interface, a length k vector of TRUE/FALSE values corresponding to enrichment or not, where k stands for the total number of GO terms at level 'GOLev' in ontology 'onto'. In the "list" interface, a boolean matrix of TRUE/FALSE values indicating enrichment or not, with k rows and s columns, where k corresponds to the total number of GO terms at level 'GOLev' in ontology 'onto' and s corresponds to the length of "list" 'x'.

**Methods (by class)**

- `enrichedIn(default)`: S3 default method
- `enrichedIn(character)`: S3 method for class "character"
- `enrichedIn(list)`: S3 method for class "list"

**Examples**

```
# Obtaining ENTREZ identifiers for the gene universe of humans:
library(org.Hs.eg.db)
humanEntrezIDs <- keys(org.Hs.eg.db, keytype = "ENTREZID")

# Gene lists to be explored for enrichment:
data(allOncoGeneLists)
?allOncoGeneLists

# Computing the cross table:
enrichd <- enrichedIn(allOncoGeneLists[["Vogelstein"]],
                      geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
                      onto = "MF", GOLevel = 6)
enrichd

# Cross table of enriched GO terms (GO ontology MF, level 6) for all gene
# lists in 'allOncoGeneLists':
enrichedAllOncoMF.6 <- enrichedIn(allOncoGeneLists,
                                 geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
                                 onto = "MF", GOLevel = 6)
enrichedAllOncoMF.6
```

---

equivTestSorensen      *Equivalence test based on the Sorensen-Dice dissimilarity*

---

**Description**

Equivalence test based on the Sorensen-Dice dissimilarity, computed either by an asymptotic normal approach or by a bootstrap approach.

**Usage**

```
equivTestSorensen(x, ...)
```

```
## S3 method for class 'table'
equivTestSorensen(
  x,
  d0 = 1/(1 + 1.25),
  conf.level = 0.95,
  boot = FALSE,
  nboot = 10000,
  check.table = TRUE,
  ...
)
```

```
## S3 method for class 'matrix'
```

```
equivTestSorensen(  
  x,  
  d0 = 1/(1 + 1.25),  
  conf.level = 0.95,  
  boot = FALSE,  
  nboot = 10000,  
  check.table = TRUE,  
  ...  
)  
  
## S3 method for class 'numeric'  
equivTestSorensen(  
  x,  
  d0 = 1/(1 + 1.25),  
  conf.level = 0.95,  
  boot = FALSE,  
  nboot = 10000,  
  check.table = TRUE,  
  ...  
)  
  
## S3 method for class 'character'  
equivTestSorensen(  
  x,  
  y,  
  d0 = 1/(1 + 1.25),  
  conf.level = 0.95,  
  boot = FALSE,  
  nboot = 10000,  
  check.table = TRUE,  
  ...  
)  
  
## S3 method for class 'list'  
equivTestSorensen(  
  x,  
  d0 = 1/(1 + 1.25),  
  conf.level = 0.95,  
  boot = FALSE,  
  nboot = 10000,  
  check.table = TRUE,  
  ...  
)  
  
## S3 method for class 'tableList'  
equivTestSorensen(  
  x,  
  d0 = 1/(1 + 1.25),  
  conf.level = 0.95,  
  boot = FALSE,  
  nboot = 10000,  
  check.table = TRUE,
```

```
    ...
  )
```

### Arguments

|                          |  |
|--------------------------|--|
| <code>x</code>           | either an object of class "table", "matrix", "numeric", "character", "list" or "tableList". See the details section for more information.  |
| <code>...</code>         | extra parameters for function <code>buildEnrichTable</code> .  |
| <code>d0</code>          | equivalence threshold for the Sorensen-Dice dissimilarity, $d$ . The null hypothesis states that $d \geq d0$ , i.e., inequivalence between the compared gene lists and the alternative that $d < d0$ , i.e., equivalence or dissimilarity irrelevance (up to a level $d0$ ). |
| <code>conf.level</code>  | confidence level of the one-sided confidence interval, a value between 0 and 1.  |
| <code>boot</code>        | boolean. If TRUE, the confidence interval and the test p-value are computed by means of a bootstrap approach instead of the asymptotic normal approach. Defaults to FALSE.   |
| <code>nboot</code>       | numeric, number of initially planned bootstrap replicates. Ignored if <code>boot == FALSE</code> . Defaults to 10000.  |
| <code>check.table</code> | Boolean. If TRUE (default), argument <code>x</code> is checked to adequately represent a 2x2 contingency table (or an aggregate of them) or gene lists producing a correct table. This checking is performed by means of function <code>nice2x2Table</code> .                |
| <code>y</code>           | an object of class "character" representing a list of gene identifiers (e.g., ENTREZ).   |

### Details

This function computes either the normal asymptotic or the bootstrap equivalence test based on the Sorensen-Dice dissimilarity, given a 2x2 arrangement of frequencies (either implemented as a "table", a "matrix" or a "numeric" object):

$$\begin{array}{cc} n_{11} & n_{10} \\ n_{01} & n_{00} \end{array}$$

The subindex '11' corresponds to those GO terms enriched in both lists, '01' to terms enriched in the second list but not in the first one, '10' to terms enriched in the first list but not enriched in the second one and '00' corresponds to those GO terms non enriched in both gene lists, i.e., to the double negatives, a value which is ignored in the computations.

In the "numeric" interface, if `length(x) >= 4`, the values are interpreted as  $(n_{11}, n_{01}, n_{10}, n_{00})$ , always in this order and discarding extra values if necessary.

If `x` is an object of class "character", then `x` (and `y`) must represent two "character" vectors of valid gene identifiers (e.g., ENTREZ). Then the equivalence test is performed between `x` and `y`, after internally summarizing them as a 2x2 contingency table of joint enrichment. This last operation is performed by function `buildEnrichTable` and "valid gene identifiers (e.g., ENTREZ)" stands for the coherency of these gene identifiers with the arguments `geneUniverse` and `orgPackg` of `buildEnrichTable`, passed by the ellipsis argument `...` in `equivTestSorensen`.

If `x` is an object of class "list", each of its elements must be a "character" vector of gene identifiers (e.g., ENTREZ). Then all pairwise equivalence tests are performed between these gene lists.

Class "tableList" corresponds to objects representing all mutual enrichment contingency tables generated in a pairwise fashion: Given gene lists  $l_1, l_2, \dots, l_k$ , an object of class "tableList" (typically

constructed by a call to function `buildEnrichTable`) is a list of lists of contingency tables  $t_{ij}$  generated from each pair of gene lists  $i$  and  $j$ , with the following structure:

```
$l2
$l2$l1$t21
$l3
$l3$l1$t31, $l3$l2$t32
...
$lk$l1$t$k1, $lk$l2$t$k2, ..., $lk$l(k-1)t(k-1)
```

If  $x$  is an object of class "tableList", the test is performed over each one of these tables.

The test is based on the fact that the studentized statistic  $(\hat{d} - d) / \hat{se}$  is approximately distributed as a standard normal.  $\hat{d}$  stands for the sample Sorensen-Dice dissimilarity,  $d$  for its true (unknown) value and  $\hat{se}$  for the estimate of its standard error. This result is asymptotically correct, but the true distribution of the studentized statistic is not exactly normal for finite samples, with a heavier left tail than expected under the Gaussian model, which may produce some type I error inflation. The bootstrap method provides a better approximation to this distribution. In the bootstrap approach, `nboot` new bootstrap contingency tables are generated from a multinomial distribution with parameters  $size = n = (n_{11} + n_{01} + n_{10} + n_{00})$  and probabilities  $(n_{11}/n, n_{01}/n, n_{10}/n, n_{00}/n)$ . Sometimes, some of these generated tables may present so low frequencies of enrichment that make them unable for Sorensen-Dice computations. As a consequence, the number of effective bootstrap samples may be lower than the number of initially planned ones, `nboot`, but our simulation studies concluded that this makes the test more conservative, less prone to reject a truly false null hypothesis of inequivalence, but in any case protects from inflating the type I error.

In a bootstrap test result, use `getNboot` to access the number of initially planned bootstrap replicates and `getEffNboot` to access the number of finally effective bootstrap replicates.

## Value

For all interfaces (except for the "list" and "tableList" interfaces) the result is a list of class "equivSDhtest" which inherits from "htest", with the following components:

- statistic** the value of the studentized statistic  $(dSorensen(x) - d0) / seSorensen(x)$
- p.value** the p-value of the test
- conf.int** the one-sided confidence interval  $(0, dUpp]$
- estimate** the Sorensen dissimilarity estimate,  $dSorensen(x)$
- null.value** the value of  $d0$
- stderr** the standard error of the Sorensen dissimilarity estimate,  $seSorensen(x)$ , used as denominator in the studentized statistic
- alternative** a character string describing the alternative hypothesis
- method** a character string describing the test
- data.name** a character string giving the names of the data
- enrichTab** the 2x2 contingency table of joint enrichment whereby the test was based

For the "list" and "tableList" interfaces, the result is an "equivSDhtestList", a list of objects with all pairwise comparisons, each one being an object of "equivSDhtest" class.

**Methods (by class)**

- equivTestSorensen(table): S3 method for class "table"
- equivTestSorensen(matrix): S3 method for class "matrix"
- equivTestSorensen(numeric): S3 method for class "numeric"
- equivTestSorensen(character): S3 method for class "character"
- equivTestSorensen(list): S3 method for class "list"
- equivTestSorensen(tableList): S3 method for class "tableList"

**See Also**

[nice2x2Table](#) for checking and reformatting data, [dSorensen](#) for computing the Sorensen-Dice dissimilarity, [seSorensen](#) for computing the standard error of the dissimilarity, [duppSorensen](#) for the upper limit of a one-sided confidence interval of the dissimilarity. [getTable](#), [getPvalue](#), [getUpper](#), [getSE](#), [getNboot](#) and [getEffNboot](#) for accessing specific fields in the result of these testing functions. [update](#) for updating the result of these testing functions with alternative equivalence limits, confidence levels or to convert a normal result in a bootstrap result or the reverse.

**Examples**

```
# Gene lists 'atlas' and 'sanger' in 'allOncoGeneLists' dataset. Table of joint enrichment
# of GO terms in ontology BP at level 3.
data(tab_atlas.sanger_BP3)
tab_atlas.sanger_BP3
equivTestSorensen(tab_atlas.sanger_BP3)
# Bootstrap test:
equivTestSorensen(tab_atlas.sanger_BP3, boot = TRUE)

# Equivalence tests from scratch, directly from gene lists:
# (These examples may be considerably time consuming due to many enrichment
# tests to build the contingency tables of mutual enrichment)
# data(allOncoGeneLists)
# ?allOncoGeneLists

# Obtaining ENTREZ identifiers for the gene universe of humans:
library(org.Hs.eg.db)
humanEntrezIDs <- keys(org.Hs.eg.db, keytype = "ENTREZID")

# Computing the equivalence test:
# equivTestSorensen(allOncoGeneLists$atlas, allOncoGeneLists$sanger,
#                   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#                   onto = "BP", GOLevel = 3)
# Bootstrap instead of normal approximation test:
# equivTestSorensen(allOncoGeneLists$atlas, allOncoGeneLists$sanger,
#                   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#                   onto = "BP", GOLevel = 3,
#                   boot = TRUE)

# Essentially, the above code makes:
# ctab_atlas.sanger_BP3 <- buildEnrichTable(allOncoGeneLists$atlas, allOncoGeneLists$sanger,
#                                           geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#                                           onto = "BP", GOLevel = 3)
# ctab_atlas.sanger_BP3
# equivTestSorensen(ctab_atlas.sanger_BP3)
# equivTestSorensen(ctab_atlas.sanger_BP3, boot = TRUE)
```

```

# (Note that building first the contingency table may be advantageous to save time!)
# The object tab_atlas.sanger_BP3 and ctab_atlas.sanger_BP3 are exactly the same

# All pairwise equivalence tests:
# equivTestSorensen(allOncoGeneLists,
#                   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#                   onto = "BP", GOLevel = 3)

# Equivalence test on a contingency table represented as a numeric vector:
equivTestSorensen(c(56, 1, 30, 47))
equivTestSorensen(c(56, 1, 30, 47), boot = TRUE)
equivTestSorensen(c(56, 1, 30))
# Error: all frequencies are needed for bootstrap:
try(equivTestSorensen(c(56, 1, 30), boot = TRUE), TRUE)

```

---

|                  |  |
|------------------|--|
| getDissimilarity | <i>Access to the estimated Sorensen-Dice dissimilarity in one or more equivalence test results</i> |
|------------------|--|

---

## Description

Given objects representing the result(s) of one or more equivalence tests (classes "equivSDhtest", "equivSDhtestList" or "allEquivSDtest", i.e., the result of functions 'equivTestSorensen' and 'allEquivTestSorensen') this function returns the estimated dissimilarities in the tests.

## Usage

```

getDissimilarity(x, ...)

## S3 method for class 'equivSDhtest'
getDissimilarity(x, ...)

## S3 method for class 'equivSDhtestList'
getDissimilarity(x, simplify = TRUE, ...)

## S3 method for class 'AllEquivSDhtest'
getDissimilarity(x, onto, GOLevel, listNames, simplify = TRUE, ...)

```

## Arguments

|           |  |
|-----------|--|
| x         | an object of class "equivSDhtest" or "equivSDhtestList" or "allEquivSDtest".                                   |
| ...       | Additional parameters.   |
| simplify  | logical, if TRUE the result is simplified, e.g., returning a vector instead of a matrix.                       |
| onto      | character, a vector with one or more of "BP", "CC" or "MF", ontologies to access.                              |
| GOLevel   | numeric or character, a vector with one or more GO levels to access. See the details section and the examples. |
| listNames | character(2), the names of a pair of gene lists.   |

## Details

Argument `GOlevel` can be of class "character" or "numeric". In the first case, the GO levels must be specified like "level 6" or `c("level 4", "level 5", "level 6")`. In the second case ("numeric"), the GO levels must be specified like `6` or `seq.int(4, 6)`.

## Value

When `x` is an object of class "equivSDhtest" (i.e., the result of a single equivalence test), the returned value is a single numeric value, the Sorensen-Dice dissimilarity. For an object of class "equivSDhtestList" (i.e. all pairwise tests for a set of gene lists), if `simplify = TRUE` (the default), the resulting value is a vector with the dissimilarities in all those tests, or the symmetric matrix of all dissimilarities if `simplify = FALSE`. If `x` is an object of class "allEquivSDhtest" (i.e., the test iterated along GO ontologies and levels), the preceding result is returned in the form of a list along the ontologies, levels and pairs of gene lists specified by the arguments `onto`, `GOlevel` and `listNames` (or all present in `x` for missing arguments).

## Methods (by class)

- `getDissimilarity(equivSDhtest)`: S3 method for class "equivSDhtest"
- `getDissimilarity(equivSDhtestList)`: S3 method for class "equivSDhtestList"
- `getDissimilarity(AllEquivSDhtest)`: S3 method for class "AllEquivSDhtest"

## Examples

```
# Dataset 'allOncoGeneLists' contains the result of the equivalence test between gene lists
# 'waldman' and 'atlas', at level 4 of the BP ontology:
data(waldman_atlas.BP.4)
waldman_atlas.BP.4
class(waldman_atlas.BP.4)
# This may correspond to the result of code like:
# waldman_atlas.BP.4 <- equivTestSorensen(
#   allOncoGeneLists[["waldman"]], allOncoGeneLists[["atlas"]],
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOlevel = 4, listNames = c("waldman", "atlas"))
# (But results may vary according to GO updating)
getDissimilarity(waldman_atlas.BP.4)

# All pairwise equivalence tests at level 4 of the BP ontology:
data(BP.4)
?BP.4
class(BP.4)
# This may correspond to a call like:
# BP.4 <- equivTestSorensen(allOncoGeneLists,
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOlevel = 4)
getDissimilarity(BP.4)
getDissimilarity(BP.4, simplify = FALSE)

# Equivalence test iterated over all GO ontologies and levels 3 to 10:
data(cancerEquivSorensen)
?cancerEquivSorensen
class(cancerEquivSorensen)
# This may correspond to code like:
# (By default, the tests are iterated over all GO ontologies and for levels 3 to 10)
# cancerEquivSorensen <- allEquivTestSorensen(allOncoGeneLists,
```



```

#                                     geneUniverse = humanEntrezIDs,
#                                     orgPackg = "org.Hs.eg.db")
# All Sorensen-Dice dissimilarities:
getDissimilarity(cancerEquivSorensen)
getDissimilarity(cancerEquivSorensen, simplify = FALSE)

# Dissimilarities only for some GO ontologies, levels or pairs of gene lists:
getDissimilarity(cancerEquivSorensen, GOLevel = "level 6")
getDissimilarity(cancerEquivSorensen, GOLevel = 6)
getDissimilarity(cancerEquivSorensen, GOLevel = seq.int(4,6))
getDissimilarity(cancerEquivSorensen, GOLevel = "level 6", simplify = FALSE)
getDissimilarity(cancerEquivSorensen, GOLevel = "level 6", listNames = c("waldman", "sanger"))
getDissimilarity(cancerEquivSorensen, GOLevel = seq.int(4,6), onto = "BP")
getDissimilarity(cancerEquivSorensen, GOLevel = seq.int(4,6), onto = "BP", simplify = FALSE)
getDissimilarity(cancerEquivSorensen, GOLevel = "level 6", onto = "BP",
                 listNames = c("waldman", "sanger"))
getDissimilarity(cancerEquivSorensen$BP$`level 4`)

```

---

getEffNboot

*Access to the number of effective bootstrap replicates in one or more equivalence test results (only for their bootstrap version)*

---

## Description

Given objects representing the result(s) of one or more equivalence tests (classes "equivSDhtest", "equivSDhtestList" or "allEquivSDtest", i.e., the result of functions 'equivTestSorensen' and 'allEquivTestSorensen'), this function returns the number of effective bootstrap replicates. Obviously, this only applies to calls of these functions with the parameter `boot = TRUE`, otherwise it returns a NA value. See the details section for further explanation.

## Usage

```

getEffNboot(x, ...)

## S3 method for class 'equivSDhtest'
getEffNboot(x, ...)

## S3 method for class 'equivSDhtestList'
getEffNboot(x, simplify = TRUE, ...)

## S3 method for class 'AllEquivSDhtest'
getEffNboot(x, onto, GOLevel, listNames, simplify = TRUE, ...)

```

## Arguments

|                       |  |
|-----------------------|--|
| <code>x</code>        | an object of class "equivSDhtest" or "equivSDhtestList" or "allEquivSDtest".             |
| <code>...</code>      | Additional parameters.   |
| <code>simplify</code> | logical, if TRUE the result is simplified, e.g., returning a vector instead of a matrix. |

|           |  |
|-----------|--|
| onto      | character, a vector with one or more of "BP", "CC" or "MF", ontologies to access.                              |
| GOLevel   | numeric or character, a vector with one or more GO levels to access. See the details section and the examples. |
| listNames | character(2), the names of a pair of gene lists.   |

### Details

In the bootstrap version of the equivalence test, resampling is performed generating new bootstrap contingency tables from a multinomial distribution based on the "real", observed, frequencies of mutual enrichment. In some bootstrap resamples, the generated contingency table of mutual enrichment may have very low frequencies of enrichment, which makes it unable for Sorensen-Dice computations. Then, the number of effective bootstrap resamples may be lower than those initially planned. To get the number of initially planned bootstrap resamples use function `getNboot`.

Argument `GOLevel` can be of class "character" or "numeric". In the first case, the GO levels must be specified like "level 6" or `c("level 4", "level 5", "level 6")` In the second case ("numeric"), the GO levels must be specified like `6` or `seq.int(4,6)`.

### Value

When `x` is an object of class "equivSDhtest" (i.e., the result of a single equivalence test), the returned value is a single numeric value, the number of effective bootstrap replicates, or NA if bootstrapping has not been performed. For an object of class "equivSDhtestList" (i.e. all pairwise tests for a set of gene lists), if `simplify = TRUE` (the default), the resulting value is a vector with the number of effective bootstrap replicates in all those tests, or the symmetric matrix of all these values if `simplify = FALSE`. If `x` is an object of class "allEquivSDhtest" (i.e., the test iterated along GO ontologies and levels), the preceding result is returned in the form of a list along the ontologies, levels and pairs of gene lists specified by the arguments `onto`, `GOlevel` and `listNames` (or all present in `x` for missing arguments).

### Methods (by class)

- `getEffNboot(equivSDhtest)`: S3 method for class "equivSDhtest"
- `getEffNboot(equivSDhtestList)`: S3 method for class "equivSDhtestList"
- `getEffNboot(AllEquivSDhtest)`: S3 method for class "AllEquivSDhtest"

### See Also

[getNboot](#)

### Examples

```
# Dataset 'allOncoGeneLists' contains the result of the equivalence test between gene lists
# 'waldman' and 'atlas', at level 4 of the BP ontology:
data(waldman_atlas.BP.4)
waldman_atlas.BP.4
class(waldman_atlas.BP.4)
# This may correspond to the result of code like:
# waldman_atlas.BP.4 <- equivTestSorensen(
#   allOncoGeneLists[["waldman"]], allOncoGeneLists[["atlas"]],
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOLevel = 4, listNames = c("waldman", "atlas"))
#
```

```

# (But results may vary according to GO updating)

# Not a bootstrap test, first upgrade to a bootstrap test:
boot.waldman_atlas.BP.4 <- upgrade(waldman_atlas.BP.4, boot = TRUE)

getEffNboot(waldman_atlas.BP.4)
getEffNboot(boot.waldman_atlas.BP.4)
getNboot(boot.waldman_atlas.BP.4)

# All pairwise equivalence tests at level 4 of the BP ontology
data(BP.4)
?BP.4
class(BP.4)
# This may correspond to a call like:
# BP.4 <- equivTestSorensen(allOncoGeneLists,
#                           geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#                           onto = "BP", GOLevel = 4)
boot.BP.4 <- upgrade(BP.4, boot = TRUE)
getEffNboot(BP.4)
getEffNboot(boot.BP.4)
getNboot(boot.BP.4)
getEffNboot(boot.BP.4, simplify = FALSE)

# Bootstrap equivalence test iterated over all GO ontologies and levels 3 to 10.
# data(cancerEquivSorensen)
# ?cancerEquivSorensen
# class(cancerEquivSorensen)
# This may correspond to code like:
# (By default, the tests are iterated over all GO ontologies and for levels 3 to 10)
# cancerEquivSorensen <- allEquivTestSorensen(allOncoGeneLists,
#                                             geneUniverse = humanEntrezIDs,
#                                             orgPackg = "org.Hs.eg.db",
#                                             boot = TRUE)
# boot.cancerEquivSorensen <- upgrade(cancerEquivSorensen, boot = TRUE)
# Number of effective bootstrap replicates for all tests:
# getEffNboot(boot.cancerEquivSorensen)
# getEffNboot(boot.cancerEquivSorensen, simplify = FALSE)

# Number of effective bootstrap replicates for specific GO ontologies, levels or pairs
# of gene lists:
# getEffNboot(boot.cancerEquivSorensen, GOLevel = "level 6")
# getEffNboot(boot.cancerEquivSorensen, GOLevel = 6)
# getEffNboot(boot.cancerEquivSorensen, GOLevel = seq.int(4,6))
# getEffNboot(boot.cancerEquivSorensen, GOLevel = "level 6", simplify = FALSE)
# getEffNboot(boot.cancerEquivSorensen, GOLevel = "level 6", listNames = c("waldman", "sanger"))
# getEffNboot(boot.cancerEquivSorensen, GOLevel = seq.int(4,6), onto = "BP")
# getEffNboot(boot.cancerEquivSorensen, GOLevel = seq.int(4,6), onto = "BP", simplify = FALSE)
# getEffNboot(boot.cancerEquivSorensen, GOLevel = "level 6", onto = "BP",
#             listNames = c("waldman", "sanger"))
# getEffNboot(boot.cancerEquivSorensen$BP$`level 4`)

```

---

getNboot

*Access to the number of initially planned bootstrap replicates in one or more equivalence test results (only in their bootstrap version)*

---

## Description

Given objects representing the result(s) of one or more equivalence tests (classes "equivSDhtest", "equivSDhtestList" or "allEquivSDtest", i.e., the result of functions 'equivTestSorensen' and 'allEquivTestSorensen' with the parameter boot = TRUE), this function returns the number of initially planned bootstrap replicates in these equivalence tests, which may be greater than the number of finally effective or valid bootstrap replicates. See the details section for more information on this.

## Usage

```
getNboot(x, ...)
```

```
## S3 method for class 'equivSDhtest'
getNboot(x, ...)
```

```
## S3 method for class 'equivSDhtestList'
getNboot(x, simplify = TRUE, ...)
```

```
## S3 method for class 'AllEquivSDhtest'
getNboot(x, onto, GOLevel, listNames, simplify = TRUE, ...)
```

## Arguments

|           |  |
|-----------|--|
| x         | an object of class "equivSDhtest" or "equivSDhtestList" or "allEquivSDtest".                                   |
| ...       | Additional parameters.   |
| simplify  | logical, if TRUE the result is simplified, e.g., returning a vector instead of a matrix.                       |
| onto      | character, a vector with one or more of "BP", "CC" or "MF", ontologies to access.                              |
| GOLevel   | numeric or character, a vector with one or more GO levels to access. See the details section and the examples. |
| listNames | character(2), the names of a pair of gene lists.   |

## Details

In the bootstrap version of the equivalence test, resampling is performed generating new bootstrap contingency tables from a multinomial distribution based on the "real", observed, frequencies of mutual enrichment. In some bootstrap iterations, the generated contingency table of mutual enrichment may have very low frequencies of enrichment, which makes it unable for Sorensen-Dice computations. Then, the number of effective bootstrap resamples may be lower than those initially planned. To get the number of effective bootstrap resamples use function getEffNboot.

Argument GOLevel can be of class "character" or "numeric". In the first case, the GO levels must be specified like "level 6" or c("level 4", "level 5", "level 6") In the second case ("numeric"), the GO levels must be specified like 6 or seq.int(4, 6).

## Value

When x is an object of class "equivSDhtest" (i.e., the result of a single equivalence test), the returned value is a single numeric value, the number of initially planned bootstrap replicates, or NA if bootstrapping has not been performed. For an object of class "equivSDhtestList" (i.e. all pairwise tests for a set of gene lists), if simplify = TRUE (the default), the resulting value is a vector with the number of initially bootstrap replicates in all those tests, or the symmetric matrix of all these values

if `simplify = TRUE`. If `x` is an object of class "allEquivSDtest" (i.e., the test iterated along GO ontologies and levels), the preceding result is returned in the form of a list along the ontologies, levels and pairs of gene lists specified by the arguments `onto`, `GOlevel` and `listNames` (or all present in `x` for missing arguments).

### Methods (by class)

- `getNboot(equivSDtest)`: S3 method for class "equivSDtest"
- `getNboot(equivSDtestList)`: S3 method for class "equivSDtestList"
- `getNboot(AllEquivSDtest)`: S3 method for class "AllEquivSDtest"

### See Also

[getEffNboot](#)

### Examples

```
# Dataset 'allOncoGeneLists' contains the result of the equivalence test between gene lists
# 'waldman' and 'atlas', at level 4 of the BP ontology:
data(waldman_atlas.BP.4)
waldman_atlas.BP.4
class(waldman_atlas.BP.4)
# This may correspond to the result of code like:
# waldman_atlas.BP.4 <- equivTestSorensen(
#   allOncoGeneLists[["waldman"]], allOncoGeneLists[["atlas"]],
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOlevel = 4, listNames = c("waldman", "atlas"))
#
# (But results may vary according to GO updating)

# Not a bootstrap test, first upgrade to a bootstrap test:
boot.waldman_atlas.BP.4 <- upgrade(waldman_atlas.BP.4, boot = TRUE)

getNboot(waldman_atlas.BP.4)
getNboot(boot.waldman_atlas.BP.4)

# All pairwise equivalence tests at level 4 of the BP ontology
data(BP.4)
?BP.4
class(BP.4)
# This may correspond to a call like:
# BP.4 <- equivTestSorensen(allOncoGeneLists,
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOlevel = 4)
boot.BP.4 <- upgrade(BP.4, boot = TRUE)
getNboot(BP.4)
getNboot(boot.BP.4)
getNboot(boot.BP.4, simplify = FALSE)

# Bootstrap equivalence test iterated over all GO ontologies and levels 3 to 10.
# data(cancerEquivSorensen)
# ?cancerEquivSorensen
# class(cancerEquivSorensen)
# This may correspond to code like:
# (By default, the tests are iterated over all GO ontologies and for levels 3 to 10)
# cancerEquivSorensen <- allEquivTestSorensen(allOncoGeneLists,
```

```

#                                     geneUniverse = humanEntrezIDs,
#                                     orgPackg = "org.Hs.eg.db",
#                                     boot = TRUE)
# boot.cancerEquivSorensen <- upgrade(cancerEquivSorensen, boot = TRUE)
# All numbers of bootstrap replicates:
# getNboot(boot.cancerEquivSorensen)
# getNboot(boot.cancerEquivSorensen, simplify = FALSE)

# Number of bootstrap replicates for specific GO ontologies, levels or pairs of gene lists:
# getNboot(boot.cancerEquivSorensen, GOLevel = "level 6")
# getNboot(boot.cancerEquivSorensen, GOLevel = 6)
# getNboot(boot.cancerEquivSorensen, GOLevel = seq.int(4,6))
# getNboot(boot.cancerEquivSorensen, GOLevel = "level 6", simplify = FALSE)
# getNboot(boot.cancerEquivSorensen, GOLevel = "level 6", listNames = c("waldman", "sanger"))
# getNboot(boot.cancerEquivSorensen, GOLevel = seq.int(4,6), onto = "BP")
# getNboot(boot.cancerEquivSorensen, GOLevel = seq.int(4,6), onto = "BP", simplify = FALSE)
# getNboot(boot.cancerEquivSorensen, GOLevel = "level 6", onto = "BP",
#         listNames = c("waldman", "sanger"))
# getNboot(boot.cancerEquivSorensen$BP$`level 4`)

```

---

getPvalue

*Access to the p-value of one or more equivalence test results*


---

### Description

Given objects representing the result(s) of one or more equivalence tests (classes "equivSDhtest", "equivSDhtestList" or "allEquivSDtest", i.e., the result of functions 'equivTestSorensen' and 'allEquivTestSorensen') this function returns the p-values of the tests.

### Usage

```

getPvalue(x, ...)

## S3 method for class 'equivSDhtest'
getPvalue(x, ...)

## S3 method for class 'equivSDhtestList'
getPvalue(x, simplify = TRUE, ...)

## S3 method for class 'AllEquivSDhtest'
getPvalue(x, onto, GOLevel, listNames, simplify = TRUE, ...)

```

### Arguments

|          |  |
|----------|--|
| x        | an object of class "equivSDhtest" or "equivSDhtestList" or "allEquivSDtest".             |
| ...      | Additional parameters.   |
| simplify | logical, if TRUE the result is simplified, e.g., returning a vector instead of a matrix. |
| onto     | character, a vector with one or more of "BP", "CC" or "MF", ontologies to access.        |

|           |  |
|-----------|--|
| GOlevel   | numeric or character, a vector with one or more GO levels to access. See the details section and the examples. |
| listNames | character(2), the names of a pair of gene lists.   |

### Details

Argument GOlevel can be of class "character" or "numeric". In the first case, the GO levels must be specified like "level 6" or c("level 4", "level 5", "level 6") In the second case ("numeric"), the GO levels must be specified like 6 or seq.int(4, 6).

### Value

When x is an object of class "equivSDhtest" (i.e., the result of a single equivalence test), the returned value is a single numeric value, the test p-value. For an object of class "equivSDhtestList" (i.e. all pairwise tests for a set of gene lists), if simplify = TRUE (the default), the resulting value is a vector with the p-values in all those tests, or the symmetric matrix of all p-values if simplify = FALSE. If x is an object of class "allEquivSDhtest" (i.e., the test iterated along GO ontologies and levels), the preceding result is returned in the form of a list along the ontologies, levels and pairs of gene lists specified by the arguments onto, GOlevel and listNames (or all present in x for missing arguments).

### Methods (by class)

- getPvalue(equivSDhtest): S3 method for class "equivSDhtest"
- getPvalue(equivSDhtestList): S3 method for class "equivSDhtestList"
- getPvalue(AllEquivSDhtest): S3 method for class "AllEquivSDhtest"

### Examples

```
# Dataset 'allOncoGeneLists' contains the result of the equivalence test between gene lists
# 'waldman' and 'atlas', at level 4 of the BP ontology:
data(waldman_atlas.BP.4)
waldman_atlas.BP.4
class(waldman_atlas.BP.4)
# This may correspond to the result of code like:
# waldman_atlas.BP.4 <- equivTestSorensen(
#   allOncoGeneLists[["waldman"]], allOncoGeneLists[["atlas"]],
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOlevel = 4, listNames = c("waldman", "atlas"))
# (But results may vary according to GO updating)
getPvalue(waldman_atlas.BP.4)

# All pairwise equivalence tests at level 4 of the BP ontology
data(BP.4)
?BP.4
class(BP.4)
# This may correspond to a call like:
# BP.4 <- equivTestSorensen(allOncoGeneLists,
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOlevel = 4)
getPvalue(BP.4)
getPvalue(BP.4, simplify = FALSE)

# Equivalence test iterated over all GO ontologies and levels 3 to 10:
data(cancerEquivSorensen)
```

```
?cancerEquivSorensen
class(cancerEquivSorensen)
# This may correspond to code like:
# (By default, the tests are iterated over all GO ontologies and for levels 3 to 10)
# cancerEquivSorensen <- allEquivTestSorensen(allOncoGeneLists,
#                                           geneUniverse = humanEntrezIDs,
#                                           orgPackg = "org.Hs.eg.db")
# All p-values:
getPvalue(cancerEquivSorensen)
getPvalue(cancerEquivSorensen, simplify = FALSE)

# P-values only for some GO ontologies, levels or pairs of gene lists:
getPvalue(cancerEquivSorensen, GOLevel = "level 6")
getPvalue(cancerEquivSorensen, GOLevel = 6)
getPvalue(cancerEquivSorensen, GOLevel = seq.int(4,6))
getPvalue(cancerEquivSorensen, GOLevel = "level 6", simplify = FALSE)
getPvalue(cancerEquivSorensen, GOLevel = "level 6", listNames = c("waldman", "sanger"))
getPvalue(cancerEquivSorensen, GOLevel = seq.int(4,6), onto = "BP")
getPvalue(cancerEquivSorensen, GOLevel = seq.int(4,6), onto = "BP", simplify = FALSE)
getPvalue(cancerEquivSorensen, GOLevel = "level 6", onto = "BP",
          listNames = c("waldman", "sanger"))
getPvalue(cancerEquivSorensen$BP$`level 4`)
```

---

getSE

*Access to the estimated standard error of the sample Sorensen-Dice dissimilarity in one or more equivalence test results*


---

### Description

Given objects representing the result(s) of one or more equivalence tests (classes "equivSDhtest", "equivSDhtestList" or "allEquivSDtest", i.e., the result of functions 'equivTestSorensen' and 'allEquivTestSorensen') this function returns the estimated standard errors of the sample dissimilarities in the tests.

### Usage

```
getSE(x, ...)

## S3 method for class 'equivSDhtest'
getSE(x, ...)

## S3 method for class 'equivSDhtestList'
getSE(x, simplify = TRUE, ...)

## S3 method for class 'AllEquivSDhtest'
getSE(x, onto, GOLevel, listNames, simplify = TRUE, ...)
```

### Arguments

x                    an object of class "equivSDhtest" or "equivSDhtestList" or "allEquivSDtest".  
...                    additional parameters.



|           |  |
|-----------|--|
| simplify  | logical, if TRUE the result is simplified, e.g., returning a vector instead of a matrix.                       |
| onto      | character, a vector with one or more of "BP", "CC" or "MF", ontologies to access.                              |
| GOlevel   | numeric or character, a vector with one or more GO levels to access. See the details section and the examples. |
| listNames | character(2), the names of a pair of gene lists.   |

### Details

Argument `GOlevel` can be of class "character" or "numeric". In the first case, the GO levels must be specified like "level 6" or `c("level 4", "level 5", "level 6")`. In the second case ("numeric"), the GO levels must be specified like `6` or `seq.int(4, 6)`.

### Value

When `x` is an object of class "equivSDhtest" (i.e., the result of a single equivalence test), the returned value is a single numeric value, the standard error of the Sorensen-Dice dissimilarity estimate. For an object of class "equivSDhtestList" (i.e. all pairwise tests for a set of gene lists), if `simplify = TRUE` (the default), the resulting value is a vector with the dissimilarity standard errors in all those tests, or the symmetric matrix of all these values if `simplify = FALSE`. If `x` is an object of class "allEquivSDhtest" (i.e., the test iterated along GO ontologies and levels), the preceding result is returned in the form of a list along the ontologies, levels and pairs of gene lists specified by the arguments `onto`, `GOlevel` and `listNames` (or all present in `x` for missing arguments).

### Methods (by class)

- `getSE(equivSDhtest)`: S3 method for class "equivSDhtest"
- `getSE(equivSDhtestList)`: S3 method for class "equivSDhtestList"
- `getSE(AllEquivSDhtest)`: S3 method for class "AllEquivSDhtest"

### Examples

```
# Dataset 'allOncoGeneLists' contains the result of the equivalence test between gene lists
# 'waldman' and 'atlas', at level 4 of the BP ontology:
data(waldman_atlas.BP.4)
waldman_atlas.BP.4
class(waldman_atlas.BP.4)
# This may correspond to the result of code like:
# waldman_atlas.BP.4 <- equivTestSorensen(
#   allOncoGeneLists[["waldman"]], allOncoGeneLists[["atlas"]],
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOlevel = 4, listNames = c("waldman", "atlas"))
# (But results may vary according to GO updating)
getSE(waldman_atlas.BP.4)

# All pairwise equivalence tests at level 4 of the BP ontology:
data(BP.4)
?BP.4
class(BP.4)
# This may correspond to a call like:
# BP.4 <- equivTestSorensen(allOncoGeneLists,
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOlevel = 4)
```

```

getSE(BP.4)
getSE(BP.4, simplify = FALSE)

# Equivalence test iterated over all GO ontologies and levels 3 to 10:
data(cancerEquivSorensen)
?cancerEquivSorensen
class(cancerEquivSorensen)
# This may correspond to code like:
# (By default, the tests are iterated over all GO ontologies and for levels 3 to 10)
# cancerEquivSorensen <- allEquivTestSorensen(allOncoGenelists,
#                                           geneUniverse = humanEntrezIDs,
#                                           orgPackg = "org.Hs.eg.db")
# All standard errors of the Sorensen-Dice dissimilarity estimates:
getSE(cancerEquivSorensen)
getSE(cancerEquivSorensen, simplify = FALSE)

# Standard errors for some GO ontologies, levels or pairs of gene lists:
getSE(cancerEquivSorensen, GOLevel = "level 6")
getSE(cancerEquivSorensen, GOLevel = 6)
getSE(cancerEquivSorensen, GOLevel = seq.int(4,6))
getSE(cancerEquivSorensen, GOLevel = "level 6", simplify = FALSE)
getSE(cancerEquivSorensen, GOLevel = "level 6", listNames = c("waldman", "sanger"))
getSE(cancerEquivSorensen, GOLevel = seq.int(4,6), onto = "BP")
getSE(cancerEquivSorensen, GOLevel = seq.int(4,6), onto = "BP", simplify = FALSE)
getSE(cancerEquivSorensen, GOLevel = "level 6", onto = "BP",
      listNames = c("waldman", "sanger"))
getSE(cancerEquivSorensen$BP$`level 4`)

```

---

|          |   |
|----------|---|
| getTable | <i>Access to the contingency table of mutual enrichment of one or more equivalence test results</i> |
|----------|---|

---

## Description

Given objects representing the result(s) of one or more equivalence tests (classes "equivSDhtest", "equivSDhtestList" or "allEquivSDtest", i.e., the result of functions 'equivTestSorensen' and 'allEquivTestSorensen') this function returns the contingency tables from which the tests were performed.

## Usage

```

getTable(x, ...)

## S3 method for class 'equivSDhtest'
getTable(x, ...)

## S3 method for class 'equivSDhtestList'
getTable(x, ...)

## S3 method for class 'AllEquivSDhtest'
getTable(x, onto, GOLevel, listNames, ...)

```

**Arguments**

|           |  |
|-----------|--|
| x         | an object of class "equivSDhtest" or "equivSDhtestList" or "allEquivSDtest".                                   |
| ...       | Additional parameters.   |
| onto      | character, a vector with one or more of "BP", "CC" or "MF", ontologies to access.                              |
| GOlevel   | numeric or character, a vector with one or more GO levels to access. See the details section and the examples. |
| listNames | character(2), the names of a pair of gene lists.   |

**Details**

Argument `GOlevel` can be of class "character" or "numeric". In the first case, the GO levels must be specified like "level 6" or `c("level 4", "level 5", "level 6")`. In the second case ("numeric"), the GO levels must be specified like `6` or `4:6`.

**Value**

An object of class "table", the 2x2 enrichment contingency table of mutual enrichment in two gene lists, built to perform the equivalence test based on the Sorensen-Dice dissimilarity.

When `x` is an object of class "equivSDhtest" (i.e., the result of a single equivalence test), the returned value is an object of class "table", the 2x2 enrichment contingency table of mutual enrichment in two gene lists, built to perform the equivalence test based on the Sorensen-Dice dissimilarity. For an object of class "equivSDhtestList" (i.e. all pairwise tests for a set of gene lists), the resulting value is a list with all the tables built in all those tests. If `x` is an object of class "allEquivSDtest" (i.e., the test iterated along GO ontologies and levels), the preceding result is returned as a list along the ontologies, levels and pairs of gene lists specified by the arguments `onto`, `GOlevel` and `listNames` (or all ontologies, levels or pairs of gene lists present in `x` if one or more of these arguments are missing).

**Methods (by class)**

- `getTable(equivSDhtest)`: S3 method for class "equivSDhtest"
- `getTable(equivSDhtestList)`: S3 method for class "equivSDhtestList"
- `getTable(AllEquivSDhtest)`: S3 method for class "AllEquivSDhtest"

**Examples**

```
# Dataset 'allOncoGeneLists' contains the result of the equivalence test between gene lists
# 'waldman' and 'atlas', at level 4 of the BP ontology:
data(waldman_atlas.BP.4)
waldman_atlas.BP.4
class(waldman_atlas.BP.4)
# This may correspond to the result of code like:
# waldman_atlas.BP.4 <- equivTestSorensen(
#   allOncoGeneLists[["waldman"]], allOncoGeneLists[["atlas"]],
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOlevel = 4, listNames = c("waldman", "atlas"))
# (But results may vary according to GO updating)
getTable(waldman_atlas.BP.4)

# All pairwise equivalence tests at level 4 of the BP ontology
data(BP.4)
```

```

?BP.4
class(BP.4)
# This may correspond to a call like:
# BP.4 <- equivTestSorensen(allOncoGeneLists,
#                           geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#                           onto = "BP", GOLevel = 4)
getTable(BP.4)

# Equivalence test iterated over all GO ontologies and levels 3 to 10:
data(cancerEquivSorensen)
?cancerEquivSorensen
class(cancerEquivSorensen)
# This may correspond to code like:
# cancerEquivSorensen <- allEquivTestSorensen(allOncoGeneLists,
#                                             geneUniverse = humanEntrezIDs,
#                                             orgPackg = "org.Hs.eg.db")
# (By default, the tests are iterated over all GO ontologies and for levels 3 to 10)
# All 2x2 contingency tables of joint enrichment:
getTable(cancerEquivSorensen)
# Contingency tables only for some GO ontologies, levels or pairs of gene lists:
getTable(cancerEquivSorensen, GOLevel = "level 6")
getTable(cancerEquivSorensen, GOLevel = 6)
getTable(cancerEquivSorensen, GOLevel = seq.int(4,6), listNames = c("waldman", "sanger"))
getTable(cancerEquivSorensen, GOLevel = "level 6", onto = "BP")
getTable(cancerEquivSorensen, GOLevel = "level 6", onto = "BP",
        listNames = c("waldman", "sanger"))

```

---

getUpper

*Access to the upper limit of the one-sided confidence intervals for the Sorensen-Dice dissimilarity in one or more equivalence test results*

---

## Description

Given objects representing the result(s) of one or more equivalence tests (classes "equivSDhtest", "equivSDhtestList" or "allEquivSDhtest", i.e., the result of functions 'equivTestSorensen' and 'allEquivTestSorensen') this function returns the upper limits of the one-sided confidence intervals [0, dU] for the Sorensen-Dice dissimilarity.

## Usage

```

getUpper(x, ...)

## S3 method for class 'equivSDhtest'
getUpper(x, ...)

## S3 method for class 'equivSDhtestList'
getUpper(x, simplify = TRUE, ...)

## S3 method for class 'AllEquivSDhtest'
getUpper(x, onto, GOLevel, listNames, simplify = TRUE, ...)

```

**Arguments**

|           |  |
|-----------|--|
| x         | an object of class "equivSDhstest" or "equivSDhstestList" or "allEquivSDtest".                                 |
| ...       | Additional parameters.   |
| simplify  | logical, if TRUE the result is simplified, e.g., returning a vector instead of a matrix.                       |
| onto      | character, a vector with one or more of "BP", "CC" or "MF", ontologies to access.                              |
| GOlevel   | numeric or character, a vector with one or more GO levels to access. See the details section and the examples. |
| listNames | character(2), the names of a pair of gene lists.   |

**Details**

Argument `GOlevel` can be of class "character" or "numeric". In the first case, the GO levels must be specified like "level 6" or `c("level 4", "level 5", "level 6")`. In the second case ("numeric"), the GO levels must be specified like `6` or `seq.int(4, 6)`.

**Value**

A numeric value, the upper limit of the one-sided confidence interval for the Sorensen-Dice dissimilarity.

When `x` is an object of class "equivSDhstest" (i.e., the result of a single equivalence test), the returned value is a single numeric value, the upper limit of the one-sided confidence interval for the Sorensen-Dice dissimilarity. For an object of class "equivSDhstestList" (i.e. all pairwise tests for a set of gene lists), if `simplify = TRUE` (the default), the resulting value is a vector with the upper limit of the one-sided confidence intervals in all those tests, or the symmetric matrix of all these values if `simplify = FALSE`. If `x` is an object of class "allEquivSDtest" (i.e., the test iterated along GO ontologies and levels), the preceding result is returned in the form of a list along the ontologies, levels and pairs of gene lists specified by the arguments `onto`, `GOlevel` and `listNames` (or all present in `x` for missing arguments).

**Methods (by class)**

- `getUpper(equivSDhstest)`: S3 method for class "equivSDhstest"
- `getUpper(equivSDhstestList)`: S3 method for class "equivSDhstestList"
- `getUpper(AllEquivSDhstest)`: S3 method for class "AllEquivSDhstest"

**Examples**

```
# Dataset 'allOncoGeneLists' contains the result of the equivalence test between gene lists
# 'waldman' and 'atlas', at level 4 of the BP ontology:
data(waldman_atlas.BP.4)
waldman_atlas.BP.4
class(waldman_atlas.BP.4)
# This may correspond to the result of code like:
# waldman_atlas.BP.4 <- equivTestSorensen(
#   allOncoGeneLists[["waldman"]], allOncoGeneLists[["atlas"]],
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOlevel = 4, listNames = c("waldman", "atlas"))
# (But results may vary according to GO updating)
getUpper(waldman_atlas.BP.4)
```

```

# All pairwise equivalence tests at level 4 of the BP ontology:
data(BP.4)
?BP.4
class(BP.4)
# This may correspond to a call like:
# BP.4 <- equivTestSorensen(allOncoGeneLists,
#                           geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#                           onto = "BP", GOLevel = 4)
getUpper(BP.4)
getUpper(BP.4, simplify = FALSE)

# Equivalence test iterated over all GO ontologies and levels 3 to 10:
data(cancerEquivSorensen)
?cancerEquivSorensen
class(cancerEquivSorensen)
# This may correspond to code like:
# (By default, the tests are iterated over all GO ontologies and for levels 3 to 10)
# cancerEquivSorensen <- allEquivTestSorensen(allOncoGeneLists,
#                                             geneUniverse = humanEntrezIDs,
#                                             orgPackg = "org.Hs.eg.db")
# All upper confidence limits for the Sorensen-Dice dissimilarities:
getUpper(cancerEquivSorensen)
getUpper(cancerEquivSorensen, simplify = FALSE)

# Upper confidence limits only for some GO ontologies, levels or pairs of gene lists:
getUpper(cancerEquivSorensen, GOLevel = "level 6")
getUpper(cancerEquivSorensen, GOLevel = 6)
getUpper(cancerEquivSorensen, GOLevel = seq.int(4,6))
getUpper(cancerEquivSorensen, GOLevel = "level 6", simplify = FALSE)
getUpper(cancerEquivSorensen, GOLevel = "level 6", listNames = c("waldman", "sanger"))
getUpper(cancerEquivSorensen, GOLevel = seq.int(4,6), onto = "BP")
getUpper(cancerEquivSorensen, GOLevel = seq.int(4,6), onto = "BP", simplify = FALSE)
getUpper(cancerEquivSorensen, GOLevel = "level 6", onto = "BP",
         listNames = c("waldman", "sanger"))
getUpper(cancerEquivSorensen$BP$`level 4`)

```

---

gosorensen

*gosorensen: A package for making inference on gene lists based on the Sorensen-Dice dissimilarity*

---

## Description

Given two lists of genes, and a set of Gene Ontology (GO) items (e.g., all GO items in a given level of a given GO ontology) one may explore some aspects of their biological meaning by constructing a 2x2 contingency table, the cross-tabulation of: number of these GO items non-enriched in both gene lists (n00), items enriched in the first list but not in the second one (n10), items non-enriched in the first list but enriched in the second (n10) and items enriched in both lists (n11). Then, one may express the degree of similarity or dissimilarity between the two lists by means of an appropriate index computed on these frequency tables of concordance or non-concordance in GO items enrichment. In our opinion, an appropriate index is the Sorensen-Dice index which ignores the double negatives n00: if the total number of candidate GO items under consideration grows (e.g., all items in a deep level of an ontology) likely n00 will also grow artificially. On the other

hand, intuitively the degree of similarity between both lists must be directly related to the degree of concordance in the enrichment,  $n11$ .

## Details

gosorensen package provides the following functions:

- enrichedIn** Build a cross-tabulation of enriched and non-enriched GO terms vs. gene lists
- buildEnrichTable** Build an enrichment contingency table from two or more gene lists
- allBuildEnrichTable** Iterate 'buildEnrichTable' along the specified GO ontologies and GO levels
- nice2x2Table** Check for validity an enrichment contingency table
- dSorensen** Compute the Sorensen-Dice dissimilarity
- seSorensen** Standard error estimate of the sample Sorensen-Dice dissimilarity
- duppSorensen** Upper limit of a one-sided confidence interval (0,dUpp] for the population dissimilarity
- equivTestSorensen** Equivalence test between two gene lists, based on the Sorensen-Dice dissimilarity
- allEquivTestSorensen** Iterate equivTestSorensen along GO ontologies and GO levels
- getDissimilarity, getPvalue, getSE, getTable, getUpper, getNboot, getEffNboot** Accessor functions to some fields of an equivalence test result
- upgrade** Updating the result of an equivalence test, e.g., changing the equivalence limit
- sorenThreshold** For a given level (2, 3, ...) in a GO ontology (BP, MF or CC), compute the equivalence threshold dissimilarity matrix.
- allSorenThreshold** Iterate 'sorenThreshold' along the specified GO ontologies and GO levels.
- hclustThreshold** From a Sorensen-Dice threshold dissimilarity matrix, generate an object of class "hclust"
- allHclustThreshold** Iterate 'hclustThreshold' along the specified GO ontologies and GO levels
- pruneClusts** Remove all NULL or unrepresentable as a dendrogram "equivClustSorensen" elements in an object of class "equivClustSorensenList"

All these functions are generic, adequate for different (S3) classes representing the before cited GO term enrichment cross-tabulations.

---

|                 |  |
|-----------------|--|
| hclustThreshold | <i>From a Sorensen-Dice threshold dissimilarity matrix, generate an object of class "hclust"</i> |
|-----------------|--|

---

## Description

From a Sorensen-Dice threshold dissimilarity matrix, generate an object of class "hclust"

## Usage

```
hclustThreshold(
  x,
  onTheFlyDev = NULL,
  method = "complete",
  jobName = paste("Equivalence cluster", method, sep = "_"),
  ylab = "Sorensen equivalence threshold dissimilarity",
  ...
)
```

**Arguments**

|             |  |
|-------------|--|
| x           | an object of class "dist" with the Sorensen-Dice equivalence threshold dissimilarities matrix  |
| onTheFlyDev | character, name of the graphical device where to immediately display the resulting diagram. The appropriate names depend on the operating system. Defaults to NULL and then nothing is displayed |
| method      | character, one of the admissible methods in function hclust. Defaults to "complete"  |
| jobName     | character, main plot name, defaults to paste("Equivalence cluster", onto, ontoLevel, method, sep = "_")  |
| ylab        | character, label of the vertical axis of the plot, defaults to "Sorensen equivalence threshold dissimilarity"  |
| ...         | additional arguments to hclust   |

**Value**

An object of class equivClustSorensen, descending from class hclust

**Examples**

```
# Gene lists to analyse:
data("allOncoGeneLists")

# Obtaining ENTREZ identifiers for the gene universe of humans:
library(org.Hs.eg.db)
humanEntrezIDs <- keys(org.Hs.eg.db, keytype = "ENTREZID")

# First, compute the Sorensen-Dice threshold equivalence dissimilarity
# for ontology BP at level 4:
# # Very time consuming, it requires building all joint enrichment contingency tables
dOncBP4 <- sorenThreshold(allOncoGeneLists, onto = "BP", GOLevel = 4,
                        geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db")
# Better (much faster), using the previously tabulated contingency tables:
data("allTabsBP.4")
dOncBP4 <- sorenThreshold(allTabsBP.4)
clust.threshold <- hclustThreshold(dOncBP4)
plot(clust.threshold, main = "AllOnco genelists, BP ontology at level 4",
     ylab = "Sorensen equivalence threshold")
# With the same data, an UPGMA dendrogram:
clust.threshold <- hclustThreshold(dOncBP4, method = "average")
plot(clust.threshold, main = "AllOnco genelists, BP ontology at level 4",
     ylab = "Sorensen equivalence threshold")
```

---

nice2x2Table

*Checks for validity data representing an enrichment contingency table generated from two gene lists*

---

**Description**

Checks for validity data representing an enrichment contingency table generated from two gene lists



**Usage**

```
nice2x2Table(x)

## S3 method for class 'table'
nice2x2Table(x)

## S3 method for class 'matrix'
nice2x2Table(x)

## S3 method for class 'numeric'
nice2x2Table(x)
```

**Arguments**

x either an object of class "table", "matrix" or "numeric".

**Details**

In the "table" and "matrix" interfaces, the input parameter x must correspond to a two-dimensional array:

$$\begin{array}{cc} n_{11} & n_{10} \\ n_{01} & n_{00}, \end{array}$$

These values are interpreted (always in this order) as n11: number of GO terms enriched in both lists, n01: GO terms enriched in the second list but not in the first one, n10: terms not enriched in the second list but enriched in the first one and double negatives, n00. The double negatives n00 are ignored in many computations concerning the Sorensen-Dice index.

In the "numeric" interface, the input x must correspond to a numeric of length 3 or more, in the same order as before.

**Value**

boolean, TRUE if x nicely represents a 2x2 contingency table interpretable as the cross-tabulation of the enriched GO terms in two gene lists: "Number of enriched terms in list 1 (TRUE, FALSE)" x "Number of enriched terms in list 2 (TRUE, FALSE)". In this function, "nicely representing a 2x2 contingency table" is interpreted in terms of computing the Sorensen-Dice dissimilarity and associated statistics. Otherwise the execution is interrupted.

**Methods (by class)**

- nice2x2Table(table): S3 method for class "table"
- nice2x2Table(matrix): S3 method for class "matrix"
- nice2x2Table(numeric): S3 method for class "numeric"

**Examples**

```
conti <- as.table(matrix(c(27, 36, 12, 501, 43, 15, 0, 0, 0), nrow = 3, ncol = 3,
                        dimnames = list(c("a1", "a2", "a3"),
                                       c("b1", "b2", "b3"))))
tryCatch(nice2x2Table(conti), error = function(e) {return(e)})
conti2 <- conti[1,seq.int(1, min(2,ncol(conti))), drop = FALSE]
```

```
conti2
tryCatch(nice2x2Table(conti2), error = function(e) {return(e)})

conti3 <- matrix(c(12, 210), ncol = 2, nrow = 1)
conti3
tryCatch(nice2x2Table(conti3), error = function(e) {return(e)})

conti4 <- c(32, 21, 81, 1439)
nice2x2Table(conti4)
conti4.mat <- matrix(conti4, nrow = 2)
conti4.mat
conti5 <- c(32, 21, 81)
nice2x2Table(conti5)

conti6 <- c(-12, 21, 8)
tryCatch(nice2x2Table(conti6), error = function(e) {return(e)})

conti7 <- c(0, 0, 0, 32)
tryCatch(nice2x2Table(conti7), error = function(e) {return(e)})
```

---

pbtGeneLists

*14 gene lists possibly related with kidney transplant rejection*

---

### Description

An object of class "list" of length 14. A non up-to-date subset of the University of Alberta pathogenesis-based transcripts sets (PBTs) that were generated by using Affymetrix Microarrays. Take them just as an illustrative example.

### Usage

```
data(pbtGeneLists)
```

### Format

An object of class "list" of length 5. Each one of its elements is a "character" vector of ENTREZ gene identifiers.

### Source

<https://www.ualberta.ca/medicine/institutes-centres-groups/atagc/research/gene-lists.html>

---

|             |  |
|-------------|--|
| pruneClusts | <i>Remove all NULL or unrepresentable as a dendrogram "equivClustSorensen" elements in an object of class "equivClustSorensenList"</i> |
|-------------|--|

---

### Description

Remove all NULL or unrepresentable as a dendrogram "equivClustSorensen" elements in an object of class "equivClustSorensenList"

### Usage

```
pruneClusts(x)
```

### Arguments

|   |  |
|---|--|
| x | An object of class "equivClustSorensenList" descending from "iterEquivClust" which itself descends from class "list". See the details section. |
|---|--|

### Details

"equivClustSorensenList" objects are lists whose components are one or more of BP, CC or MF, the GO ontologies. Each of these elements is itself a list whose elements correspond to GO levels. Finally, the elements of these lists are objects of class "equivClustSorensen", descending from "equivClust" which itself descends from "hclust".

### Value

An object of class "equivClustSorensenList".

---

|            |  |
|------------|--|
| seSorensen | <i>Standard error of the sample Sorensen-Dice dissimilarity, asymptotic approach</i> |
|------------|--|

---

### Description

Standard error of the sample Sorensen-Dice dissimilarity, asymptotic approach

### Usage

```
seSorensen(x, ...)

## S3 method for class 'table'
seSorensen(x, check.table = TRUE, ...)

## S3 method for class 'matrix'
seSorensen(x, check.table = TRUE, ...)

## S3 method for class 'numeric'
seSorensen(x, check.table = TRUE, ...)
```

```
## S3 method for class 'character'
seSorensen(x, y, check.table = TRUE, ...)

## S3 method for class 'list'
seSorensen(x, check.table = TRUE, ...)

## S3 method for class 'tableList'
seSorensen(x, check.table = TRUE, ...)
```

### Arguments

**x** either an object of class "table", "matrix" or "numeric" representing a 2x2 contingency table, or a "character" (a set of gene identifiers) or "list" or "tableList" object. See the details section for more information.

**...** extra parameters for function `buildEnrichTable`.

**check.table** Boolean. If TRUE (default), argument `x` is checked to adequately represent a 2x2 contingency table. This checking is performed by means of function `nice2x2Table`.

**y** an object of class "character" representing a vector of gene identifiers (e.g., ENTREZ).

### Details

This function computes the standard error estimate of the sample Sorensen-Dice dissimilarity, given a 2x2 arrangement of frequencies (either implemented as a "table", a "matrix" or a "numeric" object):

$$\begin{array}{cc} n_{11} & n_{10} \\ n_{01} & n_{00}, \end{array}$$

The subindex '11' corresponds to those GO terms enriched in both lists, '01' to terms enriched in the second list but not in the first one, '10' to terms enriched in the first list but not enriched in the second one and '00' corresponds to those GO terms non enriched in both gene lists, i.e., to the double negatives, a value which is ignored in the computations.

In the "numeric" interface, if `length(x) >= 3`, the values are interpreted as  $(n_{11}, n_{01}, n_{10})$ , always in this order.

If `x` is an object of class "character", then `x` (and `y`) must represent two "character" vectors of valid gene identifiers (e.g., ENTREZ). Then the standard error for the dissimilarity between lists `x` and `y` is computed, after internally summarizing them as a 2x2 contingency table of joint enrichment. This last operation is performed by function `buildEnrichTable` and "valid gene identifiers (e.g., ENTREZ)" stands for the coherency of these gene identifiers with the arguments `geneUniverse` and `orgPackg` of `buildEnrichTable`, passed by the ellipsis argument `...` in `seSorensen`.

In the "list" interface, the argument must be a list of "character" vectors, each one representing a gene list (character identifiers). Then, all pairwise standard errors of the dissimilarity between these gene lists are computed.

If `x` is an object of class "tableList", the standard error of the Sorensen-Dice dissimilarity estimate is computed over each one of these tables. Given `k` gene lists (i.e. "character" vectors of gene identifiers) `l1, l2, ..., lk`, an object of class "tableList" (typically constructed by a call to function `buildEnrichTable`) is a list of lists of contingency tables  $t(i,j)$  generated from each pair of gene lists `i` and `j`, with the following structure:

```

$12
$12$11$t(2,1)
$13
$13$11$t(3,1), $13$12$t(3,2)
...
$k
$k$11$t(k,1), $k$12$t(k,2), ..., $k$(k-1)t(k,k-1)

```

### Value

In the "table", "matrix", "numeric" and "character" interfaces, the value of the standard error of the Sorensen-Dice dissimilarity estimate. In the "list" and "tableList" interfaces, the symmetric matrix of all standard error dissimilarity estimates.

### Methods (by class)

- `seSorensen(table)`: S3 method for class "table"
- `seSorensen(matrix)`: S3 method for class "matrix"
- `seSorensen(numeric)`: S3 method for class "numeric"
- `seSorensen(character)`: S3 method for class "character"
- `seSorensen(list)`: S3 method for class "list"
- `seSorensen(tableList)`: S3 method for class "tableList"

### See Also

[buildEnrichTable](#) for constructing contingency tables of mutual enrichment, [nice2x2Table](#) for checking the validity of enrichment contingency tables, [dSorensen](#) for computing the Sorensen-Dice dissimilarity, [duppSorensen](#) for the upper limit of a one-sided confidence interval of the dissimilarity, [equivTestSorensen](#) for an equivalence test.

### Examples

```

# Gene lists 'atlas' and 'sanger' in 'Cangenes' dataset. Table of joint enrichment
# of GO terms in ontology BP at level 3.
data(tab_atlas.sanger_BP3)
tab_atlas.sanger_BP3
dSorensen(tab_atlas.sanger_BP3)
seSorensen(tab_atlas.sanger_BP3)

# Contingency table as a numeric vector:
seSorensen(c(56, 1, 30, 47))
seSorensen(c(56, 1, 30))

# (These examples may be considerably time consuming due to many enrichment
# tests to build the contingency tables of mutual enrichment)
# data(allOncoGeneLists)
# ?allOncoGeneLists

# Standard error of the sample Sorensen-Dice dissimilarity, directly from
# two gene lists, from scratch:
# seSorensen(allOncoGeneLists$atlas, allOncoGeneLists$sanger,
#           onto = "BP", GOLevel = 3,

```

```

#           geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db")
# Essentially, the above code makes the same as:
# ctab_atlas.sanger_BP3 <- buildEnrichTable(allOncoGeneLists$atlas, allOncoGeneLists$sanger,
#           onto = "BP", GOLevel = 3,
#           geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db")
# ctab_atlas.sanger_BP3
# seSorensen(ctab_atlas.sanger_BP3)
# tab_atlas.sanger_BP3 and ctab_atlas.sanger_BP3 have exactly the same result.

# All pairwise standard errors (quite time consuming):
# seSorensen(allOncoGeneLists,
#           onto = "BP", GOLevel = 3,
#           geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db")

```

---

|                |   |
|----------------|---|
| sorenThreshold | <i>For a given level (2, 3, ...) in a GO ontology (BP, MF or CC), compute the equivalence threshold dissimilarity matrix.</i> |
|----------------|---|

---

### Description

For a given level (2, 3, ...) in a GO ontology (BP, MF or CC), compute the equivalence threshold dissimilarity matrix.

### Usage

```

sorenThreshold(x, ...)

## S3 method for class 'list'
sorenThreshold(
  x,
  onto,
  GOLevel,
  geneUniverse,
  orgPackg,
  boot = FALSE,
  nboot = 10000,
  boot.seed = 6551,
  trace = TRUE,
  alpha = 0.05,
  precis = 0.001,
  ...
)

## S3 method for class 'tableList'
sorenThreshold(
  x,
  boot = FALSE,
  nboot = 10000,
  boot.seed = 6551,
  trace = TRUE,
  alpha = 0.05,
  precis = 0.001,

```

```

    ...
)

```

### Arguments

|              |  |
|--------------|--|
| x            | either an object of class "list" or class "tableList". See the details section for more information.   |
| ...          | additional arguments to buildEnrichTable   |
| onto         | character, GO ontology ("BP", "MF" or "CC") under consideration  |
| GOLevel      | integer (2, 3, ...) level of a GO ontology where the GO profiles are built   |
| geneUniverse | character vector containing the universe of genes from where geneLists have been extracted. This vector must be extracted from the annotation package declared in orgPackg. For more details see <a href="#">README File</a> . |
| orgPackg     | A string with the name of the genomic annotation package corresponding to a specific species to be analyzed, which must be previously installed and activated. For more details see <a href="#">README File</a> .              |
| boot         | boolean. If TRUE, the p-values are computed by means of a bootstrap approach instead of the asymptotic normal approach. Defaults to FALSE.   |
| nboot        | numeric, number of initially planned bootstrap replicates. Ignored if boot == FALSE. Defaults to 10000   |
| boot.seed    | starting random seed for all bootstrap iterations. Defaults to 6551. see the details section   |
| trace        | boolean, the full process must be traced? Defaults to TRUE   |
| alpha        | simultaneous nominal significance level for the equivalence tests to be repeatedly performed, defaults to 0.05   |
| precis       | numerical precision in the iterative search of the equivalence threshold dissimilarities, defaults to 0.001  |

### Details

If x is an object of class "list", each of its elements must be a "character" vector of gene identifiers (e.g., ENTREZ). Then all pairwise threshold dissimilarities between these gene lists are obtained.

Class "tableList" corresponds to objects representing all mutual enrichment contingency tables generated in a pairwise fashion: Given gene lists l1, l2, ..., lk, an object of class "tableList" (typically constructed by a call to function `buildEnrichTable`) is a list of lists of contingency tables  $t_{ij}$  generated from each pair of gene lists i and j, with the following structure:

```

$l2
$l2$l1$t21
$l3
$l3$l1$t31, $l3$l2$t32
...
$lk$l1$tk1, $lk$l2$tk2, ..., $lk$l(k-1)$tk(k-1)

```

If x is an object of class "tableList", the threshold dissimilarity is obtained over each one of these tables.

If boot == TRUE, all series of nboot bootstrap replicates start from the same random seed, provided by the argument boot.seed, except if boot == NULL.

Do not confuse the resulting threshold dissimilarity matrix with the Sorensen-Dice dissimilarities computed in each equivalence test.

The dimension of the resulting matrix may be less than the number of original gene lists being compared, as the process may not converge for some pairs of gene lists.

### Value

An object of class "dist", the equivalence threshold dissimilarity matrix based on the Sorensen-Dice dissimilarity.

### Methods (by class)

- `sorenThreshold(list)`: S3 method for class "list"
- `sorenThreshold(tableList)`: S3 method for class "tableList"

### Examples

```
# Gene lists to be explored for enrichment:
data(allOncoGeneLists)

# Obtaining ENTREZ identifiers for the gene universe of humans:
library(org.Hs.eg.db)
humanEntrezIDs <- keys(org.Hs.eg.db, keytype = "ENTREZID")

# This example is quite time consuming:
# sorenThreshold(allOncoGeneLists,
#               geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db")
# Much faster:
# Object \code{allTabsBP.4} of class "tableList" contains all the pairwise contingency
# tables of joint enrichment for the gene lists in \code{allOncoGeneLists}, for the BP
# GO ontology at level 4:
data("allTabsBP.4")
sorenThreshold(allTabsBP.4)
```

---

tab\_atlas.sanger\_BP3 *Cross-tabulation of enriched GO terms at level 3 of ontology BP in two gene lists*

---

### Description

From the "Cancer gene list" of Bushman Lab, a collection of gene lists related with cancer, for gene lists "Atlas" and "Sanger", this dataset is the cross-tabulation of all GO terms of ontology BP at level 3 which are: Enriched in both lists, enriched in sanger but not in atlas, non-enriched in sanger but enriched in atlas and non-enriched in both lists. Take it just as an illustrative example, non up-to-date for changes in the gene lists or changes in the GO. The present version was obtained under Bioconductor 3.17.

### Usage

```
data(tab_atlas.sanger_BP3)
```



**Format**

An object of class "table" representing a 2x2 contingency table.

**Source**

<http://www.bushmanlab.org/links/genelists>

---

|         |   |
|---------|---|
| upgrade | <i>Update the result of a Sorensen-Dice equivalence test.</i> |
|---------|---|

---

**Description**

Recompute the test (or tests) from an object of class "equivSDhtest", "equivSDhtestList" or "AllEquivSDhtest" (i.e., the output of functions "equivTestSorensen" or "allEquivTestSorensen"). Using the same table or tables of enrichment frequencies in 'x', obtain again the result of the equivalence test for new values of any of the parameters `d0` or `conf.level` or `boot` or `nboot` or `check.table`.

**Usage**

```
upgrade(x, ...)

## S3 method for class 'equivSDhtest'
upgrade(x, ...)

## S3 method for class 'equivSDhtestList'
upgrade(x, ...)

## S3 method for class 'AllEquivSDhtest'
upgrade(x, ...)
```

**Arguments**

`x` an object of class "equivSDhtest", "equivSDhtestList" or "AllEquivSDhtest".  
`...` any valid parameters for function "equivTestSorensen" for its interface "table", to recompute the test(s) according to these parameters.

**Value**

An object of the same class than `x`.

**Methods (by class)**

- `upgrade(equivSDhtest)`: S3 method for class "equivSDhtest"
- `upgrade(equivSDhtestList)`: S3 method for class "equivSDhtestList"
- `upgrade(AllEquivSDhtest)`: S3 method for class "allEquivSDhtest"

## Examples

```
# Result of the equivalence test between gene lists 'waldman' and 'atlas', in dataset
# 'allOncoGeneLists', at level 4 of the BP ontology:
data(waldman_atlas.BP.4)
waldman_atlas.BP.4
class(waldman_atlas.BP.4)
# This may correspond to the result of code like:
# data(allOncoGeneLists)
# library(org.Hs.eg.db)
# humanEntrezIDs <- keys(org.Hs.eg.db, keytype = "ENTREZID")
# waldman_atlas.BP.4 <- equivTestSorensen(
#   allOncoGeneLists[["waldman"]], allOncoGeneLists[["atlas"]],
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOLevel = 4, listNames = c("waldman", "atlas"))
upgrade(waldman_atlas.BP.4, d0 = 1/(1 + 10/9)) # d0 = 0.4737
upgrade(waldman_atlas.BP.4, d0 = 1/(1 + 2*1.25)) # d0 = 0.2857
upgrade(waldman_atlas.BP.4, d0 = 1/(1 + 2*1.25), conf.level = 0.99)

# All pairwise equivalence tests at level 4 of the BP ontology
data(BP.4)
?BP.4
class(BP.4)
# This may correspond to a call like:
# data(allOncoGeneLists)
# library(org.Hs.eg.db)
# humanEntrezIDs <- keys(org.Hs.eg.db, keytype = "ENTREZID")
# BP.4 <- equivTestSorensen(allOncoGeneLists,
#   geneUniverse = humanEntrezIDs, orgPackg = "org.Hs.eg.db",
#   onto = "BP", GOLevel = 4)
upgrade(BP.4, d0 = 1/(1 + 2*1.25)) # d0 = 0.2857

data(cancerEquivSorensen)
?cancerEquivSorensen
class(cancerEquivSorensen)
upgrade(cancerEquivSorensen, d0 = 1/(1 + 2*1.25)) # d0 = 0.2857
```

---

waldman\_atlas.BP.4     *An example of an object of class "equivSDhtest" resulting from a call to function 'equivSorensenTest'*

---

## Description

The Sorensen-Dice equivalence test between the gene lists "waldman" and "atlas" taken from dataset [allOncoGeneLists](#) which may be charged from this package. To perform the test, the information in these gene lists was summarized by means of contingency tables of mutual GO term enrichment, for all GO terms at level 4 of the BP ontology. The tests were performed for an equivalence limit  $d_0 = 0.4444$  and a confidence level  $conf.int = 0.95$ . Based on a version of these gene lists that may be non up-to-date, take just as an illustrative example. The present result was obtained under Bioconductor 3.17.

## Usage

```
data(waldman_atlas.BP.4)
```

**Format**

An object of class "equivSDhtest" inheriting from class "list".

**Source**

<http://www.bushmanlab.org/links/genelists>

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