

# Package ‘BioCor’

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**Title** Functional Similarities

**Version** 1.35.0

**Description** Calculates functional similarities based on the pathways described on KEGG and REACTOME or in gene sets. These similarities can be calculated for pathways or gene sets, genes, or clusters and combined with other similarities. They can be used to improve networks, gene selection, testing relationships...

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**BugReports** <https://github.com/llrs/BioCor/issues>

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BioCor-package

*BioCor: A package to calculate functional similarities*

---

## Description

Calculates a functional similarity measure between gene identifiers based on the pathways described on KEGG and REACTOME.

### Important functions

- `pathSim()`: Calculates the similarity between two pathways.
- `geneSim()`: Calculates the similarity (based on `pathSim`) between two genes.
- `clusterSim()`: Calculates the similarity between two clusters of genes by joining pathways of each gene.
- `clusterGeneSim()`: Calculates the similarity between two clusters of genes by comparing the similarity between the genes of a cluster.
- `similarities()`: Allows to combine the value of matrices of similarities.
- `conversions()`: Two functions to convert similarity measures.
- `weighted()`: Functions provided to combine similarities.

### Author(s)

**Maintainer:** Lluís Revilla Sancho <lluis.revilla@gmail.com> ([ORCID](#))

Other contributors:

- Pau Sancho-Bru ([ORCID](#)) [thesis advisor]
- Juan José Salvatella Lozano ([ORCID](#)) [thesis advisor]

### See Also

Useful links:

- <https://bioconductor.org/packages/BioCor>
- <https://biocor.llrs.dev>
- Report bugs at <https://github.com/llrs/BioCor/issues>

---

addSimilarities

*Additive integration of similarities*

---

### Description

Function that use the previously calculated similarities into a single similarity matrix.

### Usage

```
addSimilarities(x, bio_mat, weights = c(0.5, 0.18, 0.1, 0.22))
```

### Arguments

x	A matrix with the similarity of expression
bio_mat	A list of matrices of the same dimension as x.
weights	A numeric vector of weight to multiply each similarity

**Details**

The total weight can't be higher than 1 to prevent values above 1 but can be below 1. It uses `weighted.sum` with `abs = TRUE` internally.

**Value**

A square matrix of the same dimensions as the input matrices.

**Author(s)**

Lluís Revilla

**See Also**

[similarities\(\)](#), [weighted\(\)](#).

**Examples**

```
set.seed(100)
a <- seq2mat(LETTERS[1:5], rnorm(10))
b <- seq2mat(LETTERS[1:5], seq(from = 0.1, to = 1, by = 0.1))
sim <- list(b)
addSimilarities(a, sim, c(0.5, 0.5))
```

---

AintoB

*Insert a matrix into another*

---

**Description**

Insert values from a matrix into another matrix based on the rownames and colnames replacing the values.

**Usage**

```
AintoB(A, B)
```

**Arguments**

A	A matrix to be inserted.
B	A matrix to insert in.

**Details**

If all the genes with pathway information are already calculated but you would like to use more genes when performing analysis. insert the once you have calculated on the matrix of genes.

**Value**

A matrix with the values of A in the matrix B.

**Author(s)**

Lluís Revilla

**Examples**

```

B <- matrix(
  ncol = 10, nrow = 10,
  dimnames = list(letters[1:10], letters[1:10])
)
A <- matrix(c(1:15),
  byrow = TRUE, nrow = 5,
  dimnames = list(letters[1:5], letters[1:3])
)
AintoB(A, B)

# Mixed orders
colnames(A) <- c("c", "h", "e")
rownames(A) <- c("b", "a", "f", "c", "j")
AintoB(A, B)

# Missing columns or rows
colnames(A) <- c("d", "f", "k")
AintoB(A, B)

```

---

clusterGeneSim	<i>Similarity score between clusters of genes based on genes similarity</i>
----------------	---

---

**Description**

Looks for the similarity between genes of a group and then between each group's genes.

**Usage**

```

clusterGeneSim(cluster1, cluster2, info, method = c("max", "rcmax.avg"), ...)

## S4 method for signature 'character,character,GeneSetCollection'
clusterGeneSim(cluster1, cluster2, info, method = c("max", "rcmax.avg"), ...)

```

**Arguments**

cluster1, cluster2	A vector with genes.
info	A GeneSetCollection or a list of genes and the pathways they are involved.
method	A vector with two or one argument to be passed to combineScores the first one is used to summarize the similarities of genes, the second one for clusters.
...	Other arguments passed to combineScores

**Details**

Differs with `clusterSim` that first each combination between genes is calculated, and with this values then the comparison between the two clusters is done. Thus applying `combineScores` twice, one at gene level and another one at cluster level.

**Value**

Returns a similarity score between the genes of the two clusters.

**Methods (by class)**

- `clusterGeneSim(cluster1 = character, cluster2 = character, info = GeneSetCollection)`: Calculates the gene similarities in a `GeneSetCollection` and combine them using `combineScoresPar()`

**Author(s)**

Lluís Revilla

**See Also**

[mclusterGeneSim\(\)](#), [combineScores\(\)](#) and [clusterSim\(\)](#)

**Examples**

```
if (require("org.Hs.eg.db")) {
  # Extract the paths of all genes of org.Hs.eg.db from KEGG (last update in
  # data of June 31st 2011)
  genes.kegg <- as.list(org.Hs.egPATH)
  clusterGeneSim(c("18", "81", "10"), c("100", "10", "1"), genes.kegg)
  clusterGeneSim(
    c("18", "81", "10"), c("100", "10", "1"), genes.kegg,
    c("avg", "avg")
  )
  clusterGeneSim(
    c("18", "81", "10"), c("100", "10", "1"), genes.kegg,
    c("avg", "rcmax.avg")
  )
  (clus <- clusterGeneSim(
    c("18", "81", "10"), c("100", "10", "1"),
    genes.kegg, "avg"
  ))
  combineScores(clus, "rcmax.avg")
} else {
  warning("You need org.Hs.eg.db package for this example")
}
```

---

clusterSim	<i>Similarity score between clusters of genes based on pathways similarity</i>
------------	--

---

### Description

Looks for the similarity between genes in groups

### Usage

```
clusterSim(cluster1, cluster2, info, method = "max", ...)
```

```
## S4 method for signature 'character,character,GeneSetCollection'
```

```
clusterSim(cluster1, cluster2, info, method = "max", ...)
```

### Arguments

cluster1, cluster2

A vector with genes.

info

A GeneSetCollection or a list of genes and the pathways they are involved.

method

one of c("avg", "max", "rcmax", "rcmax.avg", "BMA", "reciprocal"), see Details.

...

Other arguments passed to combineScores

### Details

Once the pathways for each cluster are found they are combined using [combineScores\(\)](#).

### Value

clusterSim returns a similarity score of the two clusters

### Methods (by class)

- `clusterSim( cluster1 = character, cluster2 = character, info = GeneSetCollection )`: Calculates all the similarities of the GeneSetCollection and combine them using [combineScoresPar\(\)](#)

### Author(s)

Lluís Revilla

### See Also

For a different approach see [clusterGeneSim\(\)](#), [combineScores\(\)](#) and [conversions\(\)](#)

**Examples**

```

if (require("org.Hs.eg.db")) {
  # Extract the paths of all genes of org.Hs.eg.db from KEGG (last update in
  # data of June 31st 2011)
  genes.kegg <- as.list(org.Hs.egPATH)
  clusterSim(c("9", "15", "10"), c("33", "19", "20"), genes.kegg)
  clusterSim(c("9", "15", "10"), c("33", "19", "20"), genes.kegg, NULL)
  clusterSim(c("9", "15", "10"), c("33", "19", "20"), genes.kegg, "avg")
} else {
  warning("You need org.Hs.eg.db package for this example")
}

```

---

combinadic

*i*-th combination of *n* elements taken from *r*


---

**Description**

Function similar to `combn` but for larger vectors. To avoid allocating a big vector with all the combinations each one can be computed with this function.

**Usage**

```
combinadic(n, r, i)
```

**Arguments**

<code>n</code>	Elements to extract the combination from
<code>r</code>	Number of elements per combination
<code>i</code>	ith combination

**Value**

The combination `ith` of the elements

**Author(s)**

Joshua Ulrich

**References**

[StackOverflow answer 4494469/2886003](#)

**See Also**

[combn\(\)](#)

**Examples**

```
# Output of all combinations
combn(LETTERS[1:5], 2)
# Output of the second combination
combinadic(LETTERS[1:5], 2, 2)
```

---

combineScores	<i>Combining values</i>
---------------	-------------------------

---

**Description**

Combine several similarities into one using several methods.

**Usage**

```
combineScores(
  scores,
  method = c("max", "avg", "rcmax", "rcmax.avg", "BMA", "reciprocal"),
  round = FALSE,
  t = 0
)

combineScoresPar(scores, method, subSets = NULL, BPPARAM = NULL, ...)
```

**Arguments**

scores	Matrix of scores to be combined
method	one of c("avg", "max", "rcmax", "rcmax.avg", "BMA", "reciprocal"), see Details.
round	Should the resulting value be rounded to the third digit?
t	Numeric value to filter scores below this value. Only used in the reciprocal method.
subSets	List of combinations as info in other functions.
BPPARAM	BiocParallel back-end parameters. By default (NULL) a for loop is used.
...	Other arguments passed to combineScores

**Details**

The input matrix can be a base matrix or a matrix from package Matrix. The methods return:

- **avg**: The average or mean value.
- **max**: The max value.
- **rcmax**: The max of the column means or row means.
- **rcmax.avg**: The sum of the max values by rows and columns divided by the number of columns and rows.

- **BMA**: The same as `rcmax.avg`.
- **reciprocal**: The double of the sum of the reciprocal maximal similarities (above a threshold) divided by the number of elements. See equation 3 of the Tao *et al* 2007 article.

### Value

A numeric value as described in details.

### Note

`combineScores` is a version of the function of the same name in package `GOSemSim` (`GOSemSim::combineScores()`) with optional rounding and some internal differences.

### Author(s)

Lluís Revilla based on Guangchuang Yu.

### References

Ying Tao, Lee Sam, Jianrong Li, Carol Friedman, Yves A. Lussier; Information theory applied to the sparse gene ontology annotation network to predict novel gene function. *Bioinformatics* 2007; 23 (13): i529-i538. doi: 10.1093/bioinformatics/btm195

### See Also

[register](#) in `BiocParallel` about the arguments accepted by `BPPARAM`.

### Examples

```
(d <- structure(c(
  0.4, 0.6, 0.222222222222222, 0.4, 0.4, 0, 0.25, 0.5,
  0.285714285714286
),
  .Dim = c(3L, 3L),
  .Dimnames = list(c("a", "b", "c"), c("d", "e", "f"))
))
e <- d
sapply(c("avg", "max", "rcmax", "rcmax.avg", "BMA", "reciprocal"),
  combineScores,
  scores = d
)
d[1, 2] <- NA
sapply(c("avg", "max", "rcmax", "rcmax.avg", "BMA", "reciprocal"),
  combineScores,
  scores = d
)
colnames(e) <- rownames(e)
combineScoresPar(e, list(a = c("a", "b"), b = c("b", "c")),
  method = "max"
)
```

---

combineSources	<i>Combine different sources of pathways</i>
----------------	--

---

## Description

Given several sources of pathways with the same for the same id of the genes it merge them.

## Usage

```
combineSources(...)
```

## Arguments

...                    Lists of genes and their pathways.

## Details

It assumes that the identifier of the genes are the same for both sources but if many aren't equal it issues a warning. Only unique pathways identifiers are returned.

## Value

A single list with the pathways of each source on the same gene.

## Examples

```
DB1 <- list(g1 = letters[6:8], g2 = letters[1:5], g3 = letters[4:7])
DB2 <- list(
  g1 = c("one", "two"), g2 = c("three", "four"),
  g3 = c("another", "two")
)
combineSources(DB1, DB2)
combineSources(DB1, DB1)
DB3 <- list(
  g1 = c("one", "two"), g2 = c("three", "four"),
  g4 = c("five", "six", "seven"), g5 = c("another", "two")
)
combineSources(DB1, DB3) # A warning is expected
```

---

conversions	<i>Convert the similarities formats</i>
-------------	---

---

**Description**

Functions to convert the similarity coefficients between Jaccard and Dice. D2J is the opposite of J2D.

**Usage**

D2J(D)

J2D(J)

**Arguments**

D            Dice coefficient, as returned by `diceSim()`, `geneSim()`, `clusterSim()` and `clusterGeneSim()`

J            Jaccard coefficient

**Value**

A numeric value.

**Author(s)**

Lluís Revilla

**Examples**

```
D2J(0.5)
J2D(0.5)
D2J(J2D(0.5))
```

---

diceSim	<i>Compare pathways</i>
---------	-------------------------

---

**Description**

Function to estimate how much two list of genes overlap by looking how much of the nodes are shared. Calculates the Dice similarity

**Usage**

```
diceSim(g1, g2)
```

**Arguments**

g1, g2                    A character list with the names of the proteins in each pathway.

**Details**

It requires a vector of characters otherwise will return an NA.

**Value**

A score between 0 and 1 calculated as the double of the proteins shared by g1 and g2 divided by the number of genes in both groups.

**Author(s)**

Lluís Revilla

**See Also**

Used for [geneSim\(\)](#), see [conversions\(\)](#) help page to transform Dice score to Jaccard score.

**Examples**

```
genes.id2 <- c("52", "11342", "80895", "57654", "548953", "11586", "45985")
genes.id1 <- c(
  "52", "11342", "80895", "57654", "58493", "1164", "1163",
  "4150", "2130", "159"
)
diceSim(genes.id1, genes.id2)
diceSim(genes.id2, genes.id2)
```

---

duplicateIndices            *Finds the indices of the duplicated events of a vector*

---

**Description**

Finds the indices of duplicated elements in the vector given.

**Usage**

```
duplicateIndices(vec)
```

**Arguments**

vec                        Vector of identifiers presumably duplicated

**Details**

For each duplication it can return a list or if all the duplication events are of the same length it returns a matrix, where each column is duplicated.

**Value**

The format is determined by the `simplify2array`

**Author(s)**

Lluís Revilla

**See Also**

[removeDup\(\)](#)

**Examples**

```
duplicateIndices(c("52", "52", "53", "55")) # One repeated element
duplicateIndices(c("52", "52", "53", "55", "55")) # Repeated elements
duplicateIndices(c("52", "55", "53", "55", "52")) # Mixed repeated elements
```

---

geneSim

*Similarity score genes based on pathways similarity*

---

**Description**

Given two genes, calculates the Dice similarity between each pathway which is combined to obtain a similarity between the genes.

**Usage**

```
geneSim(gene1, gene2, info, method = "max", ...)

## S4 method for signature 'character,character,GeneSetCollection'
geneSim(gene1, gene2, info, method = "max", ...)
```

**Arguments**

gene1, gene2	Ids of the genes to calculate the similarity, to be found in genes.
info	A <code>GeneSetCollection</code> or a list of genes and the pathways they are involved.
method	one of <code>c("avg", "max", "rcmax", "rcmax.avg", "BMA", "reciprocal")</code> , see <code>Details</code> .
...	Other arguments passed to <code>combineScores</code>

**Details**

Given the information about the genes and their pathways, uses the ids of the genes to find the Dice similarity score for each pathway comparison between the genes. Later this similarities are combined using [combineScoresPar\(\)](#).

**Value**

The highest Dice score of all the combinations of pathways between the two ids compared if a method to combine scores is provided or NA if there isn't information for one gene. If an NA is returned this means that there isn't information available for any pathways for one of the genes. Otherwise a number between 0 and 1 (both included) is returned. Note that there isn't a negative value of similarity.

**Methods (by class)**

- `geneSim(gene1 = character, gene2 = character, info = GeneSetCollection)`: Calculates all the similarities of the `GeneSetCollection` and combine them using `combineScoresPar()`

**Author(s)**

Lluís Revilla

**See Also**

`mgeneSim()`, `conversions()` help page to transform Dice score to Jaccard score. For the method to combine the scores see `combineScoresPar()`.

**Examples**

```
if (require("org.Hs.eg.db") & require("reactome.db")) {
  # Extract the paths of all genes of org.Hs.eg.db from KEGG
  # (last update in data of June 31st 2011)
  genes.kegg <- as.list(org.Hs.egPATH)
  # Extracts the paths of all genes of org.Hs.eg.db from reactome
  genes.react <- as.list(reactomeEXTID2PATHID)
  geneSim("81", "18", genes.react)
  geneSim("81", "18", genes.kegg)
  geneSim("81", "18", genes.react, NULL)
  geneSim("81", "18", genes.kegg, NULL)
} else {
  warning("You need reactome.db and org.Hs.eg.db package for this example")
}
```

---

`incidence,list-method` *Creates the incidence matrix*

---

**Description**

Given a list of pathways and its genes creates an incidence matrix.

**Usage**

```
## S4 method for signature 'list'
incidence(x)
```

**Arguments**

x                    A list

**Value**

A matrix with pathways as rows and genes in columns.

**Note**

Designed to be easier to work with list and GeneSetCollection

**Author(s)**

Lluís Revilla

---

*inverseList*

*Invert a list*

---

**Description**

Calculate the pathways per gene of list

**Usage**

```
inverseList(x)
```

**Arguments**

x                    A list with genes as names and names of pathways as values of the list

**Value**

The number of pathways each gene has.

**Author(s)**

Lluís Revilla

---

mclusterGeneSim	<i>Similarity score between clusters of genes based on genes similarity</i>
-----------------	---

---

### Description

Looks for the similarity between genes of a group and then between each group's genes.

### Usage

```
mclusterGeneSim(clusters, info, method = c("max", "rcmax.avg"), ...)
```

```
## S4 method for signature 'list, GeneSetCollection'
```

```
mclusterGeneSim(clusters, info, method = c("max", "rcmax.avg"), ...)
```

### Arguments

clusters	A list of clusters of genes to be found in id.
info	A GeneSetCollection or a list of genes and the pathways they are involved.
method	A vector with two or one argument to be passed to combineScores the first one is used to summarize the similarities of genes, the second one for clusters.
...	Other arguments passed to combineScores

### Value

Returns a matrix with the similarity scores for each cluster comparison.

### Methods (by class)

- `mclusterGeneSim(clusters = list, info = GeneSetCollection)`: Calculates all the similarities of the GeneSetCollection and combine them using `combineScoresPar()`

### Author(s)

Lluís Revilla

### See Also

[clusterGeneSim\(\)](#), [clusterSim\(\)](#) and [combineScores\(\)](#)

### Examples

```
if (require("org.Hs.eg.db")) {  
  genes.kegg <- as.list(org.Hs.egPATH)  
  clusters <- list(  
    cluster1 = c("18", "81", "10"),  
    cluster2 = c("100", "594", "836"),  
    cluster3 = c("18", "10", "83")  
  )  
}
```

```

mclusterGeneSim(clusters, genes.kegg)
mclusterGeneSim(clusters, genes.kegg, c("max", "avg"))
mclusterGeneSim(clusters, genes.kegg, c("max", "BMA"))
} else {
  warning("You need org.Hs.eg.db package for this example")
}

```

---

mclusterSim	<i>Similarity score between clusters of genes based on pathways similarity</i>
-------------	--

---

### Description

Looks for the similarity between genes in groups. Once the pathways for each cluster are found they are combined using [combineScores\(\)](#).

### Usage

```

mclusterSim(clusters, info, method = "max", ...)

## S4 method for signature 'list, GeneSetCollection'
mclusterSim(clusters, info, method = "max", ...)

```

### Arguments

clusters	A list of clusters of genes to be found in id.
info	A GeneSetCollection or a list of genes and the pathways they are involved.
method	one of c("avg", "max", "rcmax", "rcmax.avg", "BMA", "reciprocal"), see Details.
...	Other arguments passed to combineScores

### Value

mclusterSim returns a matrix with the similarity scores for each cluster comparison.

### Methods (by class)

- `mclusterSim(clusters = list, info = GeneSetCollection)`: Calculates all the similarities of the GeneSetCollection and combine them using [combineScoresPar\(\)](#)

### Author(s)

Lluís Revilla

### See Also

For a different approach see [clusterGeneSim\(\)](#), [combineScores\(\)](#) and [conversions\(\)](#)

**Examples**

```

if (require("org.Hs.eg.db")) {
  # Extract the paths of all genes of org.Hs.eg.db from KEGG (last update in
  # data of June 31st 2011)
  genes.kegg <- as.list(org.Hs.egPATH)

  clusters <- list(
    cluster1 = c("18", "81", "10"),
    cluster2 = c("100", "10", "1"),
    cluster3 = c("18", "10", "83")
  )
  mclusterSim(clusters, genes.kegg)
  mclusterSim(clusters, genes.kegg, "avg")
} else {
  warning("You need org.Hs.eg.db package for this example")
}

```

---

mgeneSim

*Similarity score genes based on pathways similarity*


---

**Description**

Given two genes, calculates the Dice similarity between each pathway which is combined to obtain a similarity between the genes.

**Usage**

```

mgeneSim(genes, info, method = "max", ...)

## S4 method for signature 'character, GeneSetCollection'
mgeneSim(genes, info, method = "max", ...)

## S4 method for signature 'missing, GeneSetCollection'
mgeneSim(genes, info, method = "max", ...)

```

**Arguments**

genes	A vector of genes.
info	A GeneSetCollection or a list of genes and the pathways they are involved.
method	one of c("avg", "max", "rcmax", "rcmax.avg", "BMA", "reciprocal"), see Details.
...	Other arguments passed to combineScores

**Details**

Given the information about the genes and their pathways, uses the ids of the genes to find the Dice similarity score for each pathway comparison between the genes. Later this similarities are combined using [combineScoresPar\(\)](#).

**Value**

mgeneSim returns the matrix of similarities between the genes in the vector

**Methods (by class)**

- mgeneSim(genes = character, info = GeneSetCollection): Calculates all the similarities of the list and combine them using [combineScoresPar\(\)](#)
- mgeneSim(genes = missing, info = GeneSetCollection): Calculates all the similarities of the list and combine them using [combineScoresPar\(\)](#)

**Note**

genes accept named characters and the output will use the names of the genes.

**See Also**

[geneSim\(\)](#), [conversions\(\)](#) help page to transform Dice score to Jaccard score. For the method to combine the scores see [combineScoresPar\(\)](#).

**Examples**

```
if (require("org.Hs.eg.db") & require("reactome.db")) {
  # Extract the paths of all genes of org.Hs.eg.db from KEGG
  # (last update in data of June 31st 2011)
  genes.kegg <- as.list(org.Hs.egPATH)
  # Extracts the paths of all genes of org.Hs.eg.db from reactome
  genes.react <- as.list(reactomeEXTID2PATHID)
  mgeneSim(c("81", "18", "10"), genes.react)
  mgeneSim(c("81", "18", "10"), genes.react, "avg")
  named_genes <- structure(c("81", "18", "10"),
    .Names = c("ACTN4", "ABAT", "NAT2")
  )
  mgeneSim(named_genes, genes.react, "max")
} else {
  warning("You need reactome.db and org.Hs.eg.db package for this example")
}
```

---

mpathSim

*Calculates the Dice similarity between pathways*


---

**Description**

Calculates the similarity between several pathways using dice similarity score. If one needs the matrix of similarities between pathways set the argument methods to NULL.

**Usage**

```

mPathSim(pathways, info, method = NULL, ...)

## S4 method for signature 'character, GeneSetCollection, ANY'
mPathSim(pathways, info, method = NULL, ...)

## S4 method for signature 'missing, GeneSetCollection, ANY'
mPathSim(pathways, info, method = NULL, ...)

## S4 method for signature 'missing, list, ANY'
mPathSim(pathways, info, method = NULL, ...)

## S4 method for signature 'missing, list, missing'
mPathSim(pathways, info, method = NULL, ...)

```

**Arguments**

pathways	Pathways to calculate the similarity for
info	A list of genes and the pathways they are involved or a GeneSetCollection object
method	To combine the scores of each pathway, one of c("avg", "max", "rcmax", "rcmax.avg", "BMA"), if NULL returns the matrix of similarities.
...	Other arguments passed to <a href="#">combineScoresPar()</a>

**Value**

The similarity between those pathways or all the similarities between each comparison.

**Methods (by class)**

- `mPathSim(pathways = character, info = GeneSetCollection, method = ANY)`: Calculates the similarity between the provided pathways of the GeneSetCollection using `combineScoresPar`
- `mPathSim(pathways = missing, info = GeneSetCollection, method = ANY)`: Calculates all the similarities of the GeneSetCollection and combine them using `combineScoresPar`
- `mPathSim(pathways = missing, info = list, method = ANY)`: Calculates all the similarities of the list and combine them using `combineScoresPar`
- `mPathSim(pathways = missing, info = list, method = missing)`: Calculates all the similarities of the list

**Note**

pathways accept named characters, and then the output will have the names

**See Also**

[pathSim\(\)](#) For single pairwise comparison. [conversions\(\)](#) To convert the Dice similarity to Jaccard similarity

**Examples**

```

if (require("reactome.db")) {
  genes.react <- as.list(reactomeEXTID2PATHID)
  (pathways <- sample(unique(unlist(genes.react)), 10))
  mpathSim(pathways, genes.react, NULL)
  named_paths <- structure(
    c("R-HSA-112310", "R-HSA-112316", "R-HSA-112315"),
    .Names = c(
      "Neurotransmitter Release Cycle",
      "Neuronal System",
      "Transmission across Chemical Synapses"
    )
  )
  mpathSim(named_paths, genes.react, NULL)
  many_pathways <- sample(unique(unlist(genes.react)), 152)
  mpathSim(many_pathways, genes.react, "avg")
} else {
  warning("You need reactome.db package for this example")
}

```

---

pathSim

*Calculates the Dice similarity between pathways*


---

**Description**

Calculates the similarity between pathways using dice similarity score. `diceSim` is used to calculate similarities between the two pathways.

**Usage**

```
pathSim(pathway1, pathway2, info)
```

```
## S4 method for signature 'character,character,GeneSetCollection'
pathSim(pathway1, pathway2, info)
```

**Arguments**

```
pathway1, pathway2
```

A single pathway to calculate the similarity

```
info
```

A `GeneSetCollection` or a list of genes and the pathways they are involved.

**Value**

The similarity between those pathways or all the similarities between each comparison.

**Methods (by class)**

- `pathSim(pathway1 = character, pathway2 = character, info = GeneSetCollection)`: Calculates all the similarities of a `GeneSetCollection` and combine them using `combineScoresPar`

**Author(s)**

Lluís Revilla

**See Also**

[conversions\(\)](#) help page to transform Dice score to Jaccard score. [mpathSim\(\)](#) for multiple pairwise comparison of pathways.

**Examples**

```
if (require("reactome.db")) {
  # Extracts the paths of all genes of org.Hs.eg.db from reactome
  genes.react <- as.list(reactomeEXTID2PATHID)
  (paths <- sample(unique(unlist(genes.react)), 2))
  pathSim(paths[1], paths[2], genes.react)
} else {
  warning("You need reactome.db package for this example")
}
```

---

plot\_data

*The position of the nodes is based on the similarity between them.*

---

**Description**

The position of the nodes is based on the similarity between them.

Plot how similar are the data

**Usage**

```
plot_data(x, top)
```

```
plot_similarity(pd)
```

**Arguments**

x	Matrix with the similarities.
top	a number between 0 and 1 to select the edges relating the elements of the matrix.
pd	The plot data from plot_data() function.

**Value**

A list with two elements:

- nodes: The position and name of the nodes
- edges: The information about the selected edges

A ggplot object

## Examples

```
if (require("org.Hs.eg.db") & require("reactome.db")) {  
  # Extract the paths of all genes of org.Hs.eg.db from KEGG  
  # (last update in data of June 31st 2011)  
  genes.kegg <- as.list(org.Hs.egPATH)  
  # Extracts the paths of all genes of org.Hs.eg.db from reactome  
  genes.react <- as.list(reactomeEXTID2PATHID)  
  
  sim <- mgeneSim(c("87", "18", "10"), genes.react)  
  pd <- plot_data(sim, top = 0.25)  
  if (requireNamespace("ggplot2", quietly = TRUE)){  
    plot_similarity(pd)  
  }  
}
```

---

removeDup

*Remove duplicated rows and columns*

---

## Description

Given the indices of the duplicated entries remove the columns and rows until just one is left, it keeps the duplicated with the highest absolute mean value.

## Usage

```
removeDup(cor_mat, dupli)
```

## Arguments

cor_mat	List of matrices
dupli	List of indices with duplicated entries

## Value

A matrix with only one of the columns and rows duplicated

## Author(s)

Lluís Revilla

## See Also

[duplicateIndices\(\)](#) to obtain the list of indices with duplicated entries.

**Examples**

```
a <- seq2mat(c("52", "52", "53", "55"), runif(choose(4, 2)))
b <- seq2mat(c("52", "52", "53", "55"), runif(choose(4, 2)))
mat <- list("kegg" = a, "react" = b)
mat
dupli <- duplicateIndices(rownames(a))
remat <- removeDup(mat, dupli)
remat
```

---

seq2mat

*Transforms a vector to a symmetric matrix*

---

**Description**

Fills a matrix of `ncol = length(x)` and `nrow = length(x)` with the values in `dat` and setting the diagonal to 1.

**Usage**

```
seq2mat(x, dat)
```

**Arguments**

<code>x</code>	names of columns and rows, used to define the size of the matrix
<code>dat</code>	Data to fill with the matrix with except the diagonal.

**Details**

`dat` should be at least `choose(length(x), 2)` of length. It assumes that the data provided comes from using the row and column id to obtain it.

**Value**

A square matrix with the diagonal set to 1 and `dat` on the upper and lower triangle with the columns ids and row ids from `x`.

**Author(s)**

Lluís Revilla

**See Also**

[upper.tri\(\)](#) and [lower.tri\(\)](#)

**Examples**

```
seq2mat(LETTERS[1:5], 1:10)
seq2mat(LETTERS[1:5], seq(from = 0.1, to = 1, by = 0.1))
```

---

`similarities`*Apply a function to a list of similarities*

---

**Description**

Function to join list of similarities by a function provided by the user.

**Usage**

```
similarities(sim, func, ...)
```

**Arguments**

<code>sim</code>	list of similarities to be joined. All similarities must have the same dimensions. The genes are assumed to be in the same order for all the matrices.
<code>func</code>	function to perform on those similarities: prod, sum... It should accept as many arguments as similarities matrices are provided, and should use numbers.
<code>...</code>	Other arguments passed to the function func. Usually <code>na.rm</code> or similar.

**Value**

A matrix of the size of the similarities

**Note**

It doesn't check that the columns and rows of the matrices are in the same order or are the same.

**Author(s)**

Lluís Revilla

**See Also**

[weighted\(\)](#) for functions that can be used, and [addSimilarities\(\)](#) for a wrapper to one of them

**Examples**

```
set.seed(100)
a <- seq2mat(LETTERS[1:5], rnorm(10))
b <- seq2mat(LETTERS[1:5], seq(from = 0.1, to = 1, by = 0.1))
sim <- list(b, a)
similarities(sim, weighted.prod, c(0.5, 0.5))
# Note the differences in the sign of some values
similarities(sim, weighted.sum, c(0.5, 0.5))
```

---

weighted	<i>Weighted operations</i>
----------	----------------------------

---

### Description

Calculates the weighted sum or product of  $x$ . Each values should have its weight, otherwise it will throw an error.

### Usage

```
weighted.sum(x, w, abs = TRUE)
```

```
weighted.prod(x, w)
```

### Arguments

$x$	an object containing the values whose weighted operations is to be computed
$w$	a numerical vector of weights the same length as $x$ giving the weights to use for elements of $x$ .
$abs$	If any $x$ is negative you want the result negative too?

### Details

This functions are thought to be used with *similarities*. As some similarities might be positive and others negative the argument  $abs$  is provided for `weighted.sum`, assuming that only one similarity will be negative (usually the one coming from expression correlation).

### Value

`weighted.sum` returns the sum of the product of  $x$ \*weights removing all NA values. See parameter  $abs$  if there are any negative values.

`weighted.prod` returns the product of product of  $x$ \*weights removing all NA values.

### Author(s)

Lluís Revilla

### See Also

[weighted.mean\(\)](#), [similarities\(\)](#) and [addSimilarities\(\)](#)

**Examples**

```
expr <- c(-0.2, 0.3, 0.5, 0.8, 0.1)
weighted.sum(expr, c(0.5, 0.2, 0.1, 0.1, 0.1))
weighted.sum(expr, c(0.5, 0.2, 0.1, 0.2, 0.1), FALSE)
weighted.sum(expr, c(0.4, 0.2, 0.1, 0.2, 0.1))
weighted.sum(expr, c(0.4, 0.2, 0.1, 0.2, 0.1), FALSE)
weighted.sum(expr, c(0.4, 0.2, 0, 0.2, 0.1))
weighted.sum(expr, c(0.5, 0.2, 0, 0.2, 0.1))
# Compared to weighted.prod:
weighted.prod(expr, c(0.5, 0.2, 0.1, 0.1, 0.1))
weighted.prod(expr, c(0.4, 0.2, 0.1, 0.2, 0.1))
weighted.prod(expr, c(0.4, 0.2, 0, 0.2, 0.1))
weighted.prod(expr, c(0.5, 0.2, 0, 0.2, 0.1))
```

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