Package ‘clustComp’

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Title Clustering Comparison Package
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Imports sm, stats, graphics, grDevices
Suggests Biobase, colonCA, RUnit, BiocGenerics
biocViews GeneExpression, Clustering, Visualization
Description clustComp is a package that implements several techniques for the comparison and visualisation of relationships between different clustering results, either flat versus flat or hierarchical versus flat. These relationships among clusters are displayed using a weighted bi-graph, in which the nodes represent the clusters and the edges connect pairs of nodes with non-empty intersection; the weight of each edge is the number of elements in that intersection and is displayed through the edge thickness. The best layout of the bi-graph is provided by the barycentre algorithm, which minimises the weighted number of crossings. In the case of comparing a hierarchical and a non-hierarchical clustering, the dendrogram is pruned at different heights, selected by exploring the tree by depth-first search, starting at the root. Branches are decided to be split according to the value of a scoring function, that can be based either on the aesthetics of the bi-graph or on the mutual information between the hierarchical and the flat clusterings. A mapping between groups of clusters from each side is constructed with a greedy algorithm, and can be additionally visualised.
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barycentre

**Description**

*barycentre* provides an updated coordinate value for a node that is connected to nodes in a different layer of a bigraph. It is computed as the average of coordinates of the adjacent nodes, where weighted edges are considered as multi-edges collapsed into one.

**Usage**

```r
barycentre(edge.weight, coordinates = NULL)
```

**Arguments**

- `edge.weight` a vector containing the intersection sizes (edge weights) between a given node (from one of the partitionings) and all nodes in the other.
- `coordinates` a vector indicating the coordinates of the adjacent nodes. If it is not provided, then they are evenly spaced assuming a layout from top downwards.

**Details**

The node under consideration, from a given partitioning, is assigned a new position using the *barycentre* algorithm. The coordinates of the incident nodes are considered as many times as the corresponding edge weights indicate, and the new position for the node is given by the average over this set of coordinates.

**Value**

- `position` a number indicating the barycentre-coordinate of the node under consideration.

**Author(s)**

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**References**

**drawTreeGraph**

*See Also*

flatVSflat, flatVShier

**Examples**

```r
# simulated data
clustering1 <- c(rep(1, 5), rep(2, 10), rep(3, 10))
clustering2 <- c(rep(1, 6), rep(2, 6), rep(3, 4), rep(4, 9))
weights <- table(clustering1, clustering2)
barycentre(weights[1, ], 1:4)
barycentre(weights[1, ])
barycentre(weights[2, ], 1:4)
apply(weights, 1, barycentre, 1:4)
```

<table>
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<tr>
<td>weight</td>
<td>a contingency matrix containing the intersection sizes (edge weights) between branches in the tree and clusters from the flat partitioning.</td>
</tr>
<tr>
<td>current.order</td>
<td>a list of two components; the first one is a vector with the branches (rows of the matrix weight) in the ordering in which they are drawn; the second one provides the ordering for flat clusters (columns of weight). Both are drawn from bottom upwards.</td>
</tr>
<tr>
<td>coordinates</td>
<td>a list of two components; the first one is a vector providing the Y-coordinates, from bottom upwards, for the branches, whereas the second one provides the Y-coordinates, from bottom upwards, for the flat clusters.</td>
</tr>
<tr>
<td>tree</td>
<td>a list with two components: <code>heights</code>, a vector describing the heights at which the different branches in the tree are agglomerated, and <code>branches</code>, a matrix of 3 columns; the i-th row contains as first element the branch split at the i-th allowed splitting, and as second and third elements, the corresponding children.</td>
</tr>
<tr>
<td>dot</td>
<td>a Boolean parameter; if TRUE then the last split in the children-tree is shown with a red open circle.</td>
</tr>
<tr>
<td>line.wd</td>
<td>a number indicating the width of the thickest edge(s) in the bigraph.</td>
</tr>
</tbody>
</table>

**Description**

`drawTreeGraph` plots both a hierarchical tree, either complete or pruned, and a flat clustering, connected with edges whose thickness is proportional to the number of elements shared by branches and clusters, to form a weighted bi-graph. Its usage is mainly internal, as part of the visualisation of the `hierarchical.look.ahead` function. The size of each cluster is also displayed.

**Usage**

```r
drawTreeGraph(weight, current.order, coordinates, tree, dot = TRUE, line.wd = 3, main = NULL, expanded = FALSE, hclust.obj = NULL, labels = NULL, cex.labels = 1, expression = NULL, layout = NULL, ramp = NULL)
```

The `drawTreeGraph` function is used to plot a bi-graph determined by the branches in the tree and the flat clusters, where the thickness of the edges is proportional to the number of elements shared by branches and clusters.
**drawTreeGraph**

- **main**: a character string for the plot title.
- **expanded**: a Boolean parameter indicating whether the hierarchical tree should be plotted complete or with its branches collapsed.
- **hclust.obj**: an hclust object describing how the leaves are merged and the ordering of the branches, which might have been changed by the gravity-centre algorithm.
- **labels**: a vector indicating the labels for the leaves in the expanded tree.
- **cex.labels**: a number indicating the magnification used for the labels of the leaves.
- **expression**: a matrix containing the expression data from which the dendrogram and the flat partitioning were obtained.
- **layout**: a vector containing 3 or 2 components, depending on whether the heatmap is plotted or not. Each coordinate provides the value on the X axis for locating the heatmap, the colour bar representing pruned branches, and the bigraph. Provided vectors are increasingly ordered to keep the layout of the plot.
- **ramp**: a vector with two components containing the two colours used to define the palette for the heatmap.

**Details**

The `drawTreeGraph` function allows visualising the comparison of a hierarchical clustering, drawn on the left hand side of the plot, and a flat clustering, represented on the right hand side. The tree branches are labelled by their original labels preceded by 'B'; if the function is called as part of the `flatVShier` algorithm, then the standard notation for initial branch labels is that of `hclust` objects: if the label is a negative integer it corresponds to a leaf; if it is a positive integer, then it corresponds to a branch that agglomerates at least two elements, and the number represent the stage at which the branch was formed. The last splitting can be optionally highlighted with a red open circle upon the parent-node. The flat clusters are labelled by their original labels preceded by 'F'.

**Value**

A list of components including:

- **b.coord**: a vector indicating the Y coordinates of the nodes in the bi-graph representing the branches of the hierarchical tree.
- **f.coord**: a vector indicating the Y coordinates of the nodes in the bi-graph representing the flat clusters.
- **x.coords**: a vector of two components indicating the X coordinates at which each layer of the bi-graph is represented.

**Author(s)**

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**References**


**See Also**

`flatVShier`
Examples

```r
### simulated data
parent.clustering <- c(rep(1, 15), rep(2, 10))
# replace the branch '2' by its children '3' and '4'
children.clustering <- c(rep(1, 15), rep(3, 5), rep(4, 5))
flat.clustering <- c(rep(1, 6), rep(2, 6), rep(3, 4), rep(4, 9))
split <- rbind(c(0, 1, 2), c(2, 3, 4))
weight <- table(children.clustering, flat.clustering)
current.order <- list(c(3, 4, 1), 1:4)
coordinates <- list(c(-1, 0, 1), c(-1.5, -0.5, 0.5, 1.5))
tree <- list(heights = c(1, 0.8), branches = split)
drawTreeGraph(weight, current.order, coordinates, tree)

### expanded tree
set.seed(0)
myData <- matrix(rnorm(50), 10, 5)
myData[1:5,] <- myData[1:5, ] + 2 # two groups
flat.clustering <- kmeans(myData, 2)$cluster
hierar.clustering <- hclust(dist(myData))
weight <- matrix(c(5, 0, 0, 5), 2, 2)
colnames(weight) <- 1:2; rownames(weight) <- c(6,8)
current.order <- list(c(6, 8), 1:2)
coordinates <- list(c(0.25, 0.75), c(0.25, 0.75))
tree <- list(heights = hierar.clustering$height[9],
             branches = matrix(c(9, 6, 8), 1, 3))

# without heatmap
drawTreeGraph(weight, current.order, coordinates, tree,
              expanded = TRUE, hclust.obj = hierar.clustering,
              dot = FALSE)

# with heatmap
drawTreeGraph(weight, current.order, coordinates, tree,
              expanded = TRUE, hclust.obj = hierar.clustering,
              dot = FALSE, expression = myData)
```

dyn.cross

**Computation of the number of crossings in the bi-graph in a particular layout**

dyn.cross dynamically computes the number of edge crossings for a given node ordering of both layers of the bi-graph. This ordering is given by the rownames and colnames of the matrix of weights provided as argument. The use of this function is mainly internal.

**Usage**

dyn.cross(weights)
Arguments

weights: a matrix containing the intersection sizes (edge weights) between clusters (nodes) from the first partitioning (left or top layer of the bi-graph) and the second partitioning (right or bottom layer of the bi-graph). The rownames and colnames of the matrix provide the ordering of the nodes in the first and second layer, respectively.

Details

The number of crossings in the weighted bigraph is computed by considering multiedges between connected nodes. The specific implementation uses a modification, adapted to the case of having multiple edges, of the dynamic programming algorithm developed by Nagamochi and Yamada for counting the number of crossings in non-weighted graphs, which has reduced computational cost.

Value

crossings: the number of weighted crossings in the layout provided as argument.

Author(s)

Aurora Torrente <aurora@ebi.ac.uk> and Alvis Brazma <brazma@ebi.ac.uk>

References


See Also

barycentre, flatVSflat, flatVShier

Examples

# simulated data
clustering1 <- c(rep(1, 5), rep(2, 10), rep(3, 10))
clustering2 <- c(rep(1, 6), rep(2, 6), rep(3, 4), rep(4, 9))
dyn.cross(table(clustering1, clustering2)) # no crossings
dyn.cross(table(clustering1, clustering2)[c(2, 1, 3), ])

flatVSflat: Comparison of two flat clusterings

Description

flatVSflat carries out the comparison and visualisation of two flat clusterings. The nodes in each partitioning are represented as nodes in the two layers of a bi-graph. The sizes of the intersection between clusters are reflected in the edge thickness. The number of edge crossings is minimised heuristically using the barycentre algorithm alternatively on each side.
Usage

flatVSflat(weights, coord1 = NULL, coord2 = NULL, max.iter = 24, h.min = 0.1, 
plotting = TRUE, horiz = FALSE, offset = 0.1, line.wd = 3, point.sz = 2, 
evenly = FALSE, main = "", xlab = "", ylab = "", col = NULL, ...)

Arguments

weights a matrix containing the weights of the edges in the bigraph, which represent the overlaps between clusters in the two partitions.
coord1 a vector indicating the coordinates of the nodes in the first layer of the bi-graph. If not provided, then the nodes are initially equally spaced.
coord2 a vector indicating the coordinates of the nodes in the second layer of the bi-graph. If not provided, then the nodes are initially equally spaced.
max.iter an integer stating the maximum number of runs of the barycentre heuristic on both layers of the bi-graph.
h.min minimum separation between nodes in the same layer; if the barycentre algorithm sets two nodes to be less than this distance apart, then the second node and the following ones are shifted (downwards, in the vertical layout, and to the right, in the horizontal layout).
plotting a Boolean parameter which yields the bi-graph if TRUE.
horiz a Boolean argument for displaying a vertical (default) or horizontal layout.
offset a numerical parameter that sets the separation between the nodes and their labels. It is set to 0.1 by default.
line.wd a numerical parameter that fixes the width of the thickest edge(s); the rest are drawn proportionally to their weights; 3 by default.
point.sz a numerical parameter that fixes the size of the nodes in the bigraph; 2 by default.
evenly a Boolean parameter; if TRUE the coordinate values are ignored, and the nodes are drawn evenly spaced, according to the ordering obtained by the algorithm. It is set to FALSE by default.
main graphical parameter as in plot.
xlab graphical parameter as in plot.
ylab graphical parameters as in plot.
col graphical parameters as in plot.
... further graphical parameters.

Details

As the iterations of the algorithm run the coordinates of the nodes in a single layer are updated. For a given partition, each node is assigned a new position, the gravity-centre, using the barycentre algorithm; then, the nodes in the corresponding layer are reordered according to the new positions. If the gravity-centres cause two consecutive nodes to be less than h.min apart, the coordinates of the second and all the following ones are shifted. Additionally, to improve the results of the algorithm the following strategy is also used after running the barycentre algorithm on each side: consecutive nodes are swapped if this transposition leads to a reduction in the number of edge crossings. The algorithm runs until there is no improvement in the number of crossings or until the maximum number of iterations is reached. The rownames and colnames of matrix weights contain the cluster labels. The ordering in the layout is over-imposed by the coordinate values, therefore, the names (in the coordinates) and row-/col-names (in the contingency table) should coincide.
Value

a list of components including:

- icross: the number of edge crossings before running the barycentre algorithm.
- fcross: the number of edge crossings after running the barycentre algorithm.
- coord1: a vector containing the coordinates for each node in the first layer.
- coord2: a vector containing the coordinates for each node in the second layer.

Author(s)

Aurora Torrente <aurora@ebi.ac.uk> and Alvis Brazma <brazma@ebi.ac.uk>

References


See Also

flatVShier, barycentre

Examples

```r
# simulated data
clustering1 <- c(rep(1, 5), rep(2, 10), rep(3, 10))
clustering2 <- c(rep(1:4, 5), rep(1, 5))
weights <- table(clustering1, clustering2)
flatVSflat(table(clustering1, clustering2))
```

Description

flatVShier carries out the comparison and visualisation of the relationships between a hierarchical and a flat clusterings. The hierarchical one is shown either as a complete or pruned tree, whose collapsed branches are nodes on the left hand side layer of a bi-graph. The flat clusters are represented on the right hand side. Branches and flat clusters are connected with edges, whose thickness represents the number of elements common to both sets. The number of edge crossings is minimised using the barycentre algorithm on the right hand side; also, the children corresponding to the last split in the dendrogram when exploring it by depth-first search are swapped if this decreases the number of crossings.
Usage

flatVShier(tree, flat.clustering, flat.order = NULL, look.ahead = 2,
          score.function = "crossing", expanded = FALSE, expression = NULL,
          greedy = TRUE, layout = NULL, pausing = TRUE, verbose = TRUE,
          greedy.colours = NULL, h.min = 0.04, labels = NULL, max.branches = 100,
          line.wd = 3, cex.labels = 1, main = NULL, ramp = NULL)

Arguments

tree
  an hclust object, or structure that can be converted to hclust object, correspond-
  ing to a data set of size N.

flat.clustering
  a vector of length N containing the labels for each of the N objects clustered.

flat.order
  an optional vector containing the initial ordering for the flat clusters (from bot-
  tom upward).

look.ahead
  the number of steps allowed to look further after finding a parent-node whose
  score is better that that of its children.

score.function
  a string specifying whether the decision to split a given branch is based on the
  aesthetics ('crossing') or on the information theory ('it').

expanded
  a Boolean parameter to state whether the hierarchical tree is displayed complete
  or pruned. FALSE by default.

expression
  a matrix containing the expression data from which the dendrogram and the flat
  partitioning were obtained. If provided, and argument expanded is set to TRUE,
  the heatmap of the data is represented.

greedy
  a Boolean argument; if TRUE, the branches produced by the optimal cutoffs are
  used to construct superclusters that will be mapped to superclusters on the flat
  side with the greedy algorithm in SCmapping.

layout
  a vector containing 3 or 2 components, depending on whether the heatmap is
  plotted or not. Each coordinate provides the value on the X axis for locating
  the heatmap, the colour bar representing pruned branches, and the bigraph. Pro-
  vided vectors are increasingly ordered to keep the layout of the plot. By default,
  the X values are 1, 3, (5).

pausing
  a Boolean argument; if TRUE, each step in the comparison is plotted and fol-
  lowed by a pause.

verbose
  a Boolean argument; if TRUE, the situation in each iteration is described.

greedy.colours
  an optional vector containing the colours for each of the superclusters if the
  greedy algorithm is used; if the length of this vector is smaller than that of the
  number of resulting superclusters p, then it is recycled.

h.min
  minimum separation between nodes in the flat layer; if the barycentre algorithm
  sets two nodes to be less than this distance apart, then the second node and the
  following ones are shifted (upwards).

labels
  an optional vector containing labels for the leaves of the tree.

max.branches
  an integer stating the maximum number of branches allowed in the dendogram.

line.wd
  a numerical parameter that fixes the width of the thickest edge(s); the rest are
drawn proportionally to their weights; 3 by default.

cex.labels
  a number indicating the magnification for the labels of the flat clusters and the
  branches in the hierarchical tree.
main  an optional character string for the title of the plot.
ramp  a vector with two components containing the two colours used to define the palette for the heatmap.

Details
The method cuts different branches of the tree at ‘optimal’ levels, which may be different at different branches, to find the best matches with the flat clustering. The method explores the tree depth-first, starting from the root. In each iteration the goal is to decide whether the branch under consideration (the parent node) is to be split. To that end, the user selects a scoring function based on the bi-graph aesthetics (‘crossing’) or an alternative based on mutual information between the flat and hierarchical clusterings (‘it’). The selected score is first computed for the parent-node. Next it is replaced by its children; the barycentre algorithm, with the swapping strategy, is used on the flat side of the bi-graph. Later, the children in the tree are swapped and the positions on the flat side are likewise updated. The best score obtained by any of these layouts in the children tree is compared to the score of the parent-tree, sp. If it is better, then the splitting is allowed and the tree is subsequently explored. Otherwise, the splitting is discarded, unless it is allowed to look ahead. In that case, the score for the tree with one of the children of the parent-node replaced by its own children is compared to sp; this is repeated until we get a better score for the children or until the maximum number of looking-ahead steps is reached. After the optimal cut-offs are found, it is possible to run a greedy algorithm to determine sets of clusters from each side which have a large overlap. These sets, referred to as superclusters, determine the mapping between the two clusterings.

Value
a list of components including:

tree.partition  a vector of length N stating the branch each element belongs to.
tree.s.clustering  a vector of length N stating the supercluster on the tree side each element belongs to. If greedy=FALSE this component is not returned.
flat.s.clustering  a vector of length N stating the supercluster on the flat side each element belongs to. If greedy=FALSE this component is not returned.
tree.merging  a list of p components; the j-th element contains the labels of the tree that have been merged to produce the j-th supercluster. If greedy=FALSE this component is not returned.
flat.merging  a list of p components; the j-th element contains the labels of the flat clusters that have been merged to produce the j-th supercluster. If greedy=FALSE this component is not returned.
dendrogram  an hclust object with the appropriate ordering of the branches to minimise the number of crossings.

Author(s)
Aurora Torrente <aurora@ebi.ac.uk> and Alvis Brazma <brazma@ebi.ac.uk>

References
insert

Insert a set of values at a given position of a vector

Description

insert introduces a vector at a given position of another vector, displacing to the right all values from that position onwards.

Usage

insert(vect, position, value)

Arguments

- vect: the vector in which to insert additional values.
- position: the position of vector vect at which to insert additional values.
- value: the values to be inserted in the vector vect.

Details

The value of position does not need to be a number smaller than or equal to the length of vect, as the missing values will be denoted as NA.

Value

- new.vector: the vector resulting after inserting value at the position determined by position.
SCmapping

Author(s)
Aurora Torrente <aurora@ebi.ac.uk> and Alvis Brazma <brazma@ebi.ac.uk>

Examples

```r
# simulated data
v1 <- 1:10
v2 <- insert(v1, 4, 0)
v2 <- insert(v1, 1, rep(0, 5))
v2 <- insert(v1, 11, "A")
v2 <- insert(v1, 12, "A")
```

SCmapping

Construction of the superclusters and the one-to-one mapping between them

Description

SPmapping identifies groups of clusters from two flat partitionings that have the largest common intersections. These groups are found by following a greedy strategy: all edges incident to each cluster are removed except for the one(s) with highest weight; then the connected components in the resulting bi-graph define the correspondences of superclusters.

Usage

```r
SCmapping(clustering1, clustering2, plotting = TRUE, h.min = 0.1, line.wd = 3,
          point.sz = 3, offset = 0.1, evenly = TRUE, horiz = FALSE, max.iter = 24,
          node.col = NULL, edge.col = NULL, ...)
```

Arguments

- `clustering1`: a vector indicating the cluster in which each point is allocated in the first flat partitioning.
- `clustering2`: a vector indicating the cluster in which each point is allocated in the second flat partitioning.
- `plotting`: a Boolean parameter which leads to the representation of the bi-graph if TRUE.
- `h.min`: the minimum separation between nodes in the same layer; if the barycentre algorithm sets two nodes to be less than this distance apart, then the second node and the following ones are shifted (downwards, in the vertical layout, and to the right, in the horizontal layout).
- `line.wd`: a numerical parameter that fixes the width of the thickest edge, according to the weights; 3 by default.
- `point.sz`: a numerical parameter that fixes the size of the nodes in the bi-graph; 2 by default.
- `offset`: a numerical parameter that sets the separation between the nodes and their labels. It is set to 0.1 by default.
- `evenly`: a Boolean parameter; if TRUE the coordinate values are ignored, and the nodes are drawn evenly spaced, according to the ordering obtained by the barycentre algorithm. It is set to FALSE by default.
horiz  a Boolean argument for vertical (default) or horizontal layout.
max.iter  an integer stating the maximum number of runs of the barycentre heuristic on both layers of the bi-graph.
node.col  defines the colour of nodes from both layers.
edge.col  sets the colour of the edges.
... further graphical parameters can be passed to the function.

Details

The one-to-one mapping between groups of clusters from two different flat partitionings is computed with a greedy algorithm: firstly, for each node the edge with the highest weight is taken, and secondly, the connected components in the edge-reduced bi-graph are found, so that each connected component corresponds to a pair of superclusters with a large overlap.

Value

a list containing:
s.clustering1  a vector indicating the supercluster in which each point is allocated in the first superclustering.
s.clustering2  a vector indicating the supercluster in which each point is allocated in the second superclustering.
merging1  a list of p elements, whose j-th component contains the labels of the initial clusters from the first partitioning that have been merged to produce the j-th supercluster in the left layer of the bi-graph.
merging2  a list of p elements, whose j-th component contains the labels of the initial clusters from the second partitioning that have been merged to produce the j-th supercluster in the right layer of the bi-graph.
weights  a pxp matrix containing the size of the intersections between the superclusters.

Author(s)

Aurora Torrente <aurora@ebi.ac.uk> and Alvis Brazma <brazma@ebi.ac.uk>

References


See Also

barycentre, flatVSflat, flatVShier

Examples

```r
### computation and visualisation of superclusters
# simulated data
clustering1 <- c(rep(1, 5), rep(2, 10), rep(3, 10))
clustering2 <- c(rep(1, 6), rep(2, 6), rep(3, 4), rep(4, 9))
mapping <- SCmapping(clustering1, clustering2)
```
score.crossing

Computation of the aesthetics-based score of the parent and the children trees

Description

score.crossing computes the value of the scoring function based on the aesthetics of the bi-graph formed when comparing a dendrogram and a flat clustering, for both the parent-tree and the children-tree; the children-tree consists of the same branches as the parent-tree, except for the parent node, that has been split and replaced by some of its descendants.

Usage

score.crossing(weight.1, weight.2, N.cross)

Arguments

weight.1
a matrix of dimension \((m-1) \times n\) containing the intersection sizes (edge weights) between branches in the parent-tree and clusters from the flat partitioning. The ordering of the rows and columns is irrelevant for the computation of the score.

weight.2
a matrix of dimension \((m+k) \times n\) containing the intersection sizes (edge weights) between branches in the children-tree and clusters from the flat partitioning. \(k\) takes on values in 0, 1, ..., \(L\), where \(L\) is the maximum number of steps that the comparison algorithm is allowed to look ahead. The ordering of the rows corresponding to branches that are not descendants of the parent node must coincide with that of the matrix weight.1 after discarding the parent node. The ordering of the columns is irrelevant for the computation of the score.

N.cross
the number of edge crossings induced in the subtree formed by the descendants of the parent-node.

Details

The decision to split a given parent-node is based on achieving a better score for the children-tree than for the parent-tree. In the case of score.crossing, a better score is reflected by a larger value of the scoring function, which rewards few thicker edges, penalises many smaller edges, and accounts for the number of edge crossings in the resulting bigraph. The descendants of the parent-node considered in the children-tree are its two children if no look-ahead is carried out; otherwise, the descendants will reach subsequent generations and their number will increase by one at each look-ahead step.

Value

a list containing the following components:

sc1
the value of the scoring function for the parent-tree.

sc2
the value of the scoring function for the children-tree.

Author(s)

Aurora Torrente <aurora@ebi.ac.uk> and Alvis Brazma <brazma@ebi.ac.uk>
References

See Also
score.it, dyn.cross, flatVShier

Examples
```r
### simulated data
# replace the branch 'B2' by its children 'B4' and 'B5'
rep("B3", 10))
flat.clustering <- c(rep(1, 6), rep(2, 6), rep(3, 4), rep(4, 9))
# the ordering of flat clusters is '1','2','3' and '4'.
parent.weights <- table(parent.clustering, flat.clustering)
children.weights <- table(children.clustering, flat.clustering)
descendant.cross <- dyn.cross(children.weights[c("B4", "B5"), ])
score.crossing(parent.weights, children.weights, descendant.cross)
## better score for the parent.tree
```

See Also
cscore.it, dyn.cross, flatVShier

Examples
```r
### simulated data
# replace the branch 'B2' by its children 'B4' and 'B5'
rep("B3", 10))
flat.clustering <- c(rep(1, 6), rep(2, 6), rep(3, 4), rep(4, 9))
# the ordering of flat clusters is '1','2','3' and '4'.
parent.weights <- table(parent.clustering, flat.clustering)
children.weights <- table(children.clustering, flat.clustering)
descendant.cross <- dyn.cross(children.weights[c("B4", "B5"), ])
score.crossing(parent.weights, children.weights, descendant.cross)
## better score for the parent.tree
```

Description
score.it computes the value of the scoring function based on information theory and the mutual information shared by a dendrogram and the flat clustering which is compared to, for both the parent-tree and the children-tree; the children-tree consists of the same branches as the parent-tree, except for the parent node, that has been split and replaced by some of its descendants.

Usage
```r
score.it(weight.1, weight.2)
```

Arguments
```r
weight.1 a matrix of dimension (m-1)xn containing the intersection sizes (edge weights) between branches in the parent-tree and clusters from the flat partitioning. The ordering of the rows and columns is irrelevant for the computation of the score.
weight.2 a matrix of dimension (m+k)xn containing the intersection sizes (edge weights) between branches in the children-tree and clusters from the flat partitioning. k takes on values in 0,1,...,L, where L is the maximum number of steps that the comparison algorithm is allowed to look ahead. The ordering of the rows corresponding to branches that are not descendants of the parent node must coincide with that of the matrix weight.1 after discarding the parent node. The ordering of the columns is irrelevant for the computation of the score.
```
Details

The decision to split a given parent-node is based on achieving a better score for the children-tree than for the parent-tree. In the case of score.it, a better score is reflected by a smaller value of the scoring function, which is related to the average length of the messages that encode the information about one clustering contained in the other. The descendants of the parent-node considered in the children-tree are its two children if no look-ahead is carried out; otherwise, the descendants will reach subsequent generations and their number will increase by one at each look-ahead step.

Value

a list containing the following components:

- sc1: the value of the scoring function for the parent-tree.
- sc2: the value of the scoring function for the children-tree.

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References


See Also

score.crossing, flatVShier

Examples

```r
### simulated data
parent.clustering <- c(rep(1, 5), rep(2, 10), rep(3, 10))
# replace the branch '2' by children '4' and '5'
children.clustering<-c(rep(1,5),rep(4,3),rep(5,7),rep(3,10))
flat.clustering <- c(rep(1, 6), rep(2, 6), rep(3, 4), rep(4, 9))
score.it(table(parent.clustering, flat.clustering),
        table(children.clustering, flat.clustering))
## better score for the parent.tree
```
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