Package ‘runibic’

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Type Package

Title runibic: row-based biclustering algorithm for analysis of gene expression data in R

Version 1.24.0

Author Patryk Orzechowski, Artur Pańszczyk

Maintainer Patryk Orzechowski <patryk.orzechowski@gmail.com>

Description This package implements UbiBic algorithm in R. This biclustering algorithm for analysis of gene expression data was introduced by Zhenjia Wang et al. in 2016. It is currently considered the most promising biclustering method for identification of meaningful structures in complex and noisy data.

Depends R (>= 3.4.0), biclust, SummarizedExperiment

Imports Rcpp (>= 0.12.12), testthat, methods

Suggests knitr, rmarkdown, GEOquery, affy, airway, QUBIC

VignetteBuilder knitr

LinkingTo Rcpp

SystemRequirements C++11, GNU make

biocViews Microarray, Clustering, GeneExpression, Sequencing, Coverage

Encoding UTF-8

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NeedsCompilation yes

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BugReports http://github.com/athril/runibic/issues

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Description

This function retrieves the Longest Common Subsequence (LCS) between two integer vectors by backtracking the matrix obtained with dynamic programming.

Usage

backtrackLCS(x, y)

Arguments

x an integer vector
y an integer vector

Value

an integer vector containing the the Longest Common Subsequence (LCS) between vectors x and y (i.e. the values that appear in both x and y in the same order)

See Also

runibic pairwiseLCS calculateLCS

Examples

A <- c(1, 2, 3, 4, 5)
B <- c(1, 2, 4)
backtrackLCS(A, B)
BCUnibic-class

Class BCUnibic

Description

An S4 class to represent BCUnibic-class UniBic biclustering algorithm for numeric input. The class is intended to use with

See Also

runibic

BCUnibicD-class

Class BCUnibicD

Description

An S4 class BCUnibicD-class defines UniBic biclustering algorithm for discrete input.

calculateLCS

Calculate all Longest Common Subsequences between a matrix.

Description

This function computes unique pairwise Longest Common Subsequences between each row of input matrix. The function outputs a list sorted by Longest Common Subsequences (LCS) length. The output list contains the length of calculated LCS, indices, of the first and second rows between which LCS was calculated. The function uses two different sorting methods. The default one uses Fibonacci Heap used in original implementation of Unibic, the second one uses standard sorting algorithm from C++ STL.

Usage

calculateLCS(discreteInput, useFibHeap = TRUE)

Arguments

discreteInput is a input discrete matrix
useFibHeap boolean value for choosing which sorting method should be used in sorting of output

Value

a list with sorted values based on calculation of the length of LCS between all pairs of rows
See Also

runibic backtrackLCS pairwiseLCS

descriptions

Examples

A <- matrix(c(4, 3, 1, 2, 5, 8, 6, 7), nrow=2, byrow=TRUE)
calculateLCS(A, TRUE)

calculateLCS

cluster

Calculate biclusters from sorted list of LCS scores and row indices

Description

This function search for biclusters in the input matrix. The calculations are based on the integer matrix with indexes indicating positions of j-th smallest element in each row and the results from calculations of Longest Common Subsequence between all rows in the input matrix. The parameteres of this function can be obtained from other functions provided by this package.

Usage

cluster(discreteInput, discreteInputValues, scores, geneOne, geneTwo, rowNumber, colNumber)

Arguments

discreteInput an integer matrix with indices of sorted columns
discreteInputValues an integer matrix with discrete values
scores a numeric vector with LCS length
geneOne a numeric vector with first row indexes from pairwise LCS calculation
geneTwo a numeric vector with second row indexes from pairwise LCS calculation
rowNumber a int with number of rows in the input matrix
colNumber a int with number of columns in the input matrix

Value

a list with information of found biclusters

See Also

runibic calculateLCS unisort
**Examples**

```r
A <- matrix(c(4,3,1,2,5,8,6,7,9,10,11,12), nrow=4, byrow=TRUE)
iA <- unisort(A)
lcsResults <- calculateLCS(A)
cluster(iA, A, lcsResults$lcslen, lcsResults$a, lcsResults$b, nrow(A), ncol(A))
```

**Description**

This function calculates the matrix with Longest Common Subsequence (LCS) between two numeric vectors. From given matrix we can locate the size of the Longest Common Subsequence in the last column in the last row.

**Usage**

```r
pairwiseLCS(x, y)
```

**Arguments**

- `x`: an integer vector
- `y`: an integer vector

**Value**

A matrix computed using dynamic programming that stores the Longest Common Subsequence (LCS) between two vectors A and B.

**See Also**

`runibic`, `calculateLCS`, `backtrackLCS`

**Examples**

```r
A <- c(1, 2, 3, 4, 5)
B <- c(1, 2, 4)
pairwiseLCS(A, B)
```
**runibic**

**runibic: parallel row-based biclustering algorithm for analysis of gene expression data in R**

### Description

**runibic** is a package that contains much faster parallel version of one of the most accurate biclustering algorithms, UniBic. The original method was reimplemented from C to C++11, OpenMP was added for parallelization.

If you use this package, please cite it as: Patryk Orzechowski, Artur Pańszczyk, Xiuzhen Huang, Jason H Moore; "runibic: a Bioconductor package for parallel row-based biclustering of gene expression data"; Bioinformatics, 2018, bty512, doi: https://doi.org/10.1093/bioinformatics/bty512

Each of the following functions **BCUnibic**, **BCUnibicD**, **runibic** perform biclustering using UniBic biclustering algorithm. The major difference between the functions is that **BCUnibicD** require a discretized matrix, whilst **BCUnibic** (or **runibic**) could be applied to numeric one.

### Usage

- **BCUnibic**
  ```r
  BCUnibic(x = NULL, t = 0.95, q = 0, f = 1, nbic = 100, div = 0, useLegacy = FALSE)
  ```

- **BCUnibicD**
  ```r
  BCUnibicD(x = NULL, t = 0.95, q = 0, f = 1, nbic = 100, div = 0, useLegacy = FALSE)
  ```

- **runibic**
  ```r
  runibic(x = NULL, t = 0.95, q = 0, f = 1, nbic = 100, div = 0, useLegacy=FALSE)
  ```

### Arguments

- **x**
  numeric or integer matrix (depends on the function)

- **t**
  consistency level of the block (0.5-1.0].

- **q**
  a double value for quantile discretization

- **f**
  filtering overlapping blocks (default 1 do not remove any blocks)

- **nbic**
  maximum number of biclusters in output

- **div**
  number of ranks for up(down)-regulated genes: default: 0==ncol(x)

- **useLegacy**
  boolean value for using legacy parameter settings

### Details

For a given input matrix we first perform discretization and create index matrix using **runiDiscretize** function. The discretization is performed taking into account quantiles of the data. The resulting index matrix allows to detect order-preserving trends between each pair of the rows irrespective to the order of columns. After the ranking, the matrix is split by rows into subgroups based on the significance of the future biclusters. In each of the chunks, we calculate pairwise calculations of Longest Common Subsequence LCS between all pairs of the rows. LCS calculations are performed using dynamic programming and determine the longest order-preserving trend between each pair.
of the rows. After partitioning the matrix strict order-preserving biclusters are determined and later expanded to approximate-trend biclusters within `cluster` function.

This package provides 3 main functions: `runibic` and `BCUnibic` perform UniBic biclustering algorithm on numeric data, whilst `BCUnibicD` could be applied to integer ones. The latter two methods are compatible with `Biclust` class.

**Value**

`Biclust` object with detected biclusters

**Functions**

- `BCUnibic`: `BCUnibic` performs biclustering using UniBic on numeric matrix. It is intended to use as a method called from `biclust`.
- `BCUnibicD`: perform biclustering using UniBic on integer matrix. It is intended to use as a method called from `biclust`.
- `runibic`: perform biclustering using UniBic on numeric matrix.

**Author(s)**

Patryk Orzechowski patryk.orzechowski@gmail.com, Artur Pańszczyk panszczyk.artur@gmail.com

**References**


**See Also**

`runiDiscretize` set_runibic_params `BCUnibic-class` `BCUnibicD-class` `unisort`

**Examples**

```r
A <- matrix(replicate(100, rnorm(100)), nrow=100, byrow=TRUE)
runibic(A)
BCUnibic(A)
BCUnibic(A, t = 0.95, q = 0, f = 1, nbic = 100, div = 0)
B <- runiDiscretize(A)
runibic(B)
BCUnibicD(B, t = 0.95, q = 0, f = 1, nbic = 100, div = 0)
biclust::biclust(A, method=BCUnibic(), t = 0.95, q = 0, f = 1, nbic = 100, div = 0)
biclust::biclust(B, method=BCUnibicD(), t = 0.95, q = 0, f = 1, nbic = 100, div = 0)
```
runiDiscretize \hspace{1cm} \textit{Discretize an input matrix}

**Description**

This function discretizes the input matrix. \texttt{runiDiscretize} uses parameters: 'div' and 'q', which are set by \texttt{set_runibic_params} function. The function returns a discrete matrix with given number of ranks based on the parameter div. In contrast to \texttt{biclust::discretize} the function takes into consideration the quantile parameter 'q'. When 'q' parameter is higher or equal 0.5 a simple discretization is used with equal sizes of the levels using the quantiles. If 'q' parameter is lower than 0.5 we use up(down)-regulated discretization divided into three parts.

**Usage**

\texttt{runiDiscretize(x)}

**Arguments**

\texttt{x} \hspace{1cm} \text{a numeric matrix}

**Value**

a discretized matrix containing integers only

**See Also**

\texttt{set_runibic_params calculateLCS discretize}

**Examples**

\begin{verbatim}
A <- replicate(10, rnorm(20))
runiDiscretize(A)
\end{verbatim}

---

\texttt{set_runibic_params} \hspace{1cm} \textit{Set the parameters for runibic algorithm}

**Description**

runibic function for setting parameters

**Usage**

\texttt{set_runibic_params(t = 0.85, q = 0, f = 1, nbic = 100L, div = 0L, useLegacy = FALSE)}
unisort

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>t</td>
<td>consistency level of the block (0.5-1.0]</td>
</tr>
<tr>
<td>q</td>
<td>a double value for quantile discretization</td>
</tr>
<tr>
<td>f</td>
<td>filtering overlapping blocks, default 1 (do not remove any blocks)</td>
</tr>
<tr>
<td>nbic</td>
<td>maximum number of biclusters in output</td>
</tr>
<tr>
<td>div</td>
<td>number of ranks as which we treat the up(down)-regulated value: default: 0==ncol(x)</td>
</tr>
<tr>
<td>useLegacy</td>
<td>boolean value for legacy parameters management</td>
</tr>
</tbody>
</table>

Value

NULL (an empty value)

See Also

runibic

Examples

set_runibic_params(0.85, 0, 1, 100, 0, FALSE)

A <- matrix(c(4, 3, 1, 2, 5, 8, 6, 7), nrow=2, byrow=TRUE)
unisort(A)

Description

This function sorts separately each row of an integer matrix and returns a matrix in which the value in i-th row and j-th column represent the index of the j-th smallest value of the i-th row.

Usage

unisort(x)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>x</td>
<td>a integer matrix</td>
</tr>
</tbody>
</table>

Value

a integer matrix with indexes indicating positions of j-th smallest element in each row

See Also

runibic calculateLCS runiDiscretize

Examples

A <- matrix(c(4, 3, 1, 2, 5, 8, 6, 7), nrow=2, byrow=TRUE)
unisort(A)
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