

# Package ‘runibic’

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**Type** Package

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

**Version** 1.29.0

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**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

**License** MIT + file LICENSE

**LazyData** true

**NeedsCompilation** yes

**URL** <http://github.com/athril/runibic>

**BugReports** <http://github.com/athril/runibic/issues>

**RoxygenNote** 6.0.1

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backtrackLCS	<i>Retrieving a Longest Common Subsequence between two integer vectors.</i>
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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)
```

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BCUnibic-class	<i>Class BCUnibic</i>
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**Description**

An S4 class to represent [BCUnibic-class](#) UniBic biclustering algorithm for numeric input. The class is intended to use with

**See Also**

[runibic](#)

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BCUnibicD-class	<i>Class BCUnibicD</i>
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**Description**

An S4 class [BCUnibicD-class](#) defines UniBic biclustering algorithm for discrete input.

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calculateLCS	<i>Calculate all Longest Common Subsequences between a matrix.</i>
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**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](#)

**Examples**

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

---

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 paramteres 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**

```
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))
```

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pairwiseLCS	<i>Calculate a matrix of Longest Common Subsequence (LCS) between a pair of numeric vectors</i>
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**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**

```
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**

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

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runibic	<i>runibic: parallel row-based biclustering algorithm for analysis of gene expression data in R</i>
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## 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(x = NULL, t = 0.95, q = 0, f = 1, nbic = 100, div = 0,
         useLegacy = FALSE)
```

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

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

## Arguments

<code>x</code>	numeric or integer matrix (depends on the function)
<code>t</code>	consistency level of the block (0.5-1.0].
<code>q</code>	a double value for quantile discretization
<code>f</code>	filtering overlapping blocks (default 1 do not remove any blocks)
<code>nbic</code>	maximum number of biclusters in output
<code>div</code>	number of ranks for up(down)-regulated genes: default: $0 == \text{ncol}(x)$
<code>useLegacy</code>	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)

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## References

Wang, Zhenjia, et al. "UniBic: Sequential row-based biclustering algorithm for analysis of gene expression data." *Scientific reports* 6 (2016): 23466.

Patryk Orzechowski, Artur Pańszczyk, Xiuzhen Huang, Jason H. Moore: "runibic: a Bioconductor package for parallel row-based biclustering of gene expression data", *bioRxiv* (2017): 210682, doi: <https://doi.org/10.1101/210682>

## See Also

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

## Examples

```
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)
```

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runiDiscretize	<i>Discretize an input matrix</i>
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### Description

This function discretizes the input matrix. `runiDiscretize` uses parameters: 'div' and 'q', which are set by `set_runibic_params` function. The function returns a discrete matrix with given number of ranks based on the parameter `div`. In contrast to `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

```
runiDiscretize(x)
```

### Arguments

x                    a numeric matrix

### Value

a discretized matrix containing integers only

### See Also

[set\\_runibic\\_params](#) [calculateLCS](#) [discretize](#)

### Examples

```
A <- replicate(10, rnorm(20))
runiDiscretize(A)
```

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set_runibic_params	<i>Set the parameters for runibic algorithm</i>
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### Description

runibic function for setting parameters

### Usage

```
set_runibic_params(t = 0.85, q = 0, f = 1, nbic = 100L, div = 0L,
  useLegacy = FALSE)
```



**Arguments**

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 as which we treat the up(down)-regulated value: default: 0==ncol(x)
useLegacy	boolean value for legacy parameters management

**Value**

NULL (an empty value)

**See Also**

[runibic](#)

**Examples**

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

---

unisort

*Computing the indexes of j-th smallest values of each row*

---

**Description**

This function sorts separately each row of a 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**

x a integer matrix

**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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