Package ‘biclustermd’

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Type Package

Title Biclustering with Missing Data

Version 0.2.3

Maintainer John Reisner <`johntreisner@gmail.com`>

Description Biclustering is a statistical learning technique that simultaneously partitions and clusters rows and columns of a data matrix. Since the solution space of biclustering is in infeasible to completely search with current computational mechanisms, this package uses a greedy heuristic. The algorithm featured in this package is, to the best our knowledge, the first biclustering algorithm to work on data with missing values. Li, J., Reisner, J., Pham, H., Olafsson, S., and Vardeman, S. (2020) Biclustering with Missing Data. Information Sciences, 510, 304–316.

URL `https://github.com/jreisner/biclustermd`

BugReports `https://github.com/jreisner/biclustermd/issues`

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Author John Reisner [cre, aut, cph],
Hieu Pham [ctb, cph],
Jing Li [ctb, cph]

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`biclustermd-package` *biclustermd: A package to bicluster data with missing values*

Description

The main function is `biclustermd()`. Results can be plotted with `autoplot()` and `as.Biclust()` converts results to Biclust objects.

`as.Biclust` *Convert a* `biclustermd` *object to a* `Biclust` *object*

Description

Convert a `biclustermd` object to a `Biclust` object

Usage

```
as.Biclust(object)
```

Arguments

`object`	The `biclustermd` object to convert to a `Biclust` object

Value

Returns an object of class `Biclust`.

Examples

```
data("synthetic")

bc <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2,
                miss_val = mean(synthetic, na.rm = TRUE),
                miss_val_sd = sd(synthetic, na.rm = TRUE),
                col_min_num = 2, row_min_num = 2,
                col_num_to_move = 1, row_num_to_move = 1,
                max.iter = 10)
bc

as.Biclust(bc)

# biclust::drawHeatmap won't work since it doesn't exclude NAs
## Not run: biclust::drawHeatmap(synthetic, as.Biclust(bc), 6)

# bicluster 6 is in the top right-hand corner here:
autoplot(bc)
# compare with bicust::drawHeatmap2:
biclust::drawHeatmap2(synthetic, as.Biclust(bc), 6)

# bicluster 3 is in the bottom right-hand corner here:
autoplot(bc)
# compare with bicust::drawHeatmap2:
biclust::drawHeatmap2(synthetic, as.Biclust(bc), 3)
```

`autoplot.biclustermd` *Make a heatmap of sparse biclustering results*

Description

Make a heatmap of sparse biclustering results

Usage

```
## S3 method for class 'biclustermd'
autoplot(
  object,
  axis.text = NULL,
  reorder = FALSE,
  transform_colors = FALSE,
  c = 1/6,
  cell_alpha = 1/5,
  col_clusts = NULL,
  row_clusts = NULL,
  ...
)
```

Arguments

`object`	An object of class "biclustermd".
`axis.text`	A character vector specifying for which axes text should be drawn. Can be any of `"x"`, `"col"` for columns, `"y"`, `"row"` for rows, or any combination of the four. By default this is `NULL`; no axis text is drawn.
`reorder`	A logical. If `TRUE`, heatmap will be sorted according to the cell-average matrix, `A`.
`transform_colors`	If equals `TRUE` then the data is scaled by `c` and run through a standard normal cdf before plotting. If `FALSE` (default), raw data values are used in the heat map.
`c`	Value to scale the data by before running it through a standard normal CDF. Default is 1/6.
`cell_alpha`	A scalar defining the transparency of shading over a cell and by default this equals 1/5. The color corresponds to the cell mean.
`col_clusts`	A vector of column cluster indices to display. If `NULL` (default), all are displayed.
`row_clusts`	A vector of row cluster indices to display. If `NULL` (default), all are displayed.
`...`	Arguments to be passed to `geom_vline()` and `geom_hline()`.

Value

An object of class ggplot.

Examples

```
data("synthetic")

bc <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2,
                miss_val = mean(synthetic, na.rm = TRUE),
                miss_val_sd = sd(synthetic, na.rm = TRUE),
                col_min_num = 2, row_min_num = 2,
                col_num_to_move = 1, row_num_to_move = 1,
                max.iter = 10)
bc
autoplot(bc)

autoplot(bc, axis.text = c('x', 'row')) +
    ggplot2::scale_fill_distiller(palette = "Spectral", na.value = "white")

# Complete shading
autoplot(bc, axis.text = c('col', 'row'), cell_alpha = 1)

# Transformed values and no shading
autoplot(bc, transform_colors = TRUE, c = 1/20, cell_alpha = 0)

# Focus on row cluster 1 and column cluster 2
autoplot(bc, col_clusts = 2, row_clusts = 1)
```

`autoplot.biclustermd_sim`

Plot similarity measures between two consecutive biclusterings.

Description

Creates a ggplot of the three similarity measures used in `biclustermd::bicluster()` for both row and column dimensions.

Usage

```
## S3 method for class 'biclustermd_sim'
autoplot(object, similarity = NULL, facet = TRUE, ncol = NULL, ...)
```

Arguments

`object`	Object of class "biclustermd_sim"
`similarity`	A character vector indicating which similarity measure to plot. Can be any of `"Rand"`, `"HA"`, `"Jaccard"`, or `"used"`. If `"used"`, plot only the measure used as the stopping condition in the algorithm). By default (`NULL`) all three are plotted. When plotted, the used measure will have an asterisk.
`facet`	If `TRUE` (default), each similarity measure will be in its own plot. if `FALSE`, all three similarity measures for rows and columns are given in one plot.

`ncol`	If faceting, the number of columns to arrange the plots in.
`...`	Arguments to pass to `ggplot2::geom_point()`

Value

A ggplot object.

Examples

```
data("synthetic")

bc <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2,
                miss_val = mean(synthetic, na.rm = TRUE),
                miss_val_sd = sd(synthetic, na.rm = TRUE),
                col_min_num = 2, row_min_num = 2,
                col_num_to_move = 1, row_num_to_move = 1,
                max.iter = 10)
bc
autoplot(bc$Similarities, ncol = 1)
```

`autoplot.biclustermd_sse`

Plot sums of squared errors (SSEs) consecutive biclustering iterations.

Description

Creates a ggplot of the decrease in SSE recorded in `biclustermd::bicluster()`.

Usage

```
## S3 method for class 'biclustermd_sse'
autoplot(object, ...)
```

Arguments

`object`	Object of class "biclustermd_sse" with columns "Iteration" and "SSE"
`...`	Arguments to pass to `ggplot2::geom_point()`

Value

A ggplot object.

Examples

```
data("synthetic")

bc <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2,
                  miss_val = mean(synthetic, na.rm = TRUE),
                  miss_val_sd = sd(synthetic, na.rm = TRUE),
                  col_min_num = 2, row_min_num = 2,
                  col_num_to_move = 1, row_num_to_move = 1,
                  max.iter = 10)
bc
autoplot(bc$SSE)
```

`biclustermd` *Bicluster data with non-random missing values*

Description

Bicluster data with non-random missing values

Usage

```
biclustermd(
  data,
  row_clusters = floor(sqrt(nrow(data))),
  col_clusters = floor(sqrt(ncol(data))),
  miss_val = mean(data, na.rm = TRUE),
  miss_val_sd = 1,
  similarity = "Rand",
  row_min_num = floor(nrow(data)/row_clusters),
  col_min_num = floor(ncol(data)/col_clusters),
  row_num_to_move = 1,
  col_num_to_move = 1,
  row_shuffles = 1,
  col_shuffles = 1,
  max.iter = 100,
  verbose = FALSE
)
```

Arguments

`data`	Dataset to bicluster. Must to be a data matrix with only numbers and missing values in the data set. It should have row names and column names.
`row_clusters`	The number of clusters to partition the rows into. The default is `floor(sqrt(nrow(data)))`.
`col_clusters`	The number of clusters to partition the columns into. The default is `floor(sqrt(ncol(data)))`.
`miss_val`	Value or function to put in empty cells of the prototype matrix. If a value, a random normal variable with sd = `miss_val_sd` is used each iteration. By default, this equals the mean of `data`.

`miss_val_sd`	Standard deviation of the normal distribution `miss_val` follows if `miss_val` is a number. By default this equals 1.
`similarity`	The metric used to compare two successive clusterings. Can be "Rand" (default), "HA" for the Hubert and Arabie adjusted Rand index or "Jaccard". See RRand for details.
`row_min_num`	Minimum row prototype size in order to be eligible to be chosen when filling an empty row prototype. Default is `floor(nrow(data) / row_clusters)`.
`col_min_num`	Minimum column prototype size in order to be eligible to be chosen when filling an empty row prototype. Default is `floor(ncol(data) / col_clusters)`.
`row_num_to_move`	Number of rows to remove from the sampled prototype to put in the empty row prototype. Default is 1.
`col_num_to_move`	Number of columns to remove from the sampled prototype to put in the empty column prototype. Default is 1.
`row_shuffles`	Number of times to shuffle rows in each iteration. Default is 1.
`col_shuffles`	Number of times to shuffle columns in each iteration. Default is 1.
`max.iter`	Maximum number of iterations to let the algorithm run for.
`verbose`	Logical. If TRUE, will report progress.

Value

A list of class `biclustermd`:

`params`	a list of all arguments passed to the function, including defaults.
`data`	the inputted two way table of data.
`P0`	the initial column partition matrix.
`Q0`	the initial row partition matrix.
`InitialSSE`	the SSE of the original partitioning.
`P`	the final column partition matrix.
`Q`	the final row partition matrix.
`SSE`	a matrix of class biclustermd_sse detailing the SSE recorded at the end of each iteration.
`Similarities`	a data frame of class biclustermd_sim detailing the value of row and column similarity measures recorded at the end of each iteration. Contains information for all three similarity measures. This carries an attribute `"used"` which provides the similarity measure used as the stopping condition for the algorithm.
`iteration`	the number of iterations the algorithm ran for, whether `max.iter` was reached or convergence was achieved.
`A`	the final prototype matrix which gives the average of each bicluster.

References

Li, J., Reisner, J., Pham, H., Olafsson, S., and Vardeman, S. (2020) *Biclustering with Missing Data. Information Sciences, 510, 304–316.*

See Also

`rep_biclustermd`, `tune_biclustermd`

Examples

```
data("synthetic")
# default parameters
bc <- biclustermd(synthetic)
bc
autoplot(bc)

# providing the true number of row and column clusters
bc <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2)
bc
autoplot(bc)

# an example with the nycflights13::flights dataset
library(nycflights13)
data("flights")

library(dplyr)
flights_bcd <- flights %>%
  select(month, dest, arr_delay)

flights_bcd <- flights_bcd %>%
  group_by(month, dest) %>%
  summarise(mean_arr_delay = mean(arr_delay, na.rm = TRUE)) %>%
  spread(dest, mean_arr_delay) %>%
  as.data.frame()

rownames(flights_bcd) <- flights_bcd$month
flights_bcd <- as.matrix(flights_bcd[, -1])

flights_bc <- biclustermd(data = flights_bcd, col_clusters = 6, row_clusters = 4,
                  row_min_num = 3, col_min_num = 5,
                  max.iter = 20, verbose = TRUE)
flights_bc
```

`binary_vector_gen` *Make a binary vector with all values equal to zero except for one*

Description

Make a binary vector with all values equal to zero except for one

Usage

```
binary_vector_gen(n, i)
```

Arguments

`n`	Desired vector length.
`i`	Index whose value is one.

Value

A vector

`cell_heatmap` *Make a heat map of bicluster cell sizes.*

Description

Make a heat map of bicluster cell sizes.

Usage

```
cell_heatmap(x, ...)
```

Arguments

`x`	An object of class `biclustermd`.
`...`	Arguments to pass to `geom_tile()`

Examples

```
data("synthetic")

bc <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2,
                  miss_val = mean(synthetic, na.rm = TRUE),
                  miss_val_sd = sd(synthetic, na.rm = TRUE),
                  col_min_num = 2, row_min_num = 2,
                  col_num_to_move = 1, row_num_to_move = 1,
                  max.iter = 10)

cell_heatmap(bc)

cell_heatmap(bc) + ggplot2::scale_fill_viridis_c()
```

`cell_mse` *Make a data frame containing the MSE for each bicluster cell*

Description

Make a data frame containing the MSE for each bicluster cell

Usage

```
cell_mse(x)
```

Arguments

`x`	An object of class `biclustermd`.

Value

A data frame giving the row cluster, column cluster, the number of data points in each row and column cluster, the number of data points missing in the cell, and the cell MSE.

Examples

```
data("synthetic")
bc <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2,
                miss_val = mean(synthetic, na.rm = TRUE),
                miss_val_sd = sd(synthetic, na.rm = TRUE),
                col_min_num = 2, row_min_num = 2,
                col_num_to_move = 1, row_num_to_move = 1,
                max.iter = 10)
cell_mse(bc)
```

`cluster_iteration_sum_sse` *Calculate the sum cluster SSE in each iteration*

Description

Calculate the sum cluster SSE in each iteration

Usage

```
cluster_iteration_sum_sse(data, P, Q)
```

Arguments

`data`	The data being biclustered. Must to be a data matrix with only numbers and missing values in the data set. It should have row names and column names.
`P`	Matrix for column prototypes.
`Q`	Matrix for row prototypes.

Value

The SSE for the parameters specified.

`col.names` *A generic to gather column names*

Description

A generic to gather column names

Usage

```
col.names(x)
```

Arguments

`x`	an object to retrieve column names from

`col.names.biclustermd` *Get data matrix column names and their corresponding column cluster membership*

Description

Get data matrix column names and their corresponding column cluster membership

Usage

```
## S3 method for class 'biclustermd'
col.names(x)
```

Arguments

`x`	and object of class `biclustermd`

Value

a data frame with column names of the shuffled matrix and corresponding column cluster names.

Examples

```
data("synthetic")
# default parameters
bc <- biclustermd(synthetic)
bc
col.names(bc)
# this is a simplified version of the output for gather(bc):
library(dplyr)
gather(bc) %>% distinct(col_cluster, col_name)
```

`col_cluster_names` *Get column names in each column cluster*

Description

Get column names in each column cluster

Usage

```
col_cluster_names(x, data)
```

Arguments

`x`	Biclustering object to extract column cluster designation from
`data`	Data that contains the column names

Value

A data frame with two columns: `cluster` corresponds to the column cluster and `name` gives the column names in each cluster.

Examples

```
data("synthetic")
rownames(synthetic) <- letters[1:nrow(synthetic)]
colnames(synthetic) <- letters[1:ncol(synthetic)]
bc <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2,
                miss_val = mean(synthetic, na.rm = TRUE),
                miss_val_sd = sd(synthetic, na.rm = TRUE),
                col_min_num = 2, row_min_num = 2,
                col_num_to_move = 1, row_num_to_move = 1,
                max.iter = 10)
bc
```

`compare_biclusters` *Compare two biclusterings or a pair of partition matrices*

Description

Compare two biclusterings or a pair of partition matrices

Usage

```
compare_biclusters(bc1, bc2)
```

Arguments

`bc1`	the first biclustering or partition matrix. Must be either of class `biclustermd` or `matrix`.
`bc2`	the second biclustering or partition matrix. Must be either of class `biclustermd` or `matrix`.

Value

If comparing a pair of biclusterings, a list containing the column similarity indices and the row similarity indices, in that order. If a pair of matrices, a vector of similarity indices.

Examples

```
data("synthetic")
bc <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2)
bc2 <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2)

# compare the two biclusterings
compare_biclusters(bc, bc2)

# determine the similarity between initial and final row clusterings
compare_biclusters(bc$Q0, bc$Q)
```

`fill_empties_P` *Randomly select a column prototype to fill an empty column prototype with*

Description

Randomly select a column prototype to fill an empty column prototype with

Usage

```
fill_empties_P(data, obj, col_min_num = 10, col_num_to_move = 5)
```

Arguments

`data`	The data being biclustered. Must to be a data matrix with only numbers and missing values in the data set. It should have row names and column names.
`obj`	A matrix for column clusters, typically named P.
`col_min_num`	Minimum column prototype size in order to be eligible to be chosen when filling an empty column prototype. Default is 10.
`col_num_to_move`	Number of columns to remove from the sampled prototype to put in the empty column prototype. Default is 5.

Value

A matrix for column clusters, i.e., a P matrix.

`fill_empties_Q` *Randomly select a row prototype to fill an empty row prototype with*

Description

Randomly select a row prototype to fill an empty row prototype with

Usage

```
fill_empties_Q(data, obj, row_min_num = 10, row_num_to_move = 5)
```

Arguments

`data`	The data being biclustered. Must to be a data matrix with only numbers and missing values in the data set. It should have row names and column names.
`obj`	A matrix for row clusters, typically named Q
`row_min_num`	Minimum row prototype size in order to be eligible to be chosen when filling an empty row prototype. Default is 10.
`row_num_to_move`	Number of rows to remove from the sampled prototype to put in the empty row prototype. Default is 5.

Value

A matrix for row clusters, i.e., a Q matrix.

`format_partition` *Format a partition matrix*

Description

Formats a partition matrix so that subsets in a partition will be ordered by the value of the smallest in each subset

Usage

```
format_partition(P1)
```

Arguments

`P1`	A partition matrix.

Value

A formatted partition matrix.

`gather.biclustermd` *Gather a biclustermd object*

Description

Gather a biclustermd object

Usage

```
## S3 method for class 'biclustermd'
gather(
  data,
  key = NULL,
  value = NULL,
  ...,
  na.rm = FALSE,
  convert = FALSE,
  factor_key = FALSE
)
```

Arguments

`data`	a `biclustermd` object to gather.
`key`	unused; included for consistency with `tidyr` generic
`value`	unused; included for consistency with `tidyr` generic
`...`	unused; included for consistency with `tidyr` generic
`na.rm`	unused; included for consistency with `tidyr` generic
`convert`	unused; included for consistency with `tidyr` generic
`factor_key`	unused; included for consistency with `tidyr` generic

Value

A data frame containing the row names and column names of both the two-way table of data biclustered and the cell-average matrix.

Examples

```
data("synthetic")

bc <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2,
                miss_val = mean(synthetic, na.rm = TRUE),
                miss_val_sd = sd(synthetic, na.rm = TRUE),
                col_min_num = 2, row_min_num = 2,
                col_num_to_move = 1, row_num_to_move = 1,
                max.iter = 10)
gather(bc)

# bicluster 6 is in the top right-hand corner here:
autoplot(bc)

# bicluster 3 is in the bottom right-hand corner here:
autoplot(bc)
```

`jaccard_similarity` *Compute the Jaccard similarity coefficient for two clusterings*

Description

Compute the Jaccard similarity coefficient for two clusterings

Usage

```
jaccard_similarity(clus1, clus2)
```

Arguments

`clus1`	vector giving the first set of clusters
`clus2`	vector giving the second set of clusters

Value

a numeric

References

Milligan, G.W. and Cooper, M. C. (1986) *A study of the comparability of external criteria for hierarchical cluster analysis. Multivariate Behavioral Research, 21, 441-458.*

`mse_heatmap` *Make a heatmap of cell MSEs*

Description

Make a heatmap of cell MSEs

Usage

```
mse_heatmap(x, ...)
```

Arguments

`x`	An object of class `biclustermd`.
`...`	Arguments to pass to `geom_tile()`

Value

A ggplot object.

Examples

```
data("synthetic")
bc <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2,
                 miss_val = mean(synthetic, na.rm = TRUE),
                 miss_val_sd = sd(synthetic, na.rm = TRUE),
                 col_min_num = 2, row_min_num = 2,
                 col_num_to_move = 1, row_num_to_move = 1,
                 max.iter = 10)

mse_heatmap(bc)

mse_heatmap(bc) + ggplot2::scale_fill_viridis_c()
```

`partition_gen` *Generate an intial, random partition matrix with N objects into K subsets/groups.*

Description

This function is used to randomly generate a partition matrix and assign rows or columns to prototypes. Must be the case that N > K.

Usage

```
partition_gen(N, K)
```

Arguments

`N`	Number of objects/rows in a partition matrix
`K`	Desired number of partitions

Value

A partition matrix.

`partition_gen_by_p` *Create a partition matrix with a partition vector p*

Description

Create a partition matrix with a partition vector p

Usage

```
partition_gen_by_p(N, K, p)
```

Arguments

`N`	Rows in a partition matrix
`K`	Number of prototypes to create
`p`	Integer vector containing the cluster each row in a partition matrix is to be assigned to.

Value

A partition matrix.

`part_matrix_to_vector` *Convert a partition matrix to a vector*

Description

For each row in a partition matrix, this function gets the column index for which the row is equal to one. That is, for row i, this function returns the index of the row entry that is equal to one.

Usage

```
part_matrix_to_vector(P0)
```

Arguments

`P0`	A partition matrix

Value

An integer vector

`position_finder` *Find the index of the first nonzero value in a vector*

Description

Find the index of the first nonzero value in a vector

Usage

```
position_finder(vec)
```

Arguments

`vec`	A binary vector

Value

Position of the first nonzero value in a vector.

`print.biclustermd` *Print an object of class biclustermd*

Description

Print an object of class biclustermd

Usage

```
## S3 method for class 'biclustermd'
print(x, ...)
```

Arguments

`x`	a `biclustermd` object.
`...`	arguments passed to or from other methods

`reorder_biclust` *Reorder a bicluster object for making a heat map*

Description

Reorder a bicluster object for making a heat map

Usage

```
reorder_biclust(x)
```

Arguments

`x`	A bicluster object.

Value

A list containing the two partition matrices used by gg_bicluster.

`rep_biclustermd` *Repeat a biclustering to achieve a minimum SSE solution*

Description

Repeat a biclustering to achieve a minimum SSE solution

Usage

```
rep_biclustermd(
  data,
  nrep = 10,
  parallel = FALSE,
  ncores = 2,
  col_clusters = floor(sqrt(ncol(data))),
  row_clusters = floor(sqrt(nrow(data))),
  miss_val = mean(data, na.rm = TRUE),
  miss_val_sd = 1,
  similarity = "Rand",
  row_min_num = 5,
  col_min_num = 5,
  row_num_to_move = 1,
  col_num_to_move = 1,
  row_shuffles = 1,
  col_shuffles = 1,
  max.iter = 100
)
```

Arguments

`data`	Dataset to bicluster. Must to be a data matrix with only numbers and missing values in the data set. It should have row names and column names.
`nrep`	The number of times to repeat the biclustering. Default 10.
`parallel`	Logical indicating if the user would like to utilize the `foreach` parallel backend. Default is FALSE.
`ncores`	The number of cores to use if parallel computing. Default 2.
`col_clusters`	The number of clusters to partition the columns into.
`row_clusters`	The number of clusters to partition the rows into.
`miss_val`	Value or function to put in empty cells of the prototype matrix. If a value, a random normal variable with sd = `miss_val_sd` is used each iteration.
`miss_val_sd`	Standard deviation of the normal distribution `miss_val` follows if `miss_val` is a number. By default this equals 1.
`similarity`	The metric used to compare two successive clusterings. Can be "Rand" (default), "HA" for the Hubert and Arabie adjusted Rand index or "Jaccard". See RRand and for details.

`row_min_num`	Minimum row prototype size in order to be eligible to be chosen when filling an empty row prototype. Default is 5.
`col_min_num`	Minimum column prototype size in order to be eligible to be chosen when filling an empty row prototype. Default is 5.
`row_num_to_move`	Number of rows to remove from the sampled prototype to put in the empty row prototype. Default is 1.
`col_num_to_move`	Number of columns to remove from the sampled prototype to put in the empty column prototype. Default is 1.
`row_shuffles`	Number of times to shuffle rows in each iteration. Default is 1.
`col_shuffles`	Number of times to shuffle columns in each iteration. Default is 1.
`max.iter`	Maximum number of iterations to let the algorithm run for.

Value

A list of the minimum SSE biclustering, a vector containing the final SSE of each repeat, and the time it took the function to run.

References

Li, J., Reisner, J., Pham, H., Olafsson, S., and Vardeman, S. (2019) *Biclustering for Missing Data. Information Sciences, Submitted*

See Also

`biclustermd`, `tune_biclustermd`

Examples

```
data("synthetic")

# 20 repeats without parallelization
repeat_bc <- rep_biclustermd(synthetic, nrep = 20,
                             col_clusters = 3, row_clusters = 2,
                             miss_val = mean(synthetic, na.rm = TRUE),
                             miss_val_sd = sd(synthetic, na.rm = TRUE),
                             col_min_num = 2, row_min_num = 2,
                             col_num_to_move = 1, row_num_to_move = 1,
                             max.iter = 10)
repeat_bc
autoplot(repeat_bc$best_bc)
plot(repeat_bc$rep_sse, type = 'b', pch = 20)
repeat_bc$runtime

# 20 repeats with parallelization over 2 cores
repeat_bc <- rep_biclustermd(synthetic, nrep = 20, parallel = TRUE, ncores = 2,
                             col_clusters = 3, row_clusters = 2,
                             miss_val = mean(synthetic, na.rm = TRUE),
```

```
                          miss_val_sd = sd(synthetic, na.rm = TRUE),
                          col_min_num = 2, row_min_num = 2,
                          col_num_to_move = 1, row_num_to_move = 1,
                          max.iter = 10)
repeat_bc$runtime
```

`results_heatmap` *Make a heatmap of sparse biclustering results*

Description

Make a heatmap of sparse biclustering results

Usage

```
results_heatmap(
  x,
  reorder = FALSE,
  transform_colors = FALSE,
  c = 1/6,
  cell_alpha = 1/5,
  col_clusts = NULL,
  row_clusts = NULL,
  ...
)
```

Arguments

`x`	A `biclustermd` object.
`reorder`	A logical. If TRUE, heatmap will be sorted according to the cell-average matrix, `A`.
`transform_colors`	If equals `TRUE` then the data is scaled by `c` and run through a standard normal cdf before plotting. If `FALSE` (default), raw data values are used in the heat map.
`c`	Value to scale the data by before running it through a standard normal CDF. Default is 1/6.
`cell_alpha`	A scalar defining the transparency of shading over a cell and by default this equals 1/5. The color corresponds to the cell mean.
`col_clusts`	A vector of column cluster indices to display. If NULL (default), all are displayed.
`row_clusts`	A vector of row cluster indices to display. If NULL (default), all are displayed.
`...`	Arguments to be passed to `geom_vline()` and `geom_hline()`.

Value

An object of class ggplot.

`row.names.biclustermd` *Get data matrix row names and their corresponding row cluster membership*

Description

Get data matrix row names and their corresponding row cluster membership

Usage

```
## S3 method for class 'biclustermd'
row.names(x)
```

Arguments

`x`	and object of class `biclustermd`

Value

a data frame with row names of the shuffled matrix and corresponding row cluster names.

Examples

```
data("synthetic")
# default parameters
bc <- biclustermd(synthetic)
bc
row.names(bc)
# this is a simplified version of the output for gather(bc):
library(dplyr)
gather(bc) %>% distinct(row_cluster, row_name)
```

`row_cluster_names` *Get row names in each row cluster*

Description

Get row names in each row cluster

Usage

```
row_cluster_names(x, data)
```

Arguments

`x`	Biclustering object to extract row cluster designation from
`data`	Data that contains the row names

Value

A data frame with two columns: `cluster` corresponds to the row cluster and `name` gives the row names in each cluster.

Examples

```
data("synthetic")
rownames(synthetic) <- letters[1:nrow(synthetic)]
colnames(synthetic) <- letters[1:ncol(synthetic)]
bc <- biclustermd(synthetic, col_clusters = 3, row_clusters = 2,
                miss_val = mean(synthetic, na.rm = TRUE),
                miss_val_sd = sd(synthetic, na.rm = TRUE),
                col_min_num = 2, row_min_num = 2,
                col_num_to_move = 1, row_num_to_move = 1,
                max.iter = 10)
bc
```

`runtimes` *Algorithm run time data*

Description

This dataset stems from the R journal article introducing `biclustermd` to R users. It describes the data attributes and run time for varying data sizes and structures.

Usage

```
runtimes
```

Format

An object of class `data.frame` with 2400 rows and 13 columns.

Details

A data frame of 2400 rows and 13 variables (defined range, inclusive):

combination_no Unique identifier of a combination of parameters.

rows Number of rows in the data matrix. (50, 1500)

cols Number of columns in the data matrix. (50, 1500)

N Product of the dimensions of the data. (2500, 2250000)

row_clusts Number of clusters to partition the rows into. (4, 300)

col_clusts Number of clusters to partition the columns into. (4, 300)

avg_row_clust_size Average row cluster size. `rows / row_clusts`

avg_col_clust_size Average column cluster size. `cols / col_clusts`

sparsity Percent of data values which are missing.

user.self CPU time used executing instructions to calls (from `?proc.time`.

sys.self CPU time used executing calls (from `?proc.time`.

elapsed Amount of time in seconds it took the algorithm to converge.

iterations Number of iterations to convergence.

`synthetic` *Synthetic data for examples.*

Description

This simple dataset allows users to use data that are easy to understand while learning `biclustermd`. This is a matrix with 6 rows and 12 columns. 50% of values are missing.

Usage

```
synthetic
```

Format

An object of class `matrix` with 6 rows and 12 columns.

`tune_biclustermd` *Bicluster data over a grid of tuning parameters*

Description

Bicluster data over a grid of tuning parameters

Usage

```
tune_biclustermd(
  data,
  nrep = 10,
  parallel = FALSE,
  ncores = 2,
  tune_grid = NULL
)
```

Arguments

`data`	Dataset to bicluster. Must to be a data matrix with only numbers and missing values in the data set. It should have row names and column names.
`nrep`	The number of times to repeat the biclustering for each set of parameters. Default 10.
`parallel`	Logical indicating if the user would like to utilize the `foreach` parallel backend. Default is FALSE.
`ncores`	The number of cores to use if parallel computing. Default 2.
`tune_grid`	A data frame of parameters to tune over. The column names of this must match the arguments passed to `biclustermd()`.

Value

A list of:

`best_combn`	The best combination of parameters,
`best_bc`	The minimum SSE biclustering using the parameters in `best_combn`,
`grid`	`tune_grid` with columns giving the minimum, mean, and standard deviation of the final SSE for each parameter combination, and
`runtime`	CPU runtime & elapsed time.

References

Li, J., Reisner, J., Pham, H., Olafsson, S., and Vardeman, S. (2019) *Biclustering for Missing Data. Information Sciences, Submitted*

See Also

`biclustermd`, `rep_biclustermd`

Examples

```
library(dplyr)
library(ggplot2)
data("synthetic")
tg <- expand.grid(
miss_val = fivenum(synthetic),
similarity = c("Rand", "HA", "Jaccard"),
col_min_num = 2,
row_min_num = 2,
col_clusters = 3:5,
row_clusters = 2
)
tg

# in parallel: two cores:
tbc <- tune_biclustermd(synthetic, nrep = 2, parallel = TRUE, ncores = 2, tune_grid = tg)
tbc
```

```
tbc$grid %>%
  group_by(miss_val, col_clusters) %>%
  summarise(avg_sd = mean(sd_sse)) %>%
  ggplot(aes(miss_val, avg_sd, color = col_clusters, group = col_clusters)) +
  geom_line() +
  geom_point()

tbc <- tune_biclustermd(synthetic, nrep = 2, tune_grid = tg)
tbc

boxplot(tbc$grid$mean_sse ~ tbc$grid$similarity)
boxplot(tbc$grid$sd_sse ~ tbc$grid$similarity)

# nycflights13::flights dataset

library(nycflights13)
data("flights")

library(dplyr)
flights_bcd <- flights %>%
  select(month, dest, arr_delay)

flights_bcd <- flights_bcd %>%
  group_by(month, dest) %>%
  summarise(mean_arr_delay = mean(arr_delay, na.rm = TRUE)) %>%
  spread(dest, mean_arr_delay) %>%
  as.data.frame()

# months as rows
rownames(flights_bcd) <- flights_bcd$month
flights_bcd <- as.matrix(flights_bcd[, -1])

flights_grid <- expand.grid(
row_clusters = 4,
col_clusters = c(6, 9, 12),
miss_val = fivenum(flights_bcd),
similarity = c("Rand", "Jaccard")
)

# RUN TIME: approximately 40 seconds across two cores.
flights_tune <- tune_biclustermd(
  flights_bcd,
  nrep = 10,
  parallel = TRUE,
  ncores = 2,
  tune_grid = flights_grid
)
flights_tune
```

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