Package 'somhca'

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Type Package

Title Self-Organising Maps Coupled with Hierarchical Cluster Analysis

Version 0.1.3

Description Implements self-organising maps combined with hierarchical cluster analysis (SOM-HCA) for clustering and visualization of high-dimensional data.
The package includes functions to estimate the optimal map size based on various quality measures
and subsequently generates a model with the selected dimensions.
It also performs hierarchical clustering on the map nodes to group similar units
Documentation about the SOM-HCA method is provided in Pastorelli et al. (2024)
<doi:10.1002/xrs.3388>.

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Author Gianluca Pastorelli [aut, cre]

Maintainer Gianluca Pastorelli <gianluca.pastorelli@gmail.com>

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Contents

clusterSOM 2
finalSOM 3
generatePlot 3
getClusterData 4
optimalSOM 5
readMatrix 6

Index **7**

clusterSOM *Perform Clustering on SOM Nodes*

Description

Groups similar nodes of the SOM using hierarchical clustering and the KGS penalty function to determine the optimal number of clusters.

Usage

```
clusterSOM(model, plot_result = TRUE, file_path = NULL)
```

Arguments

model	The trained SOM model object.
plot_result	A logical value indicating whether to plot the clustering result. Default is 'TRUE'.
file_path	An optional string specifying the path to a CSV file. If provided, clusters are assigned to the observations in the original dataset, and the updated data is stored in a package environment as 'DataAndClusters'.

Value

A plot of the clusters on the SOM grid (if 'plot_result = TRUE'). If 'file_path' is specified, the clustered dataset is stored in a package environment for retrieval.

Examples

```
# Create a toy matrix with 9 columns and 100 rows
data <- matrix(rnorm(900), ncol = 9, nrow = 100)  # 900 random numbers, 100 rows, 9 columns

# Run the finalSOM function with the mock data
model <- finalSOM(data, dimension = 6, iterations = 700)

# Perform clustering using the mock model
clusterSOM(model, plot_result = TRUE)

# Load the toy data from the package's inst/extdata/ directory, perform
# clustering and retrieve the clustered dataset
file_path <- system.file("extdata", "toy_data.csv", package = "somhca")
clusterSOM(model, plot_result = FALSE, file_path)
getClusterData()
```

finalSOM *Train Final SOM Model*

Description

Re-trains the SOM using a specified optimal grid size and number of iterations.

Usage

```
finalSOM(data, dimension, iterations)
```

Arguments

data	The preprocessed data matrix containing the input data for SOM training.
dimension	An integer specifying the dimension of the square SOM grid (e.g., 5 results in a 5x5 grid).
iterations	An integer defining the number of iterations for training the SOM model. Use a large value, e.g., 500 or higher, for improved training (an error message could suggest that reducing the number of iterations might be necessary).

Value

A trained SOM model object.

Examples

```
# Create a toy matrix with 9 columns and 100 rows
data <- matrix(rnorm(900), ncol = 9, nrow = 100)  # 900 random numbers, 100 rows, 9 columns

# Run the finalSOM function with the mock data
myFinalSOM <- finalSOM(data, dimension = 6, iterations = 700)
```

generatePlot *Generate SOM Visualization Plots*

Description

Creates various types of plots to visualize and evaluate the trained SOM model.

Usage

```
generatePlot(model, plot_type, data = NULL)
```

Arguments

`model`	The trained SOM model object.
`plot_type`	An integer specifying the type of plot to generate. Options are: **1** Training progress plot (changes during training). **2** Node count plot (number of samples mapped to each node) for assessing map quality. **3** U-matrix plot (visualizing similarities between neighboring nodes). **4** Weight vector plot (patterns in the distributions of variables). **5** Kohonen heatmaps for all variables in the dataset (distribution of single variables across the map).
`data`	The preprocessed data matrix containing the input data. Required only for 'plot_type = 5'.

Value

A plot or a series of plots is generated and displayed based on the specified type.

Examples

```
# Create a toy matrix with 9 columns and 100 rows
data <- matrix(rnorm(900), ncol = 9, nrow = 100)  # 900 random numbers, 100 rows, 9 columns

# Assign column names to the data matrix
colnames(data) <- paste("Var", 1:ncol(data), sep = "_")

# Run the finalSOM function with the mock data
model <- finalSOM(data, dimension = 6, iterations = 700)

# Generate plots using the mock model
generatePlot(model, plot_type = 2)
generatePlot(model, plot_type = 5, data)
```

`getClusterData` *Retrieve Clustered Data*

Description

Access the dataset with cluster assignments stored by 'clusterSOM'.

Usage

```
getClusterData()
```

Value

A data frame with the clustered dataset.

`optimalSOM` *Estimate Optimal SOM Grid Size*

Description

Computes the optimal grid size for training a SOM using various quality measures and heuristic approaches.

Usage

```
optimalSOM(data, method = "A", increments, iterations)
```

Arguments

`data`	The preprocessed data matrix containing the input data for SOM training.
`method`	A character string indicating the method for estimating the maximum grid dimension. Options are: **"A"** Uses the heuristic formula by Vesanto et al. (default). **"B"** Applies an alternative heuristic approach. **numeric** Manually specified maximum dimension.
`increments`	An integer specifying the step size for increasing grid dimensions. For example, set increments to 2 or 5 to increment the grid size by 2 or 5 rows/columns at each step. Smaller increments lead to more granular searches but may increase computation time; larger increments risk errors if they exceed the estimated maximum SOM grid dimensions.
`iterations`	An integer defining the number of iterations for SOM training. A lower value, such as less than 500, helps reduce computation time. If the process takes too long or an error occurs, try reducing the number of iterations for quicker results.

Value

A data frame summarizing quality measures and their associated optimal grid dimensions. Use these results to select the most suitable grid size for your SOM.

Examples

```
# Create a toy matrix with 9 columns and 100 rows
data <- matrix(rnorm(900), ncol = 9, nrow = 100)  # 900 random numbers, 100 rows, 9 columns

# Run the optimalSOM function with the mock data
myOptimalSOM <- optimalSOM(data, method = "A", increments = 2, iterations = 300)
```

readMatrix *Read a CSV File and Convert to a Matrix*

Description

Reads data from a CSV file, optionally removes row headings, and applies specified normalization methods before converting the data to a matrix. In the original dataset, rows represent observations (e.g., samples), columns represent variables (e.g., features), and all cells (except for column headers and, in case, row headers) only contain numeric values.

Usage

```
readMatrix(file_path, remove_row_headings = FALSE, scaling = "no")
```

Arguments

file_path	A string specifying the path to the CSV file.
remove_row_headings	A logical value. If 'TRUE', removes the first column of the dataset. This is useful when the first column contains non-numeric identifiers (e.g., sample names) that should be excluded from the analysis. Default is 'FALSE'.
scaling	A string specifying the scaling method. Options are: **"no"** No scaling is applied (default). **"SimpleFeature"** Each column is divided by its maximum value. **"MinMax"** Each column is scaled to range [0, 1]. **"ZScore"** Each column is Z-score standardized.

Value

A matrix with the processed data.

Examples

```
# Load the toy data from the package's inst/extdata/ directory
file_path <- system.file("extdata", "toy_data.csv", package = "somhca")

# Run the readMatrix function with the mock data
myMatrix <- readMatrix(file_path, TRUE, "MinMax")
```

Index

clusterSOM, 2

finalSOM, 3

generatePlot, 3
getClusterData, 4

optimalSOM, 5

readMatrix, 6