Package ‘bibliometrix’

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Type Package

Title Comprehensive Science Mapping Analysis

Version 5.1.0

Description Tool for quantitative research in scientometrics and bibliometrics.
It implements the comprehensive workflow for science mapping analysis proposed in Aria M. and Cuccurullo C. (2017) <doi:10.1016/j.joi.2017.08.007>.
'bibliometrix' provides various routines for importing bibliographic data from 'SCOPUS', 'Clarivate Analytics Web of Science' (<`https://www.webofknowledge.com/`>), 'Digital Science Dimensions' (<`https://www.dimensions.ai/`>), 'OpenAlex' (<`https://openalex.org/`>), 'Cochrane Library' (<`https://www.cochranelibrary.com/`>), 'Lens' (<`https://lens.org`>), and 'PubMed' (<`https://pubmed.ncbi.nlm.nih.gov/`>) databases, performing bibliometric analysis and building networks for co-citation, coupling, scientific collaboration and co-word analysis.

License GPL-3

URL `https://www.bibliometrix.org`,
`https://github.com/massimoaria/bibliometrix`,
`https://www.k-synth.com`

BugReports `https://github.com/massimoaria/bibliometrix/issues`

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`bibliometrix-package` *Comprehensive Science Mapping Analysis*

Description

Tool for quantitative research in scientometrics and bibliometrics. It implements the comprehensive workflow for science mapping analysis proposed in Aria M. and Cuccurullo C. (2017) <doi:10.1016/j.joi.2017.08.007>. 'bibliometrix' provides various routines for importing bibliographic data from 'SCOPUS', 'Clarivate Analytics Web of Science' (<https://www.webofknowledge.com/>), 'Digital Science Dimensions' (<https://www.dimensions.ai/>), 'OpenAlex' (<https://openalex.org/>), 'Cochrane Library' (<https://www.cochranelibrary.com/>), 'Lens' (<https://lens.org>), and 'PubMed' (<https://pubmed.ncbi.nlm.nih.gov/>) databases, performing bibliometric analysis and building networks for co-citation, coupling, scientific collaboration and co-word analysis.

Details

INSTALLATION

- Stable version from CRAN:

install.packages("bibliometrix")

- Or development version from GitHub:

install.packages("devtools") devtools::install_github("massimoaria/bibliometrix")

- Load "bibliometrix"

library('bibliometrix')

DATA LOADING AND CONVERTING

The export file can be imported and converted by R using the function *convert2df*:

file <- ("https://www.bibliometrix.org/datasets/savedrecs.txt")

M <- convert2df(file, dbsource = "wos", format = "bibtex")

convert2df creates a bibliographic data frame with cases corresponding to manuscripts and variables to Field Tag in the original export file. Each manuscript contains several elements, such as authors' names, title, keywords and other information. All these elements constitute the bibliographic attributes of a document, also called metadata. Data frame columns are named using the standard Clarivate Analytics WoS Field Tag codify.

BIBLIOMETRIC ANALYSIS

The first step is to perform a descriptive analysis of the bibliographic data frame. The function *biblioAnalysis* calculates main bibliometric measures using this syntax:

results <- biblioAnalysis(M, sep = ";")

The function *biblioAnalysis* returns an object of class "bibliometrix".

To summarize main results of the bibliometric analysis, use the generic function *summary*. It displays main information about the bibliographic data frame and several tables, such as annual scientific production, top manuscripts per number of citations, most productive authors, most productive countries, total citation per country, most relevant sources (journals) and most relevant keywords. *summary* accepts two additional arguments. *k* is a formatting value that indicates the number of rows of each table. *pause* is a logical value (TRUE or FALSE) used to allow (or not) pause in screen scrolling. Choosing k=10 you decide to see the first 10 Authors, the first 10 sources, etc.

S <- summary(object = results, k = 10, pause = FALSE)

Some basic plots can be drawn using the generic function plot:

plot(x = results, k = 10, pause = FALSE)

BIBLIOGRAPHIC NETWORK MATRICES

Manuscript's attributes are connected to each other through the manuscript itself: author(s) to journal, keywords to publication date, etc. These connections of different attributes generate bipartite networks that can be represented as rectangular matrices (Manuscripts x Attributes). Furthermore, scientific publications regularly contain references to other scientific works. This generates a further network, namely, co-citation or coupling network. These networks are analyzed in order to capture meaningful properties of the underlying research system, and in particular to determine the influence of bibliometric units such as scholars and journals.

biblioNetwork function

The function *biblioNetwork* calculates, starting from a bibliographic data frame, the most frequently used networks: Coupling, Co-citation, Co-occurrences, and Collaboration. *biblioNetwork* uses two arguments to define the network to compute: - *analysis* argument can be "co-citation", "coupling", "collaboration", or "co-occurrences". - *network* argument can be "authors", "references", "sources", "countries", "universities", "keywords", "author_keywords", "titles" and "abstracts".

i.e. the following code calculates a classical co-citation network:

NetMatrix <- biblioNetwork(M, analysis = "co-citation", network = "references", sep = ";")

VISUALIZING BIBLIOGRAPHIC NETWORKS

All bibliographic networks can be graphically visualized or modeled. Using the function *networkPlot*, you can plot a network created by *biblioNetwork* using R routines.

The main argument of *networkPlot* is type. It indicates the network map layout: circle, kamada-kawai, mds, etc.

In the following, we propose some examples.

Country Scientific Collaboration

Create a country collaboration network

M <- metaTagExtraction(M, Field = "AU_CO", sep = ";")

NetMatrix <- biblioNetwork(M, analysis = "collaboration", network = "countries", sep = ";")

Plot the network

net=networkPlot(NetMatrix, n = dim(NetMatrix)[1], Title = "Country Collaboration", type = "circle", size=TRUE, remove.multiple=FALSE,labelsize=0.8)

Co-Citation Network

Create a co-citation network

NetMatrix <- biblioNetwork(M, analysis = "co-citation", network = "references", sep = ";")

Plot the network

net=networkPlot(NetMatrix, n = 30, Title = "Co-Citation Network", type = "fruchterman", size=T, remove.multiple=FALSE, labelsize=0.7,edgesize = 5)

Keyword co-occurrences

Create keyword co-occurrences network

NetMatrix <- biblioNetwork(M, analysis = "co-occurrences", network = "keywords", sep = ";")

Plot the network

net=networkPlot(NetMatrix, normalize="association", weighted=T, n = 30, Title = "Keyword Co-occurrences", type = "fruchterman", size=T,edgesize = 5,labelsize=0.7)

CO-WORD ANALYSIS: THE CONCEPTUAL STRUCTURE OF A FIELD

The aim of the co-word analysis is to map the conceptual structure of a framework using the word co-occurrences in a bibliographic collection. The analysis can be performed through dimensionality reduction techniques such as Multidimensional Scaling (MDS), Correspondence Analysis (CA) or Multiple Correspondence Analysis (MCA). Here, we show an example using the function *conceptualStructure* that performs a CA or MCA to draw a conceptual structure of the field and K-means clustering to identify clusters of documents which express common concepts. Results are plotted on a two-dimensional map. *conceptualStructure* includes natural language processing (NLP) routines (see the function *termExtraction*) to extract terms from titles and abstracts. In addition, it implements the Porter's stemming algorithm to reduce inflected (or sometimes derived) words to their word stem, base or root form.

Conceptual Structure using keywords (method="MCA")

CS <- conceptualStructure(M,field="ID", method="MCA", minDegree=4, clust=4 ,k.max=8, stemming=FALSE, labelsize=10, documents=10)

HISTORICAL DIRECT CITATION NETWORK

The historiographic map is a graph proposed by E. Garfield to represent a chronological network map of most relevant direct citations resulting from a bibliographic collection. The function histNetwork generates a chronological direct citation network matrix which can be plotted using *histPlot*:

```
# Create a historical citation network

histResults <- histNetwork(M, sep = ";")

# Plot a historical co-citation network

net <- histPlot(histResults, size = 10)
```

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References

Aria, M. & Cuccurullo, C. (2017). *bibliometrix*: An R-tool for comprehensive science mapping analysis, *Journal of Informetrics*, 11(4), pp 959-975, Elsevier, DOI: 10.1016/j.joi.2017.08.007 (https://doi.org/10.1016/j.joi.2017.08.007).

Cuccurullo, C., Aria, M., & Sarto, F. (2016). Foundations and trends in performance management. A twenty-five years bibliometric analysis in business and public administration domains, *Scientometrics*, DOI: 10.1007/s11192-016-1948-8 (https://doi.org/10.1007/s11192-016-1948-8).

Cuccurullo, C., Aria, M., & Sarto, F. (2015). Twenty years of research on performance management in business and public administration domains. Presentation at the *Correspondence Analysis and Related Methods conference (CARME 2015)* in September 2015 (https://www.bibliometrix.org/documents/2015Carme_cuc

Sarto, F., Cuccurullo, C., & Aria, M. (2014). Exploring healthcare governance literature: systematic review and paths for future research. *Mecosan* (https://www.francoangeli.it/Riviste/Scheda_Rivista.aspx?IDarticolo=5278

Cuccurullo, C., Aria, M., & Sarto, F. (2013). Twenty years of research on performance management in business and public administration domains. In *Academy of Management Proceedings* (Vol. 2013, No. 1, p. 14270). Academy of Management (https://doi.org/10.5465/AMBPP.2013.14270abstract).

`authorProdOverTime` *Top-Authors' Productivity over Time*

Description

It calculates and plots the author production (in terms of number of publications) over the time.

Usage

```
authorProdOverTime(M, k = 10, graph = TRUE)
```

Arguments

`M`	is a bibliographic data frame obtained by `convert2df` function.
`k`	is a integer. It is the number of top authors to analyze and plot. Default is `k = 10`.
`graph`	is logical. If TRUE the function plots the author production over time graph. Default is `graph = TRUE`.

Value

The function `authorProdOverTime` returns a list containing two objects:

`dfAU`	is a data frame
`dfpapersAU`	is a data frame
`graph`	a ggplot object

See Also

`biblioAnalysis` function for bibliometric analysis

`summary` method for class '`bibliometrix`'

Examples

```
data(scientometrics, package = "bibliometrixData")
res <- authorProdOverTime(scientometrics, k = 10)
print(res$dfAU)
plot(res$graph)
```

`biblioAnalysis` *Bibliometric Analysis*

Description

It performs a bibliometric analysis of a dataset imported from SCOPUS and Clarivate Analytics Web of Science databases.

Usage

```
biblioAnalysis(M, sep = ";")
```

Arguments

`M`	is a bibliographic data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to manuscripts and variables to Field Tag in the original SCOPUS and Clarivate Analytics Web of Science file.
`sep`	is the field separator character. This character separates strings in each column of the data frame. The default is `sep = ";"`.

Value

`biblioAnalysis` returns an object of `class` "bibliometrix".

The functions `summary` and `plot` are used to obtain or print a summary and some useful plots of the results.

An object of `class` "bibliometrix" is a list containing the following components:

Articles	the total number of manuscripts
Authors	the authors' frequency distribution
AuthorsFrac	the authors' frequency distribution (fractionalized)
FirstAuthors	corresponding author of each manuscript
nAUperPaper	the number of authors per manuscript
Appearances	the number of author appearances
nAuthors	the number of authors
AuMultiAuthoredArt	the number of authors of multi-authored articles
MostCitedPapers	the list of manuscripts sorted by citations
Years	publication year of each manuscript
FirstAffiliation	the affiliation of the first author
Affiliations	the frequency distribution of affiliations (of all co-authors for each paper)
Aff_frac	the fractionalized frequency distribution of affiliations (of all co-authors for each paper)
CO	the affiliation country of the first author
Countries	the affiliation countries' frequency distribution
CountryCollaboration	Intra-country (SCP) and intercountry (MCP) collaboration indices
TotalCitation	the number of times each manuscript has been cited
TCperYear	the yearly average number of times each manuscript has been cited
Sources	the frequency distribution of sources (journals, books, etc.)
DE	the frequency distribution of authors' keywords
ID	the frequency distribution of keywords associated to the manuscript by SCOPUS and Clarivate An

See Also

`convert2df` to import and convert an WoS or SCOPUS Export file in a bibliographic data frame.

`summary` to obtain a summary of the results.

`plot` to draw some useful plots of the results.

Examples

```
## Not run:
data(management, package = "bibliometrixData")

results <- biblioAnalysis(management)

summary(results, k = 10, pause = FALSE)

## End(Not run)
```

`biblioNetwork` *Creating Bibliographic networks*

Description

`biblioNetwork` creates different bibliographic networks from a bibliographic data frame.

Usage

```
biblioNetwork(
  M,
  analysis = "coupling",
  network = "authors",
  n = NULL,
  sep = ";",
  short = FALSE,
  shortlabel = TRUE,
  remove.terms = NULL,
  synonyms = NULL
)
```

Arguments

`M`	is a bibliographic data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to manuscripts and variables to Field Tag in the original SCOPUS and Clarivate Analytics WoS file.
`analysis`	is a character object. It indicates the type of analysis can be performed. `analysis` argument can be `"collaboration"`, `"coupling"`, `"co-occurrences"` or `"co-citation"`. Default is `analysis = "coupling"`.
`network`	is a character object. It indicates the network typology. The `network` argument can be `"authors"`, `"references"`, `"sources"`, `"countries"`,`"keywords"`, `"author_keywords"`,`"all_k` `"titles"`, or `"abstracts"`. Default is `network = "authors"`.
`n`	is an integer. It indicates the number of items to select. If `N = NULL`, all items are selected.
`sep`	is the field separator character. This character separates strings in each column of the data frame. The default is `sep = ";"`.
`short`	is a logical. If TRUE all items with frequency<2 are deleted to reduce the matrix size.
`shortlabel`	is logical. IF TRUE, reference labels are stored in a short format. Default is `shortlabel=TRUE`.
`remove.terms`	is a character vector. It contains a list of additional terms to delete from the documents before term extraction. The default is `remove.terms = NULL`.
`synonyms`	is a character vector. Each element contains a list of synonyms, separated by ";", that will be merged into a single term (the first word contained in the vector element). The default is `synonyms = NULL`.

Details

The function `biblioNetwork` can create a collection of bibliographic networks following the approach proposed by Batagelj & Cerinsek (2013) and Aria & cuccurullo (2017).

Typical networks output of `biblioNetwork` are:

Collaboration Networks
– Authors collaboration (analysis = "collaboration", network = "authors")
– University collaboration (analysis = "collaboration", network = universities")
– Country collaboration (analysis = "collaboration", network = "countries")

Co-citation Networks
– Authors co-citation (analysis = "co-citation", network = "authors")
– Reference co-citation (analysis = "co-citation", network = "references")
– Source co-citation (analysis = "co-citation", network = "sources")

Coupling Networks
– Manuscript coupling (analysis = "coupling", network = "references")
– Authors coupling (analysis = "coupling", network = "authors")
– Source coupling (analysis = "coupling", network = "sources")
– Country coupling (analysis = "coupling", network = "countries")

Co-occurrences Networks
– Authors co-occurrences (analysis = "co-occurrences", network = "authors")
– Source co-occurrences (analysis = "co-occurrences", network = "sources")
– Keyword co-occurrences (analysis = "co-occurrences", network = "keywords")
– Author-Keyword co-occurrences (analysis = "co-occurrences", network = "author_keywords")
– Title content co-occurrences (analysis = "co-occurrences", network = "titles")
– Abstract content co-occurrences (analysis = "co-occurrences", network = "abstracts")

References:
Batagelj, V., & Cerinsek, M. (2013). On bibliographic networks. Scientometrics, 96(3), 845-864.
Aria, M., & Cuccurullo, C. (2017). bibliometrix: An R-tool for comprehensive science mapping analysis. Journal of Informetrics, 11(4), 959-975.

Value

It is a squared network matrix. It is an object of class `dgMatrix` of the package `Matrix`.

See Also

`convert2df` to import and convert a SCOPUS and Thomson Reuters' ISI Web of Knowledge export file in a data frame.

`cocMatrix` to compute a co-occurrence matrix.

`biblioAnalysis` to perform a bibliometric analysis.

Examples

```
# EXAMPLE 1: Authors collaboration network

# data(scientometrics, package = "bibliometrixData")

# NetMatrix <- biblioNetwork(scientometrics, analysis = "collaboration",
# network = "authors", sep = ";")

# net <- networkPlot(NetMatrix, n = 30, type = "kamada", Title = "Collaboration",labelsize=0.5)


# EXAMPLE 2: Co-citation network

data(scientometrics, package = "bibliometrixData")

NetMatrix <- biblioNetwork(scientometrics,
  analysis = "co-citation",
  network = "references", sep = ";"
)

net <- networkPlot(NetMatrix, n = 30, type = "kamada", Title = "Co-Citation", labelsize = 0.5)
```

`biblioshiny` *Shiny UI for bibliometrix package*

Description

`biblioshiny` performs science mapping analysis using the main functions of the bibliometrix package.

Usage

```
biblioshiny(
  host = "127.0.0.1",
  port = NULL,
  launch.browser = TRUE,
  maxUploadSize = 200
)
```

Arguments

`host`	The IPv4 address that the application should listen on. Defaults to the shiny.host option, if set, or "127.0.0.1" if not.
`port`	is the TCP port that the application should listen on. If the port is not specified, and the shiny.port option is set (with options(shiny.port = XX)), then that port will be used. Otherwise, use a random port.

`launch.browser`	If true, the system's default web browser will be launched automatically after the app is started. Defaults to true in interactive sessions only. This value of this parameter can also be a function to call with the application's URL.
`maxUploadSize`	is a integer. The max upload file size argument. Default value is 200 (megabyte)

Examples

```
# biblioshiny()
```

`bibtag` *Tag list and bibtex fields.*

Description

Data frame containing a list of tags and corresponding: WoS, SCOPUS and generic bibtex fields; and Dimensions.ai csv and xlsx fields.

Format

A data frame with 44 rows and 6 variables:

TAG	Tag Fields
SCOPUS	Scopus bibtex fields
ISI	WOS/ISI bibtex fields
GENERIC	Generic bibtex fields
DIMENSIONS_OLD	DIMENSIONS cvs/xlsx old fields
DIMENSIONS	DIMENSIONS cvs/xlsx fields

`bradford` *Bradford's law*

Description

It estimates and draws the Bradford's law source distribution.

Usage

```
bradford(M)
```

Arguments

`M`	is a bibliographic dataframe.

Details

Bradford's law is a pattern first described by (*Samuel C. Bradford, 1934*) that estimates the exponentially diminishing returns of searching for references in science journals.

One formulation is that if journals in a field are sorted by number of articles into three groups, each with about one-third of all articles, then the number of journals in each group will be proportional to 1:n:n2.

Reference:
Bradford, S. C. (1934). Sources of information on specific subjects. Engineering, 137, 85-86.

Value

The function `bradford` returns a list containing the following objects:

`table`	a dataframe with the source distribution partitioned in the three zones
`graph`	the source distribution plot in ggplot2 format

See Also

`biblioAnalysis` function for bibliometric analysis

`summary` method for class '`bibliometrix`'

Examples

```
## Not run:
data(management, package = "bibliometrixData")

BR <- bradford(management)

## End(Not run)
```

`citations` *Citation frequency distribution*

Description

It calculates frequency distribution of citations.

Usage

```
citations(M, field = "article", sep = ";")
```

Arguments

`M`	is a bibliographic data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to manuscripts and variables to Field Tag in the original SCOPUS and Clarivate Analytics Web of Science file.
`field`	is a character. It can be "article" or "author" to obtain frequency distribution of cited citations or cited authors (only first authors for WoS database) respectively. The default is `field = "article"`.
`sep`	is the field separator character. This character separates citations in each string of CR column of the bibliographic data frame. The default is `sep = ";"`.

Value

an object of `class` "list" containing the following components:

Cited	the most frequent cited manuscripts or authors
Year	the publication year (only for cited article analysis)
Source	the journal (only for cited article analysis)

See Also

`biblioAnalysis` function for bibliometric analysis.

`summary` to obtain a summary of the results.

`plot` to draw some useful plots of the results.

Examples

```
## EXAMPLE 1: Cited articles

data(scientometrics, package = "bibliometrixData")

CR <- citations(scientometrics, field = "article", sep = ";")

CR$Cited[1:10]
CR$Year[1:10]
CR$Source[1:10]

## EXAMPLE 2: Cited first authors

data(scientometrics)

CR <- citations(scientometrics, field = "author", sep = ";")

CR$Cited[1:10]
```

`cocMatrix` *Bibliographic bipartite network matrices*

Description

`cocMatrix` computes occurrences between elements of a Tag Field from a bibliographic data frame. Manuscript is the unit of analysis.

Usage

```
cocMatrix(
  M,
  Field = "AU",
  type = "sparse",
  n = NULL,
  sep = ";",
  binary = TRUE,
  short = FALSE,
  remove.terms = NULL,
  synonyms = NULL
)
```

Arguments

`M`	is a data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to articles and variables to Field Tag in the original WoS or SCOPUS file.
`Field`	is a character object. It indicates one of the field tags of the standard ISI WoS Field Tag codify. Field can be equal to one of these tags:

`AU`	Authors
`SO`	Publication Name (or Source)
`JI`	ISO Source Abbreviation
`DE`	Author Keywords
`ID`	Keywords associated by WoS or SCOPUS database
`KW_Merged`	All Keywords (merged by DE and ID)
`CR`	Cited References

for a complete list of filed tags see: Field Tags used in bibliometrix

`type`	indicates the output format of co-occurrences:

`type = "matrix"`	produces an object of class `matrix`
`type = "sparse"`	produces an object of class `dgMatrix` of the package `Matrix`. "sparse" argument generates a compact

`n`	is an integer. It indicates the number of items to select. If `N = NULL`, all items are selected.
`sep`	is the field separator character. This character separates strings in each column of the data frame. The default is `sep = ";"`.
`binary`	is a logical. If TRUE each cell contains a 0/1. if FALSE each cell contains the frequency.
`short`	is a logical. If TRUE all items with frequency<2 are deleted to reduce the matrix size.
`remove.terms`	is a character vector. It contains a list of additional terms to delete from the documents before term extraction. The default is `remove.terms = NULL`.
`synonyms`	is a character vector. Each element contains a list of synonyms, separated by ";", that will be merged into a single term (the first word contained in the vector element). The default is `synonyms = NULL`.

Details

This occurrence matrix represents a bipartite network which can be transformed into a collection of bibliographic networks such as coupling, co-citation, etc..

The function follows the approach proposed by Batagelj & Cerinsek (2013) and Aria & cuccurullo (2017).

References:
Batagelj, V., & Cerinsek, M. (2013). On bibliographic networks. Scientometrics, 96(3), 845-864.
Aria, M., & Cuccurullo, C. (2017). bibliometrix: An R-tool for comprehensive science mapping analysis. Journal of Informetrics, 11(4), 959-975.

Value

a bipartite network matrix with cases corresponding to manuscripts and variables to the objects extracted from the Tag `Field`.

See Also

`convert2df` to import and convert an ISI or SCOPUS Export file in a data frame.

`biblioAnalysis` to perform a bibliometric analysis.

`biblioNetwork` to compute a bibliographic network.

Examples

```
# EXAMPLE 1: Articles x Authors occurrence matrix

data(scientometrics, package = "bibliometrixData")
WA <- cocMatrix(scientometrics, Field = "AU", type = "sparse", sep = ";")

# EXAMPLE 2: Articles x Cited References occurrence matrix
```

```
# data(scientometrics, package = "bibliometrixData")

# WCR <- cocMatrix(scientometrics, Field = "CR", type = "sparse", sep = ";")

# EXAMPLE 3: Articles x Cited First Authors occurrence matrix

# data(scientometrics, package = "bibliometrixData")
# scientometrics <- metaTagExtraction(scientometrics, Field = "CR_AU", sep = ";")
# WCR <- cocMatrix(scientometrics, Field = "CR_AU", type = "sparse", sep = ";")
```

`collabByRegionPlot` *Country Collaboration Networks by Region*

Description

A function to create and plot country collaboration networks by Region

Usage

```
collabByRegionPlot(
  NetMatrix,
  normalize = NULL,
  n = NULL,
  degree = NULL,
  type = "auto",
  label = TRUE,
  labelsize = 1,
  label.cex = FALSE,
  label.color = FALSE,
  label.n = Inf,
  halo = FALSE,
  cluster = "walktrap",
  community.repulsion = 0,
  vos.path = NULL,
  size = 3,
  size.cex = FALSE,
  curved = FALSE,
  noloops = TRUE,
  remove.multiple = TRUE,
  remove.isolates = FALSE,
  weighted = NULL,
  edgesize = 1,
  edges.min = 0,
  alpha = 0.5,
  verbose = TRUE
)
```

Arguments

`NetMatrix`	is a country collaboration matrix obtained by the function `biblioNetwork`.
`normalize`	is a character. It can be "association", "jaccard", "inclusion","salton" or "equivalence" to obtain Association Strength, Jaccard, Inclusion, Salton or Equivalence similarity index respectively. The default is type = NULL.
`n`	is an integer. It indicates the number of vertices to plot.
`degree`	is an integer. It indicates the min frequency of a vertex. If degree is not NULL, n is ignored.
`type`	is a character object. It indicates the network map layout:

`type="auto"`	Automatic layout selection
`type="circle"`	Circle layout
`type="sphere"`	Sphere layout
`type="mds"`	Multidimensional Scaling layout
`type="fruchterman"`	Fruchterman-Reingold layout
`type="kamada"`	Kamada-Kawai layout

`label`	is logical. If TRUE vertex labels are plotted.
`labelsize`	is an integer. It indicates the label size in the plot. Default is `labelsize=1`
`label.cex`	is logical. If TRUE the label size of each vertex is proportional to its degree.
`label.color`	is logical. If TRUE, for each vertex, the label color is the same as its cluster.
`label.n`	is an integer. It indicates the number of vertex labels to draw.
`halo`	is logical. If TRUE communities are plotted using different colors. Default is `halo=FALSE`
`cluster`	is a character. It indicates the type of cluster to perform among ("none", "optimal", "louvain","leiden", "infomap","edge_betweenness","walktrap", "spinglass", "leading_eigen", "fast_greedy").
`community.repulsion`	is a real. It indicates the repulsion force among network communities. It is a real number between 0 and 1. Default is `community.repulsion = 0.1`.
`vos.path`	is a character indicating the full path where VOSviewer.jar is located.
`size`	is integer. It defines the size of each vertex. Default is `size=3`.
`size.cex`	is logical. If TRUE the size of each vertex is proportional to its degree.
`curved`	is a logical or a number. If TRUE edges are plotted with an optimal curvature. Default is `curved=FALSE`. Curved values are any numbers from 0 to 1.
`noloops`	is logical. If TRUE loops in the network are deleted.
`remove.multiple`	is logical. If TRUE multiple links are plotted using just one edge.
`remove.isolates`	is logical. If TRUE isolates vertices are not plotted.

`weighted`	This argument specifies whether to create a weighted graph from an adjacency matrix. If it is NULL then an unweighted graph is created and the elements of the adjacency matrix gives the number of edges between the vertices. If it is a character constant then for every non-zero matrix entry an edge is created and the value of the entry is added as an edge attribute named by the weighted argument. If it is TRUE then a weighted graph is created and the name of the edge attribute will be weight.
`edgesize`	is an integer. It indicates the network edge size.
`edges.min`	is an integer. It indicates the min frequency of edges between two vertices. If edge.min=0, all edges are plotted.
`alpha`	is a number. Legal alpha values are any numbers from 0 (transparent) to 1 (opaque). The default alpha value usually is 0.5.
`verbose`	is a logical. If TRUE, network will be plotted. Default is `verbose = TRUE`.

Value

It is a list containing the following elements:

`graph`	a network object of the class `igraph`
`cluster_obj`	a `communities` object of the package `igraph`
`cluster_res`	a data frame with main results of clustering procedure.

Examples

```
## Not run:
data(management, package = "bibliometrixData")

management <- metaTagExtraction(management, Field = "AU_CO")

NetMatrix <- biblioNetwork(management, analysis = "collaboration", network = "countries")

net <- collabByRegionPlot(NetMatrix,
  edgesize = 4, label.cex = TRUE, labelsize = 2.5,
  weighted = TRUE, size = 0.5, size.cex = TRUE, community.repulsion = 0,
  verbose = FALSE
)

cbind(names(net))

plot(net[[4]]$graph)

## End(Not run)
```

`conceptualStructure` *Creating and plotting conceptual structure map of a scientific field*

Description

The function `conceptualStructure` creates a conceptual structure map of a scientific field performing Correspondence Analysis (CA), Multiple Correspondence Analysis (MCA) or Metric Multidimensional Scaling (MDS) and Clustering of a bipartite network of terms extracted from keyword, title or abstract fields.

Usage

```
conceptualStructure(
  M,
  field = "ID",
  ngrams = 1,
  method = "MCA",
  quali.supp = NULL,
  quanti.supp = NULL,
  minDegree = 2,
  clust = "auto",
  k.max = 5,
  stemming = FALSE,
  labelsize = 10,
  documents = 2,
  graph = TRUE,
  remove.terms = NULL,
  synonyms = NULL
)
```

Arguments

`M`	is a data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to articles and variables to Field Tag in the original ISI or SCOPUS file.
`field`	is a character object. It indicates one of the field tags of the standard ISI WoS Field Tag codify. field can be equal to one of these tags:

`ID`	Keywords Plus associated by ISI or SCOPUS database
`DE`	Author's keywords
`KW_Merged`	All keywords
`ID_TM`	Keywords Plus stemmed through the Porter's stemming algorithm
`DE_TM`	Author's Keywords stemmed through the Porter's stemming algorithm
`TI`	Terms extracted from titles
`AB`	Terms extracted from abstracts

`ngrams`	is an integer between 1 and 3. It indicates the type of n-gram to extract from texts. An n-gram is a contiguous sequence of n terms. The function can extract n-grams composed by 1, 2, 3 or 4 terms. Default value is `ngrams=1`.
`method`	is a character object. It indicates the factorial method used to create the factorial map. Use `method="CA"` for Correspondence Analysis, `method="MCA"` for Multiple Correspondence Analysis or `method="MDS"` for Metric Multidimensional Scaling. The default is `method="MCA"`
`quali.supp`	is a vector indicating the indexes of the categorical supplementary variables. It is used only for CA and MCA.
`quanti.supp`	is a vector indicating the indexes of the quantitative supplementary variables. It is used only for CA and MCA.
`minDegree`	is an integer. It indicates the minimum occurrences of terms to analyze and plot. The default value is 2.
`clust`	is an integer or a character. If clust="auto", the number of cluster is chosen automatically, otherwise clust can be an integer between 2 and 8.
`k.max`	is an integer. It indicates the maximum number of cluster to keep. The default value is 5. The max value is 20.
`stemming`	is logical. If TRUE the Porter's Stemming algorithm is applied to all extracted terms. The default is `stemming = FALSE`.
`labelsize`	is an integer. It indicates the label size in the plot. Default is `labelsize=10`
`documents`	is an integer. It indicates the number of documents per cluster to plot in the factorial map. The default value is 2. It is used only for CA and MCA.
`graph`	is logical. If TRUE the function plots the maps otherwise they are saved in the output object. Default value is TRUE
`remove.terms`	is a character vector. It contains a list of additional terms to delete from the documents before term extraction. The default is `remove.terms = NULL`.
`synonyms`	is a character vector. Each element contains a list of synonyms, separated by ";", that will be merged into a single term (the first word contained in the vector element). The default is `synonyms = NULL`.

Value

It is an object of the class `list` containing the following components:

net	bipartite network
res	Results of CA, MCA or MDS method
km.res	Results of cluster analysis
graph_terms	Conceptual structure map (class "ggplot2")
graph_documents_Contrib	Factorial map of the documents with the highest contributes (class "ggplot2")
graph_docuemnts_TC	Factorial map of the most cited documents (class "ggplot2")

See Also

`termExtraction` to extract terms from a textual field (abstract, title, author's keywords, etc.) of a bibliographic data frame.

`biblioNetwork` to compute a bibliographic network.

`cocMatrix` to compute a co-occurrence matrix.

`biblioAnalysis` to perform a bibliometric analysis.

Examples

```
# EXAMPLE Conceptual Structure using Keywords Plus

data(scientometrics, package = "bibliometrixData")

CS <- conceptualStructure(scientometrics,
  field = "ID", method = "CA",
  stemming = FALSE, minDegree = 3, k.max = 5
)
```

`convert2df` *Import and Convert bibliographic export files and API objects.*

Description

It converts a SCOPUS, Clarivate Analytics WoS, Dimensions, Lens.org, PubMed and COCHRANE Database export files or pubmedR and dimensionsR JSON/XML objects into a data frame, with cases corresponding to articles and variables to Field Tags as used in WoS.

Usage

```
convert2df(
  file,
  dbsource = "wos",
  format = "plaintext",
  remove.duplicates = TRUE
)
```

Arguments

`file`	a character array containing a sequence of filenames coming from WoS, Scopus, Dimensions, Lens.org, OpenAlex and Pubmed. Alternatively, `file` can be an object resulting from an API query fetched from Dimensions, and PubMed databases:

a)	'wos'	Clarivate Analytics WoS (in plaintext '.txt', Endnote Desktop '.ciw', or bibtex formats '.bib');
b)	'scopus'	SCOPUS (exclusively in bibtex format '.bib');
c)	'dimensions'	Digital Science Dimensions (in csv '.csv' or excel '.xlsx' formats);
d)	'lens'	Lens.org (in csv '.csv');
e)	'pubmed'	an object of the class `pubmedR (package pubmedR)` containing a collection obtained from a query perfo
f)	'dimensions'	an object of the class `dimensionsR (package dimensionsR)` containing a collection obtained from a q

g)	'openalex'	OpenAlex .csv file;
h)	'openalex_api'	the filename and path to a list object returned by openalexR package, containing a collection of works r

`dbsource`	is a character indicating the bibliographic database. `dbsource` can be `dbsource = c('cochrane','dimensions','generic','isi','openalex', 'pubmed','scopus','wos', 'lens')` . Default is `dbsource = "isi"`.
`format`	is a character indicating the SCOPUS, Clarivate Analytics WoS, and other databases export file format. `format` can be `c('api', 'bibtex', 'csv', 'endnote','excel','plaintext', 'pubmed')`. Default is `format = "plaintext"`.
`remove.duplicates`	is logical. If TRUE, the function will remove duplicated items checking by DOI and database ID.

Value

a data frame with cases corresponding to articles and variables to Field Tags in the original export file.

I.e We have three files download from Web of Science in plaintext format, file will be:

file <- c("filename1.txt", "filename2.txt", "filename3.txt")

data frame columns are named using the standard Clarivate Analytics WoS Field Tag codify. The main field tags are:

`AU`	Authors
`TI`	Document Title
`SO`	Publication Name (or Source)
`JI`	ISO Source Abbreviation
`DT`	Document Type
`DE`	Authors' Keywords
`ID`	Keywords associated by SCOPUS or WoS database
`AB`	Abstract
`C1`	Author Address
`RP`	Reprint Address
`CR`	Cited References
`TC`	Times Cited
`PY`	Year
`SC`	Subject Category
`UT`	Unique Article Identifier
`DB`	Database

for a complete list of field tags see: Field Tags used in bibliometrix

Examples

```
# Example:
# Import and convert a Web of Science collection form an export file in plaintext format:
```

```
## Not run:
files <- "https://www.bibliometrix.org/datasets/wos_plaintext.txt"

M <- convert2df(file = files, dbsource = "wos", format = "plaintext")

## End(Not run)
```

`countries` *Index of Countries.*

Description

Data frame containing a normalized index of countries.
Data are used by `biblioAnalysis` function to extract Country Field of Cited References and Authors.

Format

A data frame with 199 rows and 5 variables:

countries country names

continent continent names

iso2 country ISO 3166-1 alpha-2 code

Longitude country centroid longitude

Latitude country centroid latitude

`couplingMap` *Coupling Analysis*

Description

It performs a coupling network analysis and plots community detection results on a bi-dimensional map (Coupling Map).

Usage

```
couplingMap(
  M,
  analysis = "documents",
  field = "CR",
  n = 500,
  label.term = NULL,
  ngrams = 1,
  impact.measure = "local",
```

```
  minfreq = 5,
  community.repulsion = 0.1,
  stemming = FALSE,
  size = 0.5,
  n.labels = 1,
  repel = TRUE,
  cluster = "walktrap"
)
```

Arguments

`M`	is a bibliographic dataframe.
`analysis`	is the textual attribute used to select the unit of analysis. It can be `analysis = c("documents", "authors", "sources")`.
`field`	is the textual attribute used to measure the coupling strength. It can be `field = c("CR", "ID","DE", "TI", "AB")`.
`n`	is an integer. It indicates the number of units to include in the analysis.
`label.term`	is a character. It indicates which content metadata have to use for cluster labeling. It can be `label.term = c("ID","DE","TI","AB")`. If `label.term = NULL` cluster items will be use for labeling.
`ngrams`	is an integer between 1 and 4. It indicates the type of n-gram to extract from texts. An n-gram is a contiguous sequence of n terms. The function can extract n-grams composed by 1, 2, 3 or 4 terms. Default value is `ngrams=1`.
`impact.measure`	is a character. It indicates the impact measure used to rank cluster elements (documents, authors or sources). It can be `impact.measure = c("local", "global")`.\ With `impact.measure = "local"`, couplingMap calculates elements impact using the Normalized Local Citation Score while using `impact.measure = "global"`, the function uses the Normalized Global Citation Score to measure elements impact.
`minfreq`	is a integer. It indicates the minimum frequency (per thousand) of a cluster. It is a number in the range (0,1000).
`community.repulsion`	is a real. It indicates the repulsion force among network communities. It is a real number between 0 and 1. Default is `community.repulsion = 0.1`.
`stemming`	is logical. If it is TRUE the word (from titles or abstracts) will be stemmed (using the Porter's algorithm).
`size`	is numerical. It indicates the size of the cluster circles and is a number in the range (0.01,1).
`n.labels`	is integer. It indicates how many labels associate to each cluster. Default is `n.labels = 1`.
`repel`	is logical. If it is TRUE ggplot uses geom_label_repel instead of geom_label.
`cluster`	is a character. It indicates the type of cluster to perform among ("optimal", "louvain","leiden", "infomap","edge_betweenness","walktrap", "spinglass", "leading_eigen", "fast_greedy").

Details

The analysis can be performed on three different units: documents, authors or sources and the coupling strength can be measured using the classical approach (coupled by references) or a novel approach based on unit contents (keywords or terms from titles and abstracts)

The x-axis measures the cluster centrality (by Callon's Centrality index) while the y-axis measures the cluster impact by Mean Normalized Local Citation Score (MNLCS). The Normalized Local Citation Score (NLCS) of a document is calculated by dividing the actual count of local citing items by the expected citation rate for documents with the same year of publication.

Value

a list containing:

`map`	The coupling map as ggplot2 object
`clusters`	Centrality and Density values for each cluster.
`data`	A list of units following in each cluster
`nclust`	The number of clusters
`NCS`	The Normalized Citation Score dataframe
`net`	A list containing the network output (as provided from the networkPlot function)

See Also

`biblioNetwork` function to compute a bibliographic network.

`cocMatrix` to compute a bibliographic bipartite network.

`networkPlot` to plot a bibliographic network.

Examples

```
## Not run:
data(management, package = "bibliometrixData")
res <- couplingMap(management,
  analysis = "authors", field = "CR", n = 250, impact.measure = "local",
  minfreq = 3, size = 0.5, repel = TRUE
)
plot(res$map)

## End(Not run)
```

`customTheme` *Custom Theme variables for Biblioshiny.*

Description

List containing a set of custom theme variables for Biblioshiny.

Format

A list with 3 elements:

name object name

attribs attributes

children CSS style

`dominance` *Authors' dominance ranking*

Description

It calculates the authors' dominance ranking from an object of the class '`bibliometrix`' as proposed by Kumar & Kumar, 2008.

Usage

```
dominance(results, k = 10)
```

Arguments

`results`	is an object of the class '`bibliometrix`' for which the analysis of the authors' dominance ranking is desired.
`k`	is an integer, used for table formatting (number of authors). Default value is 10.

Value

The function `dominance` returns a data frame with cases corresponding to the first `k` most productive authors and variables to typical field of a dominance analysis.

the data frame variables are:

`Author`	Author's name
`Dominance Factor`	Dominance Factor (DF = FAA / MAA)
`Tot Articles`	N. of Authored Articles (TAA)
`Single Authored`	N. of Single-Authored Articles (SAA)
`Multi Authored`	N. of Multi-Authored Articles (MAA=TAA-SAA)
`First Authored`	N. of First Authored Articles (FAA)
`Rank by Articles`	Author Ranking by N. of Articles
`Rank by DF`	Author Ranking by Dominance Factor

See Also

`biblioAnalysis` function for bibliometric analysis

`summary` method for class '`bibliometrix`'

Examples

```
data(scientometrics, package = "bibliometrixData")
results <- biblioAnalysis(scientometrics)
DF <- dominance(results)
DF
```

`duplicatedMatching` *Searching of duplicated records in a bibliographic database*

Description

Search duplicated records in a dataframe.

Usage

```
duplicatedMatching(M, Field = "TI", exact = FALSE, tol = 0.95)
```

Arguments

`M`	is the bibliographic data frame.
`Field`	is a character object. It indicates one of the field tags used to identify duplicated records. Field can be equal to one of these tags: TI (title), AB (abstract), UT (manuscript ID).
`exact`	is logical. If exact = TRUE the function searches duplicates using exact matching. If exact=FALSE, the function uses the restricted Damerau-Levenshtein distance to find duplicated documents.
`tol`	is a numeric value giving the minimum relative similarity to match two manuscripts. Default value is `tol = 0.95`. To use the restricted Damerau-Levenshtein distance, exact argument has to be set as FALSE.

Details

A bibliographic data frame is obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to manuscripts and variables to Field Tag in the original SCOPUS and Clarivate Analytics WoS file. The function identifies duplicated records in a bibliographic data frame and deletes them. Duplicate entries are identified through the restricted Damerau-Levenshtein distance. Two manuscripts that have a relative similarity measure greater than `tol` argument are stored in the output data frame only once.

Value

the value returned from `duplicatedMatching` is a data frame without duplicated records.

See Also

`convert2df` to import and convert an WoS or SCOPUS Export file in a bibliographic data frame.

`biblioAnalysis` function for bibliometric analysis.

`summary` to obtain a summary of the results.

`plot` to draw some useful plots of the results.

Examples

```
data(scientometrics, package = "bibliometrixData")

M <- rbind(scientometrics[1:20, ], scientometrics[10:30, ])

newM <- duplicatedMatching(M, Field = "TI", exact = FALSE, tol = 0.95)

dim(newM)
```

`fieldByYear` *Field Tag distribution by Year*

Description

It calculates the median year for each item of a field tag.

Usage

```
fieldByYear(
  M,
  field = "ID",
  timespan = NULL,
  min.freq = 2,
  n.items = 5,
  labelsize = NULL,
  remove.terms = NULL,
  synonyms = NULL,
  dynamic.plot = FALSE,
  graph = TRUE
)
```

Arguments

`M`	is a bibliographic data frame obtained by `convert2df` function.
`field`	is a character object. It indicates one of the field tags of the standard ISI WoS Field Tag codify.
`timespan`	is a vector with the min and max year. If it is = NULL, the analysis is performed on the entire period. Default is `timespan = NULL`.

`min.freq`	is an integer. It indicates the min frequency of the items to include in the analysis
`n.items`	is an integer. I indicates the maximum number of items per year to include in the plot.
`labelsize`	is deprecated argument. It will be removed in the next update.
`remove.terms`	is a character vector. It contains a list of additional terms to delete from the documents before term extraction. The default is `remove.terms = NULL`.
`synonyms`	is a character vector. Each element contains a list of synonyms, separated by ";", that will be merged into a single term (the first word contained in the vector element). The default is `synonyms = NULL`.
`dynamic.plot`	is a logical. If TRUE plot aesthetics are optimized for plotly package.
`graph`	is logical. If TRUE the function plots Filed Tag distribution by Year graph. Default is `graph = TRUE`.

Value

The function `fieldByYear` returns a list containing threeobjects:

`df`	is a data frame
`df_graph`	is a data frame with data used to build the graph
`graph`	a ggplot object

See Also

`biblioAnalysis` function for bibliometric analysis

`summary` method for class '`bibliometrix`'

Examples

```
data(management, package = "bibliometrixData")
timespan <- c(2005, 2015)
res <- fieldByYear(management,
  field = "ID", timespan = timespan,
  min.freq = 5, n.items = 5, graph = TRUE
)
```

`Hindex` *h-index calculation*

Description

It calculates the authors' h-index and its variants.

Usage

```
Hindex(M, field = "author", elements = NULL, sep = ";", years = Inf)
```

Arguments

`M`	is a bibliographic data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to manuscripts and variables to Field Tag in the original SCOPUS and Clarivate Analytics WoS file.
`field`	is character. It can be equal to c("author", "source"). field indicates if H-index have to be calculated for a list of authors or for a list of sources. Default value is `field = ”author”`.
`elements`	is a character vector. It contains the authors' names list or the source list for which you want to calculate the H-index. When the field is "author", the argument has the form C("SURNAME1 N","SURNAME2 N",...), in other words, for each author: surname and initials separated by one blank space. If elements=NULL, the function calculates impact indices for all elements contained in the data frame. i.e for the authors SEMPRONIO TIZIO CAIO and ARIA MASSIMO `elements` argument is `elements = c(”SEMPRONIO TC”, ”ARIA M”)`.
`sep`	is the field separator character. This character separates authors in each string of AU column of the bibliographic data frame. The default is `sep = ”;”`.
`years`	is a integer. It indicates the number of years to consider for Hindex calculation. Default is Inf.

Value

an object of `class` "list". It contains two elements: H is a data frame with h-index, g-index and m-index for each author; CitationList is a list with the bibliographic collection for each author.

See Also

`convert2df` to import and convert an WoS or SCOPUS Export file in a bibliographic data frame.

`biblioAnalysis` function for bibliometric analysis.

`summary` to obtain a summary of the results.

`plot` to draw some useful plots of the results.

Examples

```
### EXAMPLE 1: ###

data(scientometrics, package = ”bibliometrixData”)

authors <- c(”SMALL H”, ”CHEN DZ”)

Hindex(scientometrics, field = ”author”, elements = authors, sep = ”;”)$H

Hindex(scientometrics, field = ”source”, elements = ”SCIENTOMETRICS”, sep = ”;”)$H

### EXAMPLE 2: Garfield h-index###

data(garfield, package = ”bibliometrixData”)

indices <- Hindex(garfield, field = ”author”, elements = ”GARFIELD E”, years = Inf, sep = ”;”)
```

```
# h-index, g-index and m-index of Eugene Garfield
indices$H

# Papers and total citations
head(indices$CitationList[[1]])
```

`histNetwork` *Historical co-citation network*

Description

`histNetwork` creates a historical citation network from a bibliographic data frame.

Usage

```
histNetwork(M, min.citations, sep = ";", network = TRUE, verbose = TRUE)
```

Arguments

`M`	is a bibliographic data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to manuscripts and variables to Field Tag in the original SCOPUS, OpenAlex, Lens.org and Clarivate Analytics Web of Science file.
`min.citations`	DEPRECATED. New algorithm does not use this parameters. It will be remove in the next version of bibliometrix.
`sep`	is the field separator character. This character separates strings in CR column of the data frame. The default is `sep = ";"`.
`network`	is logical. If TRUE, function calculates and returns also the direct citation network. If FALSE, the function returns only the local citation table.
`verbose`	is logical. If TRUE, results are printed on screen.

Value

`histNetwork` returns an object of `class` "list" containing the following components:

NetMatrix	the historical co-citation network matrix
histData	the set of n most cited references
M	the bibliographic data frame

See Also

`convert2df` to import and convert a supported export file in a bibliographic data frame.

`summary` to obtain a summary of the results.

`plot` to draw some useful plots of the results.

`biblioNetwork` to compute a bibliographic network.

Examples

```
## Not run:
data(management, package = "bibliometrixData")

histResults <- histNetwork(management, sep = ";")

## End(Not run)
```

`histPlot` *Plotting historical co-citation network*

Description

`histPlot` plots a historical co-citation network.

Usage

```
histPlot(
  histResults,
  n = 20,
  size = 5,
  labelsize = 5,
  remove.isolates = TRUE,
  title_as_label = FALSE,
  label = "short",
  verbose = TRUE
)
```

Arguments

`histResults`	is an object of `class` "list" containing the following components:

NetMatrix	the historical citation network matrix
Degree	the min degree of the network
histData	the set of n most cited references
M	the bibliographic data frame

is a network matrix obtained by the function `histNetwork`.

`n`	is integer. It defines the number of vertices to plot.
`size`	is an integer. It defines the point size of the vertices. Default value is 5.
`labelsize`	is an integer. It indicates the label size in the plot. Default is `labelsize=5`.
`remove.isolates`	is logical. If TRUE isolates vertices are not plotted.
`title_as_label`	is a logical. DEPRECATED

`label`	is a character. It indicates which label type to use as node id in the historiograph. It can be `label=c("short", "title", "keywords", "keywordsplus")`. Default is `label = "short"`.
`verbose`	is logical. If TRUE, results and plots are printed on screen.

Details

The function `histPlot` can plot a historical co-citation network previously created by `histNetwork`.

Value

It is list containing: a network object of the class `igraph` and a plot object of the class `ggraph`.

See Also

`histNetwork` to compute a historical co-citation network.

`cocMatrix` to compute a co-occurrence matrix.

`biblioAnalysis` to perform a bibliometric analysis.

Examples

```
# EXAMPLE Citation network
## Not run:
data(management, package = "bibliometrixData")

histResults <- histNetwork(management, sep = ";")

net <- histPlot(histResults, n = 20, labelsize = 5)

## End(Not run)
```

`idByAuthor` *Get Complete Author Information and ID from Scopus*

Description

Uses SCOPUS API author search to identify author identification information.

Usage

```
idByAuthor(df, api_key)
```

Arguments

`df`	is a dataframe composed of three columns:

`lastname`	author’s last name
`firstname`	author’s first name
`affiliation`	Part of the affiliation name (university name, city, etc.)

	i.e. df[1,1:3]<-c("aria","massimo","naples") When affiliation is not specified, the field df$affiliation have to be NA. i.e. df[2,1:3]<-c("cuccurullo","corrado", NA)
`api_key`	is a character. It contains the Elsevier API key. Information about how to obtain an API Key Elsevier API website

Value

a data frame with cases corresponding to authors and variables to author’s information and ID got from SCOPUS.

See Also

`retrievalByAuthorID` for downloading the complete author bibliographic collection from SCOPUS

Examples

```
## Request a personal API Key to Elsevier web page https://dev.elsevier.com/sc_apis.html
#
# api_key="your api key"

## create a data frame with the list of authors to get information and IDs
# i.e. df[1,1:3]<-c("aria","massimo","naples")
#      df[2,1:3]<-c("cuccurullo","corrado", NA)

## run idByAuthor function
#
# authorsID <- idByAuthor(df, api_key)
```

`keywordAssoc` *ID and DE keyword associations*

Description

It associates authors’ keywords to keywords plus.

Usage

```
keywordAssoc(M, sep = ";", n = 10, excludeKW = NA)
```

Arguments

`M`	is a bibliographic data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to manuscripts and variables to Field Tag in the original SCOPUS and Clarivate Analytics WoS file.
`sep`	is the field separator character. This character separates keywords in each string of ID and DE columns of the bibliographic data frame. The default is `sep = ";"`.
`n`	is a integer. It indicates the number of authors' keywords to associate to each keyword plus. The default is `n = 10`.
`excludeKW`	is character vector. It contains authors' keywords to exclude from the analysis.

Value

an object of `class` "list".

See Also

`convert2df` to import and convert a WoS or SCOPUS Export file in a bibliographic data frame.

`biblioAnalysis` function for bibliometric analysis.

`summary` to obtain a summary of the results.

`plot` to draw some useful plots of the results.

Examples

```
data(scientometrics, package = "bibliometrixData")

KWlist <- keywordAssoc(scientometrics, sep = ";", n = 10, excludeKW = NA)

# list of first 10 Keywords plus
names(KWlist)

# list of first 10 authors' keywords associated to the first Keyword plus
KWlist[[1]][1:10]
```

`KeywordGrowth` *Yearly occurrences of top keywords/terms*

Description

It calculates yearly occurrences of top keywords/terms.

Usage

```
KeywordGrowth(
  M,
  Tag = "ID",
  sep = ";",
  top = 10,
  cdf = TRUE,
  remove.terms = NULL,
  synonyms = NULL
)
```

Arguments

`M`	is a data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to articles and variables to Field Tag in the original WoS or SCOPUS file.
`Tag`	is a character object. It indicates one of the keyword field tags of the standard ISI WoS Field Tag codify (ID, DE, KW_Merged) or a field tag created by `termExtraction` function (TI_TM, AB_TM, etc.).
`sep`	is the field separator character. This character separates strings in each keyword column of the data frame. The default is `sep = ";"`.
`top`	is a numeric. It indicates the number of top keywords to analyze. The default value is 10.
`cdf`	is a logical. If TRUE, the function calculates the cumulative occurrences distribution.
`remove.terms`	is a character vector. It contains a list of additional terms to delete from the documents before term extraction. The default is `remove.terms = NULL`.
`synonyms`	is a character vector. Each element contains a list of synonyms, separated by ";", that will be merged into a single term (the first word contained in the vector element). The default is `synonyms = NULL`.

Value

an object of class `data.frame`

Examples

```
data(scientometrics, package = "bibliometrixData")
topKW <- KeywordGrowth(scientometrics, Tag = "ID", sep = ";", top = 5, cdf = TRUE)
topKW

# Plotting results
## Not run:
install.packages("reshape2")
library(reshape2)
library(ggplot2)
DF <- melt(topKW, id = "Year")
ggplot(DF, aes(Year, value, group = variable, color = variable)) + geom_line
```

```
## End(Not run)
```

`localCitations` *Author local citations*

Description

It calculates local citations (LCS) of authors and documents of a bibliographic collection.

Usage

```
localCitations(M, fast.search = FALSE, sep = ";", verbose = FALSE)
```

Arguments

`M`	is a bibliographic data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to manuscripts and variables to Field Tag in the original SCOPUS and Clarivate Analytics WoS file.
`fast.search`	is logical. If true, the function calculates local citations only for 25 percent top cited documents.
`sep`	is the field separator character. This character separates citations in each string of CR column of the bibliographic data frame. The default is `sep = ";"`.
`verbose`	is a logical. If TRUE, results are printed on screen.

Details

Local citations measure how many times an author (or a document) included in this collection have been cited by the documents also included in the collection.

Value

an object of `class` "list" containing author local citations and document local citations.

See Also

`citations` function for citation frequency distribution.

`biblioAnalysis` function for bibliometric analysis.

`summary` to obtain a summary of the results.

`plot` to draw some useful plots of the results.

Examples

```
data(scientometrics, package = "bibliometrixData")

CR <- localCitations(scientometrics, sep = ";")

CR$Authors[1:10, ]
CR$Papers[1:10, ]
```

`logo` *Bibliometrix logo.*

Description

The matrix contains the rgb format of the bibliometrix official logo.

Format

A matrix with 927 rows and 800 columns.

`lotka` *Lotka's law coefficient estimation*

Description

It estimates Lotka's law coefficients for scientific productivity (*Lotka A.J., 1926*).

Usage

```
lotka(M)
```

Arguments

`M`	is an object of the class '`bibliometrixDB`'.

Details

Reference: Lotka, A. J. (1926). The frequency distribution of scientific productivity. Journal of the Washington academy of sciences, 16(12), 317-323.

Value

The function `lotka` returns a list of summary statistics of the Lotka's law estimation of an object of class `bibliometrix`.

the list contains the following objects:

`Beta`	Beta coefficient
`C`	Constant coefficient
`R2`	Goodness of Fit
`fitted`	Fitted Values
`p.value`	Pvalue of two-sample Kolmogorov-Smirnov test between the empirical and the theoretical Lotka's Law dist
`AuthorProd`	Authors' Productivity frequency table
`g`	Lotka's law plot
`g_shiny`	Lotka's law plot for biblioshiny

See Also

`biblioAnalysis` function for bibliometric analysis

`summary` method for class '`bibliometrix`'

Examples

```
data(management, package = "bibliometrixData")
L <- lotka(management)
L
```

`mergeDbSources` *Merge bibliographic data frames from supported bibliogtraphic DBs*

Description

Merge bibliographic data frames from different databases (WoS,SCOPUS, Lens, Openalex, etc-) into a single one.

Usage

```
mergeDbSources(..., remove.duplicated = TRUE, verbose = TRUE)
```

Arguments

`...`	are the bibliographic data frames to merge.
`remove.duplicated`	is logical. If TRUE duplicated documents will be deleted from the bibliographic collection.
`verbose`	is logical. If TRUE, information on duplicate documents is printed on the screen.

Details

bibliographic data frames are obtained by the converting function `convert2df`. The function merges data frames identifying common tag fields and duplicated records.

Value

the value returned from `mergeDbSources` is a bibliographic data frame.

See Also

`convert2df` to import and convert an ISI or SCOPUS Export file in a bibliographic data frame.

`biblioAnalysis` function for bibliometric analysis.

`summary` to obtain a summary of the results.

`plot` to draw some useful plots of the results.

Examples

```
data(isiCollection, package = "bibliometrixData")

data(scopusCollection, package = "bibliometrixData")

M <- mergeDbSources(isiCollection, scopusCollection, remove.duplicated = TRUE)

dim(M)
```

`mergeKeywords` *Merge DE and ID Fields into a Unified Keywords Column*

Description

This function creates a new column ‘KW_Merged‘ by combining the contents of the ‘DE‘ (author keywords) and ‘ID‘ (keywords plus) fields in a bibliographic dataframe. Duplicate keywords within each record are removed, and leading/trailing spaces are trimmed. The merged keywords are separated by a semicolon (‘;‘).

Usage

```
mergeKeywords(M, force = FALSE)
```

Arguments

`M`	A dataframe containing at least the ‘DE‘ and/or ‘ID‘ columns, typically generated by ‘convert2df()‘ from the ‘bibliometrix‘ package.
`force`	Logical. If ‘TRUE‘, an existing ‘KW_Merged‘ column will be overwritten. Default is ‘FALSE‘.

Details

If the ‘KW_Merged‘ column already exists, it will not be overwritten unless ‘force = TRUE‘ is specified.

Value

A dataframe with an added (or updated) ‘KW_Merged‘ column containing deduplicated and cleaned keyword strings.

Examples

```
## Not run:
data(management, package = "bibliometrix")
M <- mergeKeywords(management)
head(M$KW_Merged)

## End(Not run)
```

`metaTagExtraction` *Meta-Field Tag Extraction*

Description

It extracts other field tags, different from the standard WoS/SCOPUS codify.

Usage

```
metaTagExtraction(M, Field = "CR_AU", sep = ";", aff.disamb = TRUE)
```

Arguments

`M`	is a data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to articles and variables to Field Tag in the original WoS or SCOPUS file.
`Field`	is a character object. New tag extracted from aggregated data is specified by this string. Field can be equal to one of these tags:

`"CR_AU"`	First Author of each cited reference
`"CR_SO"`	Source of each cited reference
`"AU_CO"`	Country of affiliation for co-authors
`"AU1_CO"`	Country of affiliation for the first author
`"AU_UN"`	University of affiliation for each co-author and the corresponding author (AU1_UN)
`"SR"`	Short tag of the document (as used in reference lists)

`sep`	is the field separator character. This character separates strings in each column of the data frame. The default is `sep = ";"`.

`aff.disamb`	is a logical. If TRUE and Field="AU_UN", then a disambiguation algorithm is used to identify and match scientific affiliations (univ, research centers, etc.). The default is `aff.disamb=TRUE`.

Value

the bibliometric data frame with a new column containing data about new field tag indicated in the argument `Field`.

See Also

`convert2df` for importing and converting bibliographic files into a data frame.

`biblioAnalysis` function for bibliometric analysis

Examples

```
# Example 1: First Authors for each cited reference

data(scientometrics, package = "bibliometrixData")
scientometrics <- metaTagExtraction(scientometrics, Field = "CR_AU", sep = ";")
unlist(strsplit(scientometrics$CR_AU[1], ";"))


# Example 2: Source for each cited reference

data(scientometrics)
scientometrics <- metaTagExtraction(scientometrics, Field = "CR_SO", sep = ";")
unlist(strsplit(scientometrics$CR_SO[1], ";"))

# Example 3: Affiliation country for co-authors

data(scientometrics)
scientometrics <- metaTagExtraction(scientometrics, Field = "AU_CO", sep = ";")
scientometrics$AU_CO[1:10]
```

`missingData` *Completeness of bibliographic metadata*

Description

It calculates the percentage of missing data in the metadata of a bibliographic data frame.

Usage

```
missingData(M)
```

Arguments

`M`	is a bibliographic data frame obtained by `convert2df` function.

Details

Each metadata is assigned a status c("Excellent," "Good," "Acceptable", "Poor", "Critical," "Completely missing") depending on the percentage of missing data. In particular, the column *status* classifies the percentage of missing value in 5 categories: "Excellent" (0 "Poor" (from 20.01

The results of the function allow us to understand which analyses can be performed with bibliometrix and which cannot based on the completeness (or status) of different metadata.

Value

The function `missingData` returns a list containing two objects:

`allTags`	is a data frame including results for all original metadata tags from the collection
`mandatoryTags`	is a data frame that included only the tags needed for analysis with bibliometrix and biblioshiny.

Examples

```
data(scientometrics, package = "bibliometrixData")
res <- missingData(scientometrics)
print(res$mandatoryTags)
```

`net2Pajek` *Save a network graph object as Pajek files*

Description

The function `net2Pajek` save a bibliographic network previously created by `networkPlot` as pajek files.

Usage

```
net2Pajek(net, filename = "my_pajek_network", path = NULL)
```

Arguments

`net`	is a network graph object returned by the function `networkPlot`.
`filename`	is a character. It indicates the filename for Pajek export files.
`path`	is a character. It indicates the path where the files will be saved. When path="NULL, the files will be saved in the current folder. Default is NULL.

Value

The function returns no object but will save three Pajek files in the folder given in the "path" argument with the name "filename.clu," "filename.vec," and "filename.net."

See Also

`net2VOSviewer` to export and plot the network with VOSviewer software.

Examples

```
## Not run:
data(management, package = "bibliometrixData")

NetMatrix <- biblioNetwork(management,
  analysis = "co-occurrences",
  network = "keywords", sep = ";"
)

net <- networkPlot(NetMatrix, n = 30, type = "auto", Title = "Co-occurrence Network", labelsize = 1)

net2Pajek(net, filename = "pajekfiles", path = NULL)

## End(Not run)
```

`net2VOSviewer` *Open a bibliometrix network in VosViewer*

Description

`net2VOSviewer` plots a network created with `networkPlot` using VOSviewer by Nees Jan van Eck and Ludo Waltman.

Usage

```
net2VOSviewer(net, vos.path = NULL)
```

Arguments

`net`	is an object created by networkPlot function.
`vos.path`	is a character indicating the full path where VOSviewer.jar is located.

Details

The function `networkPlot` can plot a bibliographic network previously created by `biblioNetwork`. The network map can be plotted using internal R routines or using VOSviewer by Nees Jan van Eck and Ludo Waltman.

Value

It write a .net file that can be open in VOSviewer

See Also

`biblioNetwork` to compute a bibliographic network.

`networkPlot` to create and plot a network object

Examples

```
# EXAMPLE

# VOSviewer.jar have to be present in the working folder

# data(scientometrics, package = "bibliometrixData")

# NetMatrix <- biblioNetwork(scientometrics, analysis = "co-citation",
# network = "references", sep = ";")

# net <- networkPlot(NetMatrix, n = 30, type = "kamada", Title = "Co-Citation",labelsize=0.5)

# net2VOSviewer(net)
```

`networkPlot` *Plotting Bibliographic networks*

Description

`networkPlot` plots a bibliographic network.

Usage

```
networkPlot(
  NetMatrix,
  normalize = NULL,
  n = NULL,
  degree = NULL,
  Title = "Plot",
  type = "auto",
  label = TRUE,
  labelsize = 1,
  label.cex = FALSE,
  label.color = FALSE,
  label.n = NULL,
  halo = FALSE,
  cluster = "walktrap",
  community.repulsion = 0.1,
  vos.path = NULL,
  size = 3,
  size.cex = FALSE,
  curved = FALSE,
  noloops = TRUE,
  remove.multiple = TRUE,
  remove.isolates = FALSE,
  weighted = NULL,
```

```
  edgesize = 1,
  edges.min = 0,
  alpha = 0.5,
  verbose = TRUE
)
```

Arguments

`NetMatrix`	is a network matrix obtained by the function `biblioNetwork`.
`normalize`	is a character. It can be "association", "jaccard", "inclusion","salton" or "equivalence" to obtain Association Strength, Jaccard, Inclusion, Salton or Equivalence similarity index respectively. The default is type = NULL.
`n`	is an integer. It indicates the number of vertices to plot.
`degree`	is an integer. It indicates the min frequency of a vertex. If degree is not NULL, n is ignored.
`Title`	is a character indicating the plot title.
`type`	is a character object. It indicates the network map layout:

`type="auto"`	Automatic layout selection
`type="circle"`	Circle layout
`type="sphere"`	Sphere layout
`type="mds"`	Multidimensional Scaling layout
`type="fruchterman"`	Fruchterman-Reingold layout
`type="kamada"`	Kamada-Kawai layout

`label`	is logical. If TRUE vertex labels are plotted.
`labelsize`	is an integer. It indicates the label size in the plot. Default is `labelsize=1`
`label.cex`	is logical. If TRUE the label size of each vertex is proportional to its degree.
`label.color`	is logical. If TRUE, for each vertex, the label color is the same as its cluster.
`label.n`	is an integer. It indicates the number of vertex labels to draw.
`halo`	is logical. If TRUE communities are plotted using different colors. Default is `halo=FALSE`
`cluster`	is a character. It indicates the type of cluster to perform among ("none", "optimal", "louvain","leiden", "infomap","edge_betweenness","walktrap", "spinglass", "leading_eigen", "fast_greedy").
`community.repulsion`	is a real. It indicates the repulsion force among network communities. It is a real number between 0 and 1. Default is `community.repulsion = 0.1`.
`vos.path`	is a character indicating the full path where VOSviewer.jar is located.
`size`	is integer. It defines the size of each vertex. Default is `size=3`.
`size.cex`	is logical. If TRUE the size of each vertex is proportional to its degree.
`curved`	is a logical or a number. If TRUE edges are plotted with an optimal curvature. Default is `curved=FALSE`. Curved values are any numbers from 0 to 1.

`noloops`	is logical. If TRUE loops in the network are deleted.
`remove.multiple`	is logical. If TRUE multiple links are plotted using just one edge.
`remove.isolates`	is logical. If TRUE isolates vertices are not plotted.
`weighted`	This argument specifies whether to create a weighted graph from an adjacency matrix. If it is NULL then an unweighted graph is created and the elements of the adjacency matrix gives the number of edges between the vertices. If it is a character constant then for every non-zero matrix entry an edge is created and the value of the entry is added as an edge attribute named by the weighted argument. If it is TRUE then a weighted graph is created and the name of the edge attribute will be weight.
`edgesize`	is an integer. It indicates the network edge size.
`edges.min`	is an integer. It indicates the min frequency of edges between two vertices. If edge.min=0, all edges are plotted.
`alpha`	is a number. Legal alpha values are any numbers from 0 (transparent) to 1 (opaque). The default alpha value usually is 0.5.
`verbose`	is a logical. If TRUE, network will be plotted. Default is `verbose = TRUE`.

Details

The function `networkPlot` can plot a bibliographic network previously created by `biblioNetwork`.

Value

It is a list containing the following elements:

`graph`	a network object of the class `igraph`
`cluster_obj`	a `communities` object of the package `igraph`
`cluster_res`	a data frame with main results of clustering procedure.

See Also

`biblioNetwork` to compute a bibliographic network.

`net2VOSviewer` to export and plot the network with VOSviewer software.

`cocMatrix` to compute a co-occurrence matrix.

`biblioAnalysis` to perform a bibliometric analysis.

Examples

```
# EXAMPLE Keywordd co-occurrence network

data(management, package = "bibliometrixData")

NetMatrix <- biblioNetwork(management,
  analysis = "co-occurrences",
```

```
  network = "keywords", sep = ";"
)

net <- networkPlot(NetMatrix, n = 30, type = "auto", Title = "Co-occurrence Network", labelsize = 1)
```

`networkStat` *Calculating network summary statistics*

Description

`networkStat` calculates main network statistics.

Usage

```
networkStat(object, stat = "network", type = "degree")
```

Arguments

`object`	is a network matrix obtained by the function `biblioNetwork` or an graph object of the class `igraph`.
`stat`	is a character. It indicates which statistics are to be calculated. `stat = "network"` calculates the statistics related to the network; `stat = "all"` calculates the statistics related to the network and the individual nodes that compose it. Default value is `stat = "network"`.
`type`	is a character. It indicates which centrality index is calculated. type values can be c("degree", "closeness", "betweenness","eigenvector","pagerank","hub","authority", "all"). Default is "degree".

Details

The function `networkStat` can calculate the main network statistics from a bibliographic network previously created by `biblioNetwork`.

Value

It is a list containing the following elements:

`graph`	a network object of the class `igraph`
`network`	a `communities` a list with the main statistics of the network
`vertex`	a data frame with the main measures of centrality and prestige of vertices.

See Also

`biblioNetwork` to compute a bibliographic network.

`cocMatrix` to compute a co-occurrence matrix.

`biblioAnalysis` to perform a bibliometric analysis.

Examples

```
# EXAMPLE Co-citation network

# to run the example, please remove # from the beginning of the following lines
# data(scientometrics, package = "bibliometrixData")

# NetMatrix <- biblioNetwork(scientometrics, analysis = "co-citation",
#      network = "references", sep = ";")

# netstat <- networkStat(NetMatrix, stat = "all", type = "degree")
```

---

normalizeCitationScore

Calculate the normalized citation score metric

Description

It calculates the normalized citation score for documents, authors and sources using both global and local citations.

Usage

```
normalizeCitationScore(M, field = "documents", impact.measure = "local")
```

Arguments

`M`	is a bibliographic data frame obtained by `convert2df` function.
`field`	is a character. It indicates the unit of analysis on which calculate the NCS. It can be equal to `field = c("documents", "authors", "sources")`. Default is `field = "documents"`.
`impact.measure`	is a character. It indicates the impact measure used to rank cluster elements (documents, authors or sources). It can be `impact.measure = c("local", "global")`.\ With `impact.measure = "local"`, normalizeCitationScore calculates elements impact using the Normalized Local Citation Score while using `impact.measure = "global"`, the function uses the Normalized Global Citation Score to measure elements impact.

Details

The document Normalized Citation Score (NCS) of a document is calculated by dividing the actual count of citing items by the expected citation rate for documents with the same year of publication.

The MNCS of a set of documents, for example the collected works of an individual, or published on a journal, is the average of the NCS values for all the documents in the set.

The NGCS is the NCS calculated using the global citations (total citations that a document received considering the whole bibliographic database).

The NLCS is the NCS calculated using the local citations (total citations that a document received from a set of documents included in the same collection).

Value

a dataframe.

Examples

```
## Not run:
data(management, package = "bibliometrixData")
NCS <- normalizeCitationScore(management, field = "authors", impact.measure = "local")

## End(Not run)
```

`normalizeSimilarity` *Calculate similarity indices*

Description

It calculates a relative measure of bibliographic co-occurrences.

Usage

```
normalizeSimilarity(NetMatrix, type = "association")
```

Arguments

`NetMatrix`	is a coupling matrix obtained by the network functions `biblioNetwork` or `cocMatrix`.
`type`	is a character. It can be "association", "jaccard", "inclusion","salton" or "equivalence" to obtain Association Strength, Jaccard, Inclusion, Salton or Equivalence similarity index respectively. The default is `type = "association"`.

Details

`couplingSimilarity` calculates Association strength, Inclusion, Jaccard or Salton similarity from a co-occurrence bibliographic matrix.

The association strength is used by Van Eck and Waltman (2007) and Van Eck et al. (2006). Several works refer to the measure as the proximity index, while Leydesdorff (2008)and Zitt et al. (2000) refer to it as the probabilistic affinity (or activity) index.

The inclusion index, also called Simpson coefficient, is an overlap measure used in information retrieval.

The Jaccard index (or Jaccard similarity coefficient) gives us a relative measure of the overlap of two sets. It is calculated as the ratio between the intersection and the union of the reference lists (of two manuscripts).

The Salton index, instead, relates the intersection of the two lists to the geometric mean of the size of both sets. The square of Salton index is also called Equivalence index.

The indices are equal to zero if the intersection of the reference lists is empty.

References

Leydesdorff, L. (2008). On the normalization and visualization of author Cocitation data: Salton's cosine versus the Jaccard index. Journal of the American Society for Information Science and Technology, 59(1), 77– 85.
Van Eck, N.J., Waltman, L., Van den Berg, J., & Kaymak, U. (2006). Visualizing the computational intelligence field. IEEE Computational Intelligence Magazine, 1(4), 6– 10.
Van Eck, N.J., & Waltman, L. (2007). Bibliometric mapping of the computational intelligence field. International Journal of Uncertainty, Fuzziness and Knowledge-Based Systems, 15(5), 625– 645
. Van Eck, N. J., & Waltman, L. (2009). How to normalize cooccurrence data? An analysis of some well-known similarity measures. Journal of the American society for information science and technology, 60(8), 1635-1651.
Zitt, M., Bassecoulard, E., & Okubo, Y. (2000). Shadows of the past in international cooperation: Collaboration profiles of the top five producers of science. Scientometrics, 47(3), 627– 657.

Value

a similarity matrix.

See Also

`biblioNetwork` function to compute a bibliographic network.

`cocMatrix` to compute a bibliographic bipartite network.

Examples

```
data(scientometrics, package = "bibliometrixData")
NetMatrix <- biblioNetwork(scientometrics,
  analysis = "co-occurrences",
  network = "keywords", sep = ";"
)
S <- normalizeSimilarity(NetMatrix, type = "association")
```

`plot.bibliodendrogram` *Plotting dendrogram resulting from Conceptual Structure Analysis*

Description

`plot` method for class '`bibliodendrogram`'

Usage

```
## S3 method for class 'bibliodendrogram'
plot(x, ...)
```

Arguments

`x`	is the object for which plots are desired.
`...`	is a generic param for plot functions.

Value

The function `plot` draws a dendrogram.

`plot.bibliometrix` *Plotting bibliometric analysis results*

Description

`plot` method for class '`bibliometrix`'

Usage

```
## S3 method for class 'bibliometrix'
plot(x, ...)
```

Arguments

`x`	is the object for which plots are desired.
`...`	can accept two arguments: `k` is an integer, used for plot formatting (number of objects). Default value is 10. `pause` is a logical, used to allow pause in screen scrolling of results. Default value is `pause = FALSE`.

Value

The function `plot` returns a list of plots of class `ggplot2`.

See Also

The bibliometric analysis function `biblioAnalysis`.

`summary` to compute a list of summary statistics of the object of class `bibliometrix`.

Examples

```
data(scientometrics, package = "bibliometrixData")

results <- biblioAnalysis(scientometrics)

plot(results, k = 10, pause = FALSE)
```

`plotThematicEvolution` *Plot Thematic Evolution Network*

Description

Visualizes the thematic evolution of clusters over time using a temporal network layout. Nodes are positioned along the x-axis according to time slices and vertically to minimize overlap. Edges represent links between themes across time periods, with customizable weights and styles. Nodes and Edges objects are the results of a Thematic Evolution Analysis performed using the `thematicEvolution` function.

Usage

```
plotThematicEvolution(
  Nodes,
  Edges,
  min.flow = 0,
  measure = "weighted",
  label_size = 5,
  edge_scale = 10,
  node_scale = 30
)
```

Arguments

`Nodes`	is a list of nodes obtained by `thematicEvolution` function.
`Edges`	is a list of edges obtained by `thematicEvolution` function.
`min.flow`	Numeric. Minimum threshold for edge weight (i.e., flow) to be included in the network visualization. Default is ‘0‘.
`measure`	Character. The method to define edge weight: ‘"inclusion"‘, ‘"stability"‘, or ‘"weighted"‘ (default is ‘"weighted"‘).
`label_size`	Numeric. Font size of the node labels. Default is ‘15‘.
`edge_scale`	Numeric. Scaling factor for edge width. Default is ‘10‘.
`node_scale`	Numeric. Scaling factor for node size. Default is ‘30‘.

Value

A ‘visNetwork‘ object displaying a time-structured thematic evolution network.

See Also

`thematicMap` function to create a thematic map based on co-word network analysis and clustering.

`thematicMap` function to perform a thematic evolution analysis.

`networkPlot` to plot a bibliographic network.

Examples

```
## Not run:
data(managemeent, package = "bibliometrixData")
years <- c(2004, 2015)

nexus <- thematicEvolution(management, field = "ID", years = years, n = 100, minFreq = 2)

plotThematicEvolution(nexus$Nodes, nexus$Edges)

## End(Not run)
```

`readFiles` *DEPRECATED: Load a sequence of ISI or SCOPUS Export files into a large character object*

Description

The function readFiled is deprecated. You can import and convert your export files directly using the function `convert2df`.

Usage

```
readFiles(...)
```

Arguments

`...`	is a sequence of names of files downloaded from WOS.(in plain text or bibtex format) or SCOPUS Export file (exclusively in bibtex format).

Value

a character vector of length the number of lines read.

See Also

`convert2df` for converting SCOPUS of ISI Export file into a dataframe

Examples

```
# WoS or SCOPUS Export files can be read using \code{\link{readFiles}} function:

# largechar <- readFiles('filename1.txt','filename2.txt','filename3.txt')

# filename1.txt, filename2.txt and filename3.txt are ISI or SCOPUS Export file
# in plain text or bibtex format.

# D <- readFiles('https://www.bibliometrix.org/datasets/bibliometrics_articles.txt')
```

`retrievalByAuthorID` *Get Author Content on SCOPUS by ID*

Description

Uses SCOPUS API search to get information about documents on a set of authors using SCOPUS ID.

Usage

```
retrievalByAuthorID(id, api_key, remove.duplicated = TRUE, country = TRUE)
```

Arguments

`id`	is a vector of characters containing the author's SCOPUS IDs. SCOPUS IDs con be obtained using the function `idByAuthor`.
`api_key`	is a character. It contains the Elsvier API key. Information about how to obtain an API Key Elsevier API website
`remove.duplicated`	is logical. If TRUE duplicated documents will be deleted from the bibliographic collection.
`country`	is logical. If TRUE authors' country information will be downloaded from SCOPUS.

Value

a list containing two objects: (i) M which is a data frame with cases corresponding to articles and variables to main Field Tags named using the standard ISI WoS Field Tag codify. M includes the entire bibliographic collection downloaded from SCOPUS. The main field tags are:

`AU`	Authors
`TI`	Document Title
`SO`	Publication Name (or Source)
`DT`	Document Type
`DE`	Authors' Keywords
`ID`	Keywords associated by SCOPUS or ISI database
`AB`	Abstract
`C1`	Author Address
`RP`	Reprint Address
`TC`	Times Cited
`PY`	Year
`UT`	Unique Article Identifier
`DB`	Database

(ii) authorDocuments which is a list containing a bibliographic data frame for each author.

LIMITATIONS: Currently, SCOPUS API does not allow to download document references. As consequence, it is not possible to perform co-citation analysis (the field CR is empty).

See Also

`idByAuthor` for downloading author information and SCOPUS ID.

Examples

```
## Request a personal API Key to Elsevier web page https://dev.elsevier.com/sc_apis.html

## api_key="your api key"

## create a data frame with the list of authors to get information and IDs
# i.e. df[1,1:3] <- c("aria","massimo","naples")
#      df[2,1:3] <- c("cuccurullo","corrado", "naples")

## run idByAuthor function
#
# authorsID <- idByAuthor(df, api_key)
#

## extract the IDs
#
# id <- authorsID[,3]
#

## create the bibliographic collection
#
# res <- retrievalByAuthorID(id, api_key)
#
# M <- res$M  # the entire bibliographic data frame
# M <- res$authorDocuments # the list containing a bibliographic data frame for each author
```

`rpys` *Reference Publication Year Spectroscopy*

Description

`rpys` computes a Reference Publication Year Spectroscopy for detecting the Historical Roots of Research Fields. The method was introduced by Marx et al., 2014.

Usage

```
rpys(M, sep = ";", timespan = NULL, median.window = "centered", graph = T)
```

Arguments

`M`	is a data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to articles and variables to Field Tag in the original ISI or SCOPUS file.
`sep`	is the cited-references separator character. This character separates cited-references in the CR column of the data frame. The default is `sep = ";"`.
`timespan`	is a numeric vector c(min year,max year). The default value is NULL (the entire timespan is considered).
`median.window`	is a character string that can be "centered" or "backward". It indicates the type of median to be used. "centered" is the default value and it uses the centered 5-year median (t-2 to t+2) as proposed by Marx et al. (2014). "backward" uses the backward 5-year median (t-4 to t) as proposed by Aria and Cuccurullo (2017).
`graph`	is a logical. If TRUE the function plot the spectroscopy otherwise the plot is created but not drawn down.

Details

References:

Marx, W., Bornmann, L., Barth, A., & Leydesdorff, L. (2014). Detecting the historical roots of research fields by reference publication year spectroscopy (RPYS). Journal of the Association for Information Science and Technology, 65(4), 751-764.

Thor A., Bornmann L., Mark W. & Mutz R.(2018). Identifying single influential publications in a research field: new analysis opportunities of the CRExplorer. Scientometrics, 116:591–608 https://doi.org/10.1007/s11192-018-2733-7

Value

a list containing the spectroscopy (class ggplot2) and three dataframes with the number of citations per year, the list of the cited references for each year, and the reference list with citations recorded year by year, respectively.

See Also

`convert2df` to import and convert an ISI or SCOPUS Export file in a data frame.

`biblioAnalysis` to perform a bibliometric analysis.

`biblioNetwork` to compute a bibliographic network.

Examples

```
## Not run:
data(management, package = "bibliometrixData")
res <- rpys(management, sep = ";", graph = TRUE)
```

```
## End(Not run)
```

---

sourceGrowth *Number of documents published annually per Top Sources*

Description

It calculates yearly published documents of the top sources.

Usage

```
sourceGrowth(M, top = 5, cdf = TRUE)
```

Arguments

`M`	is a data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to articles and variables to Field Tag in the original ISI or SCOPUS file.
`top`	is a numeric. It indicates the number of top sources to analyze. The default value is 5.
`cdf`	is a logical. If TRUE, the function calculates the cumulative occurrences distribution.

Value

an object of class `data.frame`

Examples

```
data(scientometrics, package = "bibliometrixData")
topSO <- sourceGrowth(scientometrics, top = 1, cdf = TRUE)
topSO

# Plotting results
## Not run:
install.packages("reshape2")
library(reshape2)
library(ggplot2)
DF <- melt(topSO, id = "Year")
ggplot(DF, aes(Year, value, group = variable, color = variable)) +
  geom_line()

## End(Not run)
```

`splitCommunities` *Splitting Network communities*

Description

`networkPlot` Create a network plot with separated communities.

Usage

```
splitCommunities(graph, n = NULL)
```

Arguments

`graph`	is a network plot obtained by the function `networkPlot`.
`n`	is an integer. It indicates the number of vertices to plot for each community.

Details

The function `splitCommunities` splits communities in separated subnetworks from a bibliographic network plot previously created by `networkPlot`.

Value

It is a network object of the class `igraph`

See Also

`biblioNetwork` to compute a bibliographic network.

`networkPlot` to plot a bibliographic network.

`net2VOSviewer` to export and plot the network with VOSviewer software.

`cocMatrix` to compute a co-occurrence matrix.

`biblioAnalysis` to perform a bibliometric analysis.

Examples

```
# EXAMPLE Keywordd co-occurrence network

data(management, package = "bibliometrixData")

NetMatrix <- biblioNetwork(management,
  analysis = "co-occurrences",
  network = "keywords", sep = ";"
)

net <- networkPlot(NetMatrix,
  n = 30, type = "auto",
  Title = "Co-occurrence Network", labelsize = 1, verbose = FALSE
```

```
)

graph <- splitCommunities(net$graph, n = 30)
```

`stopwords` *List of English stopwords.*

Description

A character vector containing a complete list of English stopwords
Data are used by `biblioAnalysis` function to extract Country Field of Cited References and Authors.

Format

A character vector with 665 rows.

`summary.bibliometrix` *Summarizing bibliometric analysis results*

Description

`summary` method for class '`bibliometrix`'

Usage

```
## S3 method for class 'bibliometrix'
summary(object, ...)
```

Arguments

`object`	is the object for which a summary is desired.
`...`	can accept two arguments: `k` integer, used for table formatting (number of rows). Default value is 10. `pause` logical, used to allow pause in screen scrolling of results. Default value is `pause = FALSE`. `width` integer, used to define screen output width. Default value is `width = 120`. `verbose` logical, used to allow screen output. Default is TRUE.

Value

The function summary computes and returns a list of summary statistics of the object of class `bibliometrics`.

the list contains the following objects:

`MainInformation`	Main Information about Data
`AnnualProduction`	Annual Scientific Production
`AnnualGrowthRate`	Annual Percentage Growth Rate
`MostProdAuthors`	Most Productive Authors
`MostCitedPapers`	Top manuscripts per number of citations
`MostProdCountries`	Corresponding Author's Countries
`TCperCountries`	Total Citation per Countries
`MostRelSources`	Most Relevant Sources
`MostRelKeywords`	Most Relevant Keywords

See Also

`biblioAnalysis` function for bibliometric analysis

`plot` to draw some useful plots of the results.

Examples

```
data(scientometrics, package = "bibliometrixData")

results <- biblioAnalysis(scientometrics)

summary(results)
```

`summary.bibliometrix_netstat`
Summarizing network analysis results

Description

`summary` method for class '`bibliometrix_netstat`'

Usage

```
## S3 method for class 'bibliometrix_netstat'
summary(object, ...)
```

Arguments

`object`	is the object for which a summary is desired.
`...`	can accept two arguments: `k` integer, used for table formatting (number of rows). Default value is 10.

Value

The function `summary` computes and returns on display several statistics both at network and vertex level.

Examples

```
# to run the example, please remove # from the beginning of the following lines
# data(scientometrics, package = "bibliometrixData")

# NetMatrix <- biblioNetwork(scientometrics, analysis = "collaboration",
#                    network = "authors", sep = ";")
# netstat <- networkStat(NetMatrix, stat = "all", type = "degree")
# summary(netstat)
```

`tableTag` *Tabulate elements from a Tag Field column*

Description

It tabulates elements from a Tag Field column of a bibliographic data frame.

Usage

```
tableTag(
  M,
  Tag = "CR",
  sep = ";",
  ngrams = 1,
  remove.terms = NULL,
  synonyms = NULL
)
```

Arguments

`M`	is a data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to articles and variables to Field Tag in the original WoS or SCOPUS file.
`Tag`	is a character object. It indicates one of the field tags of the standard ISI WoS Field Tag codify.
`sep`	is the field separator character. This character separates strings in each column of the data frame. The default is `sep = ";"`.
`ngrams`	is an integer between 1 and 3. It indicates the type of n-gram to extract from titles or abstracts.
`remove.terms`	is a character vector. It contains a list of additional terms to delete from the documents before term extraction. The default is `remove.terms = NULL`.

`synonyms`	is a character vector. Each element contains a list of synonyms, separated by ";", that will be merged into a single term (the first word contained in the vector element). The default is `synonyms = NULL`.

Details

`tableTag` is an internal routine of main function `biblioAnalysis`.

Value

an object of class `table`

Examples

```
data(scientometrics, package = "bibliometrixData")
Tab <- tableTag(scientometrics, Tag = "CR", sep = ";")
Tab[1:10]
```

`termExtraction` *Term extraction tool from textual fields of a manuscript*

Description

It extracts terms from a text field (abstract, title, author's keywords, etc.) of a bibliographic data frame.

Usage

```
termExtraction(
  M,
  Field = "TI",
  ngrams = 1,
  stemming = FALSE,
  language = "english",
  remove.numbers = TRUE,
  remove.terms = NULL,
  keep.terms = NULL,
  synonyms = NULL,
  verbose = TRUE
)
```

Arguments

`M`	is a data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to articles and variables to Field Tag in the original WoS or SCOPUS file.

`Field`	is a character object. It indicates the field tag of textual data : `"TI"` Manuscript title `"AB"` Manuscript abstract `"ID"` Manuscript keywords plus `"DE"` Manuscript author's keywords The default is `Field = "TI"`.
`ngrams`	is an integer between 1 and 3. It indicates the type of n-gram to extract from texts. An n-gram is a contiguous sequence of n terms. The function can extract n-grams composed by 1, 2, 3 or 4 terms. Default value is `ngrams=1`.
`stemming`	is logical. If TRUE the Porter Stemming algorithm is applied to all extracted terms. The default is `stemming = FALSE`.
`language`	is a character. It is the language of textual contents ("english", "german","italian","french","spanish"). The default is `language="english"`.
`remove.numbers`	is logical. If TRUE all numbers are deleted from the documents before term extraction. The default is `remove.numbers = TRUE`.
`remove.terms`	is a character vector. It contains a list of additional terms to delete from the corpus after term extraction. The default is `remove.terms = NULL`.
`keep.terms`	is a character vector. It contains a list of compound words "formed by two or more terms" to keep in their original form in the term extraction process. The default is `keep.terms = NULL`.
`synonyms`	is a character vector. Each element contains a list of synonyms, separated by ";", that will be merged into a single term (the first word contained in the vector element). The default is `synonyms = NULL`.
`verbose`	is logical. If TRUE the function prints the most frequent terms extracted from documents. The default is `verbose=TRUE`.

Value

the bibliometric data frame with a new column containing terms about the field tag indicated in the argument `Field`.

See Also

`convert2df` to import and convert an WoS or SCOPUS Export file in a bibliographic data frame.

`biblioAnalysis` function for bibliometric analysis

Examples

```
# Example 1: Term extraction from titles

data(scientometrics, package = "bibliometrixData")

# vector of compound words
keep.terms <- c("co-citation analysis", "bibliographic coupling")
```

```
# term extraction
scientometrics <- termExtraction(scientometrics,
  Field = "TI", ngrams = 1,
  remove.numbers = TRUE, remove.terms = NULL, keep.terms = keep.terms, verbose = TRUE
)

# terms extracted from the first 10 titles
scientometrics$TI_TM[1:10]


# Example 2: Term extraction from abstracts

data(scientometrics)

# term extraction
scientometrics <- termExtraction(scientometrics,
  Field = "AB", ngrams = 2,
  stemming = TRUE, language = "english",
  remove.numbers = TRUE, remove.terms = NULL, keep.terms = NULL, verbose = TRUE
)

# terms extracted from the first abstract
scientometrics$AB_TM[1]

# Example 3: Term extraction from keywords with synonyms

data(scientometrics)

# vector of synonyms
synonyms <- c("citation; citation analysis", "h-index; index; impact factor")

# term extraction
scientometrics <- termExtraction(scientometrics,
  Field = "ID", ngrams = 1,
  synonyms = synonyms, verbose = TRUE
)
```

`thematicEvolution` *Perform a Thematic Evolution Analysis*

Description

It performs a Thematic Evolution Analysis based on co-word network analysis and clustering. The methodology is inspired by the proposal of Cobo et al. (2011).

Usage

```
thematicEvolution(
  M,
```

```
  field = "ID",
  years,
  n = 250,
  minFreq = 2,
  size = 0.5,
  ngrams = 1,
  stemming = FALSE,
  n.labels = 1,
  repel = TRUE,
  remove.terms = NULL,
  synonyms = NULL,
  cluster = "walktrap"
)
```

Arguments

`M`	is a bibliographic data frame obtained by the converting function `convert2df`.
`field`	is a character object. It indicates the content field to use. Field can be one of c=("ID","DE","KW_Merged","TI","AB"). Default value is `field="ID"`.
`years`	is a numeric vector of one or more unique cut points.
`n`	is numerical. It indicates the number of words to use in the network analysis
`minFreq`	is numerical. It indicates the min frequency of words included in to a cluster.
`size`	is numerical. It indicates del size of the cluster circles and is a number in the range (0.01,1).
`ngrams`	is an integer between 1 and 4. It indicates the type of n-gram to extract from texts. An n-gram is a contiguous sequence of n terms. The function can extract n-grams composed by 1, 2, 3 or 4 terms. Default value is `ngrams=1`.
`stemming`	is logical. If it is TRUE the word (from titles or abstracts) will be stemmed (using the Porter's algorithm).
`n.labels`	is integer. It indicates how many labels associate to each cluster. Default is `n.labels = 1`.
`repel`	is logical. If it is TRUE ggplot uses geom_label_repel instead of geom_label.
`remove.terms`	is a character vector. It contains a list of additional terms to delete from the documents before term extraction. The default is `remove.terms = NULL`.
`synonyms`	is a character vector. Each element contains a list of synonyms, separated by ";", that will be merged into a single term (the first word contained in the vector element). The default is `synonyms = NULL`.
`cluster`	is a character. It indicates the type of cluster to perform among ("optimal", "louvain","leiden", "infomap","edge_betweenness","walktrap", "spinglass", "leading_eigen", "fast_greedy").

Details

`thematicEvolution` starts from two or more thematic maps created by `thematicMap` function.

Reference:
Cobo, M. J., Lopez-Herrera, A. G., Herrera-Viedma, E., & Herrera, F. (2011). An approach for detecting, quantifying, and visualizing the evolution of a research field: A practical application to the fuzzy sets theory field. Journal of Informetrics, 5(1), 146-166.

Value

a list containing:

`nets`	The thematic nexus graph for each comparison
`incMatrix`	Some useful statistics about the thematic nexus

See Also

`thematicMap` function to create a thematic map based on co-word network analysis and clustering.

`cocMatrix` to compute a bibliographic bipartite network.

`networkPlot` to plot a bibliographic network.

Examples

```
## Not run:
data(management, package = "bibliometrixData")
years <- c(2004, 2015)

nexus <- thematicEvolution(management, field = "ID", years = years, n = 100, minFreq = 2)

## End(Not run)
```

`thematicMap` *Create a thematic map*

Description

It creates a thematic map based on co-word network analysis and clustering. The methodology is inspired by the proposal of Cobo et al. (2011).

Usage

```
thematicMap(
  M,
  field = "ID",
  n = 250,
  minfreq = 5,
  ngrams = 1,
  stemming = FALSE,
  size = 0.5,
```

```
  n.labels = 1,
  community.repulsion = 0.1,
  repel = TRUE,
  remove.terms = NULL,
  synonyms = NULL,
  cluster = "walktrap",
  subgraphs = FALSE
)
```

Arguments

`M`	is a bibliographic dataframe.
`field`	is the textual attribute used to build up the thematic map. It can be `field = c("ID","DE","KW_Merged","TI", "AB")`. `biblioNetwork` or `cocMatrix`.
`n`	is an integer. It indicates the number of terms to include in the analysis.
`minfreq`	is a integer. It indicates the minimum frequency (per thousand) of a cluster. It is a number in the range (0,1000).
`ngrams`	is an integer between 1 and 4. It indicates the type of n-gram to extract from texts. An n-gram is a contiguous sequence of n terms. The function can extract n-grams composed by 1, 2, 3 or 4 terms. Default value is `ngrams=1`.
`stemming`	is logical. If it is TRUE the word (from titles or abstracts) will be stemmed (using the Porter's algorithm).
`size`	is numerical. It indicates del size of the cluster circles and is a number in the range (0.01,1).
`n.labels`	is integer. It indicates how many labels associate to each cluster. Default is `n.labels = 1`.
`community.repulsion`	is a real. It indicates the repulsion force among network communities. It is a real number between 0 and 1. Default is `community.repulsion = 0.1`.
`repel`	is logical. If it is TRUE ggplot uses geom_label_repel instead of geom_label.
`remove.terms`	is a character vector. It contains a list of additional terms to delete from the documents before term extraction. The default is `remove.terms = NULL`.
`synonyms`	is a character vector. Each element contains a list of synonyms, separated by ";", that will be merged into a single term (the first word contained in the vector element). The default is `synonyms = NULL`.
`cluster`	is a character. It indicates the type of cluster to perform among ("optimal", "louvain","leiden", "infomap","edge_betweenness","walktrap", "spinglass", "leading_eigen", "fast_greedy").
`subgraphs`	is a logical. If TRUE cluster subgraphs are returned.

Details

`thematicMap` starts from a co-occurrence keyword network to plot in a two-dimensional map the typological themes of a domain.

Reference:
Cobo, M. J., Lopez-Herrera, A. G., Herrera-Viedma, E., & Herrera, F. (2011). An approach for detecting, quantifying, and visualizing the evolution of a research field: A practical application to the fuzzy sets theory field. Journal of Informetrics, 5(1), 146-166.

Value

a list containing:

`map`	The thematic map as ggplot2 object
`clusters`	Centrality and Density values for each cluster.
`words`	A list of words following in each cluster
`nclust`	The number of clusters
`net`	A list containing the network output (as provided from the networkPlot function)

See Also

`biblioNetwork` function to compute a bibliographic network.

`cocMatrix` to compute a bibliographic bipartite network.

`networkPlot` to plot a bibliographic network.

Examples

```
## Not run:
data(scientometrics, package = "bibliometrixData")
res <- thematicMap(scientometrics, field = "ID", n = 250, minfreq = 5, size = 0.5, repel = TRUE)
plot(res$map)

## End(Not run)
```

`threeFieldsPlot` *Three Fields Plot*

Description

Visualize the main items of three fields (e.g. authors, keywords, journals), and how they are related through a Sankey diagram.

Usage

```
threeFieldsPlot(M, fields = c("DE", "AU", "SO"), n = c(20, 20, 20))
```

Arguments

`M`	is a bibliographic data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to manuscripts and variables to Field Tag in the original SCOPUS and Clarivate Analytics WoS file.
`fields`	is a character vector. It indicates the fields to analyze using the standard WoS field tags. Default is `fields = c("AU","DE", "SO")`.
`n`	is a integer vector. It indicates how many items to plot, for each of the three fields. Default is `n = c(20, 20, 20)`

Value

a sankeyPlot

Examples

```
# data(scientometrics, package = "bibliometrixData")

# threeFieldsPlot(scientometrics, fields=c("DE","AU","CR"),n=c(20,20,20))
```

`timeslice` *Bibliographic data frame time slice*

Description

Divide a bibliographic data frame into time slice

Usage

```
timeslice(M, breaks = NA, k = 5)
```

Arguments

`M`	is a bibliographic data frame obtained by the converting function `convert2df`. It is a data matrix with cases corresponding to manuscripts and variables to Field Tag in the original SCOPUS and Clarivate Analytics WoS file.
`breaks`	is a numeric vector of two or more unique cut points.
`k`	is an integer value giving the number of intervals into which the data frame is to be cut. `k` is used only in case `breaks` argument is not provided. The default is `k = 5`.

Value

the value returned from `split` is a list containing the data frames for each sub-period.

See Also

`convert2df` to import and convert an ISI or SCOPUS Export file in a bibliographic data frame.

`biblioAnalysis` function for bibliometric analysis.

`summary` to obtain a summary of the results.

`plot` to draw some useful plots of the results.

Examples

```
data(scientometrics, package = "bibliometrixData")

list_df <- timeslice(scientometrics, breaks = c(1995, 2005))

names(list_df)
```

`trim` *Deleting leading and ending white spaces*

Description

Deleting leading and ending white spaces from a `character` object.

Usage

```
trim(x)
```

Arguments

x	is a `character` object.

Details

`tableTag` is an internal routine of `bibliometrics` package.

Value

an object of class `character`

Examples

```
char <- c("  Alfred", "Mary", " John")
char
trim(char)
```

`trim.leading` *Deleting leading white spaces*

Description

Deleting leading white spaces from a `character` object.

Usage

```
trim.leading(x)
```

Arguments

`x`	is a `character` object.

Details

`tableTag` is an internal routine of `bibliometrics` package.

Value

an object of class `character`

Examples

```
char <- c("  Alfred", "Mary", " John")
char
trim.leading(char)
```

`trimES` *Deleting extra white spaces*

Description

Deleting extra white spaces from a `character` object.

Usage

```
trimES(x)
```

Arguments

`x`	is a `character` object.

Details

`tableTag` is an internal routine of `bibliometrics` package.

Value

an object of class `character`

Examples

```
char <- c("Alfred  BJ", "Mary    Beth", "John      John")
char
trimES(char)
```

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