Package 'screenmedR'

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Type Package

Title Filtering Pubmed Articles for a meta-analysis.

Version 0.1.0

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Description screenmedR is a package for automatizing the screening of publications in order to minimize the manual work needed to extract the proper publications for a meta-analysis project.

License GPL(>=2)

Encoding UTF-8

LazyData true

RoxygenNote 7.2.2

Imports rentrez,
 XML,
 dplyr,
 purrr,
 tm,
 stringr,
 RISmed,
 tidyr,
 proxy,
 lsa

Suggests knitr,
 rmarkdown

VignetteBuilder knitr

Depends R (>= 2.10)

R topics documented:

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abstractsofgroup	*A Function that collects the PMID's of a specific clustering group, after clustering with screenmed function.*

Description

Gathering the PMIDs of abstracts which belong to a specific cluster.

Usage

```
abstractsofgroup(clustering, group_number)
```

Arguments

clustering	The $clustering output of the screemed function.
group_number	The number of the group the screenmed divided the initial_search.

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diagnosis_clean	*A function that cleans and manipulates the abstracts*

Description

By Using tm functions works for cleaning, stemming, removing special words etc.

Usage

```
diagnosis_clean(x)
```

Arguments

x

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mesh_by_name	*A function that provides the PMID numbers of publications in terms of the names of their Descriptors & Qualifiers*

Description

It can provide all the PMIDS of publications with specific Descriptors and Qualifiers. It has a 300 Abstracts input limit ($x < 300$)

Usage

```
mesh_by_name(x, Descriptor, Qualifier)
```

Arguments

x	A character vector containing the PMID numbers of the articles of our search
Descriptor	A character vector containing the mesh Descriptors.
Qualifier	A character vector containing the mesh Qualifiers.

| mesh_by_name_bq | *A function that provides the PMID numbers of publications in terms of the names of their Descriptors & Qualifiers* |

Description

It can provide all the PMIDS of publications with specific Descriptors and Qualifiers.

Usage

```
mesh_by_name_bq(x, d, q)
```

Arguments

x	A character vector containing the PMID numbers of the articles of our search
Descriptor	A character vector containing the mesh Descriptors.
Qualifier	A character vector containing the mesh Qualifiers.

Examples

```
initial_search <- read.csv(system.file("extdata", "csv-randomized-set.csv", package = "screenmedR"))
initialPMID<-initial_search$PMID
Descriptor<-c("Blood Pressure","Dobutamine","Humans","Infant, Newborn")
Qualifier<-c("administration & dosage")
mesh_by_name_bq(initialPMID,Descriptor,Qualifier)
```

| mesh_clean | *A function that screens relevant publications in terms of common numbers of mesh terms.* |

Description

It provides the PMID numbers of a set of publications x which have at least d descriptors and q qualifiers in common with a small default set y. It has a limit of 300 Abstracts (x< 300).

Usage

```
mesh_clean(x, y, d, q)
```

Arguments

x	A character vector containing the PMID numbers of the articles of our search
y	A character vector containing the pmid numbers of publications that the user would like to compare with x.
d	An integer that describes the number of Descriptors that the user wants the two vectors to have at least in common.
q	An integer that describes the number of Qualifiers that the user wants the two vectors to have at least in common.

Value

result_final

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mesh_clean_bq	*Screening-cleaning relevant publications in terms of number of mesh terms.*

Description

It provides the PMID numbers of a set of publications x which have at least d descriptors and q qualifiers in common with a small default set y.

Usage

```
mesh_clean_bq(x, y, d, q)
```

Arguments

x	A character vector containing the PMID numbers of the articles of our search
y	A character vector containing the pmid numbers of publications that the user would like to compare with x.
d	An integer that describes the number of Descriptors that the user wants the two vectors to have at least in common.
q	An integer that describes the number of Qualifiers that the user wants the two vectors to have at least in common.

Examples

```
initial_search <- read.csv(system.file("extdata", "csv-randomized-set.csv", package = "screenmedR"))
initialPMID<-initial_search$PMID
knownPMID<-c("18822428","8276025","16452355","17329276","8346957")
mesh_clean_bq(initialPMID,knownPMID,11,2)
```

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screenmed	*A Function which is grouping abstracts in terms of similarity with a small group of relevant publications.*

Description

It provides the following: 1) The number of groups the user choose to split the initial search 2) The cosine similarities between the small group of publications and each of the clustered groups of abstracts 3) A list of the clustered abstracts and the cluster they belong to. 4) The PMIDS of the publications that no abstract was found in Pubmed.

Usage

```
screenmed(initial_search, filtered, sparsity, group_number)
```

Arguments

`initial_search`	A character vector containing the PMID numbers of the articles of our search.
`filtered`	A character vector containing the pmid numbers of abstracts (4 or 5 typically) that belong to the study.
`sparsity`	A number typically in (0,99,1) that defines the sparsity of the abstracts for clustering.
`group_number`	The number of groups the user would like to divide the initial number of publications from pubmed search.

Value

group_number,cosine_similarity,clustering,missing_abstracts

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