Package ‘MeSHSim’

November 3, 2016

Type Package

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Title MeSH (Medical Subject Headings) Semantic Similarity Measures

Version 1.6.0

Date 2015-01-12

Imports XML, RCurl

Depends R(>= 3.0.0)

Description Provide for measuring semantic similarity over MeSH headings and MEDLINE documents

License GPL-2

biocViews Clustering, Software

NeedsCompilation no

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**docInfo**

*Get details of documents*

**Description**

Fetch information of a given article from PubMed.

**Usage**

```
docInfo(pmid, verbose=FALSE, major=FALSE)
```

**Arguments**

- **pmid**: pmid of the desired article.
- **verbose**: whether the title and abstract of the article should be print out.
- **major**: whether only major terms should be returned.

**Value**

Document information of given PMID including title, abstract, MeSH headings

**Note**

Network connection is required for using this function.

**Examples**

```
docInfo("1111111")
```

---

**docSim**

*Similarity between articles*

**Description**

Calculate the similarity between two articles.

**Usage**

```
docSim(pmid1, pmid2, method="SP", frame="node", major=FALSE, env=NULL)
```

**Arguments**

- **pmid1, pmid2**: pmids of two articles whose similarity is needed to be calculated.
- **method**: similarity measurement method, see Details for available methods.
- **frame**: available options are node and heading, decide whether using node-based or heading-based methods.
- **env**: the dataset to use.
- **major**: whether the calculation should only be based on major terms
headingSetSim

Details

Value
Semantic similarity between two MEDLINE documents, whose value is between 0 and 1.

Note
Network connection is required for using this function.

Examples

```
docSim("1111113","1111111")
```

headingSetSim

Similarity between two MeSH heading sets

Description
Calculate similarity between two MeSH heading sets.

Usage

```
headingSetSim(headingSet1, headingSet2, method="SP", frame="node", env=NULL)
```

Arguments

- `headingSet1, headingSet2` two lists of headings
- `method` similarity measurment method, see Details for available methods.
- `frame` available options are node and heading, decide whether using node-based or heading-based methods.
- `env` the dataset to use.

Details

Value
Semantic similarity between two MeSH heading sets, whose value is between 0 and 1.

Examples

```
headingSet1<-c("Lumbosacral Region", "Body Regions")
headingSet2<-c("Body Regions", "Abdomen", "Abdominal Cavity")
headingSetSim(headingSet1,headingSet2,'SP','node')
```
headingSim  

*Similarity between headings*

**Description**

Calculate similarity between two headings.

**Usage**

```
headingSim(heading1, heading2, method="SP", frame="node", env=NULL)
```

**Arguments**

- `heading1`, `heading2`  
  two headings or two lists of headings
- `method`  
  similarity measurement method, see Details for available methods.
- `frame`  
  available options are node and heading, decide whether using node-based or heading-based methods.
- `env`  
  the dataset to use.

**Details**


**Value**

Semantic similarity between two MeSH headings, whose value is between 0 and 1.

**Examples**

```
headingSim("Lumbosacral Region", "Body Regions")
```

---

**MeshSimData**  

*MeSH Dataset*

**Description**

These contents data of the whole MeSH tree, as well as information contents for every node and term.

This dataset will be auto loaded by the first invoked function of this package, if no other dataset is specified.
**mheadingSim**

*Similarity between heading lists*

**Description**
Calculate similarity matrix between two heading lists.

**Usage**
mheadingSim(headingList1, headingList2, method="SP", frame="node", env=NULL)

**Arguments**
- headingList1, headingList2: two headings or two lists of headings
- method: similarity measurement method, see Details for available methods.
- frame: available options are node and heading, decide whether using node-based or heading-based methods.
- env: the dataset to use.

**Details**

**Value**
Semantic similarity matrix between two MeSH heading lists.

**Examples**
```r
headingList1<-c("Body Regions", "Abdomen", "Abdominal Cavity")
headingList2<-c("Lumbosacral Region", "Body Regions")
mheadingSim(headingList1,headingList2)
```

**mnodeSim**

*Similarity between node lists*

**Description**
Calculate similarity matrix between two MeSH node lists.

**Usage**
mnodeSim(nodeList1, nodeList2, method="SP", frame="node", env=NULL)

**Arguments**
- nodeList1, nodeList2: two headings or two lists of headings
- method: similarity measurement method, see Details for available methods.
- frame: available options are node and heading, decide whether using node-based or heading-based methods.
- env: the dataset to use.

**Details**

**Value**
Semantic similarity matrix between two MeSH node lists.

**Examples**
```r
headingList1<-c("Body Regions", "Abdomen", "Abdominal Cavity")
headingList2<-c("Lumbosacral Region", "Body Regions")
mnodeSim(nodeList1, nodeList2)
```
nodeInfo

Arguments

nodeList1, nodeList2
  two nodes or two lists of nodes
method
  similarity measurement method, see Details for available methods.
frame
  available options are node and heading, decide whether using node-based or
  heading-based methods.
env
  the dataset to use.

Details


Value

Semantic similarity matrix between two MeSH node lists.

Examples

```r
default <- c("B03.440.400.425.340.590", "B03.440.400.425.117.800.200")
nodeList2 <- c("B03.440.400.425.340.590", "B03.440.400.425.117.800.200", "B03.440.400.425.127.100")
mnodeSim(nodeList1, nodeList2)
```

nodeInfo

Details of nodes

Description

This function returns a tree contains the given node.

Usage

```r
nodeInfo(node, brief, env=NULL)
```

Arguments

node
  a node name.
brevi
  brief model for nodeInfo
e
  the dataset to use.

Value

Hierarchy information of node a

Examples

```r
nodeInfo("B03.440.400.425.127")
nodeInfo("B03.440.400", brief=TRUE)
```
**nodeSim**

*Similarity between nodes*

**Description**

Calculate similarity between two MeSH nodes.

**Usage**

```r
nodeSim(node1, node2, method="SP", frame="node", env=NULL)
```

**Arguments**

- `node1, node2`: two nodes or two lists of nodes
- `method`: similarity measurement method, see Details for available methods.
- `frame`: available options are node and heading, decide whether using node-based or heading-based methods.
- `env`: the dataset to use.

**Details**


**Value**

Semantic similarity between two MeSH nodes, whose value is between 0 and 1.

**Examples**

```r
nodeSim("B03.440.400.425.340.590", "B03.440.400.425.117.800.200")
```

**termInfo**

*Details of MeSH terms*

**Description**

This function returns a tree contains the given term.

**Usage**

```r
termInfo(term, brief, env=NULL)
```

**Arguments**

- `term`: a term name.
- `brief`: whether to retrieve brief tree information of MeSH term
- `env`: the dataset to use.
termInfo

Value

Hierarchy information of a given term

Examples

termInfo("Body Regions")
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