Package ‘textreuse’

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Description Tools for measuring similarity among documents and detecting passages which have been reused. Implements shingled n-gram, skip n-gram, and other tokenizers; similarity/dissimilarity functions; pairwise comparisons; minhash and locality sensitive hashing algorithms; and a version of the Smith-Waterman local alignment algorithm suitable for natural language.

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Author Lincoln Mullen [aut, cre] (<https://orcid.org/0000-0001-5103-6917>)

Maintainer Lincoln Mullen <lincoln@lincolnmullen.com>

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R topics documented:

<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>textreuse-package</td>
<td>2</td>
</tr>
<tr>
<td>align_local</td>
<td>3</td>
</tr>
<tr>
<td>as.matrix.textreuse_candidates</td>
<td>5</td>
</tr>
<tr>
<td>filenames</td>
<td>5</td>
</tr>
<tr>
<td>hash_string</td>
<td>6</td>
</tr>
<tr>
<td>lsh</td>
<td>7</td>
</tr>
<tr>
<td>lsh_candidates</td>
<td>8</td>
</tr>
<tr>
<td>lsh_compare</td>
<td>9</td>
</tr>
<tr>
<td>lsh_probability</td>
<td>10</td>
</tr>
<tr>
<td>lsh_query</td>
<td>11</td>
</tr>
<tr>
<td>lsh_subset</td>
<td>12</td>
</tr>
<tr>
<td>minhash_generator</td>
<td>12</td>
</tr>
<tr>
<td>pairwise_candidates</td>
<td>13</td>
</tr>
<tr>
<td>pairwise_compare</td>
<td>14</td>
</tr>
<tr>
<td>rehash</td>
<td>15</td>
</tr>
<tr>
<td>similarity-functions</td>
<td>16</td>
</tr>
<tr>
<td>TextReuseCorpus</td>
<td>18</td>
</tr>
<tr>
<td>TextReuseTextDocument</td>
<td>19</td>
</tr>
<tr>
<td>TextReuseTextDocument-accessors</td>
<td>22</td>
</tr>
<tr>
<td>tokenize</td>
<td>22</td>
</tr>
<tr>
<td>tokenizers</td>
<td>23</td>
</tr>
<tr>
<td>wordcount</td>
<td>24</td>
</tr>
</tbody>
</table>

Index 26

Description

Tools for measuring similarity among documents and detecting passages which have been reused. Implements shingled n-gram, skip n-gram, and other tokenizers; similarity/dissimilarity functions; pairwise comparisons; minhash and locality sensitive hashing algorithms; and a version of the Smith-Waterman local alignment algorithm suitable for natural language.

Details

The best place to begin with this package in the introductory vignette.

```r
vignette("textreuse-introduction",package = "textreuse")
```

After reading that vignette, the "pairwise" and "minhash" vignettes introduce specific paths for working with the package.

```r
vignette("textreuse-pairwise",package = "textreuse")
vignette("textreuse-minhash",package = "textreuse")
vignette("textreuse-alignment",package = "textreuse")
```
Another good place to begin with the package is the documentation for loading documents (`TextReuseTextDocument` and `TextReuseCorpus`), for tokenizers, similarity functions, and locality-sensitive hashing.

**Author(s)**

**Maintainer:** Lincoln Mullen <lincoln@lincolnmullen.com> (ORCID)

**References**

The sample data provided in the `extdata/legal` directory is taken from a corpus of American Tract Society publications from the nineteenth-century, gathered from the Internet Archive.

The sample data provided in the `extdata/legal` directory, are taken from the following nineteenth-century codes of civil procedure from California and New York.


**See Also**

Useful links:

- [https://docs.ropensci.org/textreuse](https://docs.ropensci.org/textreuse)
- [https://github.com/ropensci/textreuse](https://github.com/ropensci/textreuse)
- Report bugs at [https://github.com/ropensci/textreuse/issues](https://github.com/ropensci/textreuse/issues)

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**align_local**

*Local alignment of natural language texts*

**Description**

This function takes two texts, either as strings or as `TextReuseTextDocument` objects, and finds the optimal local alignment of those texts. A local alignment finds the best matching subset of the two documents. This function adapts the Smith-Waterman algorithm, used for genetic sequencing, for use with natural language. It compare the texts word by word (the comparison is case-insensitive) and scores them according to a set of parameters. These parameters define the score for a match, and the penalties for a mismatch and for opening a gap (i.e., the first mismatch in a potential sequence). The function then reports the optimal local alignment. Only the subset of the documents that is a match is included. Insertions or deletions in the text are reported with the `edit_mark` character.
Usage

```r
align_local(
  a,
  b,
  match = 2L,
  mismatch = -1L,
  gap = -1L,
  edit_mark = "#",
  progress = interactive()
)
```

Arguments

- `a`: A character vector of length one, or a `TextReuseTextDocument`.
- `b`: A character vector of length one, or a `TextReuseTextDocument`.
- `match`: The score to assign a matching word. Should be a positive integer.
- `mismatch`: The score to assign a mismatching word. Should be a negative integer or zero.
- `gap`: The penalty for opening a gap in the sequence. Should be a negative integer or zero.
- `edit_mark`: A single character used for displaying insertions/deletions in the documents.
- `progress`: Display a progress bar and messages while computing the alignment.

Details

The compute time of this function is proportional to the product of the lengths of the two documents. Thus, longer documents will take considerably more time to compute. This function has been tested with pairs of documents containing about 25 thousand words each.

If the function reports that there were multiple optimal alignments, then it is likely that there is no strong match in the document.

The score reported for the local alignment is dependent on both the size of the documents and on the strength of the match, as well as on the parameters for match, mismatch, and gap penalties, so the scores are not directly comparable.

Value

A list with the class `textreuse_alignment`. This list contains several elements:

- `a_edit` and `b_edit`: Character vectors of the sequences with edits marked.
- `score`: The score of the optimal alignment.

References

For a useful description of the algorithm, see this post. For the application of the Smith-Waterman algorithm to natural language, see David A. Smith, Ryan Cordell, and Elizabeth Maddock Dillon, "Infectious Texts: Modeling Text Reuse in Nineteenth-Century Newspapers." IEEE International Conference on Big Data, 2013, [http://hdl.handle.net/2047/d20004858](http://hdl.handle.net/2047/d20004858).
Examples

```r
align_local("The answer is blowin' in the wind.",
             "As the Bob Dylan song says, the answer is blowing in the wind.")

# Example of matching documents from a corpus
dir <- system.file("extdata/legal", package = "textreuse")
corpus <- TextReuseCorpus(dir = dir, progress = FALSE)
alignment <- align_local(corpus[["ca1851-match"]], corpus[["ny1850-match"]])
str(alignment)
```

### as.matrix.textreuse_candidates

Convert candidates data frames to other formats

**Description**

These S3 methods convert a `textreuse_candidates` object to a matrix.

**Usage**

```r
## S3 method for class 'textreuse_candidates'
as.matrix(x, ...)
```

**Arguments**

- `x` An object of class `textreuse_candidates`
- `...` Additional arguments.

**Value**

A similarity matrix with row and column names containing document IDs.

### filenames

Filenames from paths

**Description**

This function takes a character vector of paths and returns just the file name, by default without the extension. A `TextReuseCorpus` uses the paths to the files in the corpus as the names of the list. This function is intended to turn those paths into more manageable identifiers.

**Usage**

```r
filenames(paths, extension = FALSE)
```
hash_string

Arguments

paths A character vector of paths.
extension Should the file extension be preserved?

See Also

basename

Examples

paths <- c("corpus/one.txt", "corpus/two.md", "corpus/three.text")
filenames(paths)
filenames(paths, extension = TRUE)

hash_string

Hash a string to an integer

Description

Hash a string to an integer

Usage

hash_string(x)

Arguments

x A character vector to be hashed.

Value

A vector of integer hashes.

Examples

s <- c("How", "many", "roads", "must", "a", "man", "walk", "down")
hash_string(s)
Locality sensitive hashing (LSH) discovers potential matches among a corpus of documents quickly, so that only likely pairs can be compared.

Usage

\texttt{lsh(x, bands, progress = interactive())}

Arguments

\begin{description}
\item[x] A \texttt{TextReuseCorpus} or \texttt{TextReuseTextDocument}.
\item[bands] The number of bands to use for locality sensitive hashing. The number of hashes in the documents in the corpus must be evenly divisible by the number of bands. See \texttt{lsh\_threshold} and \texttt{lsh\_probability} for guidance in selecting the number of bands and hashes.
\item[progress] Display a progress bar while comparing documents.
\end{description}

Details

Locality sensitive hashing is a technique for detecting document similarity that does not require pairwise comparisons. When comparing pairs of documents, the number of pairs grows rapidly, so that only the smallest corpora can be compared pairwise in a reasonable amount of computation time. Locality sensitive hashing, on the other hand, takes a document which has been tokenized and hashed using a minhash algorithm. (See \texttt{minhash\_generator}.) Each set of minhash signatures is then broken into bands comprised of a certain number of rows. (For example, 200 minhash signatures might be broken down into 20 bands each containing 10 rows.) Each band is then hashed to a bucket. Documents with identical rows in a band will be hashed to the same bucket. The likelihood that a document will be marked as a potential duplicate is proportional to the number of bands and inversely proportional to the number of rows in each band.

This function returns a data frame with the additional class \texttt{lsh\_buckets}. The LSH technique only requires that the signatures for each document be calculated once. So it is possible, as long as one uses the same minhash function and the same number of bands, to combine the outputs from this function at different times. The output can thus be treated as a kind of cache of LSH signatures.

To extract pairs of documents from the output of this function, see \texttt{lsh\_candidates}.

Value

A data frame (with the additional class \texttt{lsh\_buckets}), containing a column with the document IDs and a column with their LSH signatures, or buckets.
References


See Also

minhash_generator, lsh_candidates, lsh_query, lsh_probability, lsh_threshold

Examples

dir <- system.file("extdata/legal", package = "textreuse")
minhash <- minhash_generator(200, seed = 235)
corpus <- TextReuseCorpus(dir = dir,
                           tokenizer = tokenize_ngrams, n = 5,
                           minhash_func = minhash)
buckets <- lsh(corpus, bands = 50)
buckets

lsh_candidates

Candidate pairs from LSH comparisons

Description

Given a data frame of LSH buckets returned from `lsh`, this function returns the potential candidates.

Usage

lsh_candidates(buckets)

Arguments

buckets A data frame returned from `lsh`.

Value

A data frame of candidate pairs.

Examples

dir <- system.file("extdata/legal", package = "textreuse")
minhash <- minhash_generator(200, seed = 234)
corpus <- TextReuseCorpus(dir = dir,
                          tokenizer = tokenize_ngrams, n = 5,
                          minhash_func = minhash)
buckets <- lsh(corpus, bands = 50)
lsh_candidates(buckets)
$lsh\_compare$

$Compare\ candidates\ identified\ by\ LSH$

Description

The $lsh\_candidates$ only identifies potential matches, but cannot estimate the actual similarity of the documents. This function takes a data frame returned by $lsh\_candidates$ and applies a comparison function to each of the documents in a corpus, thereby calculating the document similarity score. Note that since your corpus will have minhash signatures rather than hashes for the tokens itself, you will probably wish to use $tokenize$ to calculate new hashes. This can be done for just the potentially similar documents. See the package vignettes for details.

Usage

lsh_compare(candidates, corpus, f, progress = interactive())

Arguments

candidates A data frame returned by $lsh\_candidates$.
corpus The same TextReuseCorpus corpus which was used to generate the candidates.
f A comparison function such as jaccard_similarity.
progress Display a progress bar while comparing documents.

Value

A data frame with values calculated for score.

Examples

dir <- system.file("extdata/legal", package = "textreuse")
minhash <- minhash_generator(200, seed = 234)
corpus <- TextReuseCorpus(dir = dir,
  tokenizer = tokenize_ngrams, n = 5,
  minhash_func = minhash)
buckets <- lsh(corpus, bands = 50)
candidates <- lsh_candidates(buckets)
lsh_compare(candidates, corpus, jaccard_similarity)
**lsh_probability**  
*Probability that a candidate pair will be detected with LSH*

**Description**

Functions to help choose the correct parameters for the `lsh` and `minhash_generator` functions. Use `lsh_threshold` to determine the minimum Jaccard similarity for two documents for them to likely be considered a match. Use `lsh_probability` to determine the probability that a pair of documents with a known Jaccard similarity will be detected.

**Usage**

```python
lsh_probability(h, b, s)
```

```python
lsh_threshold(h, b)
```

**Arguments**

- `h`: The number of minhash signatures.
- `b`: The number of LSH bands.
- `s`: The Jaccard similarity.

**Details**

Locality sensitive hashing returns a list of possible matches for similar documents. How likely is it that a pair of documents will be detected as a possible match? If `h` is the number of minhash signatures, `b` is the number of bands in the LSH function (implying then that the number of rows `r = h / b`), and `s` is the actual Jaccard similarity of the two documents, then the probability `p` that the two documents will be marked as a candidate pair is given by this equation.

\[
p = 1 - (1 - s^{r})^{b}
\]

According to MMDS, that equation approximates an S-curve. This implies that there is a threshold (`t`) for `s` approximated by this equation.

\[
t = \frac{1}{b}
\]

**References**

Examples

# Threshold for default values
lsh_threshold(h = 200, b = 40)

# Probability for varying values of s
lsh_probability(h = 200, b = 40, s = .25)
lsh_probability(h = 200, b = 40, s = .50)
lsh_probability(h = 200, b = 40, s = .75)

Description

This function retrieves the matches for a single document from an lsh_buckets object created by lsh. See lsh_candidates to retrieve all pairs of matches.

Usage

lsh_query(buckets, id)

Arguments

buckets An lsh_buckets object created by lsh.
id The document ID to find matches for.

Value

An lsh_candidates data frame with matches to the document specified.

See Also

lsh, lsh_candidates

Examples

dir <- system.file("extdata/legal", package = "textreuse")
minhash <- minhash_generator(200, seed = 235)
corpus <- TextReuseCorpus(dir = dir,
    tokenizer = tokenize_ngrams, n = 5,
    minhash_func = minhash)
buckets <- lsh(corpus, bands = 50)
lsh_query(buckets, "ny1850-match")
lsh_subset  
List of all candidates in a corpus

Description
List of all candidates in a corpus

Usage
lsh_subset(candidates)

Arguments
candidates  
A data frame of candidate pairs from lsh_candidates.

Value
A character vector of document IDs from the candidate pairs, to be used to subset the TextReuseCorpus.

Examples

dir <- system.file("extdata/legal", package = "textreuse")
minhash <- minhash_generator(200, seed = 234)
corpus <- TextReuseCorpus(dir = dir,
    tokenizer = tokenize_ngrams, n = 5,
    minhash_func = minhash)
buckets <- lsh(corpus, bands = 50)
candidates <- lsh_candidates(buckets)
lsh_subset(candidates)
corpus[lsh_subset(candidates)]

minhash_generator  
Generate a minhash function

Description
A minhash value is calculated by hashing the strings in a character vector to integers and then selecting the minimum value. Repeated minhash values are generated by using different hash functions: these different hash functions are created by using performing a bitwise XOR operation (bitwXor) with a vector of random integers. Since it is vital that the same random integers be used for each document, this function generates another function which will always use the same integers. The returned function is intended to be passed to the hash_func parameter of TextReuseTextDocument.

Usage
minhash_generator(n = 200, seed = NULL)
Arguments

n
The number of minhashes that the returned function should generate.

seed
An option parameter to set the seed used in generating the random numbers to ensure that the same minhash function is used on repeated applications.

Value

A function which will take a character vector and return n minhashes.

References


See Also

lsh

Examples

```
set.seed(253)
minhash <- minhash_generator(10)

# Example with a TextReuseTextDocument
file <- system.file("extdata/legal/ny1850-match.txt", package = "textreuse")
doc <- TextReuseTextDocument(file = file, hash_func = minhash,
                           keep_tokens = TRUE)
hashes(doc)

# Example with a character vector
is.character(tokens(doc))
minhash(tokens(doc))
```

Description

Converts a comparison matrix generated by pairwise_compare into a data frame of candidates for matches.

Usage

`pairwise_candidates(m, directional = FALSE)`
pairwise_compare

Arguments

- **m**: A matrix from `pairwise_compare`.
- **directional**: Should be set to the same value as in `pairwise_compare`.

Value

A data frame containing all the non-NA values from `m`. Columns `a` and `b` are the IDs from the original corpus as passed to the comparison function. Column `score` is the score returned by the comparison function.

Examples

```r
dir <- system.file("extdata/legal", package = "textreuse")
corpus <- TextReuseCorpus(dir = dir)

m1 <- pairwise_compare(corpus, ratio_of_matches, directional = TRUE)
pairwise_candidates(m1, directional = TRUE)

m2 <- pairwise_compare(corpus, jaccard_similarity)
pairwise_candidates(m2)
```

Description

Pairwise comparisons among documents in a corpus

Given a `TextReuseCorpus` containing documents of class `TextReuseTextDocument`, this function applies a comparison function to every pairing of documents, and returns a matrix with the comparison scores.

Usage

```r
pairwise_compare(corpus, f, ..., directional = FALSE, progress = interactive())
```

Arguments

- **corpus**: A `TextReuseCorpus`.
- **f**: The function to apply to `x` and `y`.
- **...**: Additional arguments passed to `f`.
- **directional**: Some comparison functions are commutative, so that `f(a, b) == f(b, a)` (e.g., `jaccard_similarity`). Other functions are directional, so that `f(a, b)` measures `a`’s borrowing from `b`, which may not be the same as `f(b, a)` (e.g., `ratio_of_matches`). If `directional` is `FALSE`, then only the minimum number of comparisons will be made, i.e., the upper triangle of the matrix. If `directional` is `TRUE`, then both directional comparisons will be measured. In no case, however, will documents be compared to themselves, i.e., the diagonal of the matrix.
- **progress**: Display a progress bar while comparing documents.
Value

A square matrix with dimensions equal to the length of the corpus, and row and column names set by the names of the documents in the corpus. A value of NA in the matrix indicates that a comparison was not made. In cases of directional comparisons, then the comparison reported is \( f(\text{row}, \text{column}) \).

See Also

See these document comparison functions, \texttt{jaccard_similarity}, \texttt{ratio_of_matches}.

Examples

```r
dir <- system.file("extdata/legal", package = "textreuse")
corpus <- TextReuseCorpus(dir = dir)
names(corpus) <- filenames(names(corpus))

# A non-directional comparison
pairwise_compare(corpus, jaccard_similarity)

# A directional comparison
pairwise_compare(corpus, ratio_of_matches, directional = TRUE)
```

---

### rehash

\textit{Recompute the hashes for a document or corpus}

Description

Given a \texttt{TextReuseTextDocument} or a \texttt{TextReuseCorpus}, this function recomputes either the hashes or the minhashes with the function specified. This implies that you have retained the tokens with the \texttt{keep_tokens = TRUE} parameter.

Usage

```r
rehash(x, func, type = c("hashes", "minhashes"))
```

Arguments

- \textbf{x} \hspace{1cm} A \texttt{TextReuseTextDocument} or \texttt{TextReuseCorpus}.
- \textbf{func} \hspace{1cm} A function to either hash the tokens or to generate the minhash signature. See \texttt{hash_string}, \texttt{minhash_generator}.
- \textbf{type} \hspace{1cm} Recompute the hashes or minhashes?

Value

The modified \texttt{TextReuseTextDocument} or \texttt{TextReuseCorpus}.
Examples

dir <- system.file("extdata/legal", package = "textreuse")
minhash1 <- minhash_generator(seed = 1)
corpus <- TextReuseCorpus(dir = dir, minhash_func = minhash1, keep_tokens = TRUE)
head(minhashes(corpus[[1]]))
minhash2 <- minhash_generator(seed = 2)
corpus <- rehash(corpus, minhash2, type = "minhashes")
head(minhashes(corpus[[2]]))

similarity-functions  Measure similarity/dissimilarity in documents

Description

A set of functions which take two sets or bag of words and measure their similarity or dissimilarity.

Usage

jaccard_similarity(a, b)

jaccard_dissimilarity(a, b)

jaccard_bag_similarity(a, b)

ratio_of_matches(a, b)

Arguments

a  The first set (or bag) to be compared. The origin bag for directional comparisons.
b  The second set (or bag) to be compared. The destination bag for directional comparisons.

Details

The functions jaccard_similarity and jaccard_dissimilarity provide the Jaccard measures of similarity or dissimilarity for two sets. The coefficients will be numbers between 0 and 1. For the similarity coefficient, the higher the number the more similar the two sets are. When applied to two documents of class TextReuseTextDocument, the hashes in those documents are compared. But this function can be passed objects of any class accepted by the set functions in base R. So it is possible, for instance, to pass this function two character vectors comprised of word, line, sentence, or paragraph tokens, or those character vectors hashed as integers.

The Jaccard similarity coefficient is defined as follows:

\[
J(A, B) = \frac{|A \cap B|}{|A \cup B|}
\]
The Jaccard dissimilarity is simply

\[ 1 - J(A, B) \]

The function `jaccard_bag_similarity` treats \(a\) and \(b\) as bags rather than sets, so that the result is a fraction where the numerator is the sum of each matching element counted the minimum number of times it appears in each bag, and the denominator is the sum of the lengths of both bags. The maximum value for the Jaccard bag similarity is \(0.5\).

The function `ratio_of_matches` finds the ratio between the number of items in \(b\) that are also in \(a\) and the total number of items in \(b\). Note that this similarity measure is directional: it measures how much \(b\) borrows from \(a\), but says nothing about how much of \(a\) borrows from \(b\).

References


Examples

```
jaccard_similarity(1:6, 3:10)
jaccard_dissimilarity(1:6, 3:10)

a <- c("a", "a", "a", "b")
b <- c("a", "a", "b", "b", "c")
jaccard_similarity(a, b)
jaccard_bag_similarity(a, b)
ratio_of_matches(a, b)
ratio_of_matches(b, a)
```

```
ny <- system.file("extdata/legal/ny1850-match.txt", package = "textreuse")
ca_match <- system.file("extdata/legal/ca1851-match.txt", package = "textreuse")
ca_nomatch <- system.file("extdata/legal/ca1851-nomatch.txt", package = "textreuse")

ny <- TextReuseTextDocument(file = ny,
                           meta = list(id = "ny"))
ca_match <- TextReuseTextDocument(file = ca_match,
                                   meta = list(id = "ca_match"))
ca_nomatch <- TextReuseTextDocument(file = ca_nomatch,
                                    meta = list(id = "ca_nomatch"))

# These two should have higher similarity scores
jaccard_similarity(ny, ca_match)
ratio_of_matches(ny, ca_match)

# These two should have lower similarity scores
jaccard_similarity(ny, ca_nomatch)
ratio_of_matches(ny, ca_nomatch)
```
This is the constructor function for a TextReuseCorpus, modeled on the virtual S3 class Corpus from the tm package. The object is a TextReuseCorpus, which is basically a list containing objects of class TextReuseTextDocument. Arguments are passed along to that constructor function. To create the corpus, you can pass either a character vector of paths to text files using the paths = parameter, a directory containing text files (with any extension) using the dir = parameter, or a character vector of documents using the text = parameter, where each element in the character vector is a document. If the character vector passed to text = has names, then those names will be used as the document IDs. Otherwise, IDs will be assigned to the documents. Only one of the paths, dir, or text parameters should be specified.

Usage

```
TextReuseCorpus(
  paths,
  dir = NULL,
  text = NULL,
  meta = list(),
  progress = interactive(),
  tokenizer = tokenize_ngrams,
  ...
  hash_func = hash_string,
  minhash_func = NULL,
  keep_tokens = FALSE,
  keep_text = TRUE,
  skip_short = TRUE
)
```

```
is.TextReuseCorpus(x)

skipped(x)
```

Arguments

- **paths** A character vector of paths to files to be opened.
- **dir** The path to a directory of text files.
- **text** A character vector (possibly named) of documents.
- **meta** A list with named elements for the metadata associated with this corpus.
- **progress** Display a progress bar while loading files.
- **tokenizer** A function to split the text into tokens. See tokenizers. If value is NULL, then tokenizing and hashing will be skipped.
... Arguments passed on to the tokenizer.

hash_func A function to hash the tokens. See hash_string.

minhash_func A function to create minhash signatures of the document. See minhash_generator.

keep_tokens Should the tokens be saved in the documents that are returned or discarded?

keep_text Should the text be saved in the documents that are returned or discarded?

skip_short Should short documents be skipped? (See details.)

x An R object to check.

Details

If skip_short = TRUE, this function will skip very short or empty documents. A very short document is one where there are two few words to create at least two n-grams. For example, if five-grams are desired, then a document must be at least six words long. If no value of n is provided, then the function assumes a value of n = 3. A warning will be printed with the document ID of each skipped document. Use skipped() to get the IDs of skipped documents.

This function will use multiple cores on non-Windows machines if the "mc.cores" option is set. For example, to use four cores: options("mc.cores" = 4L).

See Also

Accessors for TextReuse objects.

Examples

dir <- system.file("extdata/legal", package = "textreuse")
corpus <- TextReuseCorpus(dir = dir, meta = list("description" = "Field Codes"))
# Subset by position or file name
corpus[[1]]
names(corpus)
corpus[["ca1851-match"]]

Description

This is the constructor function for TextReuseTextDocument objects. This class is used for comparing documents.
Usage

TextReuseTextDocument(
  text,
  file = NULL,
  meta = list(),
  tokenizer = tokenize_ngrams,
  ..., 
  hash_func = hash_string,
  minhash_func = NULL,
  keep_tokens = FALSE,
  keep_text = TRUE,
  skip_short = TRUE
)

is.TextReuseTextDocument(x)

has_content(x)

has_tokens(x)

has_hashes(x)

has_minhashes(x)

Arguments

text A character vector containing the text of the document. This argument can be skipped if supplying file.

file The path to a text file, if text is not provided.

meta A list with named elements for the metadata associated with this document. If a document is created using the text parameter, then you must provide an id field, e.g., meta = list(id = "my_id"). If the document is created using file, then the ID will be created from the file name.

tokenizer A function to split the text into tokens. See tokenizers. If value is NULL, then tokenizing and hashing will be skipped.

... Arguments passed on to the tokenizer.

hash_func A function to hash the tokens. See hash_string.

minhash_func A function to create minhash signatures of the document. See minhash_generator.

keep_tokens Should the tokens be saved in the document that is returned or discarded?

keep_text Should the text be saved in the document that is returned or discarded?

skip_short Should short documents be skipped? (See details.)

x An R object to check.
Details

This constructor function follows a three-step process. It reads in the text, either from a file or from memory. It then tokenizes that text. Then it hashes the tokens. Most of the comparison functions in this package rely only on the hashes to make the comparison. By passing FALSE to keep_tokens and keep_text, you can avoid saving those objects, which can result in significant memory savings for large corpora.

If `skip_short = TRUE`, this function will return NULL for very short or empty documents. A very short document is one where there are two few words to create at least two n-grams. For example, if five-grams are desired, then a document must be at least six words long. If no value of \( n \) is provided, then the function assumes a value of \( n = 3 \). A warning will be printed with the document ID of a skipped document.

Value

An object of class `TextReuseTextDocument`. This object inherits from the virtual S3 class `TextDocument` in the NLP package. It contains the following elements:

- `content` The text of the document.
- `tokens` The tokens created from the text.
- `hashes` Hashes created from the tokens.
- `minhashes` The minhash signature of the document.
- `metadata` The document metadata, including the filename (if any) in `file`.

See Also

`Accessors for TextReuse objects`.

Examples

```r
file <- system.file("extdata/legal/ny1850-match.txt", package = "textreuse")
doc <- TextReuseTextDocument(file = file, meta = list(id = "ny1850"))
print(doc)
meta(doc)
head(tokens(doc))
head(hashes(doc))
## Not run:
content(doc)
## End(Not run)
```
TextReuseTextDocument-accessors

Accessors for TextReuse objects

Description

Accessor functions to read and write components of `TextReuseTextDocument` and `TextReuseCorpus` objects.

Usage

tokens(x)

tokens(x) <- value

hashes(x)

hashes(x) <- value

minhashes(x)

minhashes(x) <- value

Arguments

x The object to access.

value The value to assign.

Value

Either a vector or a named list of vectors.

---

tokenize Recompute the tokens for a document or corpus

Description

Given a `TextReuseTextDocument` or a `TextReuseCorpus`, this function recomputes the tokens and hashes with the functions specified. Optionally, it can also recompute the minhash signatures.
tokenizers

Usage
tokenize(
  x,
  tokenizer,
  ...,  
  hash_func = hash_string,
  minhash_func = NULL,
  keep_tokens = FALSE,
  keep_text = TRUE
)

Arguments

  x A TextReuseTextDocument or TextReuseCorpus.
  tokenizer A function to split the text into tokens. See tokenizers.
  ... Arguments passed on to the tokenizer.
  hash_func A function to hash the tokens. See hash_string.
  minhash_func A function to create minhash signatures. See minhash_generator.
  keep_tokens Should the tokens be saved in the document that is returned or discarded?
  keep_text Should the text be saved in the document that is returned or discarded?

Value

The modified TextReuseTextDocument or TextReuseCorpus.

Examples

dir <- system.file("extdata/legal", package = "textreuse")
corpus <- TextReuseCorpus(dir = dir, tokenizer = NULL)
corpus <- tokenize(corpus, tokenize_ngrams)
head(tokens(corpus[[1]]))

<table>
<thead>
<tr>
<th>tokenizers</th>
<th>Split texts into tokens</th>
</tr>
</thead>
</table>

Description

These functions each turn a text into tokens. The tokenize_ngrams functions returns shingled n-grams.
Usage

tokenize_words(string, lowercase = TRUE)

tokenize_sentences(string, lowercase = TRUE)

tokenize_ngrams(string, lowercase = TRUE, n = 3)

tokenize_skip_ngrams(string, lowercase = TRUE, n = 3, k = 1)

Arguments

string A character vector of length 1 to be tokenized.
lowercase Should the tokens be made lower case?
n For n-gram tokenizers, the number of words in each n-gram.
k For the skip n-gram tokenizer, the maximum skip distance between words. The function will compute all skip n-grams between 0 and k.

Details

These functions will strip all punctuation.

Value

A character vector containing the tokens.

Examples

dylan <- "How many roads must a man walk down? The answer is blowin' in the wind."
tokenize_words(dylan)
tokenize_sentences(dylan)
tokenize_ngrams(dylan, n = 2)
tokenize_skip_ngrams(dylan, n = 3, k = 2)

wordcount

Count words

Description

This function counts words in a text, for example, a character vector, a TextReuseTextDocument, some other object that inherits from TextDocument, or a all the documents in a TextReuseCorpus.

Usage

wordcount(x)

Arguments

x The object containing a text.
**wordcount**

**Value**

An integer vector for the word count.
Index

Accessors for TextReuse objects, 19, 21
align_local, 3
as.matrix.textreuse_candidates, 5
basename, 6
bitwXor, 12
Corpus, 18
filenames, 5
has_content (TextReuseTextDocument), 19
has hashes (TextReuseTextDocument), 19
has_minhashes (TextReuseTextDocument), 19
has_tokens (TextReuseTextDocument), 19
hash_string, 6, 15, 19, 20, 23
hashes (TextReuseTextDocument-accessors), 22
hashes<- (TextReuseTextDocument-accessors), 22
is.TextReuseCorpus (TextReuseCorpus), 18
is.TextReuseTextDocument (TextReuseTextDocument), 19
jaccard_bag_similarity (similarity-functions), 16
jaccard_dissimilarity (similarity-functions), 16
jaccard_similarity, 9, 14, 15
jaccard_similarity (similarity-functions), 16
locality-sensitive hashing, 3
lsh, 7, 8, 10, 11, 13
lsh_candidates, 7, 8, 9, 11, 12
lsh_compare, 9
lsh_probability, 7, 8, 10
lsh_query, 8, 11
lsh_subset, 12
lsh_threshold, 7, 8
lsh_threshold (lsh_probability), 10
minhash_generator, 7, 8, 10, 12, 15, 19, 20, 23
minhashes (TextReuseTextDocument-accessors), 22
minhashes<- (TextReuseTextDocument-accessors), 22
pairwise_candidates, 13
pairwise_compare, 13, 14, 14
ratio_of_matches, 14, 15
ratio_of_matches (similarity-functions), 16
rehash, 15
similarity functions, 3
similarity-functions, 16
skipped (TextReuseCorpus), 18
TextDocument, 21, 24
textreuse (textreuse-package), 2
textreuse-package, 2
textreuse_candidates, 5
TextReuseCorpus, 3, 5, 7, 9, 12, 14, 15, 18, 22–24
TextReuseTextDocument, 3, 4, 7, 12, 14–16, 18, 19, 22–24
TextReuseTextDocument-accessors, 22
tokenize, 9, 22
tokenize_ngrams (tokenizers), 23
tokenize_sentences (tokenizers), 23
tokenize_skip_ngrams (tokenizers), 23
tokenize_words (tokenizers), 23
tokenizers, 3, 18, 20, 23, 23
tokens
  (TextReuseTextDocument-accessors),
  22
tokens<-  
  (TextReuseTextDocument-accessors),
  22

wordcount, 24