Package ‘quanteda’

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Title Quantitative Analysis of Textual Data

Description A fast, flexible, and comprehensive framework for quantitative text analysis in R. Provides functionality for corpus management, creating and manipulating tokens and ngrams, exploring keywords in context, forming and manipulating sparse matrices of documents by features and feature co-occurrences, analyzing keywords, computing feature similarities and distances, applying content dictionaries, applying supervised and unsupervised machine learning, visually representing text and text analyses, and more.

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'character-methods.R' 'convert.R' 'corpus-methods-base.R'
'corpus-methods-quanteda.R' 'corpus-methods-tm.R' 'corpus.R'
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'tokens_subset.R' 'tokens_sample.R' 'utils.R' 'wordstem.R'
'zzz.R'

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Description

A set of functions for creating and managing text corpora, extracting features from text corpora, and analyzing those features using quantitative methods.

*quanteda* makes it easy to manage texts in the form of a corpus, defined as a collection of texts that includes document-level variables specific to each text, as well as meta-data for documents and for the collection as a whole. *quanteda* includes tools to make it easy and fast to manipulate the texts in a corpus, by performing the most common natural language processing tasks simply and quickly, such as tokenizing, stemming, or forming ngrams. *quanteda*’s functions for tokenizing texts and forming multiple tokenized documents into a document-feature matrix are both extremely fast and extremely simple to use. *quanteda* can segment texts easily by words, paragraphs, sentences, or even user-supplied delimiters and tags.

Built on the text processing functions in the *stringi* package, which is in turn built on C++ implementation of the ICU libraries for Unicode text handling, *quanteda* pays special attention to fast and correct implementation of Unicode and the handling of text in any character set.

*quanteda* is built for efficiency and speed, through its design around three infrastructures: the *stringi* package for text processing, the *data.table* package for indexing large documents efficiently, and the *Matrix* package for sparse matrix objects. If you can fit it into memory, *quanteda* will handle it quickly. (And eventually, we will make it possible to process objects even larger than available memory.)

*quanteda* is principally designed to allow users a fast and convenient method to go from a corpus of texts to a selected matrix of documents by features, after defining what the documents and features. The package makes it easy to redefine documents, for instance by splitting them into sentences or paragraphs, or by tags, as well as to group them into larger documents by document variables, or to subset them based on logical conditions or combinations of document variables. The package also implements common NLP feature selection functions, such as removing stopwords and stemming in numerous languages, selecting words found in dictionaries, treating words as equivalent based on a user-defined "thesaurus", and trimming and weighting features based on document frequency, feature frequency, and related measures such as tf-idf.

Once constructed, a *quanteda* document-feature matrix ("dfm") can be easily analyzed using either *quanteda*’s built-in tools for scaling document positions, or used with a number of other text analytic tools, such as: topic models (including converters for direct use with the topicmodels, LDA, and stm packages) document scaling (using *quanteda*’s own functions for the "wordfish" and "Wordscores" models, direct use with the *ca* package for correspondence analysis, or scaling with the austin package) machine learning through a variety of other packages that take matrix or matrix-like inputs.

Additional features of *quanteda* include:

- powerful, flexible tools for working with *dictionaries*;
- the ability to identify *keywords* associated with documents or groups of documents;
quanteda-package

- the ability to explore texts using key-words-in-context;
- fast computation of a variety of readability indexes;
- fast computation of a variety of lexical diversity measures;
- quick computation of word or document similarities, for clustering or to compute distances for other purposes;
- a comprehensive suite of descriptive statistics on text such as the number of sentences, words, characters, or syllables per document; and
- flexible, easy to use graphical tools to portray many of the analyses available in the package.

Source code and additional information

http://github.com/quanteda/quanteda

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See Also

Useful links:

- https://quanteda.io
- Report bugs at https://github.com/quanteda/quanteda/issues
as.corpus.corpuszip Coerce a compressed corpus to a standard corpus

Description

Recast a compressed corpus object into a standard (uncompressed) corpus object.

Usage

```r
## S3 method for class 'corpuszip'
as.corpus(x)
```

Arguments

- `x` a compressed `corpus` object

as.dfm Coercion and checking functions for dfm objects

Description

Convert an eligible input object into a dfm, or check whether an object is a dfm. Current eligible inputs for coercion to a dfm are: `matrix`, (sparse) `Matrix`, `TermDocumentMatrix`, `DocumentTermMatrix`, `data.frame`, and other `dfm` objects.

Usage

```r
as.dfm(x)

is.dfm(x)
```

Arguments

- `x` a candidate object for checking or coercion to `dfm`

Value

- `as.dfm` converts an input object into a `dfm`. Row names are used for docnames, and column names for featnames, of the resulting dfm.
- `is.dfm` returns `TRUE` if and only if its argument is a `dfm`.

See Also

`as.data.frame.dfm, as.matrix.dfm, convert`
as.dictionary

Coercion and checking functions for dictionary objects

Description

Convert a dictionary from a different format into a **quanteda** dictionary, or check to see if an object is a dictionary.

Usage

```r
as.dictionary(x)

is.dictionary(x)
```

Arguments

- `x` object to be coerced or checked; current legal values are a data.frame with the fields `word` and `sentiment` (as per the `tidytext` package)

Value

- `as.dictionary` returns a dictionary object. This conversion function differs from the `dictionary` constructor function in that it converts an existing object rather than creates one from components or from a file.
- `is.dictionary` returns `TRUE` if an object is a **quanteda** dictionary.

Examples

```r
## Not run:
data(sentiments, package = "tidytext")

as.dictionary(subset(sentiments, lexicon == "nrc"))
as.dictionary(subset(sentiments, lexicon == "bing"))

# to convert AFINN into polarities - adjust thresholds if desired
afinn <- subset(sentiments, lexicon == "AFINN")
afinn[,"sentiment"] <-
  with(afinn,
      sentiment <- ifelse(score < 0, "negative",
                         ifelse(score > 0, "positive", "neutral"))
  )

with(afinn, table(score, sentiment))
as.dictionary(afinn)

## End(Not run)

is.dictionary(dictionary(list(key1 = c("val1", "val2"), key2 = "val3")))
## [1] TRUE
is.dictionary(dictionary(list(key1 = c("val1", "val2"), key2 = "val3")))
## [1] FALSE
```
Coerce a dist object into a list

Description
Coerce a dist matrix into a list of selected target terms and similar terms, in descending order of similarity. Can be used after calling `textstat_simil` or `textstat_dist`.

Usage
```r
## S3 method for class 'dist'
as.list(x, sorted = TRUE, n = NULL, ...)
```

Arguments
- `x`: dist class object
- `sorted`: sort results in descending order if TRUE
- `n`: the top `n` highest-ranking items will be returned. If `n` is NULL, return all items.
- `...`: unused

Coerce a dfm to a matrix or data.frame

Description
Methods for coercing a dfm object to a matrix or data.frame object.

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

Arguments
- `x`: dfm to be coerced
- `...`: unused

Examples
```r
# coercion to matrix
as.matrix(data_dfm_lbgexample[, 1:10])
```
as.tokens

Coercion, checking, and combining functions for tokens objects

Description

Coercion functions to and from tokens objects, checks for whether an object is a tokens object, and functions to combine tokens objects.

Usage

as.tokens(x, concatenator = "_", ...)  
## S3 method for class 'list'
as.tokens(x, concatenator = "_", ...)

## S3 method for class 'spacyr_parsed'
as.tokens(x, concatenator = "/", 
    include_pos = c("none", "pos", "tag"), use_lemma = FALSE, ...)

## S3 method for class 'tokens'
as.list(x, ...)

## S3 method for class 'tokens'
unlist(x, recursive = FALSE, use.names = TRUE)

## S3 method for class 'tokens'
as.character(x, use.names = FALSE, ...)

is.tokens(x)

## S3 method for class 'tokens'
t1 + t2

## S3 method for class 'tokens'
c(...)

Arguments

x object to be coerced or checked
concatenator character between multi-word expressions, default is the underscore character. See Details.
... additional arguments used by specific methods. For c.tokens, these are the tokens objects to be concatenated.
include_pos character; whether and which part-of-speech tag to use: "none" do not use any part of speech indicator, "pos" use the pos variable, "tag" use the tag variable. The POS will be added to the token after "concatenator".
as.tokens

use_lemma logical; if TRUE, use the lemma rather than the raw token
recursive a required argument for unlist but inapplicable to tokens objects
use.names logical; preserve names if TRUE. For as.character and unlist only.
t1 tokens one to be added
t2 tokens two to be added

Details

The concatenator is used to automatically generate dictionary values for multi-word expressions in tokens_lookup and dfm_lookup. The underscore character is commonly used to join elements of multi-word expressions (e.g. "piece_of_cake", "New_York"), but other characters (e.g. whitespace " " or a hyphen ".") can also be used. In those cases, users have to tell the system what is the concatenator in your tokens so that the conversion knows to treat this character as the inter-word delimiter, when reading in the elements that will become the tokens.

Value

as.tokens returns a quanteda tokens object.

as.list returns a simple list of characters from a tokens object.

unlist returns a simple vector of characters from a tokens object.

as.character returns a character vector from a tokens object.

is.tokens returns TRUE if the object is of class tokens, FALSE otherwise.

c(...) and + return a tokens object whose documents have been added as a single sequence of documents.

Examples

# create tokens object from list of characters with custom concatenator
dict <- dictionary(list(country = "United States",
                     sea = c("Atlantic Ocean", "Pacific Ocean")))
lis <- list(c("The", "United-States", "has", "the", "Atlantic-Ocean",
             "and", "the", "Pacific-Ocean", "."))
toks <- as.tokens(lis, concatenator = "-")
tokens_lookup(toks, dict)

# combining tokens
toks1 <- tokens(c(doc1 = "a b c d e", doc2 = "f g h"))
toks2 <- tokens(c(doc3 = "1 2 3"))
toks1 + toks2
c(toks1, toks2)
**as.nyaml**

_Convert quanteda dictionary objects to the YAML format_

**Description**

Converts a _quanteda_ dictionary object constructed by the _dictionary_ function into the YAML format. The YAML files can be edited in text editors and imported into _quanteda_ again.

**Usage**

```r
as.nyaml(x)
```

**Arguments**

- `x` a dictionary object

**Value**

- `as.nyaml` a dictionary in the YAML format, as a character object

**Examples**

```r
## Not run:
dict <- dictionary(list(one = c("a", "b", "c"), two = c("x", "y", "z??")))
cat(yaml <- as.nyaml(dict))
cat(yaml, file = yamlfile <- paste(tempfile(), ".yml"))
dictionary(file = yamlfile)
## End(Not run)
```

---

**bootstrap_dfm**

_Bootstrap a dfm_

**Description**

Create an array of resampled dfms.

**Usage**

```r
bootstrap_dfm(x, n = 10, ..., verbose = quanteda_options("verbose"))
```

**Arguments**

- `x` a character or _corpus_ object
- `n` number of resamples
- `...` additional arguments passed to _dfm_
- `verbose` if TRUE print status messages
**char_tolower**

**Details**

Function produces multiple, resampled dfm objects, based on resampling sentences (with replacement) from each document, recombining these into new "documents" and computing a dfm for each. Resampling of sentences is done strictly within document, so that every resampled document will contain at least some of its original tokens.

**Value**

A named list of dfm objects, where the first, dfm_0, is the dfm from the original texts, and subsequent elements are the sentence-resampled dfms.

**Author(s)**

Kenneth Benoit

**Examples**

```r
# bootstrapping from the original text
txt <- c(textone = "This is a sentence. Another sentence. Yet another.",
          texttwo = "Premiere phrase. Deuxieme phrase."
) bootstrap_dfm(txt, n = 3)
```

---

**char_tolower**  
*Convert the case of character objects*

**Description**

char_tolower and char_toupper are replacements for tolower and toupper based on the stringi package. The stringi functions for case conversion are superior to the base functions because they correctly handle case conversion for Unicode. In addition, the *_tolower functions provide an option for preserving acronyms.

**Usage**

```r
char_tolower(x, keep_acronyms = FALSE, ...)
char_toupper(x, ...)
```

**Arguments**

- **x**  
The input object whose character/tokens/feature elements will be case-converted
- **keep_acronyms**  
Logical; if TRUE, do not lowercase any all-uppercase words (applies only to *_tolower functions)
- **...**  
Additional arguments passed to stringi functions, (e.g. stri_trans_tolower), such as locale
Examples

txt <- c(txt1 = "b A A", txt2 = "C C a b B")
char_tolower(txt)
char_toupper(txt)

# with acronym preservation
txt2 <- c(txt1 = "England and France are members of NATO and UNESCO",
       txt2 = "NASA sent a rocket into space.")
char_tolower(txt2)
char_tolower(txt2, keep_acronyms = TRUE)
char_toupper(txt2)

convert

Convert a dfm to a non-quanteda format

Description

Convert a quanteda dfm object to a format useable by other text analysis packages. The general function convert provides easy conversion from a dfm to the document-term representations used in all other text analysis packages for which conversions are defined.

Usage

convert(x, to = c("lda", "tm", "stm", "austin", "topicmodels", "lsa",
                  "matrix", "data.frame", "tripletlist"), docvars = NULL)

Arguments

x a dfm to be converted
to target conversion format, consisting of the name of the package into whose
document-term matrix representation the dfm will be converted:
"lda" a list with components "documents" and "vocab" as needed by the function
lda.collapsed.gibbs.sampler from the lda package
"tm" a DocumentTermMatrix from the tm package
"stm" the format for the stm package
"austin" the wfm format from the austin package
"topicmodels" the "dtm" format as used by the topicmodels package
"lsa" the "textmatrix" format as used by the lsa package
"data.frame" a data.frame where each feature is a variable
"tripletlist" a named "triplet" format list consisting of document, feature,
and frequency
docvars optional data.frame of document variables used as the meta information in conversion to the stm package format. This aids in selecting the document variables only corresponding to the documents with non-zero counts.
corpus

Value

A converted object determined by the value of to (see above). See conversion target package documentation for more detailed descriptions of the return formats.

Examples

```r
mycorpus <- corpus_subset(data_corpus_inaugural, Year > 1970)
quantdfm <- dfm(mycorpus, verbose = FALSE)

# austin's wfm format
identical(dim(quantdfm), dim(convert(quantdfm, to = "austin")))

# stm package format
stmdfm <- convert(quantdfm, to = "stm")
str(stmdfm)

#' # triplet
triplet <- convert(quantdfm, to = "tripletlist")
str(triplet)

# illustrate what happens with zero-length documents
quantdfm2 <- dfm(c(punctOnly = "!!!", mycorpus[-1]), verbose = FALSE)
rowSums(quantdfm2)
stmdfm2 <- convert(quantdfm2, to = "stm", docvars = docvars(mycorpus))
str(stmdfm2)

## Not run:
# tm's DocumentTermMatrix format
tmdfm <- convert(quantdfm, to = "tm")
str(tmdfm)

# topicmodels package format
str(convert(quantdfm, to = "topicmodels"))

# lda package format
ldadfm <- convert(quantdfm, to = "lda")
str(ldadfm)

## End(Not run)
```

---

### corpus

**Construct a corpus object**

**Description**

Creates a corpus object from available sources. The currently available sources are:

- a character vector, consisting of one document per element; if the elements are named, these names will be used as document names.
• a data.frame (or a tibble tbl_df), whose default document id is a variable identified by docid_field; the text of the document is a variable identified by textid_field; and other variables are imported as document-level meta-data. This matches the format of data.frames constructed by the readtext package.
• a kwic object constructed by kwic.
• a tm VCorpus or SimpleCorpus class object, with the fixed metadata fields imported as docvars and corpus-level metadata imported as metacorpus information.
• a corpus object.

Usage

corpus(x, ...)

```r
## S3 method for class 'corpus'
corpus(x, docnames = quanteda::docnames(x),
       docvars = quanteda::docvars(x), metacorpus = quanteda::metacorpus(x),
       compress = FALSE, ...)
```

```r
## S3 method for class 'character'
corpus(x, docnames = NULL, docvars = NULL,
        metacorpus = NULL, compress = FALSE, ...)
```

```r
## S3 method for class 'data.frame'
corpus(x, docid_field = "doc_id",
        text_field = "text", metacorpus = NULL, compress = FALSE, ...)
```

```r
## S3 method for class 'kwic'
corpus(x, split_context = TRUE, extract_keyword = TRUE,
         ...
```

```r
## S3 method for class 'Corpus'
corpus(x, metacorpus = NULL, compress = FALSE, ...)
```

Arguments

- **x**: a valid corpus source object
- **...**: not used directly
- **docnames**: Names to be assigned to the texts. Defaults to the names of the character vector (if any); doc_id for a data.frame; the document names in a tm corpus; or a vector of user-supplied labels equal in length to the number of documents. If none of these are round, then "text1", "text2", etc. are assigned automatically.
- **docvars**: a data.frame of document-level variables associated with each text
- **metacorpus**: a named list containing additional (character) information to be added to the corpus as corpus-level metadata. Special fields recognized in the summary.corpus are:
  - **source**: a description of the source of the texts, used for referencing;
The texts and document variables of corpus objects can also be accessed using index notation. Indexing a corpus object as a vector will return its text, equivalent to `texts(x)`. Note that this is not the same as subsetting the entire corpus – this should be done using the `subset` method for a corpus.

Indexing a corpus using two indexes (integers or column names) will return the document variables, equivalent to `docvars(x)`. It is also possible to access, create, or replace docvars using list notation, e.g.

```r
myCorpus[["newSerialDocvar"]]<- paste0("tag", 1:ndoc(myCorpus)).
```

For details, see `corpus-class`.

Value

A `corpus-class` class object containing the original texts, document-level variables, document-level metadata, corpus-level metadata, and default settings for subsequent processing of the corpus.

A warning on accessing corpus elements

A corpus currently consists of an S3 specially classed list of elements, but **you should not access these elements directly**. Use the extractor and replacement functions instead, or else your code is not only going to be uglier, but also likely to break should the internal structure of a corpus object change (as it inevitably will as we continue to develop the package, including moving corpus objects to the S4 class system).

Author(s)

Kenneth Benoit and Paul Nulty
corpus_reshape

Recast the document units of a corpus

See Also
corpus-class, docvars, metadoc, metacorpus, settings, texts, ndoc, docnames

Examples

# create a corpus from texts
corpus(data_char_ukimmig2010)

# create a corpus from texts and assign meta-data and document variables
summary(corpus(data_char_ukimmig2010,
               docvars = data.frame(party = names(data_char_ukimmig2010))), 5)
corpus(texts(data_corpus_irishbudget2010))

# import a tm VCorpus
if (requireNamespace("tm", quietly = TRUE)) {
  data(crude, package = "tm") # load in a tm example VCorpus
  mytmCorpus <- corpus(crude)
  summary(mytmCorpus, showmeta=TRUE)

data(acq, package = "tm")
summary(corpus(acq), 5, showmeta=TRUE)

tmCorp <- tm::VCorpus(tm::VectorSource(data_char_ukimmig2010))
quantCorp <- corpus(tmCorp)
summary(quantCorp)
}

# construct a corpus from a data.frame
mydf <- data.frame(letter_factor = factor(rep(letters[1:3], each = 2)),
                   some_ints = 1L:6L,
                   some_text = paste0("This is text number ", 1:6, "."),
                   stringsAsFactors = FALSE,
                   row.names = paste0("fromdf_", 1:6))
mydf
summary(corpus(mydf, text_field = "some_text",
               metacorpus = list(source = "from a data.frame called mydf.")))

# construct a corpus from a kwic object
mykwic <- kwic(data_corpus_inaugural, "southern")
summary(corpus(mykwic))

# from a kwic
kw <- kwic(data_char_sampletext, "econom")
summary(corpus(kw))
split_context = FALSE)
texts(corpus(kw, split_context = FALSE))
corpus_reshape

Description

For a corpus, reshape (or recast) the documents to a different level of aggregation. Units of aggre-
gation can be defined as documents, paragraphs, or sentences. Because the corpus object records
its current "units" status, it is possible to move from recast units back to original units, for example
from documents, to sentences, and then back to documents (possibly after modifying the sentences).

Usage

corpus_reshape(x, to = c("sentences", "paragraphs", "documents"),
               use_docvars = TRUE, ...)

Arguments

x            corpus whose document units will be reshaped

  to          new document units in which the corpus will be recast

  use_docvars if TRUE, repeat the docvar values for each segmented text; if FALSE, drop the
docvars in the segmented corpus. Dropping the docvars might be useful in order
to conserve space or if these are not desired for the segmented corpus.

  ...         additional arguments passed to tokens, since the syntactic segmenter uses this
              function)

Value

A corpus object with the documents defined as the new units, including document-level meta-data
identifying the original documents.

Examples

# simple example
corp <- corpus(c(textone = "This is a sentence. Another sentence. Yet another.",
                texttwo = "Premiere phrase. Deuxieme phrase."),
               docvars = data.frame(country=c("UK", "USA"), year=c(1990, 2000)),
               metacorpus = list(notes = "Example showing how corpus_reshape() works."))
summary(corp)
summary(corpus_reshape(corp, to = "sentences"), showmeta = TRUE)

# example with inaugural corpus speeches
(corp2 <- corpus_subset(data_corpus_inaugural, Year>2004))
corp2_para <- corpus_reshape(corp2, to="paragraphs")
corp2_para
summary(corp2_para, 100, showmeta = TRUE)
## Note that Bush 2005 is recorded as a single paragraph because that text
## used a single \n to mark the end of a paragraph.
corpus_sample

Randomly sample documents from a corpus

Description

Take a random sample of documents of the specified size from a corpus, with or without replacement. Works just as sample works for the documents and their associated document-level variables.

Usage

```
corpus_sample(x, size = ndoc(x), replace = FALSE, prob = NULL, 
    by = NULL, ...)```

Arguments

- `x`: a corpus object whose documents will be sampled
- `size`: a positive number, the number of documents to select
- `replace`: Should sampling be with replacement?
- `prob`: A vector of probability weights for obtaining the elements of the vector being sampled.
- `by`: a grouping variable for sampling. Useful for resampling sub-document units such as sentences, for instance by specifying `by = "document"
- `...`: unused

Value

A corpus object with number of documents equal to `size`, drawn from the corpus `x`. The returned corpus object will contain all of the meta-data of the original corpus, and the same document variables for the documents selected.

Examples

```
# sampling from a corpus
summary(corpus_sample(data_corpus_inaugural, 5))
summary(corpus_sample(data_corpus_inaugural, 10, replace = TRUE))

# sampling sentences within document
doccorpus <- corpus(c(one = "Sentence one. Sentence two. Third sentence.",
    two = "First sentence, doc2. Second sentence, doc2."))
sentcorpus <- corpus_reshape(doccorpus, to = "sentences")
texts(sentcorpus)
texts(corpus_sample(sentcorpus, replace = TRUE, by = "document"))
```
corpus_segment

Segment texts on a pattern match

Description

Segment corpus text(s) or a character vector, splitting on a pattern match. This is useful for breaking the texts into smaller documents based on a regular pattern (such as a speaker identifier in a transcript) or a user-supplied annotation.

Usage

corpus_segment(x, pattern = "***", valuetype = c("glob", "regex", "fixed"), case_insensitive = TRUE, extract_pattern = TRUE, pattern_position = c("before", "after"), use_docvars = TRUE)

cchar_segment(x, pattern = "***", valuetype = c("glob", "regex", "fixed"), case_insensitive = TRUE, remove_pattern = TRUE, pattern_position = c("before", "after"))

Arguments

x character or corpus object whose texts will be segmented
pattern a character vector, list of character vectors, dictionary, collocations, or dfm. See pattern for details.
valuetype the type of pattern matching: "glob" for "glob"-style wildcard expressions; "regex" for regular expressions; or "fixed" for exact matching. See valuetype for details.
case_insensitive ignore case when matching, if TRUE
extract_pattern extracts matched patterns from the texts and save in docvars if TRUE
pattern_position either "before" or "after", depending on whether the pattern precedes the text (as with a user-supplied tag, such as ##INTRO in the examples below) or follows the text (as with punctuation delimiters)
use_docvars if TRUE, repeat the docvar values for each segmented text; if FALSE, drop the docvars in the segmented corpus. Dropping the docvars might be useful in order to conserve space or if these are not desired for the segmented corpus.
remove_pattern removes matched patterns from the texts if TRUE

Details

For segmentation into syntactic units defined by the locale (such as sentences), use corpus_reshape instead. In cases where more fine-grained segmentation is needed, such as that based on commas or semi-colons (phrase delimiters within a sentence), corpus_segment offers greater user control than corpus_reshape.
value

corpus_segment returns a corpus of segmented texts
char_segment returns a character vector of segmented texts

Boundaries and segmentation explained

The pattern acts as a boundary delimiter that defines the segmentation points for splitting a text into new "document" units. Boundaries are always defined as the pattern matches, plus the end and beginnings of each document. The new "documents" that are created following the segmentation will then be the texts found between boundaries.

The pattern itself will be saved as a new document variable named pattern. This is most useful when segmenting a text according to tags such as names in a transcript, section titles, or user-supplied annotations. If the beginning of the file precedes a pattern match, then the extracted text will have a NA for the extracted pattern document variable (or when pattern_position = "after", this will be true for the text split between the last pattern match and the end of the document).

To extract syntactically defined sub-document units such as sentences and paragraphs, use corpus_reshape instead.

Using patterns

One of the most common uses for corpus_segment is to partition a corpus into sub-documents using tags. The default pattern value is designed for a user-annotated tag that is a term beginning with double "hash" signs, followed by a whitespace, for instance as #INTRODUCTION The text. Glob and fixed pattern types use a whitespace character to signal the end of the pattern.

For more advanced pattern matches that could include whitespace or newlines, a regex pattern type can be used, for instance a text such as

Mr. Smith: Text
Mrs. Jones: More text

could have as pattern = "\b[A-Z]+\s[A-Z][a-z]+:", which would catch the title, the name, and the colon.

For custom boundary delimitation using punctuation characters that come come at the end of a clause or sentence (such as , and ., these can be specified manually and pattern_position set to "after". To keep the punctuation characters in the text (as with sentence segmentation), set extract_pattern = FALSE. (With most tag applications, users will want to remove the patterns from the text, as they are annotations rather than parts of the text itself.)

See Also

corpus_reshape, for segmenting texts into pre-defined syntactic units such as sentences, paragraphs, or fixed-length chunks

Examples

## segmenting a corpus

# segmenting a corpus using tags
corp <- corpus(c("##INTRO This is the introduction."
corpus_subset

Extract a subset of a corpus

Description

Returns subsets of a corpus that meet certain conditions, including direct logical operations on
docvars (document-level variables). corpus_subset functions identically to subset.data.frame,
using non-standard evaluation to evaluate conditions based on the docvars in the corpus.

Usage

corpus_subset(x, subset, select, ...)

Arguments

x corpus object to be subsetted
subset logical expression indicating the documents to keep: missing values are taken
as false
select expression, indicating the docvars to keep
... not used
corpus_trim

**Value**

corpus object, with a subset of documents (and docvars) selected according to arguments

**See Also**

subset.data.frame

**Examples**

```
summary(corpus_subset(data_corpus_inaugural, Year > 1980))
summary(corpus_subset(data_corpus_inaugural, Year > 1930 & President == "Roosevelt", 
                      select = Year))
```

---

**corpus_trim**

*Remove sentences based on their token lengths or a pattern match*

**Description**

Removes sentences from a corpus or a character vector shorter than a specified length.

**Usage**

```
corpus_trim(x, what = c("sentences", "paragraphs", "documents"),
            min_ntoken = 1, max_ntoken = NULL, exclude_pattern = NULL)
char_trim(x, what = c("sentences", "paragraphs", "documents"),
          min_ntoken = 1, max_ntoken = NULL, exclude_pattern = NULL)
```

**Arguments**

- **x**: corpus or character object whose sentences will be selected.
- **what**: units of trimming, "sentences" or "paragraphs", or "documents"
- **min_ntoken, max_ntoken**: minimum and maximum lengths in word tokens (excluding punctuation)
- **exclude_pattern**: a string regular expression whose match (at the sentence level) will be used to exclude sentences

**Value**

a corpus or character vector equal in length to the input. If the input was a corpus, then the all docvars and metadata are preserved. For documents whose sentences have been removed entirely, a null string (""") will be returned.
data_char_sampletext

Examples

txt <- c("PAGE 1. This is a single sentence. Short sentence. Three word sentence.",
"PAGE 2. Very short! Shorter.",
"Very long sentence, with multiple parts, separated by commas. PAGE 3."
mycorp <- corpus(txt, docvars = data.frame(serial = 1:3))
texts(mycorp)

# exclude sentences shorter than 3 tokens
texts(corpus_trim(mycorp, min_ntoken = 3))
# exclude sentences that start with "PAGE <digit(s)>"
texts(corpus_trim(mycorp, exclude_pattern = "\dPAGE\d+"))

# trimming character objects
char_trim(txt, "sentences", min_ntoken = 3)
char_trim(txt, "sentences", exclude_pattern = "sentence\.")

data_char_sampletext  A paragraph of text for testing various text-based functions

Description

This is a long paragraph (2,914 characters) of text taken from a debate on Joe Higgins, delivered December 8, 2011.

Usage

data_char_sampletext

Format

character vector with one element

Source


Examples

tokens(data_char_sampletext, remove_punct = TRUE)
data_char_ukimmig2010  
*Immigration-related sections of 2010 UK party manifestos*

**Description**

Extracts from the election manifestos of 9 UK political parties from 2010, related to immigration or asylum-seekers.

**Usage**

`data_char_ukimmig2010`

**Format**

A named character vector of plain ASCII texts

**Examples**

```r
data_corpus_ukimmig2010 <- corpus(data_char_ukimmig2010, 
    docvars = data.frame(party = names(data_char_ukimmig2010)))
metadoc(data_corpus_ukimmig2010, "language") <- "english"
summary(data_corpus_ukimmig2010, showmeta = TRUE)
```

---

data_corpus_dailnoconf1991  
*Confidence debate from 1991 Irish Parliament*

**Description**

Texts of speeches from a no-confidence motion debated in the Irish Dáil from 16-18 October 1991 over the future of the Fianna Fail-Progressive Democrat coalition. (See Laver and Benoit 2002 for details.)

**Usage**

`data_corpus_dailnoconf1991`

**Format**

`data_corpus_dailnoconf1991` is a corpus with 58 texts, including docvars for name, party, and position.

**Source**

References


Examples

```r
## Not run:
data_dfm_dailnoconf1991 <- dfm(data_corpus_dailnoconf1991, removePunct = TRUE)
fitted <- textmodel_mixfit(data_dfm_dailnoconf1991,
c("Govt", "Opp", "Opp", rep(NA, 55)))
(pred <- predict(fitted))
tmpdf <-
  data.frame(party = as.character(docvars(data_corpus_dailnoconf1991, "party")),
             govt = coef(pred)["Govt"],
             position = as.character(docvars(data_corpus_dailnoconf1991, "position")),
             stringsAsFactors = FALSE)
bymedian <- with(tmpdf, reorder(paste(party, position), govt, median))
par(mar = c(5, 6, 4, 2)+.1)
boxplot(govt ~ bymedian, data = tmpdf,
        horizontal = TRUE, las = 1,
        xlab = "Degree of support for government")
abline(h = 7.5, col = "red", lty = "dashed")
text(c(0.9, 0.9), c(8.5, 6.5), c("Government", "Opposition"))
## End(Not run)
```

data_corpus_inaugural

US presidential inaugural address texts

Description

US presidential inaugural address texts, and metadata (for the corpus), from 1789 to present.

Usage

data_corpus_inaugural

Format

a corpus object with the following docvars:

- Year a four-digit integer year
- President character; President’s last name
- FirstName character; President’s first name (and possibly middle initial)
Details

data_corpus_inaugural is the quanteda-package corpus object of US presidents' inaugural addresses since 1789. Document variables contain the year of the address and the last name of the president.

Source


Examples

# some operations on the inaugural corpus
summary(data_corpus_inaugural)
head(docvars(data_corpus_inaugural), 10)

__________________________________________
data_corpus_irishbudget2010
Irish budget speeches from 2010

Description

Speeches and document-level variables from the debate over the Irish budget of 2010.

Usage

data_corpus_irishbudget2010

Format

The corpus object for the 2010 budget speeches, with document-level variables for year, debate, serial number, first and last name of the speaker, and the speaker's party.

Source


References


Examples

summary(data_corpus_irishbudget2010)
**data_dfm_lbgexample**

_dfm from data in Table 1 of Laver, Benoit, and Garry (2003)_

**Description**

Constructed example data to demonstrate the Wordscores algorithm, from Laver Benoit and Garry (2003), Table 1.

**Usage**

```r
data_dfm_lbgexample
```

**Format**

A _dfm_ object with 6 documents and 37 features.

**Details**

This is the example word count data from Laver, Benoit and Garry's (2003) Table 1. Documents R1 to R5 are assumed to have known positions: -1.5, -0.75, 0, 0.75, 1.5. Document V1 is assumed unknown, and will have a raw text score of approximately -0.45 when computed as per LBG (2003).

**References**


**data_dictionary_lsdRP1U**

_Lexicoder Sentiment Dictionary (2015)_

**Description**

The 2015 Lexicoder Sentiment Dictionary in _quanteda_ dictionary format.

**Usage**

```r
data_dictionary_lsdRP1U
```
Format

A dictionary of four keys containing glob-style pattern matches.

- negative: 2,858 word patterns indicating negative sentiment
- positive: 1,709 word patterns indicating positive sentiment
- neg_positive: 1,721 word patterns indicating a positive word preceded by a negation (used to convey negative sentiment)
- neg_negative: 2,860 word patterns indicating a negative word preceded by a negation (used to convey positive sentiment)

Details

The dictionary consists of 2,858 "negative" sentiment words and 1,709 "positive" sentiment words. A further set of 2,860 and 1,721 negations of negative and positive words, respectively, is also included. While many users will find the non-negation sentiment forms of the LSD adequate for sentiment analysis, Young and Soroka (2012) did find a small, but non-negligible increase in performance when accounting for negations. Users wishing to test this or include the negations are encouraged to subtract negated positive words from the count of positive words, and subtract the negated negative words from the negative count.

Young and Soroka (2012) also suggest the use of a pre-processing script to remove specific cases of some words (i.e., "good bye", or "nobody better", which should not be counted as positive). Pre-processing scripts are available at http://lexicoder.com.

License and Conditions

The LSD is available for non-commercial academic purposes only. By using data_dictionary_LSD2015, you accept these terms. Please cite the references below when using the dictionary.

References

The objectives, development and reliability of the dictionary are discussed in detail in Young and Soroka (2012). Please cite this article when using the Lexicoder Sentiment Dictionary and related resources. Young, Lori and Stuart Soroka. 2012. Lexicoder Sentiment Dictionary. Available at http://lexicoder.com.


Examples

```r
# simple example
txt <- "This aggressive policy will not win friends."
tokens_lookup(tokens(txt), dictionary = data_dictionary_LSD2015, exclusive = FALSE)
# tokens from 1 document.
## text1 :
## [1] "This" "NEGATIVE" "policy" "will" "NEG_POSITIVE" "POSITIVE" "."

# on larger examples - notice that few negations are used
```
dfm

Create a document-feature matrix

Description

Construct a sparse document-feature matrix, from a character, corpus, tokens, or even other dfm object.

Usage

dfm(x, tolower = TRUE, stem = FALSE, select = NULL, remove = NULL,
dictionary = NULL, thesaurus = NULL, valuetype = c("glob", "regex",
"fixed"), groups = NULL, verbose = quanteda_options("verbose"), ...)

Arguments

x character, corpus, tokens, or dfm object
tolower convert all features to lowercase
stem if TRUE, stem words
select a pattern of user-supplied features to keep, while excluding all others. This can be used in lieu of a dictionary if there are only specific features that a user wishes to keep. To extract only Twitter usernames, for example, set select = "@*" and make sure that remove_twitter = FALSE as an additional argument passed to tokens. Note: select = "^@\w+\b" would be the regular expression version of this matching pattern. The pattern matching type will be set by valuetype. See also tokens_remove.
remove a pattern of user-supplied features to ignore, such as "stop words". To access one possible list (from any list you wish), use stopwords(). The pattern matching type will be set by valuetype. See also tokens_select. For behaviour of remove with ngrams > 1, see Details.
dictionary a dictionary object to apply to the tokens when creating the dfm
thesaurus a dictionary object that will be applied as if exclusive = FALSE. See also tokens_lookup. For more fine-grained control over this and other aspects of converting features into dictionary/thesaurus keys from pattern matches to values, consider creating the dfm first, and then applying dfm_lookup separately, or using tokens_lookup on the tokenized text before calling dfm.
valuetype the type of pattern matching: "glob" for "glob"-style wildcard expressions; "regex" for regular expressions; or "fixed" for exact matching. See valuetye for details.

groups either: a character vector containing the names of document variables to be used for grouping; or a factor or object that can be coerced into a factor equal in length or rows to the number of documents. See groups for details.

verbose display messages if TRUE

... additional arguments passed to tokens; not used when x is a dfm

Details

The default behaviour for remove/select when constructing ngrams using dfm(x, ngrams > 1) is to remove/select any ngram constructed from a matching feature. If you wish to remove these before constructing ngrams, you will need to first tokenize the texts with ngrams, then remove the features to be ignored, and then construct the dfm using this modified tokenization object. See the code examples for an illustration.

To select on and match the features of a another dfm, x must also be a dfm.

Value

a dfm-class object

Note

When x is a dfm, groups provides a convenient and fast method of combining and refactoring the documents of the dfm according to the groups.

See Also

dfm_select, dfm-class

Examples

```r
## for a corpus
corpus_post@inaug <- corpus_subset(data_corpus_inaugural, Year > 1980)
dfm(corpus_post@inaug)
dfm(corpus_post@inaug, tolower = FALSE)

# grouping documents by docvars in a corpus
dfm(corpus_post@inaug, groups = "President", verbose = TRUE)

# with English stopwords and stemming
dfm(corpus_post@inaug, remove = stopwords("english"), stem = TRUE, verbose = TRUE)
# works for both words in ngrams too
dfm("Banking industry", stem = TRUE, ngrams = 2, verbose = FALSE)

# with dictionaries
corpus_post1900@inaug <- corpus_subset(data_corpus_inaugural, Year > 1900)
mydict <- dictionary(list(christmas = c("Christmas", "Santa", "holiday"),
opposition = c("Opposition", "reject", "notincorpus"),
```
taxing = "taxing",
taxation = "taxation",
taxregex = "tax*",
country = "states")
dfm(corpus_post1900inaug, dictionary = mydict)

# removing stopwords
test_text <- "The quick brown fox named Seamus jumps over the lazy dog also named Seamus, with the newspaper from a boy named Seamus, in his mouth."
test_corpus <- corpus(test_text)
# note: "also" is not in the default stopwords("english")
featnames(dfm(test_corpus, select = stopwords("english")))
# for ngrams
featnames(dfm(test_corpus, ngrams = 2, select = stopwords("english"), remove_punct = TRUE))
featnames(dfm(test_corpus, ngrams = 1:2, select = stopwords("english"), remove_punct = TRUE))

# removing stopwords before constructing ngrams
tokens_all <- tokens(char_tolower(test_text), remove_punct = TRUE)
tokens_no_stopwords <- tokens_remove(tokens_all, stopwords("english"))
tokens_ngrams_no_stopwords <- tokens_ngrams(tokens_no_stopwords, 2)
featnames(dfm(tokens_ngrams_no_stopwords, verbose = FALSE))

# keep only certain words
dfm(test_corpus, select = "*s", verbose = FALSE)  # keep only words ending in "s"
dfm(test_corpus, select = "$", valuetype = "regex", verbose = FALSE)

# testing Twitter functions
test_tweets <- c("My homie @justinbieber #justinbieber shopping in LA yesterday #beliebers",
"2all the ha8ers including my bro #justinbieber #emabiggestfansjustinbieber",
"Justin Bieber #justinbieber #belieber #fetusjustin #EMABiggestFansJustinBieber")
dfm(test_tweets, select = "#*", remove_twitter = FALSE)  # keep only hashtags
dfm(test_tweets, select = "#.*$", valuetype = "regex", remove_twitter = FALSE)

# for a dfm
dfm1 <- dfm(data_corpus_irishbudget2010)
dfm2 <- dfm(dfm1,
groups = ifelse(docvars(data_corpus_irishbudget2010, "party") %in% c("FF", "Green"),
   "Govt", "Opposition"),
tolower = FALSE, verbose = TRUE)

dfm_compress

Recombine a dfm or fcm by combining identical dimension elements

Description

"Compresses" or groups a dfm or fcm whose dimension names are the same, for either documents or features. This may happen, for instance, if features are made equivalent through application of a thesaurus. It could also be needed after a cbind.dfm or rbind.dfm operation. In most cases, you
dfm_compress

will not need to call 'dfm_compress', since it is called automatically by functions that change the dimensions of the dfm, e.g. dfm_tolower.

Usage

dfm_compress(x, margin = c("both", "documents", "features"))

fcm_compress(x)

Arguments

x input object, a dfm or fcm

margin character indicating on which margin to compress a dfm, either "documents", "features", or "both" (default). For fcm objects, "documents" has no effect.

... additional arguments passed from generic to specific methods

Value

dfm_compress returns a dfm whose dimensions have been recombed by summing the cells across identical dimension names (docnames or featnames). The docvars will be preserved for combining by features but not when documents are combined.

fcm_compress returns an fcm whose features have been recombed by combining counts of identical features, summing their counts.

Note

fcm_compress works only when the fcm was created with a document context.

Examples

# dfm_compress examples
mat <- rbind(dfm(c("b A A", "C C a b B"), tolower = FALSE),
              dfm("A C C C C", tolower = FALSE))
colnames(mat) <- char_tolower(featnames(mat))
mat
dfm_compress(mat, margin = "documents")
dfm_compress(mat, margin = "features")
dfm_compress(mat)

# no effect if no compression needed
compactdfm <- dfm(data_corpus_inaugural[1:5])
dim(compactdfm)
dim(dfm_compress(compactdfm))

# compress an fcm
myfcm <- fcm(tokens("A D a C E a d F e B A C E D"),
            context = "window", window = 3)
## this will produce an error:
# fcm_compress(myfcm)
dfm_group

Description
Combine documents in a dfm by a grouping variable, which can also be one of the docvars attached to the dfm. This is identical in functionality to using the "groups" argument in dfm.

Usage
    dfm_group(x, groups = NULL, fill = FALSE)

Arguments
x    a dfm
groups    either: a character vector containing the names of document variables to be used for grouping; or a factor or object that can be coerced into a factor equal in length or rows to the number of documents. See groups for details.
fill    logical; if TRUE and groups is a factor, then use all levels of the factor when forming the new "documents" of the grouped dfm. This will result in documents with zero feature counts for levels not observed. Has no effect if the groups variable(s) are not factors.

Value
    dfm_group returns a dfm whose documents are equal to the unique group combinations, and whose cell values are the sums of the previous values summed by group. Document-level variables that have no variation within groups are saved in docvars.

Setting the fill = TRUE offers a way to "pad" a dfm with document groups that may not have been observed, but for which an empty document is needed, for various reasons. If groups is a factor of dates, for instance, then using fill = TRUE ensures that the new documents will consist of one row of the dfm per date, regardless of whether any documents previously existed with that date.
dfm_lookup

Apply a dictionary to a dfm

Description
Apply a dictionary to a dfm by looking up all dfm features for matches in a set of dictionary values, and replace those features with a count of the dictionary’s keys. If exclusive = FALSE then the behaviour is to apply a “thesaurus”, where each value match is replaced by the dictionary key, converted to capitals if capkeys = TRUE (so that the replacements are easily distinguished from features that were terms found originally in the document).

Usage

dfm_lookup(x, dictionary, levels = 1:5, exclusive = TRUE, valuetype = c("glob", "regex", "fixed"), caseInsensitive = TRUE, capkeys = !exclusive, nomatch = NULL, verbose = quanteda_options("verbose"))

Arguments

x the dfm to which the dictionary will be applied
dictionary a dictionary class object
levels levels of entries in a hierarchical dictionary that will be applied
exclusive if TRUE, remove all features not in dictionary, otherwise, replace values in dictionary with keys while leaving other features unaffected
valuetype the type of pattern matching: "glob" for "glob"-style wildcard expressions; "regex" for regular expressions; or "fixed" for exact matching. See valuetype for details.
caseInsensitive ignore the case of dictionary values if TRUE
capkeys if TRUE, convert dictionary keys to uppercase to distinguish them from other features
nomatch an optional character naming a new feature that will contain the counts of features of x not matched to a dictionary key. If NULL (default), do not tabulate unmatched features.
verbose print status messages if TRUE

Examples

mycorpus <- corpus(c("a a b", "a b c", "a c d d", "a c c d"),
                    docvars = data.frame(grp = c("grp1", "grp1", "grp2", "grp2")))
mydfm <- dfm(mycorpus)
dfm_group(mydfm, groups = "grp")
dfm_group(mydfm, groups = c(1, 1, 2, 2))

# equivalent
dfm(mydfm, groups = "grp")
dfm(mydfm, groups = c(1, 1, 2, 2))
**dfm_replace**

**Note**

If using `dfm_lookup` with dictionaries containing multi-word values, matches will only occur if the features themselves are multi-word or formed from ngrams. A better way to match dictionary values that include multi-word patterns is to apply `tokens_lookup` to the tokens, and then construct the dfm.

**See Also**

`dfm_replace`

**Examples**

```r
my_dict <- dictionary(list(christmas = c("Christmas", "Santa", "holiday"),
                           opposition = c("Opposition", "reject", "notincorpus"),
                           taxglob = "tax*",
                           taxregex = "tax.+$",
                           country = c("United_States", "Sweden")))
my_dfm <- dfm(c("My Christmas was ruined by your opposition tax plan.",
                "Does the United_States or Sweden have more progressive taxation?"),
                remove = stopwords("english"), verbose = FALSE)
my_dfm

# glob format
dfm_lookup(my_dfm, my_dict, valuetype = "glob")
dfm_lookup(my_dfm, my_dict, valuetype = "glob", case_insensitive = FALSE)

# regex v. glob format: note that "united_states" is a regex match for "tax*"
dfm_lookup(my_dfm, my_dict, valuetype = "glob")
dfm_lookup(my_dfm, my_dict, valuetype = "regex", case_insensitive = TRUE)

# fixed format: no pattern matching
dfm_lookup(my_dfm, my_dict, valuetype = "fixed")
dfm_lookup(my_dfm, my_dict, valuetype = "fixed", case_insensitive = FALSE)

# show unmatched tokens
dfm_lookup(my_dfm, my_dict, nomatch = "_UNMATCHED")
```

---

**dfm_replace**  
*Replace features in dfm*

**Description**

Substitute features based on vectorized one-to-one matching for lemmatization or user-defined stemming.

**Usage**

```r
dfm_replace(x, pattern, replacement = NULL, case_insensitive = TRUE, verbose = quanteda_options("verbose"))
```
dfm_sample

Arguments

x
  dfm whose features will be replaced

pattern
  a character vector or dictionary. See pattern for more details.

replacement
  if pattern is a character vector, then replacement must be character vector of
  equal length, for a 1:1 match. If pattern is a dictionary, then replacement
  should not be used.

case_insensitive
  ignore case when matching, if TRUE

verbose
  print status messages if TRUE

Examples

mydfm <- dfm(data_corpus_irishbudget2010)

# lemmatization
infle <- c("foci", "focus", "focussed", "focuses", "focusing", "focussed", "focusses")
 lemma <- rep("focus", length(infle))
mydfm2 <- dfm_replace(mydfm, infle, lemma)
 featnames(dfm_select(mydfm2, infle))

# stemming
feat <- featnames(mydfm)
 stem <- char_wordstem(feat, "porter")
mydfm3 <- dfm_replace(mydfm, feat, stem, case_insensitive = FALSE)
 identical(mydfm3, dfm_wordstem(mydfm, "porter"))

dfm_sample

Randomly sample documents or features from a dfm

Description

Sample randomly from a dfm object, from documents or features.

Usage

dfm_sample(x, size = ndoc(x), replace = FALSE, prob = NULL,
margin = c("documents", "features"))

Arguments

x
  the dfm object whose documents or features will be sampled

size
  a positive number, the number of documents or features to select

replace
  logical; should sampling be with replacement?

prob
  a vector of probability weights for obtaining the elements of the vector being
  sampled.

margin
  dimension (of a dfm) to sample: can be documents or features
Value

A dfm object with number of documents or features equal to size, drawn from the dfm x.

See Also

sample

Examples

set.seed(10)
myDfm <- dfm(data_corpus_inaugural[1:10])
head(myDfm)
head(dfm_sample(myDfm))
head(dfm_sample(myDfm, replace = TRUE))
head(dfm_sample(myDfm, margin = "features"))

---

**dfm_select**

Select features from a dfm or fcm

Description

This function selects or removes features from a dfm or fcm, based on feature name matches with pattern. The most common usages are to eliminate features from a dfm already constructed, such as stopwords, or to select only terms of interest from a dictionary.

Usage

```r
dfm_select(x, pattern = NULL, selection = c("keep", "remove"),
valuetype = c("glob", "regex", "fixed"), caseInsensitive = TRUE,
min_nchar = 1L, max_nchar = 79L,
verbose = quanteda_options("verbose"))
```

```r
dfm_remove(x, ...)
```

```r
dfm_keep(x, ...)
```

```r
fcm_select(x, pattern = NULL, selection = c("keep", "remove"),
valuetype = c("glob", "regex", "fixed"), caseInsensitive = TRUE,
verbose = quanteda_options("verbose"), ...)
```

```r
fcm_remove(x, pattern = NULL, ...)
```

```r
fcm_keep(x, pattern = NULL, ...)
```
Arguments

- **x**: the dfm or fcm object whose features will be selected.
- **pattern**: a character vector, list of character vectors, dictionary, collocations, or dfm. See `pattern` for details.
- **selection**: whether to keep or remove the features.
- **valuetype**: the type of pattern matching: "glob" for "glob"-style wildcard expressions; "regex" for regular expressions; or "fixed" for exact matching. See `valuetype` for details.
- **case_insensitive**: ignore the case of dictionary values if TRUE.
- **min_nchar, max_nchar**: numerics specifying the minimum and maximum length in characters for features to be removed or kept; defaults are 1 and 79. (Set max_nchar to NULL for no upper limit.) These are applied after (and hence, in addition to) any selection based on pattern matches.
- **verbose**: if TRUE print message about how many pattern were removed.
- **...**: used only for passing arguments from dfm_remove or dfm_keep to dfm_select. Cannot include selection.

Details

- `dfm_remove` and `fcm_remove` are simply a convenience wrappers to calling `dfm_select` and `fcm_select` with `selection = "remove"`.
- `dfm_keep` and `fcm_keep` are simply a convenience wrappers to calling `dfm_select` and `fcm_select` with `selection = "keep"`.

Value

A dfm or fcm object, after the feature selection has been applied.

When `pattern` is a dfm object and `selection = "keep"`, then the returned object will be identical in its feature set to the dfm supplied as the `pattern` argument. This means that any features in `x` not in the dfm provided as `pattern` will be discarded, and that any features in found in the dfm supplied as `pattern` but not found in `x` will be added with all zero counts. Because selecting on a dfm is designed to produce a selected dfm with an exact feature match, when `pattern` is a dfm object, then the following settings are always used: `case_insensitive = FALSE`, and `valuetype = "fixed"`.

Selecting on a dfm is useful when you have trained a model on one dfm, and need to project this onto a test set whose features must be identical. It is also used in `bootstrap_dfm`. See examples.

When `pattern` is a dfm object and `selection = "keep"`, the returned object will simply be the dfm without the featnames matching those of the selection dfm.

Note

This function selects features based on their labels. To select features based on the values of the document-feature matrix, use `dfm_trim`. 


dfm_sort

Examples

my_dfm <- dfm(c("My Christmas was ruined by your opposition tax plan.",
               "Does the United States or Sweden have more progressive taxation?"),
              tolower = FALSE, verbose = FALSE)
my_dict <- dictionary(list(countries = c("United States", "Sweden", "France"),
                           wordsEndingInY = c("by", "my"),
                           notintext = "blahblah"))
dfm_select(my_dfm, my_dict)
dfm_select(my_dfm, my_dict, case_insensitive = FALSE)
dfm_select(my_dfm, c("s$", ".y"), selection = "keep", valuetype = "regex")
dfm_select(my_dfm, c("s$", ".y"), selection = "remove", valuetype = "regex")
dfm_select(my_dfm, stopwords("english"), selection = "keep", valuetype = "fixed")
dfm_select(my_dfm, stopwords("english"), selection = "remove", valuetype = "fixed")

# select based on character length
dfm_select(my_dfm, min_nchar = 5)

# selecting on a dfm
txts <- c("This is text one", "The second text", "This is text three")
(dfm1 <- dfm(txts[1:2]))
(dfm2 <- dfm(txts[2:3]))
(dfm3 <- dfm_select(dfm1, dfm2, valuetype = "fixed", verbose = TRUE))
setequal(featnames(dfm2), featnames(dfm3))
tmpdfm <- dfm(c("This is a document with lots of stopwords.",
               "No if, and, or but about it: lots of stopwords.",
               verbose = FALSE)
tmpdfm

dfm_remove(tmpdfm, stopwords("english"))
toks <- tokens(c("this contains lots of stopwords",
                "no if, and, or but about it: lots"),
                remove_punct = TRUE)
tmpfcm <- fcm(toks)
tmpfcm
fcm_remove(tmpfcm, stopwords("english"))

dfm_sort  Sort a dfm by frequency of one or more margins

Description  
Sorts a dfm by descending frequency of total features, total features in documents, or both.

Usage

dfm_sort(x, decreasing = TRUE, margin = c("features", "documents",
                                         "both"))
Arguments

- **x**: Document-feature matrix created by `dfm`
- **decreasing**: logical; if TRUE, the sort will be in descending order, otherwise sort in increasing order
- **margin**: which margin to sort on features to sort by frequency of features, documents to sort by total feature counts in documents, and both to sort by both

Value

A sorted `dfm` matrix object

Author(s)

Ken Benoit

Examples

```r
dtm <- dfm(data_corpus_inaugural)
head(dtm)
head(dfm_sort(dtm))
head(dfm_sort(dtm, decreasing = FALSE, "both"))
```

____

### dfm_subset

*Extract a subset of a dfm*

Description

Returns document subsets of a dfm that meet certain conditions, including direct logical operations on docvars (document-level variables). `dfm_subset` functions identically to `subset.data.frame`, using non-standard evaluation to evaluate conditions based on the `docvars` in the dfm.

Usage

```r
dfm_subset(x, subset, select, ...)
```

Arguments

- **x**: `dfm` object to be subsetted
- **subset**: logical expression indicating the documents to keep: missing values are taken as false
- **select**: expression, indicating the docvars to select from the dfm; or a `dfm` object, in which case the returned dfm will contain the same documents as the original dfm, even if these are empty. See Details.
- **...**: not used
**dfm_tfidf**  

**Details**  

To select or subset features, see `dfm_select` instead.

When `select` is a `dfm`, then the returned `dfm` will be equal in document dimension and order to the `dfm` used for selection. This is the document-level version of using `dfm_select` where pattern is a `dfm`: that function matches features, while `dfm_subset` will match documents.

**Value**

`dfm` object, with a subset of documents (and docvars) selected according to arguments

**See Also**

`subset.data.frame`

**Examples**

```r
library(kubix)

testcorp <- corpus(c(d1 = "a b c d", d2 = "a a b e",  
  d3 = "b b c e", d4 = "e e f a b"),  
  docvars = data.frame(grp = c(1, 1, 2, 3)))

testdfm <- dfm(testcorp)  
# selecting on a docvars condition  
dfm_subset(testdfm, grp > 1)  
# selecting on a supplied vector  
dfm_subset(testdfm, c(TRUE, FALSE, TRUE, FALSE))

# selecting on a dfm  
dfm1 <- dfm(c(d1 = "a b b c", d2 = "b b c d"))  
dfm2 <- dfm(c(d1 = "x y z", d2 = "a b c c d", d3 = "x x x"))  
dfm_subset(dfm1, subset = dfm2)  
dfm_subset(dfm1, subset = dfm2[c(3,1,2), ])
```

---

**dfm_tfidf**  

**Weight a dfm by tf-idf**

**Description**

Weight a dfm by term frequency-inverse document frequency (tf-idf), with full control over options. Uses fully sparse methods for efficiency.

**Usage**

```r
dfm_tfidf(x, scheme_tf = "count", scheme_df = "inverse", base = 10,  
  ...)```
Arguments

- **x** object for which idf or tf-idf will be computed (a document-feature matrix)
- **scheme_tf** scheme for `dfm_weight`; defaults to "count"
- **scheme_df** scheme for `docfreq`; defaults to "inverse". Other options to `docfreq` can be passed through the ellipsis (...).
- **base** the base for the logarithms in the `tf` and `docfreq` calls; default is 10
- **...** additional arguments passed to `docfreq`.

Details

dfm_tfidf computes term frequency-inverse document frequency weighting. The default is to use counts instead of normalized term frequency (the relative term frequency within document), but this can be overridden using `scheme_tf = "prop"`.

References


See Also

dfm_weight, docfreq

Examples

```r
mydfm <- as.dfm(data_dfm_lbgexample)
head(mydfm[, 5:10])
head(dfm_tfidf(mydfm)[, 5:10])
docfreq(mydfm)[5:15]
head(dfm_weight(mydfm)[, 5:10])

# replication of worked example from
# https://en.wikipedia.org/wiki/Tf-idf#Example_of_tfidf
wiki_dfm <-
  matrix(c(1,1,2,1,0,0, 1,1,0,0,2,3),
         byrow = TRUE, nrow = 2,
         dimnames = list(docs = c("document1", "document2"),
                         features = c("this", "is", "a", "sample",
                                      "another", "example")))

   as.dfm()
wiki_dfm
docfreq(wiki_dfm)
dfm_tfidf(wiki_dfm, scheme_tf = "prop") %>% round(digits = 2)

## Not run:
# comparison with tm
if (requireNamespace("tm")) {
  convert(wiki_dfm, to = "tm") %>% weightTfIdf() %>% as.matrix()
  # same as:
  dfm_tfidf(wiki_dfm, base = 2, scheme_tf = "prop")
```
**Description**

`dfm_tolower` and `dfm_toupper` convert the features of the dfm or fcm to lower and upper case, respectively, and then recombine the counts.

**Usage**

```r
dfm_tolower(x, keep_acronyms = FALSE, ...)
dfm_toupper(x, ...)
fcm_tolower(x, keep_acronyms = FALSE, ...)
fcm_toupper(x, ...)
```

**Arguments**

- `x`: the input object whose character/tokens/feature elements will be case-converted
- `keep_acronyms`: logical; if TRUE, do not lowercase any all-uppercase words (applies only to *_tolower functions)
- `...`: additional arguments passed to stringi functions, (e.g. `stri_trans_tolower`), such as locale

**Details**

`fcm_tolower` and `fcm_toupper` convert both dimensions of the fcm to lower and upper case, respectively, and then recombine the counts. This works only on fcm objects created with `context = "document"`.

**Examples**

```r
# for a document-feature matrix
mydfm <- dfm(c("b A A", "C C a b B"),
             toLower = FALSE, verbose = FALSE)
mydfm
dfm_tolower(mydfm)
dfm_toupper(mydfm)

# for a feature co-occurrence matrix
myfcm <- fcm(tokens(c("b A A d", "C C a b B e")),
             context = "document")
```
dfm_trim

Trim a dfm using frequency threshold-based feature selection

Description

Returns a document by feature matrix reduced in size based on document and term frequency, usually in terms of a minimum frequency, but may also be in terms of maximum frequencies. Setting a combination of minimum and maximum frequencies will select features based on a range.

Feature selection is implemented by considering features across all documents, by summing them for term frequency, or counting the documents in which they occur for document frequency. Rank and quantile versions of these are also implemented, for taking the first \( n \) features in terms of descending order of overall global counts or document frequencies, or as a quantile of all frequencies.

Usage

\[
dfm\_trim(x, \text{min\_termfreq} = \text{NULL}, \text{max\_termfreq} = \text{NULL}, 
\text{termfreq\_type} = \text{c("count", "prop", "rank", "quantile")}, 
\text{min\_docfreq} = \text{NULL}, \text{max\_docfreq} = \text{NULL}, \text{docfreq\_type} = \text{c("count", "prop", "rank", "quantile")}, \text{sparsity} = \text{NULL}, 
\text{verbose} = \text{quanteda\_options("verbose")}, \ldots)
\]

Arguments

\( x \)  

a dfm object

\( \text{min\_termfreq}, \text{max\_termfreq} \)  

minimum/maximum values of feature frequencies across all documents, below/above which features will be removed

\( \text{termfreq\_type} \)  

how \( \text{min\_termfreq} \) and \( \text{max\_termfreq} \) are interpreted. "count" sums the frequencies; "prop" divides the term frequencies by the total sum; "rank" is matched against the inverted ranking of features in terms of overall frequency, so that 1, 2, ... are the highest and second highest frequency features, and so on; "quantile" sets the cutoffs according to the quantiles (see \textbf{quantile}) of term frequencies.

\( \text{min\_docfreq}, \text{max\_docfreq} \)  

minimum/maximum values of a feature’s document frequency, below/above which features will be removed

\( \text{docfreq\_type} \)  

specify how \( \text{min\_docfreq} \) and \( \text{max\_docfreq} \) are interpreted. "count" is the same as \( \text{docfreq}(x, \text{scheme} = \text{"count"}) \); "prop" divides the document frequencies by the total sum; "rank" is matched against the inverted ranking of document frequency, so that 1, 2, ... are the features with the highest and second highest document frequencies, and so on; "quantile" sets the cutoffs according to the quantiles (see \textbf{quantile}) of document frequencies.
dfm_trim

sparsity equivalent to 1 - min_docfreq, included for comparison with tm
verbose print messages
... not used

Value

A dfm reduced in features (with the same number of documents)

Note

Trimming a dfm object is an operation based on the values in the document-feature matrix. To select subsets of a dfm based on the features themselves (meaning the feature labels from featnames) – such as those matching a regular expression, or removing features matching a stopword list, use dfm_select.

See Also

dfm_select, dfm_sample

Examples

(mydfm <- dfm(data_corpus_inaugural[1:5]))

# keep only words occurring >= 10 times and in > 2 documents
dfm_trim(mydfm, min_termfreq = 10, min_docfreq = 2)

# keep only words occurring >= 10 times and in at least 0.4 of the documents
dfm_trim(mydfm, min_termfreq = 10, min_docfreq = 0.4)

# keep only words occurring <= 10 times and in <=2 documents
dfm_trim(mydfm, max_termfreq = 10, max_docfreq = 2)

# keep only words occurring <= 10 times and in at most 3/4 of the documents
dfm_trim(mydfm, max_termfreq = 10, max_docfreq = 0.75)

# keep only words occurring 5 times in 1000, and in 2 of 5 of documents
dfm_trim(mydfm, min_docfreq = 0.4, min_termfreq = 0.005, termfreq_type = "prop")

# keep only words occurring frequently (top 20%) and in <=2 documents
dfm_trim(mydfm, min_termfreq = 0.2, max_docfreq = 2, termfreq_type = "quantile")

## Not run:
# compare to removeSparseTerms from the tm package
(mydfm_tm <- convert(mydfm, "tm"))
tm::removeSparseTerms(mydfm_tm, 0.7)
dfm_trim(mydfm, min_docfreq = 0.3)
dfm_trim(mydfm, sparsity = 0.7)

## End(Not run)
dfm_weight

Weight the feature frequencies in a dfm

Description

Weight the feature frequencies in a dfm

Usage

```r
dfm_weight(x, scheme = c("count", "prop", "propmax", "logcount", "boolean", "augmented", "logave"), weights = NULL, base = 10, K = 0.5)
dfm_smooth(x, smoothing = 1)
```

Arguments

- **x**: document-feature matrix created by `dfm`
- **scheme**: a label of the weight type:
  - `count`: $tf_{ij}$, an integer feature count (default when a dfm is created)
  - `prop`: the proportion of the feature counts of total feature counts (aka relative frequency), calculated as $tf_{ij} / \sum_j tf_{ij}$
  - `propmax`: the proportion of the feature counts of the highest feature count in a document, $tf_{ij} / \max_j tf_{ij}$
  - `logcount`: take the logarithm of $1 +$ each count, for the given base: $\log_{base}(1 + tf_{ij})$
  - `boolean`: recode all non-zero counts as 1
  - `augmented`: equivalent to $K + (1 - K) \ast dfm\_weight(x, \ "propmax")$
  - `logave`: 1 + the log of the counts) / (1 + log of the counts / the average count within document), or
    $$\frac{1 + \log_{base} tf_{ij}}{1 + \log_{base}(\sum_j tf_{ij}/N_i)}$$
- **weights**: if scheme is unused, then weights can be a named numeric vector of weights to be applied to the dfm, where the names of the vector correspond to feature labels of the dfm, and the weights will be applied as multipliers to the existing feature counts for the corresponding named features. Any features not named will be assigned a weight of 1.0 (meaning they will be unchanged).
- **base**: base for the logarithm when scheme is "logcount" or logave
- **K**: the K for the augmentation when scheme = "augmented"
- **smoothing**: constant added to the dfm cells for smoothing, default is 1
Value

dfm_weight returns the dfm with weighted values. Note the because the default weighting scheme is "count", simply calling this function on an unweighted dfm will return the same object. Many users will want the normalized dfm consisting of the proportions of the feature counts within each document, which requires setting scheme = "prop".

dfm_smooth returns a dfm whose values have been smoothed by adding the smoothing amount. Note that this effectively converts a matrix from sparse to dense format, so may exceed memory requirements depending on the size of your input matrix.

References


See Also

dfm_tfidf, docfreq

Examples

```r
my_dfm <- dfm(data_corpus_inaugural)
x <- apply(my_dfm, 1, function(tf) tf/max(tf))
topfeatures(my_dfm)
norm_dfm <- dfm_weight(my_dfm, "prop")
topfeatures(norm_dfm)
max_tf_dfm <- dfm_weight(my_dfm)
topfeatures(max_tf_dfm)
log(tf_dfm) <- dfm_weight(my_dfm, scheme = "logcount")
topfeatures(log(tf_dfm))
log_ave_dfm <- dfm_weight(my_dfm, scheme = "logave")
topFeatures(log_ave_dfm)

# combine these methods for more complex dfm weightings, e.g. as in Section 6.4
# of Introduction to Information Retrieval
head(dfm_tfidf(my_dfm, scheme_tf = "logcount"))

# apply numeric weights
str <- c("apple is better than banana", "banana banana apple much better")
(my_dfm <- dfm(str, remove = stopwords("english")))
dfm_weight(my_dfm, weights = c(apple = 5, banana = 3, much = 0.5))

# smooth the dfm
dfm_smooth(my_dfm, 0.5)
```
Create a dictionary class object, either from a list or by importing from a foreign format. Currently supported input file formats are the Wordstat, LIWC, Lexicoder v2 and v3, and Yoshikoder formats. The import using the LIWC format works with all currently available dictionary files supplied as part of the LIWC 2001, 2007, and 2015 software (see References).

Usage

dictionary(x, file = NULL, format = NULL, separator = " ",
  tolower = TRUE, encoding = "auto")

Arguments

x a named list of character vector dictionary entries, including valuetype pattern matches, and including multi-word expressions separated by concatenator. See examples. This argument may be omitted if the dictionary is read from file.

file file identifier for a foreign dictionary

format character identifier for the format of the foreign dictionary. If not supplied, the format is guessed from the dictionary file’s extension. Available options are:
  "wordstat" format used by Provalis Research’s Wordstat software
  "LIWC" format used by the Linguistic Inquiry and Word Count software
  "yoshikoder" format used by Yoshikoder software
  "lexicoder" format used by Lexicoder
  "YAML" the standard YAML format

separator the character in between multi-word dictionary values. This defaults to " ".

tolower if TRUE, convert all dictionary values to lowercase

encoding additional optional encoding value for reading in imported dictionaries. This uses the iconv labels for encoding. See the "Encoding" section of the help for file.

Details

Dictionaries can be subsetted using [ and [[, operating the same as the equivalent list operators.

Dictionaries can be coerced from lists using as.dictionary, coerced to named lists of characters using as.list, and checked using is.dictionary.

Value

A dictionary class object, essentially a specially classed named list of characters.
dictionary

References


Yoshikoder page, from Will Lowe http://conjugateprior.org/software/yoshikoder/.

Lexicoder format, http://www.lexicoder.com

See Also

dfm, as.dictionary, as.list, is.dictionary

Examples

```r
mycorpus <- corpus_subset(data_corpus_inaugural, Year>1900)
mydict <- dictionary(list(christmas = c("Christmas", "Santa", "holiday"),
                         opposition = c("Opposition", "reject", "notincorpus"),
                         taxing = "taxing",
                         taxation = "taxation",
                         taxregex = "tax+",
                         country = "america"))

head(dfm(mycorpus, dictionary = mydict))

# subset a dictionary
mydict[1:2]
mydict[c("christmas", "opposition")]
mydict[["opposition"]]

# combine dictionaries
c(mydict["christmas"], mydict["country"])

## Not run:
# import the Laver-Garry dictionary from Provalis Research
dictfile <- tempfile()
download.file("https://provalisresearch.com/Download/LaverGarry.zip",
               dictfile, mode = "wb")
unzip(dictfile, exdir = (td <- tempdir()))
lgdict <- dictionary(file = paste(td, "LaverGarry.cat", sep = "/"))
head(dfm(data_corpus_inaugural, dictionary = lgdict))

# import a LIWC formatted dictionary from http://www.moralfoundations.org
download.file("https://goo.gl/5gmxXq", tf <- tempfile())
mfdict <- dictionary(file = tf, format = "LIWC")
head(dfm(data_corpus_inaugural, dictionary = mfdict))

## End(Not run)
```
**Description**

For a dfm object, returns a (weighted) document frequency for each term. The default is a simple count of the number of documents in which a feature occurs more than a given frequency threshold. (The default threshold is zero, meaning that any feature occurring at least once in a document will be counted.)

**Usage**

```r
docfreq(x, scheme = c("count", "inverse", "inversemax", "inverseprob", "unary"), smoothing = 0, k = 0, base = 10, threshold = 0, use.names = TRUE)
```

**Arguments**

- `x` a dfm
- `scheme` type of document frequency weighting, computed as follows, where $N$ is defined as the number of documents in the dfm and $s$ is the smoothing constant:
  - `count df_j`, the number of documents for which $n_{ij} > threshold$
  - `inverse` $\log_{base} \left( s + \frac{N}{k + df_j} \right)$
  - `inversemax` $\log_{base} \left( s + \frac{\max(df_j)}{k + df_j} \right)$
  - `inverseprob` $\log_{base} \left( \frac{N - df_j}{k + df_j} \right)$
  - `unary` 1 for each feature
- `smoothing` added to the quotient before taking the logarithm
- `k` added to the denominator in the "inverse" weighting types, to prevent a zero document count for a term
- `base` the base with respect to which logarithms in the inverse document frequency weightings are computed; default is 10 (see Manning, Raghavan, and Schütze 2008, p123).
- `threshold` numeric value of the threshold above which a feature will considered in the computation of document frequency. The default is 0, meaning that a feature’s document frequency will be the number of documents in which it occurs greater than zero times.
- `use.names` logical; if TRUE attach feature labels as names of the resulting numeric vector
- `...` not used
**Value**

a numeric vector of document frequencies for each feature

**References**


**Examples**

```r
mydfm <- dfm(data_corpus_inaugural[1:2])
docfreq(mydfm[, 1:22])

# replication of worked example from
wiki_dfm <-
  matrix(c(1,1,2,1,0,0, 1,1,0,0,2,3),
         byrow = TRUE, nrow = 2,
         dimnames = list(docs = c("document1", "document2"),
                         features = c("this", "is", "a", "sample",
                                      "another", "example")))
  as.dfmc()
wiki_dfm
docfreq(wiki_dfm)
docfreq(wiki_dfm, scheme = "inverse")
docfreq(wiki_dfm, scheme = "inverse", k = 1, smoothing = 1)
docfreq(wiki_dfm, scheme = "unary")
docfreq(wiki_dfm, scheme = "inversemax")
docfreq(wiki_dfm, scheme = "inverseprob")
```

---

**docnames**  
*Get or set document names*

**Description**

Get or set the document names of a corpus, tokens, or dfm object.

**Usage**

docnames(x)

docnames(x) <- value

**Arguments**

- **x**  
  the object with docnames

- **value**  
  a character vector of the same length as x
Value

docnames returns a character vector of the document names
docnames <- assigns new values to the document names of an object.

See Also

featnames

Examples

# get and set document names to a corpus
mycorp <- data_corpus_inaugural
docnames(mycorp) <- char_tolower(docnames(mycorp))

# get and set document names to a tokens
mytoks <- tokens(data_corpus_inaugural)
docnames(mytoks) <- char_tolower(docnames(mytoks))

# get and set document names to a dfm
mydfm <- dfm(data_corpus_inaugural[1:5])
docnames(mydfm) <- char_tolower(docnames(mydfm))

# reassign the document names of the inaugural speech corpus
docnames(data_corpus_inaugural) <- paste("Speech", 1:ndoc(data_corpus_inaugural), sep="")
Value

docvars returns a data.frame of the document-level variables, dropping the second dimension to form a vector if a single docvar is returned.

docvars <- assigns value to the named field

Index access to docvars in a corpus

Another way to access and set docvars is through indexing of the corpus j element, such as data_corpus_irishbudget2010[, c("foren", "name"); or for a single docvar, data_corpus_irishbudget2010["name"). The latter also permits assignment, including the easy creation of new document variables, e.g. data_corpus_irishbudget2010["newvar"] <- 1:nrow(data_corpus_irishbudget2010). See [.corpus for details.

Note

Reassigning document variables for a tokens or dfm object is allowed, but discouraged. A better, more reproducible workflow is to create your docvars as desired in the corpus, and let these continue to be attached "downstream" after tokenization and forming a document-feature matrix. Recognizing that in some cases, you may need to modify or add document variables to downstream objects, the assignment operator is defined for tokens or dfm objects as well. Use with caution.

Examples

# retrieving docvars from a corpus
head(docvars(data_corpus_inaugural))
tail(docvars(data_corpus_inaugural, "President"), 10)

# assigning document variables to a corpus
corp <- data_corpus_inaugural
docvars(corp, "President") <- paste("prez", 1:nrow(corp), sep = "")
head(docvars(corp))

# alternative using indexing
head(corp[, "Year"])
corp["President2"] <- paste("prezTwo", 1:nrow(corp), sep = "")
head(docvars(corp))

fcm

Create a feature co-occurrence matrix

Description

Create a sparse feature co-occurrence matrix, measuring co-occurrences of features within a user-defined context. The context can be defined as a document or a window within a collection of documents, with an optional vector of weights applied to the co-occurrence counts.
Usage

```r
fcm(x, context = c("document", "window"), count = c("frequency", "boolean", "weighted"), window = 5L, weights = 1L, ordered = FALSE, span_sentence = TRUE, tri = TRUE, ...)
```

Arguments

- `x` character, corpus, tokens, or dfm object from which to generate the feature co-occurrence matrix
- `context` the context in which to consider term co-occurrence: "document" for co-occurrence counts within document; "window" for co-occurrence within a defined window of words, which requires a positive integer value for window. Note: if `x` is a dfm object, then `context` can only be "document".
- `count` how to count co-occurrences:
  - "frequency" count the number of co-occurrences within the context
  - "boolean" count only the co-occurrence or not within the context, irrespective of how many times it occurs.
  - "weighted" count a weighted function of counts, typically as a function of distance from the target feature. Only makes sense for context = "window".
- `window` positive integer value for the size of a window on either side of the target feature, default is 5, meaning 5 words before and after the target feature
- `weights` a vector of weights applied to each distance from 1:window, strictly decreasing by default; can be a custom-defined vector of the same length as length(weights)
- `ordered` if TRUE the number of times that a term appears before or after the target feature are counted separately. Only makes sense for context = "window".
- `span_sentence` if FALSE, then word windows will not span sentences
- `tri` if TRUE return only upper triangle (including diagonal). Ignored if ordered = TRUE
- ... not used here

Details

The function `fcm` provides a very general implementation of a "context-feature" matrix, consisting of a count of feature co-occurrence within a defined context. This context, following Momtazi et. al. (2010), can be defined as the document, sentences within documents, syntactic relationships between features (nouns within a sentence, for instance), or according to a window. When the context is a window, a weighting function is typically applied that is a function of distance from the target word (see Jurafsky and Martin 2015, Ch. 16) and ordered co-occurrence of the two features is considered (see Church & Hanks 1990).

`fcm` provides all of this functionality, returning a V * V matrix (where V is the vocabulary size, returned by `nfeat`). The tri = TRUE option will only return the upper part of the matrix.

Unlike some implementations of co-occurrences, `fcm` counts feature co-occurrences with themselves, meaning that the diagonal will not be zero.

`fcm` also provides "boolean" counting within the context of "window", which differs from the counting within "document".

is.fcm(x) returns TRUE if and only if its x is an object of type `fcm`. 
**Author(s)**
Kenneth Benoit (R), Haiyan Wang (R, C++), Kohei Watanabe (C++)

**References**


**Examples**

# see http://bit.ly/29b2zOA

txt <- "A D A C E A D F E B A C E D"

fcm(txt, context = "window", window = 2)

fcm(txt, context = "window", count = "weighted", window = 3)

fcm(txt, context = "window", count = "weighted", window = 3,
weights = c(3, 2, 1), ordered = TRUE, tri = FALSE)

# with multiple documents
txts <- c("a a a b b c", "a a c e", "a c e f g")

fcm(txts, context = "document", count = "frequency")

fcm(txts, context = "document", count = "boolean")

fcm(txts, context = "window", window = 2)

# from tokens

txt <- c("The quick brown fox jumped over the lazy dog.",
"The dog jumped and ate the fox.")

toks <- tokens(char_tolower(txt), remove_punct = TRUE)

fcm(toks, context = "document")

fcm(toks, context = "window", window = 3)

---

**fcm_sort**

*Sort an fcm in alphabetical order of the features*

**Description**

Sorts an fcm in alphabetical order of the features.

**Usage**

fcm_sort(x)
Arguments

\( x \) \hspace{1cm} fcm object

Value

A \texttt{fcm} object whose features have been alphabetically sorted. Differs from \texttt{fcm_sort} in that this function sorts the fcm by the feature labels, not the counts of the features.

Author(s)

Ken Benoit

Examples

\begin{verbatim}
# with tri = FALSE
myfcm <- fcm(tokens(c("A X Y C B A", "X Y C A B B")), tri = FALSE)
rownames(myfcm)[3] <- colnames(myfcm)[3] <- "Z"
myfcm
fcm_sort(myfcm)

# with tri = TRUE
myfcm <- fcm(tokens(c("A X Y C B A", "X Y C A B B")), tri = TRUE)
rownames(myfcm)[3] <- colnames(myfcm)[3] <- "Z"
myfcm
fcm_sort(myfcm)
\end{verbatim}

---

\textbf{featnames} \hspace{2cm} \textit{Get the feature labels from a dfm}

Description

Get the features from a document-feature matrix, which are stored as the column names of the dfm object.

Usage

\texttt{featnames(x)}

Arguments

\( x \) \hspace{1cm} the dfm whose features will be extracted

Value

character vector of the feature labels
**Examples**

```r
inaugDfm <- dfm(data_corpus_inaugural, verbose = FALSE)

# first 50 features (in original text order)
head(featnames(inaugDfm), 50)

# first 50 features alphabetically
head(sort(featnames(inaugDfm)), 50)

# contrast with descending total frequency order from topfeatures()
head(names(topfeatures(inaugDfm, 50)))
```

---

**Description**

For a `corpus` object, returns the first or last n documents.

**Usage**

```r
## S3 method for class 'corpus'
head(x, n = 6L, ...)

## S3 method for class 'corpus'
tail(x, n = 6L, ...)
```

**Arguments**

- `x`: a dfm object
- `n`: a single integer. If positive, the number of documents for the resulting object: number of first/last documents for the dfm. If negative, all but the n last/first number of documents of x.
- `...`: additional arguments passed to other functions

**Value**

A `corpus` class object corresponding to the subset defined by n.

**Examples**

```r
head(data_corpus_irishbudget2010, 3) %>% summary()

tail(data_corpus_irishbudget2010, 3) %>% summary()
```
head.dfm

*Return the first or last part of a dfm*

### Description

For a `dfm` object, returns the first or last \( n \) documents and first \( n_{\text{feat}} \) features.

### Usage

```r
## S3 method for class 'dfm'
head(x, n = 6L, nf = nfeat(x), ...)
```

```r
## S3 method for class 'dfm'
tail(x, n = 6L, nf = nfeat(x), ...)
```

### Arguments

- **x**
  - A `dfm` object
- **n**
  - A single, positive integer. If positive, size for the resulting object: number of first/last documents for the `dfm`. If negative, all but the \( n \) last/first number of documents of `x`.
- **nf**
  - The number of features to return, where the resulting object will contain the first \( n_{\text{col}} \) features; default is all features
- **...**
  - Additional arguments passed to other functions

### Value

A `dfm` class object corresponding to the subset defined by `n` and `n_{\text{feat}}`.

### Examples

```r
head(data_dfm_lbgexample, 3, nf = 5)
head(data_dfm_lbgexample, -4)

tail(data_dfm_lbgexample)
tail(data_dfm_lbgexample, n = 3, nf = 4)
```
**kwic**  

**Locate keywords-in-context**

**Description**

For a text or a collection of texts (in a quanteda corpus object), return a list of a keyword supplied by the user in its immediate context, identifying the source text and the word index number within the source text. (Not the line number, since the text may or may not be segmented using end-of-line delimiters.)

**Usage**

```r
kwic(x, pattern, window = 5, valuetype = c("glob", "regex", "fixed"),
     separator = " ", case_insensitive = TRUE, ...)

is.kwic(x)
```

**Arguments**

- `x`: a character, corpus, or tokens object
- `pattern`: a character vector, list of character vectors, dictionary, collocations, or dfm. See `pattern` for details.
- `window`: the number of context words to be displayed around the keyword.
- `valuetype`: the type of pattern matching: "glob" for "glob"-style wildcard expressions; "regex" for regular expressions; or "fixed" for exact matching. See `valuetype` for details.
- `separator`: character to separate words in the output
- `case_insensitive`: match without respect to case if TRUE
- `...`: additional arguments passed to `tokens`, for applicable object types

**Value**

A `kwic` classed data.frame, with the document name (docname), the token index positions (from and to, which will be the same for single-word patterns, or a sequence equal in length to the number of elements for multi-word phrases), the context before (pre), the keyword in its original format (keyword, preserving case and attached punctuation), and the context after (post). The return object has its own `print` method, plus some special attributes that are hidden in the print view. If you want to turn this into a simple data.frame, simply wrap the result in `data.frame`.

**Note**

`pattern` will be a keyword pattern or phrase, possibly multiple patterns, that may include punctuation. If a pattern contains whitespace, it is best to wrap it in `phrase` to make this explicit. However if `pattern` is a `collocations` or `dictionary` object, then the collocations or multi-word dictionary keys will automatically be considered phrases where each whitespace-separated element matches a token in sequence.
Examples

head(kwic(data_corpus_inaugural, "secure\*", window = 3, valuetype = "glob"))
head(kwic(data_corpus_inaugural, "secur", window = 3, valuetype = "regex"))
head(kwic(data_corpus_inaugural, "security", window = 3, valuetype = "fixed"))

toks <- tokens(data_corpus_inaugural)
kwic(data_corpus_inaugural, phrase("war against"))
kwic(data_corpus_inaugural, phrase("war against"), valuetype = "regex")

mykwic <- kwic(data_corpus_inaugural, "provident\*")
is.kwic(mykwic)
is.kwic("Not a kwic")

metacorpus

Get or set corpus metadata

Description

Get or set the corpus-level metadata in a corpus object.

Usage

metacorpus(x, field = NULL)

metacorpus(x, field) <- value

Arguments

x 
  a corpus object

field 
  metadata field name(s); if NULL (default), return all metadata names

value 
  new value of the corpus metadata field

Value

For metacorpus, a named list of the metadata fields in the corpus.

For metacorpus <-, the corpus with the updated metadata.

Examples

metacorpus(data_corpus_inaugural)
metacorpus(data_corpus_inaugural, "source")
metacorpus(data_corpus_inaugural, "citation") <- "Presidential Speeches Online Project (2014)."
metacorpus(data_corpus_inaugural, "citation")
Get or set document-level meta-data

Description

Get or set document-level meta-data. Document-level meta-data are a special type of docvars, meant to contain information about documents that would not be used as a "variable" for analysis. An example could be the source of the document, or notes pertaining to its transformation, copyright information, etc.

Document-level meta-data differs from corpus-level meta-data in that the latter pertains to the collection of texts as a whole, whereas the document-level version can differ with each document.

Usage

```r
metadoc(x, field = NULL)

metadoc(x, field = NULL) <- value
```

Arguments

- `x`: a corpus object
- `field`: character, the name of the metadata field(s) to be queried or set
- `value`: the new value of the new meta-data field

Value

For `texts`, a character vector of the texts in the corpus.
For `texts <-`, the corpus with the updated texts.

Note

Document-level meta-data names are preceded by an underscore character, such as `_language`, but when named in in the `field` argument, do not need the underscore character.

See Also

- `metacorpus`

Examples

```r
mycorp <- corpus_subset(data_corpus_inaugural, Year > 1990)
summary(mycorp, showmeta = TRUE)
metadoc(mycorp, "encoding") <- "UTF-8"
metadoc(mycorp)
metadoc(mycorp, "language") <- "english"
summary(mycorp, showmeta = TRUE)
```
**ndoc**

*Count the number of documents or features*

**Description**

Get the number of documents or features in an object.

**Usage**

```r
ndoc(x)
```

```r
nfeat(x)
```

```r
nfeature(x)
```

**Arguments**

- `x` a quanted object: a corpus, dfm, or tokens object, or a readtext object from the readtext package.

**Details**

`ndoc` returns the number of documents in an object whose texts are organized as "documents" (a corpus, dfm, or tokens object, a readtext object from the readtext package).

`nfeat` returns the number of features from a dfm; it is an alias for `ntype` when applied to dfm objects. This function is only defined for dfm objects because only these have "features". (To count tokens, see `ntoken`.)

`nfeature` is the deprecated form of `nfeat`.

**Value**

an integer (count) of the number of documents or features

**See Also**

`ntoken`

**Examples**

```r
# number of documents
ndoc(data_corpus_inaugural)
nfeat(corpus_subset(data_corpus_inaugural, Year > 1980))
ndoc(tokens(data_corpus_inaugural))
nfeat(dfm(corpus_subset(data_corpus_inaugural, Year > 1980)))
```

```
# number of features
nfeat(dfm(corpus_subset(data_corpus_inaugural, Year > 1980), remove_punct = FALSE))
nfeat(dfm(corpus_subset(data_corpus_inaugural, Year > 1980), remove_punct = TRUE))
```
nscrabble

Count the Scrabble letter values of text

Description

Tally the Scrabble letter values of text given a user-supplied function, such as the sum (default) or mean of the character values.

Usage

nscrabble(x, FUN = sum)

Arguments

  x       a character vector
  FUN     function to be applied to the character values in the text; default is sum, but could also be mean or a user-supplied function

Value

a (named) integer vector of Scrabble letter values, computed using FUN, corresponding to the input text(s)

Note

Character values are only defined for non-accented Latin a-z, A-Z letters. Lower-casing is unnecessary.

We would be happy to add more languages to this *extremely useful function* if you send us the values for your language!

Author(s)

Kenneth Benoit

Examples

nscrabble(c("muzjiks", "excellency"))
nscrabble(data_corpus_inaugural[1:5], mean)
nsentence Count the number of sentences

Description

Return the count of sentences in a corpus or character object.

Usage

nsentence(x, ...)

Arguments

x a character or corpus whose sentences will be counted
... additional arguments passed to tokens

Value

count(s) of the total sentences per text

Note

nsentence() relies on the boundaries definitions in the stringi package (see stri_opts_brkiter). It does not count sentences correctly if the text has been transformed to lower case, and for this reason nsentence() will issue a warning if it detects all lower-cased text.

Examples

# simple example
txt <- c(text1 = "This is a sentence: second part of first sentence.",
text2 = "A word. Repeated repeated.",
text3 = "Mr. Jones has a PhD from the LSE. Second sentence.")
nsentence(txt)
	nsyllable Count syllables in a text

Description

Returns a count of the number of syllables in texts. For English words, the syllable count is exact and looked up from the CMU pronunciation dictionary, from the default syllable dictionary data_int_syllables. For any word not in the dictionary, the syllable count is estimated by counting vowel clusters.

data_int_syllables is a quanteda-supplied data object consisting of a named numeric vector of syllable counts for the words used as names. This is the default object used to count English syllables. This object that can be accessed directly, but we strongly encourage you to access it only through the nsyllable() wrapper function.
### Usage

```r
nsyllable(x, syllable_dictionary = quanteda::data_int_syllables,
           use.names = FALSE)
```

### Arguments

- **x**: character vector or tokens object whose syllables will be counted. This will count all syllables in a character vector without regard to separating tokens, so it is recommended that `x` be individual terms.

- **syllable_dictionary**: optional named integer vector of syllable counts where the names are lower case tokens. When set to `NULL` (default), then the function will use the quanteda data object `data_int_syllables`, an English pronunciation dictionary from CMU.

- **use.names**: logical; if `TRUE`, assign the tokens as the names of the syllable count vector.

### Value

If `x` is a character vector, a named numeric vector of the counts of the syllables in each element. If `x` is a `tokens` object, return a list of syllable counts where each list element corresponds to the tokens in a document.

### Note

All tokens are automatically converted to lowercase to perform the matching with the syllable dictionary, so there is no need to perform this step prior to calling `nsyllable()`.

`nsyllable()` only works reliably for English, as the only syllable count dictionary we could find is the freely available CMU pronunciation dictionary at `http://www.speech.cs.cmu.edu/cgi-bin/cmudict`. If you have a dictionary for another language, please email the package maintainer as we would love to include it.

### Examples

```r
# character
nsyllable(c("cat", "syllable", "supercalifragilisticexpialidocious",
          "Brexit", "Administration"), use.names = TRUE)

# tokens
txt <- c(doc1 = "This is an example sentence.",
         doc2 = "Another of two sample sentences.")
nsyllable(tokens(txt, remove_punct = TRUE))
```

# punctuation is not counted
nsyllable(tokens(txt), use.names = TRUE)
Description
Get the count of tokens (total features) or types (unique tokens).

Usage
ntoken(x, ...)
ntype(x, ...)

Arguments
x a quanted object: a character, corpus, tokens, or dfm object
... additional arguments passed to tokens

Details
The precise definition of "tokens" for objects not yet tokenized (e.g. character or corpus objects) can be controlled through optional arguments passed to tokens through ....
For dfm objects, ntype will only return the count of features that occur more than zero times in the dfm.

Value
named integer vector of the counts of the total tokens or types

Note
Due to differences between raw text tokens and features that have been defined for a dfm, the counts may be different for dfm objects and the texts from which the dfm was generated. Because the method tokenizes the text in order to count the tokens, your results will depend on the options passed through to tokens.

Examples
```r
# simple example
txt <- c(text1 = "This is a sentence, this.", text2 = "A word. Repeated repeated.")
ntoken(txt)
ntype(txt)
ntoken(char_tolower(txt))  # same
ntype(char_tolower(txt))   # fewer types
ntoken(char_tolower(txt), remove_punct = TRUE)
ntype(char_tolower(txt), remove_punct = TRUE)

# with some real texts
```
phrase

Declare a compound character to be a sequence of separate pattern matches

Description

Declares that a whitespace-separated expression consists of multiple patterns, separated by whitespace. This is typically used as a wrapper around pattern to make it explicit that the pattern elements are to be used for matches to multi-word sequences, rather than individual, unordered matches to single words.

Usage

phrase(x)
n
is.phrase(x)

Arguments

x the sequence, as a character object containing whitespace separating the patterns

Value

phrase returns a specially classed list whose white-spaced elements have been parsed into separate character elements.

is.phrase returns TRUE if the object was created by phrase; FALSE otherwise.

Examples

# make phrases from characters
phrase(c("a b", "c d e", "f"))

# from a dictionary
phrase(dictionary(list(catone = c("a b"), cattwo = "c d e", catthree = "f")))

# from a collocations object
(coll <- textstat_collocations(tokens("a b c a b d e b d a b")))
phrase(coll)
quanteda_options

Get or set package options for quanteda

Description
Get or set global options affecting functions across quanteda.

Usage
quanteda_options(..., reset = FALSE, initialize = FALSE)

Arguments
... options to be set, as key-value pair, same as options. This may be a list of valid key-value pairs, useful for setting a group of options at once (see examples).
reset logical; if TRUE, reset all quanteda options to their default values
initialize logical; if TRUE, reset only the quanteda options that are not already defined. Used for setting initial values when some have been defined previously, such as in `.Rprofile`.

Details
Currently available options are:

- verbose logical; if TRUE then use this as the default for all functions with a verbose argument
- threads integer; specifies the number of threads to use in parallelized functions
- print_dfm_max_ndoc integer; specifies the number of documents to display when using the defaults for printing a dfm
- print_dfm_max_nfeat integer; specifies the number of features to display when using the defaults for printing a dfm
- base_docname character; stem name for documents that are unnamed when a corpus, tokens, or dfm are created or when a dfm is converted from another object
- base_featname character; stem name for features that are unnamed when they are added, for whatever reason, to a dfm through an operation that adds features
- base_compname character; stem name for components that are created by matrix factorization
- language_stemmer character; language option for char_wordstem, tokens_wordstem, and dfm_wordstem

Value
When called using a key = value pair (where key can be a label or quoted character name), the option is set and TRUE is returned invisibly.
When called with no arguments, a named list of the package options is returned.
When called with reset = TRUE as an argument, all arguments are options are reset to their default values, and TRUE is returned invisibly.
Examples

```r
(opt <- quanteda_options())

quanteda_options(verbos = TRUE)
quanteda_options("verbos" = FALSE)
quanteda_options("threads")
quanteda_options(print_dfm_max_ndoc = 50L)
  # reset to defaults
quanteda_options(reset = TRUE)
  # reset to saved options
quanteda_options(opt)
```

spacyr-methods  Extensions for and from spacy_parse objects

Description

These functions provide `quanteda` methods for `spacyr` objects, and also extend `spacy_parse` to work with `corpus` objects.

Usage

```r
## S3 method for class 'corpus'
spacy_parse(x, ...)
```

Arguments

- `x` an object returned by `spacy_parse`, or (for `spacy_parse`) a `corpus` object
- `...` unused except for `spacy_parse`, in which case it passes through extra arguments to that function

Usage

- `docnames(x)` returns the document names
- `ndoc(x)` returns the number of documents
- `ntoken(x, ...)` returns the number of tokens by document
- `ntype(x, ...)` returns the number of types (unique tokens) by document
- `spacy_parse(x, ...)` is also defined for a `quanteda corpus`
\textbf{Examples} \\

```r
## Not run:
library("spacyr")
spacy_initialize()

txt <- c(doc1 = "And now, now, now for something completely different.",
        doc2 = "Jack and Jill are children."
)
parsed <- spacy\_parse(txt)
ntype(parsed)
ntoken(parsed)
ndoc(parsed)
docnames(parsed)

corpus\_subset(data\_corpus\_inaugural, Year <= 1793) \%\% spacy\_parse()

## End(Not run)
```

---

\textbf{sparsity}  
\textit{Compute the sparsity of a document-feature matrix}

\section*{Description}

Return the proportion of sparseness of a document-feature matrix, equal to the proportion of cells that have zero counts.

\section*{Usage}

\texttt{sparsity(x)}

\section*{Arguments}

\texttt{x} \hspace{1cm} the document-feature matrix

\section*{Examples}

```r
inaug\_dfm <- dfm(data\_corpus\_inaugural, verbose = FALSE)
sparsity(inaug\_dfm)
sparsity(dfm\_trim(inaug\_dfm, min\_termfreq = 5))
```
**Description**

`textmodel_affinity` implements the maximum likelihood supervised text scaling method described in Perry and Benoit (2017).

**Usage**

```r
textmodel_affinity(x, y, exclude = NULL, smooth = 0.5, ref_smooth = 0.5, verbose = TRUE)
```

**Arguments**

- `x`: the `dfm` or `bootstrap_dfm` object on which the model will be fit. Does not need to contain only the training documents, since the index of these will be matched automatically.
- `y`: vector of training classes/scores associated with each document identified in `data`
- `exclude`: a set of words to exclude from the model
- `smooth`: a smoothing parameter for class affinities; defaults to 0.5 (Jeffreys prior). A plausible alternative would be 1.0 (Laplace prior).
- `ref_smooth`: a smoothing parameter for token distributions; defaults to 0.5
- `verbose`: logical; if TRUE print diagnostic information during fitting.

**Author(s)**

Patrick Perry and Kenneth Benoit

**References**


**See Also**

`predict.textmodel_affinity` for methods of applying a fitted `textmodel_affinity` model object to predict quantities from (other) documents.
Examples

```r
(af <- textmodel_affinity(data_dfm_lbgexample, y = c("L", NA, NA, NA, "R", NA))
predict(af)
predict(af, newdata = data_dfm_lbgexample[6, ])

## Not run:
# compute bootstrapped SEs
bs_dfm <- bootstrap_dfm(data_corpus_dailnoconf1991, n = 10, remove_punct = TRUE)
textmodel_affinity(bs_dfm, y = c("Govt", "Opp", "Opp", rep(NA, 55)))

## End(Not run)
```

---

**textmodel_ca**

*Correspondence analysis of a document-feature matrix*

**Description**

textmodel_ca implements correspondence analysis scaling on a dfm. The method is a fast/sparse version of function `ca`.

**Usage**

```r
textmodel_ca(x, smooth = 0, nd = NA, sparse = FALSE, residual_floor = 0.1)
```

**Arguments**

- `x` the dfm on which the model will be fit
- `smooth` a smoothing parameter for word counts; defaults to zero.
- `nd` Number of dimensions to be included in output; if NA (the default) then the maximum possible dimensions are included.
- `sparse` retains the sparsity if set to TRUE; set it to TRUE if x (the dfm) is too big to be allocated after converting to dense
- `residual_floor` specifies the threshold for the residual matrix for calculating the truncated svd. Larger value will reduce memory and time cost but might reduce accuracy; only applicable when sparse = TRUE

**Details**

svds in the **RSpectra** package is applied to enable the fast computation of the SVD.

**Value**

textmodel_ca() returns a fitted CA textmodel that is a special class of `ca` object.
Note

You may need to set sparse = \texttt{TRUE} and increase the value of residual_floor to ignore less important information and hence to reduce the memory cost when you have a very big dfm. If your attempt to fit the model fails due to the matrix being too large, this is probably because of the memory demands of computing the $V \times V$ residual matrix. To avoid this, consider increasing the value of residual_floor by 0.1, until the model can be fit.

Author(s)

Kenneth Benoit and Haiyan Wang

References


See Also

\texttt{coef.textmodel_lsa}, \texttt{ca}

Examples

ieDfm <- dfm(data_corpus_irishbudget2010)
wca <- textmodel_ca(ieDfm)
summary(wca)

\begin{verbatim}
textmodel_lsa  Latent Semantic Analysis
\end{verbatim}

Description

Fit the Latent Semantic Analysis scaling model to a dfm, which may be weighted (for instance using \texttt{dfm_tfidf}).

Usage

textmodel_lsa(x, nd = 10, margin = c("both", "documents", "features"))

Arguments

\begin{itemize}
  \item \texttt{x} \hspace{1cm} the \texttt{dfm} on which the model will be fit
  \item \texttt{nd} \hspace{1cm} the number of dimensions to be included in output
  \item \texttt{margin} \hspace{1cm} margin to be smoothed by the SVD
\end{itemize}

Details

\texttt{svds} in the \texttt{RSpectra} package is applied to enable the fast computation of the SVD.
Note

The number of dimensions nd retained in LSA is an empirical issue. While a reduction in k can remove much of the noise, keeping too few dimensions or factors may lose important information.

Author(s)

Haiyan Wang and Kohei Watanabe

References


See Also

predict.textmodel_lsa, coef.textmodel_lsa

Examples

```
ie_dfm <- dfm(data_corpus_irishbudget2010)
# create an LSA space and return its truncated representation in the low-rank space
ie_lsa <- textmodel_lsa(ie_dfm[1:10, ])
head(ie_lsa$docs)

# matrix in low_rank LSA space
ie_lsa$matrix_low_rank[,1:5]

# fold queries into the space generated by ie_dfm[1:10,]
# and return its truncated versions of its representation in the new low-rank space
new_lsa <- predict(ie_lsa, ie_dfm[11:14, ])
new_lsa$docs_newspace
```

textmodel_nb

Naive Bayes classifier for texts

Description

Fit a multinomial or Bernoulli Naive Bayes model, given a dfm and some training labels.

Usage

```
textmodel_nb(x, y, smooth = 1, prior = c("uniform", "docfreq", "termfreq"), distribution = c("multinomial", "Bernoulli"))
```
Arguments

- **x**
  - the `dfm` on which the model will be fit. Does not need to contain only the training documents.

- **y**
  - vector of training labels associated with each document identified in `train`. (These will be converted to factors if not already factors.)

- **smooth**
  - smoothing parameter for feature counts by class

- **prior**
  - prior distribution on texts; one of "uniform", "docfreq", or "termfreq". See Prior Distributions below.

- **distribution**
  - count model for text features, can be multinomial or Bernoulli. To fit a "binary multinomial" model, first convert the `dfm` to a binary matrix using `dfm_weight(x, scheme = "boolean")`.

Value

textmodel_nb() returns a list consisting of the following (where `I` is the total number of documents, `J` is the total number of features, and `k` is the total number of training classes):

- **call**
  - original function call

- **PwGc**
  - `k × J`; probability of the word given the class (empirical likelihood)

- **Pc**
  - `k`-length named numeric vector of class prior probabilities

- **Pcw**
  - `k × J`; posterior class probability given the word

- **Pw**
  - `J × 1`; baseline probability of the word

- **x**
  - the `I × J` training `dfm`

- **y**
  - the `I`-length `y` training class vector

- **distribution**
  - the distribution argument

- **prior**
  - the prior argument

- **smooth**
  - the value of the smoothing parameter

Prior distributions

Prior distributions refer to the prior probabilities assigned to the training classes, and the choice of prior distribution affects the calculation of the fitted probabilities. The default is uniform priors, which sets the unconditional probability of observing the one class to be the same as observing any other class.

"Document frequency" means that the class priors will be taken from the relative proportions of the class documents used in the training set. This approach is so common that it is assumed in many examples, such as the worked example from Manning, Raghavan, and Schütze (2008) below. It is not the default in quanteda, however, since there may be nothing informative in the relative numbers of documents used to train a classifier other than the relative availability of the documents. When training classes are balanced in their number of documents (usually advisable), however, then the empirically computed "docfreq" would be equivalent to "uniform" priors.

Setting **prior** to "termfreq" makes the priors equal to the proportions of total feature counts found in the grouped documents in each training class, so that the classes with the largest number of features are assigned the largest priors. If the total count of features in each training class was the same, then "uniform" and "termfreq" would be the same.
Author(s)
Kenneth Benoit

References

See Also
predict.textmodel_nb

Examples
```r
## Example from 13.1 of _An Introduction to Information Retrieval_
txt <- c(d1 = "Chinese Beijing Chinese", 
d2 = "Chinese Chinese Shanghai", 
d3 = "Chinese Macao", 
d4 = "Tokyo Japan Chinese", 
d5 = "Chinese Chinese Chinese Tokyo Japan")
trainingset <- dfm(txt, tolower = FALSE)
trainingclass <- factor(c("Y", "Y", "Y", "N", NA), ordered = TRUE)

## replicate IIR p261 prediction for test set (document 5)
(nb <- textmodel_nb(trainingset, trainingclass, prior = "docfreq"))
summary(nb)
coef(nb)
predict(nb)

# contrast with other priors
predict(textmodel_nb(trainingset, trainingclass, prior = "uniform"))
predict(textmodel_nb(trainingset, trainingclass, prior = "termfreq"))

## replicate IIR p264 Bernoulli Naive Bayes
nb_bern <- textmodel_nb(trainingset, trainingclass, distribution = "Bernoulli", 
                        prior = "docfreq")
predict(nb_bern, newdata = trainingset[5,])
```

Description
textmodel_wordfish

Usage

textmodel_wordfish(x, dir = c(1, 2), priors = c(Inf, Inf, 3, 1),
                   tol = c(1e-06, 1e-08),
                   dispersion = c("poisson", "quasipoisson"),
                   dispersion_level = c("feature", "overall"),
                   dispersion_floor = 0,
                   sparse = FALSE, abs_err = FALSE, svd_sparse = TRUE,
                   residual_floor = 0.5)

Arguments

x
set global identification by specifying the indexes for a pair of documents such that \( \hat{\theta}_{dir[1]} < \hat{\theta}_{dir[2]} \).

dir

priors

prior precisions for the estimated parameters \( \alpha_i, \psi_j, \beta_j, \) and \( \theta_i \), where \( i \) indexes documents and \( j \) indexes features.

tol

tolerances for convergence. The first value is a convergence threshold for the log-posterior of the model, the second value is the tolerance in the difference in parameter values from the iterative conditional maximum likelihood (from conditionally estimating document-level, then feature-level parameters).

dispersion

sets whether a quasi-Poisson quasi-likelihood should be used based on a single dispersion parameter ("poisson"), or quasi-Poisson ("quasipoisson")

dispersion_level

sets the unit level for the dispersion parameter, options are "feature" for term-level variances, or "overall" for a single dispersion parameter.

dispersion_floor

constraint for the minimal underdispersion multiplier in the quasi-Poisson model. Used to minimize the distorting effect of terms with rare term or document frequencies that appear to be severely underdispersed. Default is 0, but this only applies if dispersion = "quasipoisson".

sparse

specifies whether the "dfm" is coerced to dense. While setting this to TRUE will make it possible to handle larger dfm objects (and make execution faster), it will generate slightly different results each time, because the sparse SVD routine has a stochastic element.

abs_err

specifies how the convergence is considered.

svd_sparse

uses svd to initialize the starting values of theta, only applies when sparse = TRUE.

residual_floor

specifies the threshold for residual matrix when calculating the svds, only applies when sparse = TRUE.

Details

The returns match those of Will Lowe’s R implementation of wordfish (see the austin package), except that here we have renamed words to be features. (This return list may change.) We have also followed the practice begun with Slapin and Proksch’s early implementation of the model that used a regularization parameter of \( \text{se}(\sigma) = 3 \), through the third element in priors.
Value

An object of class textmodel_fitted_wordfish. This is a list containing:

- dir: global identification of the dimension
- theta: estimated document positions
- alpha: estimated document fixed effects
- beta: estimated feature marginal effects
- psi: estimated word fixed effects
- docs: document labels
- features: feature labels
- sigma: regularization parameter for betas in Poisson form
- ll: log likelihood at convergence
- se.theta: standard errors for theta-hats
- x: dfm to which the model was fit

Note

In the rare situation where a warning message of "The algorithm did not converge." shows up, removing some documents may work.

Author(s)

Benjamin Lauderdale, Haiyan Wang, and Kenneth Benoit

References


See Also

predict.textmodel_wordfish

Examples

```r
(wf <- textmodel_wordfish(data_dfm_lbgexample, dir = c(1,5)))
summary(wf, n = 10)
coef(wf)
predict(wf)
predict(wf, se.fit = TRUE)
predict(wf, interval = "confidence")
```

## Not run:
```
ie2010dfw <- dfm(data_corpus_irishbudget2010, verbose = FALSE)
```
textmodel_wordscores implements Laver, Benoit and Garry's (2003) "Wordscores" method for scaling texts on a single dimension, given a set of anchoring or reference texts whose values are set through reference scores. This scale can be fitted in the linear space (as per LBG 2003) or in the logit space (as per Beauchamp 2012). Estimates of virgin or unknown texts are obtained using the predict() method to score documents from a fitted textmodel_wordscores object.

Usage

```
textmodel_wordscores(x, y, scale = c("linear", "logit"), smooth = 0)
```

Arguments

- `x`  
  the dfm on which the model will be trained

- `y`  
  vector of training scores associated with each document in `x`

- `scale`  
  scale on which to score the words; "linear" for classic LBG linear posterior weighted word class differences, or "logit" for log posterior differences

- `smooth`  
  a smoothing parameter for word counts; defaults to zero for the to match the LBG (2003) method. See Value below for additional information on the behaviour of this argument.
Details

The `textmodel_wordscores()` function and the associated `predict()` method are designed to function in the same manner as `predict.lm`. `coef()` can also be used to extract the word coefficients from the fitted `textmodel_wordscores` object, and `summary()` will print a nice summary of the fitted object.

Value

A fitted `textmodel_wordscores` object. This object will contain a copy of the input data, but in its original form without any smoothing applied. Calling `predict.textmodel_wordscores` on this object without specifying a value for `newdata`, for instance, will predict on the unsmoothed object. This behaviour differs from versions of quanteda <= 1.2.

Author(s)

Kenneth Benoit

References


See Also

`predict.textmodel_wordscores` for methods of applying a fitted `textmodel_wordscores` model object to predict quantities from (other) documents.

Examples

```r
(ws <- textmodel_wordscores(data_dfm_lbgexample, c(seq(-1.5, 1.5, .75), NA)))
summary(ws)
coef(ws)
predict(ws)
predict(ws, rescaling = "lbglbgr")
predict(ws, se.fit = TRUE, interval = "confidence", rescaling = "mv")
```
textplot_influence  

Influence plot for text scaling models

Description

Plot the results of a fitted scaling model, from (e.g.) a predicted `textmodel_affinity` model.

Usage

textplot_influence(x, n = 30, ...)

Arguments

x  
the object output from `influence()` run on the fitted or predicted scaling model object to be plotted

n  
the number of features whose influence will be plotted

...  
additional arguments passed to `plot`

Author(s)

Patrick Perry and Kenneth Benoit

See Also

`textmodel_affinity`

`influence.predict.textmodel_affinity`

Examples

```r
af <- textmodel_affinity(data_dfm_lbgexample, y = c("L", NA, NA, NA, "R", NA))
afpred <- predict(af)
textplot_influence(influence(afpred))
```

textplot_keyness  

Plot word keyness

Description

Plot the results of a "keyword" of features comparing their differential associations with a target and a reference group, after calculating keyness using `textstat_keyness`.

Usage

textplot_keyness(x, show_reference = TRUE, show_legend = TRUE, 
n = 20L, min_count = 2L, margin = 0.05, color = c("darkblue", "gray"), labelcolor = "gray30", labelsize = 4, font = NULL)
Arguments

- **x**: a return object from `textstat_keyness`
- **show_reference**: logical; if TRUE, show key reference features in addition to key target features
- **show_legend**: logical; if TRUE, show legend
- **n**: integer; number of features to plot
- **min_count**: numeric; minimum total count of feature across the target and reference categories, for a feature to be included in the plot
- **margin**: numeric; size of margin where feature labels are shown
- **color**: character or integer; colors of bars for target and reference documents. color must have two elements when `show_reference = TRUE`. See color.
- **labelcolor**: character; color of feature labels.
- **labelsize**: numeric; size of feature labels and bars. See size.
- **font**: character; font-family of texts. Use default font if NULL.

Value

A `ggplot2` object

Author(s)

Haiyan Wang and Kohei Watanabe

See Also

textstat_keyness

Examples

```r
# compare Trump speeches to other Presidents by chi^2
dem_dfm <- data_corpus_inaugural %>%
  corpus_subset(Year > 1980) %>%
  dfm(groups = "President", remove = stopwords("english"), remove_punct = TRUE)

dem_key <- textstat_keyness(dem_dfm, target = "Trump")
textplot_keyness(dem_key, margin = 0.2, n = 10)

# compare contemporary Democrats v. Republicans
pres_corp <- data_corpus_inaugural %>%
  corpus_subset(Year > 1960)
docvars(pres_corp, "party") <-
  ifelse(docvars(pres_corp, "President") %in% c("Nixon", "Reagan", "Bush", "Trump"),
  "Republican", "Democrat")

pres_dfm <- dfm(pres_corp, groups = "party", remove = stopwords("english"),
  remove_punct = TRUE)

pres_key <- textstat_keyness(pres_dfm, target = "Democrat", measure = "lr")
textplot_keyness(pres_key, color = c("blue", "red"), n = 10)
```
Description

Plot an fcm object as a network, where edges show co-occurrences of features.

Usage

textplot_network(x, min_freq = 0.5, omit_isolated = TRUE, 
edge_color = "#1f78b4", edge_alpha = 0.5, edge_size = 2, 
vertex_color = "#404040", vertex_size = 2, 
vertex_labelcolor = NULL, vertex_labelfont = NULL, offset = NULL, 
...)

## S3 method for class 'fcm'
as.network(x, min_freq = 0.5, omit_isolated = TRUE, ...)

## S3 method for class 'fcm'
as.igraph(x, min_freq = 0.5, omit_isolated = TRUE, ...)

Arguments

x          a fcm or dfm object
min_freq   a frequency count threshold or proportion for co-occurrence frequencies of features to be included.
omit_isolated if TRUE, features do not occur more frequent than min_freq will be omitted.
edge_color  color of edges that connect vertices.
edge_alpha  opacity of edges ranging from 0 to 1.0.
edge_size   size of edges for most frequent co-occurrence. The size of other edges are determined proportionally to the 99th percentile frequency instead of the maximum to reduce the impact of outliers.
vertex_color color of vertices.
vertex_size  size of vertices.
vertex_labelcolor color of texts. Defaults to the same as vertex_color. If NA is given, texts are not rendered.
vertex_labelfont font-family of texts. Use default font if NULL.
offset      if NULL, the distance between vertices and texts are determined automatically.
...         additional arguments passed to network or graph_from_adjacency_matrix. Not used for as.igraph.
Details

Currently the size of the network is limited to 1000, because of the computationally intensive nature of network formation for larger matrices. When the fcm is large, users should select features using fcm_select, set the threshold using min_freq, or implement own plotting function using as_network.

Author(s)

Kohei Watanabe and Stefan Müller

See Also

fcm
network
graph_from_adjacency_matrix

Examples

toks <- corpus_subset(data_corpus_irishbudget2010) %>%	oks(remove_punct = TRUE) %>%	oks_tolower() %>%	oks_remove(stopwords("english"), padding = FALSE)
myfcm <- fcm(toks, context = "window", tri = FALSE)
feat <- names(topfeatures(myfcm, 30))
fcm_select(myfcm, feat, verbose = FALSE) %>%
textplot_network(min_freq = 0.5)
fcm_select(myfcm, feat, verbose = FALSE) %>%
textplot_network(min_freq = 0.8)
fcm_select(myfcm, feat, verbose = FALSE) %>%
textplot_network(min_freq = 0.8, vertex_labelcolor = rep(c('gray40', NA), 15))

# as.igraph
if (requireNamespace("igraph", quietly = TRUE)) {
  txt <- c("a a a b b c", "a a c e", "a c e f g")
  mat <- fcm(txt)
  as.igraph(mat, min_freq = 1, omit_isolated = FALSE)
}

textplot_scale1d

Plot a fitted scaling model

Description

Plot the results of a fitted scaling model, from (e.g.) a predicted textmodel_wordscores model or a fitted textmodel_wordfish or textmodel_ca model. Either document or feature parameters may be plotted: an ideal point-style plot (estimated document position plus confidence interval on the x-axis, document labels on the y-axis) with optional renaming and sorting, or as a plot of estimated
feature-level parameters (estimated feature positions on the x-axis, and a measure of relative frequency or influence on the y-axis, with feature names replacing plotting points with some being chosen by the user to be highlighted).

Usage

textplot_scale1d(x, margin = c("documents", "features"),
                 doclabels = NULL, sort = TRUE, groups = NULL, highlighted = NULL,
                 alpha = 0.7, highlighted_color = "black")

Arguments

x the fitted or predicted scaling model object to be plotted

margin "documents" to plot estimated document scores (the default) or "features" to plot estimated feature scores by a measure of relative frequency

doclabels a vector of names for document; if left NULL (the default), docnames will be used

sort if TRUE (the default), order points from low to high score. If a vector, order according to these values from low to high. Only applies when margin = "documents".

groups either: a character vector containing the names of document variables to be used for grouping; or a factor or object that can be coerced into a factor equal in length or rows to the number of documents. See groups for details.

highlighted a vector of feature names to draw attention to in a feature plot; only applies if margin = "features"

alpha A number between 0 and 1 (default 0.5) representing the level of alpha transparency used to overplot feature names in a feature plot; only applies if margin = "features"

highlighted_color color for highlighted terms in highlighted

Value

a ggplot2 object

Note

The groups argument only applies when margin = "documents".

Author(s)

Kenneth Benoit, Stefan Müller, and Adam Obeng

See Also

textmodel_wordfish, textmodel_wordscores, textmodel_ca
Examples

```r
## Not run:
ie_dfm <- dfm(data_corpus_irishbudget2010)
doclab <- apply(docvars(data_corpus_irishbudget2010, c("name", "party")),
  1, paste, collapse = " ")

## wordscores
refscores <- c(rep(NA, 4), 1, -1, rep(NA, 8))
ws <- textmodel_wordscores(ie_dfm, refscores, smooth = 1)
# plot estimated word positions
textplot_scale1d(ws, highlighted = c("minister", "have", "our", "budget"))
# plot estimated document positions
textplot_scale1d(predict(ws, se.fit = TRUE), doclabels = doclab,
  groups = docvars(data_corpus_irishbudget2010, "party"))

## wordfish
wf <- textmodel_wordfish(dfm(data_corpus_irishbudget2010), dir = c(6, 5))
# plot estimated document positions
textplot_scale1d(wf, doclabels = doclab)
textplot_scale1d(wf, doclabels = doclab,
  groups = docvars(data_corpus_irishbudget2010, "party"))
# plot estimated word positions
textplot_scale1d(wf, margin = "features",
  highlighted = c("government", "global", "children",
    "bank", "economy", "the", "citizenship",
    "productivity", "deficit"))

## correspondence analysis
c <- textmodel_ca(ie_dfm)
# plot estimated document positions
textplot_scale1d(ca, margin = "documents",
  doclabels = doclab,
  groups = docvars(data_corpus_irishbudget2010, "party"))

## End(Not run)
```

---

**textplot_wordcloud**

Plot features as a wordcloud

**Description**

Plot a dfm object as a wordcloud, where the feature labels are plotted with their sizes proportional to their numerical values in the dfm. When comparison = TRUE, it plots comparison word clouds by document.

**Usage**

```r
textplot_wordcloud(x, min_size = 0.5, max_size = 4, min_count = 3,
  max_words = 500, color = "darkblue", font = NULL, adjust = 0,
```
Arguments

x       a dfm object
min_size size of the smallest word
max_size size of the largest word
min_count words with frequency below min_count will not be plotted
max_words maximum number of words to be plotted. least frequent terms dropped.
color   color of words from least to most frequent
font    font-family of words and labels. Use default font if NULL.
adjust  adjust sizes of words by a constant. Useful for non-English words for which R fails to obtain correct sizes.
rotation proportion of words with 90 degree rotation
random_order plot words in random order. If FALSE, they will be plotted in decreasing frequency.
random_color choose colors randomly from the colors. If FALSE, the color is chosen based on the frequency
ordered_color if TRUE, then colors are assigned to words in order.
labelcolor color of group labels. Only used when comparison=TRUE.
labels size of group labels. Only used when comparison=TRUE.
labeloffset position of group labels. Only used when comparison=TRUE.
fixed_aspect if TRUE, the aspect ratio is fixed. Variable aspect ratio only supported if rotation = 0.
...     additional parameters. Only used to make it compatible with wordcloud
comparison if TRUE, plot a wordcloud that compares documents in the same way as comparison.cloud

Details

The default is to plot the word cloud of all features, summed across documents. To produce word cloud plots for specific document or set of documents, you need to slice out the document(s) from the dfm object.

Comparison wordcloud plots may be plotted by setting comparison = TRUE, which plots a separate grouping for each document in the dfm. This means that you will need to slice out just a few documents from the dfm, or to create a dfm where the "documents" represent a subset or a grouping of documents by some document variable.

Author(s)

Kohei Watanabe, building on code from Ian Fellows’s wordcloud package.
**Examples**

```r
# plot the features (without stopwords) from Obama's inaugural addresses
set.seed(10)
obama_dfm <-
dfm(corpus_subset(data_corpus_inaugural, President == "Obama"),
    remove = stopwords("english"), remove_punct = TRUE) %>%
dfm_trim(min_termfreq = 3)

# basic wordcloud
textplot_wordcloud(obama_dfm)

# plot in colors with some additional options
textplot_wordcloud(obama_dfm, rotation = 0.25,
    color = rev(RColorBrewer::brewer.pal(10, "RdBu")))

# other display options
col <- sapply(seq(0.1, 1, 0.1), function(x) adjustcolor("#F78B4", x))
textplot_wordcloud(obama_dfm, adjust = 0.5, random_order = FALSE,
    color = col, rotation = FALSE)

# comparison plot of Obama v. Trump
obama_trump_dfm <-
dfm(corpus_subset(data_corpus_inaugural, President %in% c("Obama", "Trump")),
    remove = stopwords("english"), remove_punct = TRUE, groups = "President") %>%
dfm_trim(min_termfreq = 3)
textplot_wordcloud(obama_trump_dfm, comparison = TRUE, max_words = 300,
    color = c("blue", "red"))
```

---

**Description**

Plots a dispersion or "x-ray" plot of selected word pattern(s) across one or more texts. The format of the plot depends on the number of `kwic` class objects passed: if there is only one document, keywords are plotted one below the other. If there are multiple documents the documents are plotted one below the other, with keywords shown side-by-side. Given that this returns a `ggplot2` object, you can modify the plot by adding `ggplot2` layers (see example).

**Usage**

```r
textplot_xray(..., scale = c("absolute", "relative"), sort = FALSE)
```

**Arguments**

```r
... any number of `kwic` class objects
```
texts

scale whether to scale the token index axis by absolute position of the token in the document or by relative position. Defaults are absolute for single document and relative for multiple documents.

sort whether to sort the rows of a multiple document plot by document name

Value

a ggplot2 object

Author(s)

Adam Obeng

Examples

```r
## Not run:
data_corpus_inauguralPost70 <- corpus_subset(data_corpus_inaugural, Year > 1970)
# compare multiple documents
textplot_xray(kwic(data_corpus_inauguralPost70, "american"))
textplot_xray(kwic(data_corpus_inauguralPost70, "american"), scale = "absolute")
# compare multiple terms across multiple documents
textplot_xray(kwic(data_corpus_inauguralPost70, "america"),
             kwic(data_corpus_inauguralPost70, "people"))

# how to modify the ggplot with different options
library(ggplot2)
g <- textplot_xray(kwic(data_corpus_inauguralPost70, "american"),
                   kwic(data_corpus_inauguralPost70, "people"))
g + aes(color = keyword) + scale_color_manual(values = c('red', 'blue'))

# adjust the names of the document names
docnames(data_corpus_inauguralPost70) <- apply(docvars(data_corpus_inauguralPost70, 
                                                   c("Year", "President")), 
                                                1, paste, collapse = ", ")
textplot_xray(kwic(data_corpus_inauguralPost70, "america"),
              kwic(data_corpus_inauguralPost70, "people"))

## End(Not run)
```

texts

Get or assign corpus texts

Description

Get or replace the texts in a corpus, with grouping options. Works for plain character vectors too, if groups is a factor.
Usage

texts(x, groups = NULL, spacer = " ")

texts(x) <- value

## S3 method for class 'corpus'
as.character(x, ...)

Arguments

x a corpus or character object
groups either: a character vector containing the names of document variables to be used for grouping; or a factor or object that can be coerced into a factor equal in length or rows to the number of documents. See groups for details.
spacer when concatenating texts by using groups, this will be the spacing added between texts. (Default is two spaces.)
value character vector of the new texts
... unused

Details

as.character(x) where x is a corpus is equivalent to calling texts(x)

Value

For texts, a character vector of the texts in the corpus.
For texts <-, the corpus with the updated texts.
For texts <-, a corpus with the texts replaced by value
as.character(x) is equivalent to texts(x)

Note

The groups will be used for concatenating the texts based on shared values of groups, without any specified order of aggregation.
You are strongly encouraged as a good practice of text analysis workflow not to modify the substance of the texts in a corpus. Rather, this sort of processing is better performed through downstream operations. For instance, do not lowercase the texts in a corpus, or you will never be able to recover the original case. Rather, apply tokens_tolower after applying tokens to a corpus, or use the option tolower = TRUE in dfm.

Examples

nchar(texts(corpus_subset(data_corpus_inaugural, Year < 1806)))

# grouping on a document variable
nchar(texts(corpus_subset(data_corpus_inaugural, Year < 1806), groups = "President"))
# grouping a character vector using a factor
nchar(data_char_ukimmig2010[1:5])
nchar(texts(data_corpus_inaugural[1:5],
    groups = as.factor(data_corpus_inaugural[1:5, "President"))))

BritCorpus <- corpus(c("We must prioritise honour in our neighbourhood.",
    "Aluminium is a valourous metal."))
texts(BritCorpus) <-
    stringi::stri_replace_all_regex(texts(BritCorpus),
        c("ise", "([nlb])our", "nium"),
        c("ize", "$lor", "num"),
        vectorize_all = FALSE)
texts(BritCorpus)
texts(BritCorpus)[2] <- "New text number 2."
texts(BritCorpus)

---

### textstat_collocations

**Identify and score multi-word expressions**

**Description**

Identify and score multi-word expressions, or adjacent fixed-length collocations, from text.

**Usage**

```r
textstat_collocations(x, method = "lambda", size = 2, min_count = 2,
    smoothing = 0.5, tolower = TRUE, ...)
```

```r
is.collocations(x)
```

**Arguments**

- **x**: a character, corpus, or tokens object whose collocations will be scored. The tokens object should include punctuation, and if any words have been removed, these should have been removed with `padding = TRUE`. While identifying collocations for tokens objects is supported, you will get better results with character or corpus objects due to relatively imperfect detection of sentence boundaries from texts already tokenized.

- **method**: association measure for detecting collocations. Currently this is limited to "lambda". See Details.

- **size**: integer; the length of the collocations to be scored

- **min_count**: numeric; minimum frequency of collocations that will be scored

- **smoothing**: numeric; a smoothing parameter added to the observed counts (default is 0.5)

- **tolower**: logical; if TRUE, form collocations as lower-cased combinations

- **...**: additional arguments passed to `tokens`, if `x` is not a tokens object already
Details

Documents are grouped for the purposes of scoring, but collocations will not span sentences. If \( x \) is a tokens object and some tokens have been removed, this should be done using tokens_remove(\( x \), pattern, padding = TRUE) so that counts will still be accurate, but the pads will prevent those collocations from being scored.

The \( \lambda \) computed for a size = \( K \)-word target multi-word expression the coefficient for the \( K \)-way interaction parameter in the saturated log-linear model fitted to the counts of the terms forming the set of eligible multi-word expressions. This is the same as the "lambda" computed in Blaheta and Johnson’s (2001), where all multi-word expressions are considered (rather than just verbs, as in that paper). The \( z \) is the Wald \( z \)-statistic computed as the quotient of \( \lambda \) and the Wald statistic for \( \lambda \) as described below.

In detail:

Consider a \( K \)-word target expression \( x \), and let \( z \) be any \( K \)-word expression. Define a comparison function \( c(x, z) = (j_1, \ldots, j_K) = c \) such that the \( k \)th element of \( c \) is 1 if the \( k \)th word in \( z \) is equal to the \( k \)th word in \( x \), and 0 otherwise. Let \( c_i = (j_{i1}, \ldots, j_{iK}), i = 1, \ldots, 2^K = M, \) be the possible values of \( c(x, z) \), with \( c_M = (1, 1, \ldots, 1) \). Consider the set of \( c(x, z) \) across all expressions \( z_r \) in a corpus of text, and let \( n_i \), for \( i = 1, \ldots, M \), denote the number of the \( c(x, z) \) which equal \( c_i \), plus the smoothing constant smoothing.

The \( n_i \) are the counts in a \( 2^K \) contingency table whose dimensions are defined by the \( c_i \).

\( \lambda \) is the \( K \)-way interaction parameter in the saturated log-linear model fitted to the \( n_i \). It can be calculated as:

\[
\lambda = \sum_{i=1}^{M} (-1)^{K-b_i} \ast \log n_i
\]

where \( b_i \) is the number of the elements of \( c_i \) which are equal to 1.

Wald test \( z \)-statistic \( z \) is calculated as:

\[
z = \frac{\lambda}{\left[\sum_{i=1}^{M} n_i^{-1}\right]^{(1/2)}}
\]

Value

textstat_collocations returns a data.frame of collocations and their scores and statistics. This consists of the collocations, their counts, length, and \( \lambda \) and \( z \) statistics. When size is a vector, then count_nested counts the lower-order collocations that occur within a higher-order collocation (but this does not affect the statistics).
is.collocation returns TRUE if the object is of class collocations, FALSE otherwise.

Note

This function is under active development, with more measures to be added in the the next release of quanteda.

Author(s)

Kenneth Benoit, Jouni Kuha, Haiyan Wang, and Kohei Watanabe
textstat_frequency

References

Examples

txts <- data_corpus_inaugural[1:2]
head(cols <- textstat_collocations(txts, size = 2, min_count = 2), 10)
head(cols <- textstat_collocations(txts, size = 3, min_count = 2), 10)

# extracting multi-part proper nouns (capitalized terms)
toks2 <- tokens(data_corpus_inaugural)
toks2 <- tokens_remove(toks2, stopwords("english"), padding = TRUE)
toks2 <- tokens_select(toks2, "^[A-Z][a-z]\s\{2,}\$", valuetype = "regex",
                     case_insensitive = FALSE, padding = TRUE)
seqs <- textstat_collocations(toks2, size = 3, tolower = FALSE)
head(seqs, 10)

# vectorized size
txt <- c("... a b c ... a b c ... c d e",
          "a b ... a b ... a b ... a b ... a b",
          "b c d ... b c ... b c ... b c")
textstat_collocations(txt, size = 2:3)

---

textstat_frequency  Tabulate feature frequencies

Description
Produces counts and document frequencies summaries of the features in a dfm, optionally grouped by a docvars variable or other supplied grouping variable.

Usage
textstat_frequency(x, n = NULL, groups = NULL)

Arguments

x  a dfm object
n  (optional) integer specifying the top n features to be returned, within group if groups is specified

groups  either: a character vector containing the names of document variables to be used for grouping; or a factor or object that can be coerced into a factor equal in length or rows to the number of documents. See groups for details.
Value

a data.frame containing the following variables:

feature (character) the feature
frequency count of the feature
rank rank of the feature, where 1 indicates the greatest frequency
docfreq document frequency of the feature, as a count (the number of documents in which this feature occurred at least once)
docfreq document frequency of the feature, as a count
group (only if groups is specified) the label of the group. If the features have been grouped, then all counts, ranks, and document frequencies are within group. If groups is not specified, the group column is omitted from the returned data.frame.

textstat_frequency returns a data.frame of features and their term and document frequencies within groups.

Examples

dfm1 <- dfm(c("a a b b c d", "a d d d", "a a a"))
textstat_frequency(dfm1)
textstat_frequency(dfm1, groups = c("one", "two", "one"))

obamadfm <-
corpus_subset(data_corpus_inaugural, President == "Obama")
 dfm(remov_punct = TRUE, remove = stopwords("english"))
freq <- textstat_frequency(obamadfm)
head(freq, 10)

# plot 20 most frequent words
library("ggplot2")
ggplot(freq[1:20, ], aes(x = reorder(feature, frequency), y = frequency)) +
geom_point() +
coord_flip() +
labs(x = NULL, y = "Frequency")

# plot relative frequencies by group
dfm_weight_pres <- data_corpus_inaugural %>%
corpus_subset(Year > 2000) %>%
 dfm(remove = stopwords("english"), remove_punct = TRUE) %>%
dfm_group(groups = "President") %>%
dfm_weight(scheme = "prop")

# calculate relative frequency by president
freq_weight <- textstat_frequency(dfm_weight_pres, n = 10,
groups = "President")

# plot frequencies
ggplot(data = freq_weight, aes(x = nrow(freq_weight):1, y = frequency)) +
geom_point() +
**textstat_keyness**

Calculate keyness statistics

**Description**

Calculate "keyness", a score for features that occur differentially across different categories. Here, the categories are defined by reference to a "target" document index in the dfm, with the reference group consisting of all other documents.

**Usage**

```r
textstat_keyness(x, target = 1L, measure = c("chi2", "exact", "lr", "pmi"), sort = TRUE, correction = c("default", "yates", "williams", "none"))
```

**Arguments**

- `x` a dfm containing the features to be examined for keyness
- `target` the document index (numeric, character or logical) identifying the document forming the "target" for computing keyness; all other documents’ feature frequencies will be combined for use as a reference
- `measure` (signed) association measure to be used for computing keyness. Currently available: "chi2"; "exact" (Fisher’s exact test); "lr" for the likelihood ratio; "pmi" for pointwise mutual information.
- `sort` logical; if TRUE sort features scored in descending order of the measure, otherwise leave in original feature order
- `correction` if "default", Yates correction is applied to "chi2"; William’s correction is applied to "lr"; and no correction is applied for the "exact" and "pmi" measures. Specifying a value other than the default can be used to override the defaults, for instance to apply the Williams correction to the chi2 measure. Specifying a correction for the "exact" and "pmi" measures has no effect and produces a warning.

**Value**

a data.frame of computed statistics and associated p-values, where the features scored name each row, and the number of occurrences for both the target and reference groups. For `measure = "chi2"` this is the chi-squared value, signed positively if the observed value in the target exceeds its expected value; for `measure = "exact"` this is the estimate of the odds ratio; for `measure = "lr"` this is the likelihood ratio $G^2$ statistic; for `pmi" this is the pointwise mutual information statistics.

textstat_keyness returns a data.frame of features and their keyness scores and frequency counts.
References


Examples

```r
# compare pre- v. post-war terms using grouping
period <- ifelse(docvars(data_corpus_inaugural, "Year") < 1945, "pre-war", "post-war")
mydfm <- dfm(data_corpus_inaugural, groups = period)
head(mydfm) # make sure 'post-war' is in the first row
head(result <- textstat_keyness(mydfm), 10)
tail(result, 10)

# compare pre- v. post-war terms using logical vector
mydfm2 <- dfm(data_corpus_inaugural)
textstat_keyness(mydfm2, docvars(data_corpus_inaugural, "Year") >= 1945)

# compare Trump 2017 to other post-war presidents
pwdfm <- dfm(corpus_subset(data_corpus_inaugural, period == "post-war"))
head(textstat_keyness(pwdfm, target = "2017-Trump"), 10)
# using the likelihood ratio method
head(textstat_keyness(dfm_smooth(pwdfm), measure = "lr", target = "2017-Trump"), 10)
```

textstat_lexdiv

---

**Calculate lexical diversity**

**Description**

Calculate the lexical diversity or complexity of text(s).

**Usage**

```r
```

**Arguments**

- `x` an input dfm
- `measure` a character vector defining the measure to calculate.
- `log.base` a numeric value defining the base of the logarithm (for measures using logs)
- `...` not used
Details

textstat_lexdiv calculates a variety of proposed indices for lexical diversity. In the following formulas, \( N \) refers to the total number of tokens, \( V \) to the number of types, and \( f_v(i, N) \) to the numbers of types occurring \( i \times \) times in a sample of length \( N \).

"TTR": The ordinary Type-Token Ratio:

\[
TTR = \frac{V}{N}
\]

"C": Herdan’s \( C \) (Herdan, 1960, as cited in Tweedie & Baayen, 1998; sometimes referred to as LogTTR):

\[
C = \frac{\log V}{\log N}
\]

"R": Guiraud’s Root TTR (Guiraud, 1954, as cited in Tweedie & Baayen, 1998):

\[
R = \frac{V}{\sqrt{N}}
\]

"CTTR": Carroll’s Corrected TTR:

\[
CTTR = \frac{V}{\sqrt{2N}}
\]

"U": Dugast’s Uber Index (Dugast, 1978, as cited in Tweedie & Baayen, 1998):

\[
U = \frac{(\log N)^2}{\log N - \log V}
\]

"S": Summer’s index:

\[
S = \frac{\log \log V}{\log \log N}
\]

"K": Yule’s \( K \) (Yule, 1944, as presented in Tweedie & Baayen, 1998, Eq. 16) is calculated by:

\[
K = 10^4 \times \left[ -\frac{1}{N} + \sum_{i=1}^{V} f_v(i, N) \left( \frac{i}{N} \right)^2 \right]
\]

"D": Simpson’s \( D \) (Simpson 1949, as presented in Tweedie & Baayen, 1998, Eq. 17) is calculated by:

\[
D = \sum_{i=1}^{V} f_v(i, N) \frac{i(i-1)}{N(N-1)}
\]

"Vm": Herdan’s \( V_m \) (Herdan 1955, as presented in Tweedie & Baayen, 1998, Eq. 18) is calculated by:

\[
V_m = \sqrt{\sum_{i=1}^{V} f_v(i, N)(i/N)^2 - \frac{i}{V}}
\]

"Maas": Maas’ indices \( a, \log V_0, \log V_0 \):

\[
a^2 = \frac{\log N - \log V}{\log N^2}
\]
\[ \log V_0 = \frac{\log V}{\sqrt{1 - \frac{\log V}{\log N}}} \]

The measure was derived from a formula by Mueller (1969, as cited in Maas, 1972). \(\log e V_0\) is equivalent to \(\log V_0\), only with \(e\) as the base for the logarithms. Also calculated are \(a\), \(\log V_0\) (both not the same as before) and \(V'\) as measures of relative vocabulary growth while the text progresses. To calculate these measures, the first half of the text and the full text will be examined (see Maas, 1972, p. 67 ff. for details). Note: for the current method (for a dfm) there is no computation on separate halves of the text.

**Value**

textstat_lexdiv returns a data.frame of documents and their lexical diversity scores.

**Note**

This implements only the static measures of lexical diversity, not more complex measures based on windows of text such as the Mean Segmental Type-Token Ratio, the Moving-Average Type-Token Ratio (Covington & McFall, 2010), the MLTD or MLTD-MA (Moving-Average Measure of Textual Lexical Diversity) proposed by McCarthy & Jarvis (2010) or Jarvis (no year), or the HD-D version of vocd-D (see McCarthy & Jarvis, 2007). These are available from the package korRpus.

**Author(s)**

Kenneth Benoit, adapted from the S4 class implementation written by Meik Michalke in the korRpus package.

**References**


Michalke, Meik. (2014) korRpus: An R Package for Text Analysis. Version 0.05-5. [http://reaktanz.de/?c=hacking&s=korRpus](http://reaktanz.de/?c=hacking&s=korRpus)


textstat_readability

Calculate readability

Description

Calculate the readability of text(s) using one of a variety of computed indexes.

Usage


Arguments

x                     a character or corpus object containing the texts
measure               character vector defining the readability measure to calculate. Matches are case-insensitive.
remove_hyphens        if TRUE, treat constituent words in hyphenated as separate terms, for purposes of computing word lengths, e.g. "decision-making" as two terms of lengths 8 and 6 characters respectively, rather than as a single word of 15 characters
min_sentence_length, max_sentence_length
set the minimum and maximum sentence lengths (in tokens, excluding punctuation) to include in the computation of readability. This makes it easy to exclude "sentences" that may not really be sentences, such as section titles, table elements, and other cruft that might be in the texts following conversion. For finer-grained control, consider filtering sentences prior first, including through pattern-matching, using corpus_trim.
intermediate           if TRUE, include intermediate quantities in the output
...
not used
Value

textstat_readability returns a data.frame of documents and their readability scores.

Author(s)

Kenneth Benoit, re-engineered from Meik Michalke’s koRpus package.

Examples

txt <- c(doc1 = "Readability zero one. Ten, Eleven.",
         doc2 = "The cat in a dilapidated tophat."
)    
textstat_readability(txt, "Flesch")

textstat_readability(txt, c("FOG", "FOG.PSK", "FOG.NRI"))

textstat_readability(data_corpus_inaugural[48:58],
                     measure = c("Flesch.Kincaid", "Dale.Chall.old"))

textstat_simil

Similarity and distance computation between documents or features

Description

These functions compute matrixes of distances and similarities between documents or features from a dfm and return a dist object (or a matrix if specific targets are selected). They are fast and robust because they operate directly on the sparse dfm objects.

Usage

textstat_simil(x, selection = NULL, margin = c("documents", "features"),
               method = c("correlation", "cosine", "jaccard", "ejaccard",
                          "dice", "edice", "hamman", "simple matching", "faith"),
               upper = FALSE, diag = FALSE)

textstat_dist(x, selection = NULL, margin = c("documents", "features"),
              method = c("euclidean", "kullback", "manhattan", "maximum", "canberra",
                       "minkowski"), upper = FALSE, diag = FALSE, p = 2)

Arguments

x                  a dfm object
selection          a valid index for document or feature names (depending on margin) from x, to be selected for comparison
margin             identifies the margin of the dfm on which similarity or difference will be computed: "documents" for documents or "features" for word/term features.
method             method the similarity or distance measure to be used; see Details.
upper              whether the upper triangle of the symmetric $V \times V$ matrix is recorded. Only used when value = "dist".
textstat_simil

diag
  whether the diagonal of the distance matrix should be recorded. Only used when value = "dist".

p
  The power of the Minkowski distance.

Details

textstat_simil options are: "correlation" (default), "cosine", "jaccard", "ejaccard", "dice", "edice", "simple matching", "hamman", and "faith".

textstat_dist options are: "euclidean" (default), "kullback", "manhattan", "maximum", "canberra", and "minkowski".

Value

By default, textstat_simil and textstat_dist return dist class objects if selection is NULL, otherwise, a matrix is returned matching distances to the documents or features identified in the selection.

These can be transformed into a list format using as_list.dist, if that format is preferred.

Note

If you want to compute similarity on a "normalized" dfm object (controlling for variable document lengths, for methods such as correlation for which different document lengths matter), then wrap the input dfm in dfm_weight(x, "prop").

References

"kullback" is the Kullback-Leibler distance, which assumes that \( P(x_i) = 0 \) implies \( P(y_i) = 0 \), and in case either \( P(x_i) \) or \( P(y_i) \) equals to zero, then \( P(x_i) \ast \log(p(x_i)/p(y_i)) \) is assumed to be zero as the limit value. The formula is:

\[
\sum P(x) \ast \log(P(x)/p(y))
\]

All other measures are described in the proxy package.

See Also

textstat_dist, as.matrix.simil, as.list.dist, dist, as.dist

Examples

# similarities for documents
mt <- dfm(data_corpus_inaugural, remove_punct = TRUE, remove = stopwords("english"))
(s1 <- textstat_simil(mt, method = "cosine", margin = "documents"))
as.matrix(s1)
as.list(s1)

# similarities for for specific documents
textstat_simil(mt, "2017-Trump", margin = "documents")
textstat_simil(mt, "2017-Trump", method = "cosine", margin = "documents")
textstat_simil(mt, c("2009-Obama", "2013-Obama"), margin = "documents")
tokens

Tokenize a set of texts

description

Tokenize the texts from a character vector or from a corpus.

usage

tokens(x, what = c("word", "sentence", "character", "fastestword", "fasterword"), remove_numbers = FALSE, remove_punct = FALSE, remove_symbols = FALSE, remove_separators = TRUE, remove_twitter = FALSE, remove_hyphens = FALSE, remove_url = FALSE, ngrams = 1L, skip = 0L, concatenator = "\_", verbose = quanteda_options("verbose"), include_docvars = TRUE, ...)

Arguments

x a character, corpus, or tokens object to be tokenized
what the unit for splitting the text, available alternatives are:
word (recommended default) smartest, but slowest, word tokenization method; see stringi-search-boundaries for details.
fasterword dumber, but faster, word tokenization method, uses stri_split_charclass(x, \p{z}\p{c})
fastestword dumbest, but fastest, word tokenization method, calls stri_split_fixed(x, "")
character tokenization into individual characters
remove_numbers: remove tokens that consist only of numbers, but not words that start with digits, e.g. 2day
remove_punct: if TRUE, remove all characters in the Unicode "Punctuation" [P] class
remove_symbols: if TRUE, remove all characters in the Unicode "Symbol" [S] class
remove_separators: if TRUE, remove separators and separator characters (Unicode "Separator" [Z] and "Control [C]" categories). Only applicable for what = "character" (when you probably want it to be FALSE) and for what = "word" (when you probably want it to be TRUE).
remove_twitter: remove Twitter characters @ and #; set to TRUE if you wish to eliminate these. Note that this will always be set to FALSE if remove_punct = FALSE.
remove_hyphens: if TRUE, split words that are connected by hyphenation-like characters in between words, e.g. "self-storage" becomes c("self", "storage"). Default is FALSE to preserve such words as is, with the hyphens. Only applies if what = "word" or what = "fasterword".
remove_url: if TRUE, find and eliminate URLs beginning with http(s) – see section "Dealing with URLs".

ngrams: integer vector of the n for n-grams, defaulting to 1 (unigrams). For bigrams, for instance, use 2; for bigrams and unigrams, use 1:2. You can even include irregular sequences such as 2:3 for bigrams and trigrams only. See tokens_ngrams.
skip: integer vector specifying the skips for skip-grams, default is 0 for only immediately neighbouring words. Only applies if ngrams is different from the default of 1. See tokens_skipgrams.
concatenator: character to use in concatenating n-grams, default is ".", which is recommended since this is included in the regular expression and Unicode definitions of "word" characters
verbose: if TRUE, print timing messages to the console; off by default
include_docvars: if TRUE, pass docvars and metadoc fields through to the tokens object. Only applies when tokenizing corpus objects.

Details

The tokenizer is designed to be fast and flexible as well as to handle Unicode correctly. Most of the time, users will construct dfm objects from texts or a corpus, without calling tokens() as an intermediate step. Since tokens() is most likely to be used by more technical users, we have set its options to default to minimal intervention. This means that punctuation is tokenized as well, and that nothing is removed by default from the text being tokenized except inter-word spacing and equivalent characters.

Note that a tokens constructor also works on tokens objects, which allows setting additional options that will modify the original object. It is not possible, however, to change a setting to "un-remove" something that was removed from the input tokens object, however. For instance,
tokens(tokens("Hello!", remove_punct = TRUE), remove_punct = FALSE) will not restore the "!" token. No warning is currently issued about this, so the user should use tokens(tokens()) with caution.

Value

quanteda tokens class object, by default a serialized list of integers corresponding to a vector of types.

Dealing with URLs

URLs are tricky to tokenize, because they contain a number of symbols and punctuation characters. If you wish to remove these, as most people do, and your text contains URLs, then you should set what = "fasterword" and remove_url = TRUE. If you wish to keep the URLs, but do not want them mangled, then your options are more limited, since removing punctuation and symbols will also remove them from URLs. We are working on improving this behaviour.

See the examples below.

See Also
tokens_ngrams, tokens_skipgrams, as.list.tokens

Examples

txt <- c(doc1 = "This is a sample: of tokens.",
   doc2 = "Another sentence, to demonstrate how tokens works.")
tokens(txt)
   # removing punctuation marks and lowcasing texts
tokens(char_tolower(txt), remove_punct = TRUE)
   # keeping versus removing hyphens
tokens("quanteda data objects are auto-loading.", remove_punct = TRUE)
tokens("quanteda data objects are auto-loading.", remove_punct = TRUE, remove_hyphens = TRUE)
   # keeping versus removing symbols
tokens("<tags> and other + symbols.", remove_symbols = FALSE)
tokens("<tags> and other + symbols.", remove_symbols = TRUE)
tokens("<tags> and other + symbols.", remove_symbols = FALSE, what = "fasterword")
tokens("<tags> and other + symbols.", remove_symbols = TRUE, what = "fasterword")

## examples with URLs - hardly perfect!
tokens(txt, remove_url = TRUE, remove_punct = TRUE)
tokens(txt, remove_url = FALSE, remove_punct = TRUE)
tokens(txt, remove_url = FALSE, remove_punct = TRUE, what = "fasterword")
tokens(txt, remove_url = FALSE, remove_punct = TRUE, what = "fasterword")

## MORE COMPARISONS

##textanalysis is my <3 4U @myhandle gr8 #stuff :-)"
tokens(txt, remove_punct = TRUE)
tokens(txt, remove_punct = TRUE, remove_twitter = TRUE)
tokens("great website http://textastodata.com", remove_url = FALSE)
tokens_compound

## Convert token sequences into compound tokens

### Description

Replace multi-token sequences with a multi-word, or "compound" token. The resulting compound tokens will represent a phrase or multi-word expression, concatenated with concatenator (by default, the "_" character) to form a single "token". This ensures that the sequences will be processed subsequently as single tokens, for instance in constructing a dfm.
Usage

tokens_compound(x, pattern, concatenator = " ", valuetype = c("glob", "regex", "fixed"), case_insensitive = TRUE, join = TRUE)

Arguments

x an input tokens object

pattern a character vector, list of character vectors, dictionary, collocations, or dfm. See pattern for details.

concatenator the concatenation character that will connect the words making up the multi-word sequences. The default _ is recommended since it will not be removed during normal cleaning and tokenization (while nearly all other punctuation characters, at least those in the Unicode punctuation class [P] will be removed).

valuetype the type of pattern matching: "glob" for "glob"-style wildcard expressions; "regex" for regular expressions; or "fixed" for exact matching. See valuetye for details.

case_insensitive logical; if TRUE, ignore case when matching

join logical; if TRUE, join overlapping compounds

Value

a tokens object in which the token sequences matching pattern have been replaced by compound "tokens" joined by the concatenator

Author(s)

Kenneth Benoit and Kohei Watanabe

Examples

mytexts <- c("The new law included a capital gains tax, and an inheritance tax.", "New York City has raised taxes: an income tax and inheritance taxes.")
mytoks <- tokens(mytexts, remove_punct = TRUE)

# for lists of sequence elements
myseqs <- list(c("tax"), c("income", "tax"), c("capital", "gains", "tax"), c("inheritance", "tax"))
(cw <- tokens_compound(mytoks, myseqs))
dfm(cw)

# when used as a dictionary for dfm creation
mydict1 <- dictionary(list(tax=c("tax", "income tax", "capital gains tax", "inheritance tax")))
(cw2 <- tokens_compound(mytoks, mydict1))

# to pick up "taxes" in the second text, set valuetye = "regex"
(cw3 <- tokens_compound(mytoks, mydict1, valuetye = "regex"))

# dictionaries w/glob matches
mydict2 <- dictionary(list(negative = c("bad\* word\*", "negative", "awful text"),

"tokens\_compound"
tokens_lookup

positive = c("good stuff", "like? th??")
toks <- tokens(c(txt1 = "I liked this, when we can use bad words, in awful text.",
              txt2 = "Some damn good stuff, like the text, she likes that too."))
tokens_compound(toks, mydict2)

# with collocations
cols <-
textstat_collocations(tokens("capital gains taxes are worse than inheritance taxes"),
 size = 2, min_count = 1)
toks <- tokens("The new law included capital gains taxes and inheritance taxes.")
tokens_compound(toks, cols)

---

**tokens_lookup**

Apply a dictionary to a tokens object

**Description**

Convert tokens into equivalence classes defined by values of a dictionary object.

**Usage**

```r
tokens_lookup(x, dictionary, levels = 1:5, valuetype = c("glob", "regex", "fixed"),
              case_insensitive = TRUE, capkeys = !exclusive,
              exclusive = TRUE, nomatch = NULL,
              verbose = quanteda_options("verbose"))
```

**Arguments**

- **x**: tokens object to which dictionary or thesaurus will be supplied
- **dictionary**: the dictionary-class object that will be applied to `x`
- **levels**: integers specifying the levels of entries in a hierarchical dictionary that will be applied. The top level is 1, and subsequent levels describe lower nesting levels. Values may be combined, even if these levels are not contiguous, e.g. `levels = c(1:3)` will collapse the second level into the first, but record the third level (if present) collapsed below the first (see examples).
- **valuetype**: the type of pattern matching: "glob" for "glob"-style wildcard expressions; "regex" for regular expressions; or "fixed" for exact matching. See `valuetype` for details.
- **case_insensitive**: ignore the case of dictionary values if TRUE uppercase to distinguish them from other features
- **capkeys**: if TRUE, convert dictionary keys to uppercase to distinguish them from other features
- **exclusive**: if TRUE, remove all features not in dictionary, otherwise, replace values in dictionary with keys while leaving other features unaffected
- **nomatch**: an optional character naming a new key for tokens that do not matched to a dictionary values If `null` (default), do not record unmatched tokens.
- **verbose**: print status messages if TRUE
See Also
tokens_replace

Examples

toks <- tokens(data_corpus_inaugural)
dict <- dictionary(list(country = "united states",
    law = c('law', 'constitution'),
    freedom = c('freedom', 'liberty')))
dfm(tokens_lookup(toks, dict, valuetype='glob', verbose = TRUE))
dfm(tokens_lookup(toks, dict, valuetype='glob', verbose = TRUE, nomatch = 'NONE'))

dict_fix <- dictionary(list(country = "united states",
    law = c('law', 'constitution'),
    freedom = c('freedom', 'liberty')))
# dfm(applyDictionary(toks, dict_fix, valuetype='fixed'))
dfm(tokens_lookup(toks, dict_fix, valuetype='fixed'))

# hierarchical dictionary example
txt <- c(d1 = "The United States has the Atlantic Ocean and the Pacific Ocean.",
    d2 = "Britain and Ireland have the Irish Sea and the English Channel.")
toks <- tokens(txt)
dict <- dictionary(list(US = list(Countries = c("States"),
    oceans = c("Atlantic", "Pacific")),
    Europe = list(Countries = c("Britain", "Ireland"),
    oceans = list(west = "Irish Sea",
    east = "English Channel"))))
tokens_lookup(toks, dict, levels = 1)
tokens_lookup(toks, dict, levels = 2)
tokens_lookup(toks, dict, levels = 1:2)
tokens_lookup(toks, dict, levels = 3)
tokens_lookup(toks, dict, levels = c(1,3))
tokens_lookup(toks, dict, levels = c(2,3))

# show unmatched tokens
tokens_lookup(toks, dict, nomatch = "_UNMATCHED")

---

tokens_ngrams Create ngrams and skipgrams from tokens

Description

Create a set of ngrams (tokens in sequence) from already tokenized text objects, with an optional skip argument to form skipgrams. Both the ngram length and the skip lengths take vectors of arguments to form multiple lengths or skips in one pass. Implemented in C++ for efficiency.
tokens_ngrams

Usage

tokens_ngrams(x, n = 2L, skip = 0L, concatenator = "_")

char_ngrams(x, n = 2L, skip = 0L, concatenator = "_")

tokens_skipgrams(x, n, skip, concatenator = "_")

Arguments

x  a tokens object, or a character vector, or a list of characters
n  integer vector specifying the number of elements to be concatenated in each ngram. Each element of this vector will define a n in the n-gram(s) that are produced.
skip  integer vector specifying the adjacency skip size for tokens forming the ngrams, default is 0 for only immediately neighbouring words. For skipgrams, skip can be a vector of integers, as the "classic" approach to forming skip-grams is to set skip = k where k is the distance for which k or fewer skips are used to construct the n-gram. Thus a "4-skip-n-gram" defined as skip = 0:4 produces results that include 4 skips, 3 skips, 2 skips, 1 skip, and 0 skips (where 0 skips are typical n-grams formed from adjacent words). See Guthrie et al (2006).
concatenator  character for combining words, default is _ (underscore) character

Details

Normally, these functions will be called through tokens_ngrams, but these functions are provided in case a user wants to perform lower-level ngram construction on tokenized texts.

tokens_skipgrams is a wrapper to tokens_ngrams that requires arguments to be supplied for both n and skip. For k-skip skipgrams, set skip to 0:k, in order to conform to the definition of skip-grams found in Guthrie et al (2006): A k skip-gram is an ngram which is a superset of all ngrams and each (k - i) skipgram until (k - i) == 0 (which includes 0 skip-grams).

Value

a tokens object consisting a list of character vectors of ngrams, one list element per text, or a character vector if called on a simple character vector

Note

char_ngrams is a convenience wrapper for a (non-list) vector of characters, so named to be consistent with quanteda’s naming scheme.

Author(s)

Kohei Watanabe (C++) and Ken Benoit (R)

References

Examples

```r
# ngrams
tokens_ngrams(tokens(c("a b c d e", "c d e f g"), n = 2:3))

toks <- tokens(c(text1 = "the quick brown fox jumped over the lazy dog"))
tokens_ngrams(toks, n = 1:3)
tokens_ngrams(toks, n = c(2,4), concatenator = " ")
tokens_ngrams(toks, n = c(2,4), skip = 1, concatenator = " ")

# on character
char_ngrams(letters[1:3], n = 1:3)

# skipgrams
toks <- tokens("insurgents killed in ongoing fighting")
tokens_skipgrams(toks, n = 2, skip = 0:1, concatenator = " ")
tokens_skipgrams(toks, n = 2, skip = 0:2, concatenator = " ")
tokens_skipgrams(toks, n = 3, skip = 0:2, concatenator = " ")
```

### tokens_replace

*Replace types in tokens object*

**Description**

Substitute token types based on vectorized one-to-one matching. Since this function is created for lemmatization or user-defined stemming, it does not support multi-word features, or glob and regex patterns. Please use `tokens_lookup` with `exclusive = FALSE` for substitutions of more complex patterns.

**Usage**

```r
tokens_replace(x, pattern, replacement = NULL, case_insensitive = TRUE, verbose = quanteda_options("verbose"))
```

**Arguments**

- `x`: `tokens` object whose token elements will be replaced
- `pattern`: a character vector or dictionary. See `pattern` for more details.
- `replacement`: if pattern is a character vector, then replacement must be character vector of equal length, for a 1:1 match. If pattern is a dictionary, then replacement should not be used.
- `case_insensitive`: ignore case when matching, if TRUE
- `verbose`: print status messages if TRUE
**tokens_sample**

Randomly sample documents from a tokens object

**Description**

Sample tokenized documents randomly from a tokens object, with or without replacement. Works just as `sample` works, for document-level units (and their associated document-level variables).

**Usage**

```r
tokens_sample(x, size = ndoc(x), replace = FALSE, prob = NULL)
```

**Arguments**

- **x**: the `tokens` object whose documents will be sampled
- **size**: a positive number, the number of documents or features to select
- **replace**: logical; should sampling be with replacement?
- **prob**: a vector of probability weights for obtaining the elements of the vector being sampled.

**Value**

A `tokens` object with number of documents or features equal to `size`, drawn from the `tokens x`.

**See Also**

`sample`
Examples

```r
set.seed(10)
toks <- tokens(data_corpus_inaugural[1:10])
head(toks)
head(tokens.sample(toks))
head(tokens.sample(toks, replace = TRUE))
```

tokens_select  
Select or remove tokens from a tokens object

Description

These function select or discard tokens from a tokens objects. For convenience, the functions `tokens_remove` and `tokens_keep` are defined as shortcuts for `tokens_select(x, pattern, selection = "remove")` and `tokens_select(x, pattern, selection = "keep")`, respectively. The most common usage for `tokens_remove` will be to eliminate stop words from a text or text-based object, while the most common use of `tokens_select` will be to select tokens with only positive pattern matches from a list of regular expressions, including a dictionary.

Usage

```r
tokens_select(x, pattern, selection = c("keep", "remove"),
              valuetype = c("glob", "regex", "fixed"), case_insensitive = TRUE,
              padding = FALSE, window = 0, min_nchar = 1L, max_nchar = 79L,
              verbose = quanteda_options("verbose"))

tokens_remove(x, ...)

tokens_keep(x, ...)
```

Arguments

- `x` tokens object whose token elements will be removed or kept
- `pattern` a character vector, list of character vectors, dictionary, collocations, or dfm. See `pattern` for details.
- `selection` whether to "keep" or "remove" the tokens matching pattern
- `valuetype` the type of pattern matching: "glob" for "glob"-style wildcard expressions; "regex" for regular expressions; or "fixed" for exact matching. See `valuetype` for details.
- `case_insensitive` ignore case when matching, if TRUE
- `padding` if TRUE, leave an empty string where the removed tokens previously existed. This is useful if a positional match is needed between the pre- and post-selected tokens, for instance if a window of adjacency needs to be computed.
window  integer of length 1 or 2; the size of the window of tokens adjacent to pattern that will be selected. The window is symmetric unless a vector of two elements is supplied, in which case the first element will be the token length of the window before pattern, and the second will be the token length of the window after pattern. The default is 0, meaning that only the pattern matched token(s) are selected, with no adjacent terms. Terms from overlapping windows are never double-counted, but simply returned in the pattern match. This is because tokens_select never redefines the document units; for this, see kwic.

min_nchar, max_nchar  numerics specifying the minimum and maximum length in characters for tokens to be removed or kept; defaults are 1 and 79. (Set max_nchar to NULL for no upper limit.) These are applied after (and hence, in addition to) any selection based on pattern matches.

verbose  if TRUE print messages about how many tokens were selected or removed

additional arguments passed by tokens_remove and tokens_keep to tokens_select. Cannot include selection.

Value  
a tokens object with tokens selected or removed based on their match to pattern

Examples

```r
## tokens_select with simple examples
toks <- tokens(c("This is a sentence.", "This is a second sentence."),
               remove_punct = TRUE)
tokens_select(toks, c("is", "a", "this"), selection = "keep", padding = FALSE)
tokens_select(toks, c("is", "a", "this"), selection = "keep", padding = TRUE)
tokens_select(toks, c("is", "a", "this"), selection = "remove", padding = FALSE)
tokens_select(toks, c("is", "a", "this"), selection = "remove", padding = TRUE)

# how case_insensitive works
tokens_select(toks, c("is", "a", "this"), selection = "remove", case_insensitive = TRUE)
tokens_select(toks, c("is", "a", "this"), selection = "remove", case_insensitive = FALSE)

# use window
tokens_select(toks, "second", selection = "keep", window = 1)
tokens_select(toks, "second", selection = "remove", window = 1)
tokens_remove(toks, "is", window = c(0, 1))

# tokens_remove example: remove stopwords
txt <- c(wash1 <- "Fellow citizens, I am again called upon by the voice of my country to execute the functions of its Chief Magistrate.",
         wash2 <- "When the occasion proper for it shall arrive, I shall endeavor to express the high sense I entertain of this distinguished honor.")
tokens_remove(tokens(txt, remove_punct = TRUE), stopwords("english"))

# token_keep example: keep two-letter words
tokens_keep(tokens(txt, remove_punct = TRUE), "??")
```
tokens_subset

Extract a subset of a tokens

description

Returns document subsets of a tokens that meet certain conditions, including direct logical operations on docvars (document-level variables). tokens_subset functions identically to subset.data.frame, using non-standard evaluation to evaluate conditions based on the docvars in the tokens.

Usage

tokens_subset(x, subset, select, ...)

Arguments

x: tokens object to be subsetted
subset: logical expression indicating the documents to keep: missing values are taken as false
select: expression, indicating the docvars to select from the tokens; or a tokens object, in which case the returned tokens will contain the same documents in the same order as the original tokens, even if these are empty.
...: not used

Value

tokens object, with a subset of documents (and docvars) selected according to arguments

See Also

subset.data.frame

Examples

corp <- corpus(c(d1 = "a b c d", d2 = "a a b e", d3 = "b b c e", d4 = "e e f a b"),
docvars = data.frame(grp = c(1, 1, 2, 3)))
toks <- tokens(corp)
# selecting on a docvars condition
tokens_subset(toks, grp > 1)
# selecting on a supplied vector
tokens_subset(toks, c(TRUE, FALSE, TRUE, FALSE))

# selecting on a tokens
toks1 <- tokens(c(d1 = "a b b c", d2 = "b b c d"))
toks2 <- tokens(c(d1 = "x y z", d2 = "a b c c d", d3 = "x x x"))
tokens_subset(toks1, subset = toks2)
tokens_subset(toks1, subset = toks2[c(3,1,2)])
**tokens_tolower**  
*Convert the case of tokens*

**Description**

`tokens_tolower` and `tokens_toupper` convert the features of a `tokens` object and re-index the types.

**Usage**

```r
tokens_tolower(x, keep_acronyms = FALSE, ...)
tokens_toupper(x, ...)
```

**Arguments**

- `x`  
  the input object whose character/tokens/feature elements will be case-converted

- `keep_acronyms`  
  logical; if `TRUE`, do not lowercase any all-uppercase words (applies only to *_tolower functions)

- `...`  
  additional arguments passed to `stringi` functions, (e.g. `stri_trans_tolower`), such as `locale`

**Examples**

```r
# for a document-feature matrix
toks <- tokens(c(txt1 = "b A A", txt2 = "C a b B"))
tokens_tolower(toks)
tokens_toupper(toks)
```

**tokens_tortl**  
*([Experimental] Change direction of words in tokens)*

**Description**

This function adds a Unicode direction mark to tokens types for punctuations and symbols to correct how right-to-left languages (e.g. Arabic, Hebrew, Persian, and Urdu) are printed in HTML-based consoles (e.g. R Studio). This is an experimental function subject to future change.

**Usage**

```r
tokens_tortl(x)
char_tortl(x)
```

**Arguments**

- `x`  
  the input object whose punctuation marks will be modified by the direction mark
Stem the terms in an object

Description

Apply a stemmer to words. This is a wrapper to `wordStem` designed to allow this function to be called without loading the entire `SnowballC` package. `wordStem` uses Martin Porter’s stemming algorithm and the C libstemmer library generated by Snowball.

Usage

```r
tokens_wordstem(x, language = quanteda_options("language_stemmer"))
char_wordstem(x, language = quanteda_options("language_stemmer"))
dfm_wordstem(x, language = quanteda_options("language_stemmer"))
```

Arguments

- `x`: a character, tokens, or dfm object whose word stems are to be removed. If tokenized texts, the tokenization must be word-based.
- `language`: the name of a recognized language, as returned by `getStemLanguages`, or a two- or three-letter ISO-639 code corresponding to one of these languages (see references for the list of codes).

Value

- `tokens_wordstem` returns a `tokens` object whose word types have been stemmed.
- `char_wordstem` returns a `character` object whose word types have been stemmed.
- `dfm_wordstem` returns a `dfm` object whose word types (features) have been stemmed, and recombined to consolidate features made equivalent because of stemming.

References

- http://snowball.tartarus.org/
- http://www.iso.org/iso/home/standards/language_codes.htm for the ISO-639 language codes

See Also

- `wordStem`
Examples

# example applied to tokens
txt <- c(one = "eating eater eaters eats ate",
         two = "taxing taxes taxed my tax return")
th <- tokens(txt)
tokens_wordstem(th)

# simple example
char_wordstem(c("win", "winning", "wins", "won", "winner"))

# example applied to a dfm
(origdfm <- dfm(txt))
dfm_wordstem(origdfm)

---

**topfeatures**

*Identify the most frequent features in a dfm*

**Description**

List the most (or least) frequently occurring features in a dfm, either as a whole or separated by document.

**Usage**

```r
topfeatures(x, n = 10, decreasing = TRUE, scheme = c("count",
                "docfreq"), groups = NULL)
```

**Arguments**

- `x` the object whose features will be returned
- `n` how many top features should be returned
- `decreasing` If `TRUE`, return the `n` most frequent features; otherwise return the `n` least frequent features
- `scheme` one of `count` for total feature frequency (within group if applicable), or `docfreq` for the document frequencies of features
- `groups` either: a character vector containing the names of document variables to be used for grouping; or a factor or object that can be coerced into a factor equal in length or rows to the number of documents. See `groups` for details.

**Value**

A named numeric vector of feature counts, where the names are the feature labels, or a list of these if `groups` is given.
Examples

```r
mydfm <- corpus_subset(data_corpus_inaugural, Year > 1980)
  dfm(remove_punct = TRUE)
mydfm_nostopw <- dfm_remove(mydfm, stopwords("english"))

# most frequent features
topfeatures(mydfm)
topfeatures(mydfm_nostopw)

# least frequent features
topfeatures(mydfm_nostopw, decreasing = FALSE)

# top features of individual documents
topfeatures(mydfm_nostopw, n = 5, groups = docnames(mydfm_nostopw))

# grouping by president last name
topfeatures(mydfm_nostopw, n = 5, groups = "President")

# features by document frequencies
tail(topfeatures(mydfm, scheme = "docfreq", n = 200))
```

---

**types**  
*Get word types from a tokens object*

**Description**

Get unique types of tokens from a tokens object.

**Usage**

```r
types(x)
```

**Arguments**

- `x` a tokens object

**See Also**

- `featnames`

**Examples**

```r
toks <- tokens(data_corpus_inaugural)
types(toks)
```
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