Package 'quanteda'

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Version 1.3.4

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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Depends R (>= 3.1.0), methods

Imports data.table (>= 1.9.6), extrafont, fastmatch, ggplot2 (>= 2.2.0), ggrepel, lubridate, magrittr, Matrix (>= 1.2), network, RSpectra, Rcpp (>= 0.12.12), RcppParallel, sna, SnowballC, spacyr, stopwords, stringi, xml2, yaml

LinkingTo Rcpp, RcppParallel, RcppArmadillo (>= 0.7.600.1.0)

Suggests ca, dplyr, DT, e1071, ExPosition, koRpus, lda, lsa, proxy, purrr, RColorBrewer, rmarkdown, slam, stm, svs, testthat, text2vec, tibble, tidytext, tm (>= 0.6), topicmodels, xtable, knitr, igraph

URL http://quanteda.io

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BugReports https://github.com/quanteda/quanteda/issues

LazyData TRUE

VignetteBuilder knitr

Collate 'RcppExports.R' 'View.R' 'bootstrap_dfm.R' 'casechange-functions.R' 'directionchange-functions.R' 'character-methods.R' 'convert.R' 'corpus-methods-base.R' 'corpus-methods-quanteda.R' 'corpus-methods-tm.R' 'corpus.R' 'corpus_reshape.R' 'corpus_sample.R' 'corpus_segment.R' 'corpus_subset.R' 'corpus_trim.R' 'corpuszip.R' 'data-deprecated.R' 'data-documentation.R' 'defunct-functions.R' 'dfm-classes.R' 'dfm-methods.R' 'dfm-print.R' 'dfm-subsetting.R' 'dfm.R' 'dfm_compress.R'

'dfm_group.R' 'dfm_lookup.R' 'dfm_replace.R' 'dfm_sample.R'
'dfm_select.R' 'dfm_sort.R' 'dfm_subset.R' 'dfm_trim.R'
'dfm_weight.R' 'dictionaries.R' 'docnames.R' 'docvars.R'
'fcm-classes.R' 'fcm-methods.R' 'fcm-subsetting.R' 'fcm.R'
'kwic.R' 'nfunctions.R' 'nscrabble.R' 'nsyllable.R'
'pattern2fixed.R' 'phrases.R' 'quanteda-documentation.R'
'quanteda_options.R' 'readtext-methods.R' 'settings.R'
'spacyr-methods.R' 'stopwords.R' 'textmodel-methods.R'
'textmodel_affinity.R' 'textmodel_ca.R' 'textmodel_lsa.R'
'textmodel_nb.R' 'textmodel_wordfish.R'
'textmodel_wordscores.R' 'textplot_influence.R'
'textplot_keyness.R' 'textplot_network.R' 'textplot_scale1d.R'
'textplot_wordcloud.R' 'textplot_xray.R' 'textstat-methods.R'
'textstat_collocations.R' 'textstat_dist.R'
'textstat_frequency.R' 'textstat_keyness.R' 'textstat_lexdiv.R'
'textstat_readability.R' 'textstat_simil.R' 'tokens.R'
'tokens_compound.R' 'tokens_group.R' 'tokens_lookup.R'
'tokens_ngrams.R' 'tokens_replace.R' 'tokens_segment.R'
'tokens_select.R' 'tokens_subset.R' 'utils.R' 'wordstem.R'
'zzz.R'

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`quanteda-package` *An R package for the quantitative analysis of textual data*

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;
- 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:

- http://quanteda.io
- Report bugs at https://github.com/quanteda/quanteda/issues

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as.corpus.corpuszip *Coerce a compressed corpus to a standard corpus*

Description

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

Usage

```
## 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

```
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

```
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

```
## 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", "netural"))
    )
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(list(key1 = c("val1", "val2"), key2 = "val3"))
## [1] FALSE
```

---

as.list.dist *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

```
## 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

Examples

```
## Not run:
## compare to tm

# tm version
require(tm)
data("crude")
crude <- tm_map(crude, content_transformer(tolower))
crude <- tm_map(crude, remove_punctuation)
crude <- tm_map(crude, remove_numbers)
crude <- tm_map(crude, stemDocument)
tdm <- TermDocumentMatrix(crude)
findAssocs(tdm, c("oil", "opec", "xyz"), c(0.75, 0.82, 0.1))

# in quanteda
quantedaDfm <- as.dfm(t(as.matrix(tdm)))
as.list(textstat_dist(quantedaDfm, c("oil", "opec", "xyz"), margin = "features"), n = 14)

# in base R
corMat <- as.matrix(proxy::simil(as.matrix(quantedaDfm), by_rows = FALSE))
round(head(sort(corMat[, "oil"], decreasing = TRUE), 14), 2)
round(head(sort(corMat[, "opec"], decreasing = TRUE), 9), 2)

## End(Not run)
```

---

as.matrix.dfm *Coerce a dfm to a matrix or data.frame*

Description

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

Usage

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

Arguments

x	dfm to be coerced
...	unused

Examples

```
# 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".
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.yaml *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

```
as.yaml(x)
```

Arguments

x	a dictionary object

Value

as.yaml a dictionary in the YAML format, as a character object

Examples

```
## Not run:
dict <- dictionary(list(one = c("a b", "c*"), two = c("x", "y", "z??")))
cat(yaml <- as.yaml(dict))
cat(yaml, file = (yamlfile <- paste0(tempfile(), ".yml")))
dictionary(file = yamlfile)

## End(Not run)
```

---

bootstrap_dfm *Bootstrap a dfm*

Description

Create an array of resampled dfms.

Usage

```
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

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

```
# 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

```
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(text1 = "England and France are members of NATO and UNESCO",
          text2 = "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.

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

```
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 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, ...)

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

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

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

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

## 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; • citation information on how to cite the corpus; and • notes any additional information about who created the text, warnings, to do lists, etc.
compress	logical; if TRUE, compress the texts in memory using gzip compression. This significantly reduces the size of the corpus in memory, but will slow down operations that require the texts to be extracted.
docid_field	optional column index of a document identifier; defaults to "doc_id", but if this is not found, then will use the rownames of the data.frame; if the rownames are not set, it will use the default sequence based on (quanteda_options("base_docname").
text_field	the character name or numeric index of the source data.frame indicating the variable to be read in as text, which must be a character vector. All other variables in the data.frame will be imported as docvars. This argument is only used for data.frame objects (including those created by **readtext**).
split_context	logical; if TRUE, split each kwic row into two "documents", one for "pre" and one for "post", with this designation saved in a new docvar context and with the new number of documents therefore being twice the number of rows in the kwic.
extract_keyword	logical; if TRUE, save the keyword matching pattern as a new docvar keyword

Details

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.

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

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))
summary(corpus(kw, split_context = FALSE))
texts(corpus(kw, split_context = FALSE))
```

`corpus_reshape` *Recast the document units of a corpus*

Description

For a corpus, reshape (or recast) the documents to a different level of aggregation. Units of aggregation 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.",
                 textwo = "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 or documents of the specified size from a corpus or document-feature matrix, 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)

char_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.
                 ##DOC1 This is the first document.  Second sentence in Doc 1.
                 ##DOC3 Third document starts here.  End of third document.",
                "##INTRO Document ##NUMBER Two starts before ##NUMBER Three."))
corp_seg <- corpus_segment(corp, "##*")
cbind(texts(corp_seg), docvars(corp_seg), metadoc(corp_seg))

# segmenting a transcript based on speaker identifiers
corp2 <- corpus("Mr. Smith: Text.\nMrs. Jones: More text.\nMr. Smith: I'm speaking, again.")
corp_seg2 <- corpus_segment(corp2, pattern = "\\b[A-Z].+\\s[A-Z][a-z]+:",
                            valuetype = "regex")
cbind(texts(corp_seg2), docvars(corp_seg2), metadoc(corp_seg2))

# segmenting a corpus using crude end-of-sentence segmentation
corp_seg3 <- corpus_segment(corp, pattern = ".", valuetype = "fixed",
                            pattern_position = "after", extract_pattern = FALSE)
cbind(texts(corp_seg3), docvars(corp_seg3), metadoc(corp_seg3))

## segmenting a character vector

# segment into paragraphs and removing the "- " bullet points
cat(data_char_ukimmig2010[4])
char_segment(data_char_ukimmig2010[4],
             pattern = "\\n\\n(\\-\\s){0,1}", valuetype = "regex",
             remove_pattern = TRUE)

# segment a text into clauses
txt <- c(d1 = "This, is a sentence?  You: come here.", d2 = "Yes, yes okay.")
char_segment(txt, pattern = "\\p{P}", valuetype = "regex",
             pattern_position = "after", remove_pattern = FALSE)
```

`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

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))
```

---

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

Dáil Éireann Debate, Financial Resolution No. 13: General (Resumed). 7 December 2011. vol. 749, no. 1.

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

```
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

https://www.oireachtas.ie/en/debates/debate/dail/1991-10-16/10/

References

Laver, Michael, and Kenneth Benoit. 2002. "Locating TDs in Policy Spaces: Wordscoring Dáil Speeches." *Irish Political Studies* 17 (Summer): 59-73.

Laver, Michael, Kenneth Benoit, and John Garry. 2003. "Estimating policy positions from political text using words as data." *American Political Science Review* 97(2): 311-331.

Examples

```
## 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("Goverment", "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

https://archive.org/details/Inaugural-Address-Corpus-1789-2009 and http://www.presidency.ucsb.edu/inaugurals.php.

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

Dáil Éireann Debate, Budget Statement 2010. 9 December 2009. vol. 697, no. 3.

References

Lowe, Will, and Kenneth R Benoit. 2013. "Validating Estimates of Latent Traits From Textual Data Using Human Judgment as a Benchmark." *Political Analysis* 21: 298-313.

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

```
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

Laver, Michael, Kenneth Benoit, and John Garry. 2003. "Estimating policy positions from political text using words as data." *American Political Science Review* 97(2): 311-331.

data_dictionary_LSD2015 *Lexicoder Sentiment Dictionary (2015)*

Description

The 2015 Lexicoder Sentiment Dictionary in **quanteda** dictionary format.

Usage

```
data_dictionary_LSD2015
```

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.

Young, Lori and Stuart Soroka. 2012. "Affective News: The Automated Coding of Sentiment in Political Texts." *Political Communication* 29(2): 205-231.

Examples

```
# 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(data_char_ukimmig2010, dictionary = data_dictionary_LSD2015)
kwic(data_char_ukimmig2010, "not")

# compound neg_negative and neg_positive tokens before creating a dfm object
toks <- tokens_compound(tokens(txt), data_dictionary_LSD2015)

dfm_lookup(dfm(toks), data_dictionary_LSD2015)
```

---

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 valuetype 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 behavior 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

```
## for a corpus
corpus_post80inaug <- corpus_subset(data_corpus_inaugural, Year > 1980)
dfm(corpus_post80inaug)
dfm(corpus_post80inaug, tolower = FALSE)

# grouping documents by docvars in a corpus
dfm(corpus_post80inaug, groups = "President", verbose = TRUE)

# with English stopwords and stemming
dfm(corpus_post80inaug, 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_post1900inaug <- 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 = "s$", 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 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 recombined 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 recombined 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 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)

txt <- c("The fox JUMPED over the dog.",
         "The dog jumped over the fox.")
toks <- tokens(txt, remove_punct = TRUE)
myfcm <- fcm(toks, context = "document")
colnames(myfcm) <- rownames(myfcm) <- tolower(colnames(myfcm))
colnames(myfcm)[5] <- rownames(myfcm)[5] <- "fox"
myfcm
fcm_compress(myfcm)
```

---

dfm_group *Combine documents in a dfm by a grouping variable*

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.

Examples

```
mycorpus <- corpus(c("a a b", "a b c 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_lookup *Apply a dictionary to a dfm*

Description

Apply a dictionary to a dfm by looking up all dfm features for matches in a 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"), case_insensitive = 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.

`case_insensitive`
: 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`

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

```
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

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

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", "focused", "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

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

dfm_remove(x, ...)

dfm_keep(x, ...)

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

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

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. For dfm_select, pattern may also be a dfm; see Value below.
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.

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

```
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

```
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

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

```
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

```
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

Manning, C. D., Raghavan, P., & Schutze, H. (2008). *Introduction to Information Retrieval*. Cambridge University Press.

See Also

dfm_weight, docfreq

Examples

```
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_tf.E2.80.93idf
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")
}

## End(Not run)
```

`dfm_tolower` *Convert the case of the features of a dfm and combine*

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

```
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

```
# 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")
myfcm
fcm_tolower(myfcm)
fcm_toupper(myfcm)
```

---

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, min_termfreq = NULL, max_termfreq = NULL,
  termfreq_type = c("count", "prop", "rank", "quantile"),
  min_docfreq = NULL, max_docfreq = NULL, docfreq_type = c("count",
  "prop", "rank", "quantile"), sparsity = NULL,
  verbose = quanteda_options("verbose"), ...)
```

Arguments

x a dfm object

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

termfreq_type — how min_termfreq and max_termfreq are intepreted. "count" sums the frequencies; "prop" devides the term frequences 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 quantile) of term frequencies.

min_docfreq, max_docfreq — minimum/maximum values of a feature's document frequency, below/above which features will be removed

docfreq_type — specify how min_docfreq and max_docfreq are intepreted. "count" is the same as docfreq(x, scheme = "count"); "prop" devides the document frequences 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 quantile) of document frequencies.

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

```
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 $K + (1 - K) *$ `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

Manning, Christopher D., Prabhakar Raghavan, and Hinrich Schutze. *Introduction to Information Retrieval*. Vol. 1. Cambridge: Cambridge University Press, 2008.

See Also

dfm_tfidf, docfreq

Examples

```
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)
```

`dictionary` *Create a dictionary*

Description

Create a **quanteda** 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.

References

Wordstat dictionaries page, from Provalis Research http://provalisresearch.com/products/content-analysis-software/wordstat-dictionary/.

Pennebaker, J.W., Chung, C.K., Ireland, M., Gonzales, A., & Booth, R.J. (2007). The development and psychometric properties of LIWC2007. [Software manual]. Austin, TX (www.liwc.net).

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

```
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/5gmwXq", tf <- tempfile())
mfdict <- dictionary(file = tf, format = "LIWC")
head(dfm(data_corpus_inaugural, dictionary = mfdict))

## End(Not run)
```

---

docfreq *Compute the (weighted) document frequency of a feature*

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

```
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 Schutze 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

Manning, C. D., Raghavan, P., & Schutze, H. (2008). *Introduction to Information Retrieval*. Cambridge University Press.

Examples

```
mydfm <- dfm(data_corpus_inaugural[1:2])
docfreq(mydfm[, 1:20])

# replication of worked example from
# https://en.wikipedia.org/wiki/Tf-idf#Example_of_tf.E2.80.93idf
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)
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 doument names to a corpus
mycorp <- data_corpus_inaugural
docnames(mycorp) <- char_tolower(docnames(mycorp))

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

# get and set doument 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="")
```

---

docvars *Get or set document-level variables*

Description

Get or set variables associated with a document in a corpus, tokens or dfm object.

Usage

```
docvars(x, field = NULL)

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

Arguments

x	corpus, tokens, or dfm object whose document-level variables will be read or set
field	string containing the document-level variable name
value	the new values of the document-level variable

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[["`. The latter also permits assignment, including the easy creation of new document variables, e.g. `data_corpus_irishbudget2010[["newvar"]] <-1:ndoc(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:ndoc(corp), sep = "")
head(docvars(corp))

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

```
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)
...	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

Momtazi, S., Khudanpur, S., & Klakow, D. (2010). "A comparative study of word co-occurrence for term clustering in language model-based sentence retrieval." *Human Language Technologies: The 2010 Annual Conference of the North American Chapter of the ACL*, Los Angeles, California, June 2010, pp. 325-328.

Daniel Jurafsky & James H. Martin. (2015) *Speech and Language Processing*. Draft of April 11, 2016. Chapter 16, Semantics with Dense Vectors.

Church, K. W. & P. Hanks (1990) "Word association norms, mutual information, and lexicography" *Computational Linguistics*, 16(1):22–29.

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	fcm object

Value

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

Author(s)

Ken Benoit

Examples

```
# 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)
```

featnames *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

```
featnames(x)
```

Arguments

x	the dfm whose features will be extracted

Value

character vector of the feature labels

Examples

```
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()
names(topfeatures(inaugDfm, 50))
```

head.corpus *Return the first or last part of a corpus*

Description

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

Usage

```
## 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

```
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 nfeat features.

Usage

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

## 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 ncol features; default is all features
...	additional arguments passed to other functions

Value

A dfm class object corresponding to the subset defined by n and nfeat.

Examples

```
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

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

Author(s)

Kenneth Benoit and Kohei Watanabe

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.

Replacement function for corpus-level data

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")
```

---

metadoc *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

```
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

```
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

```
ndoc(x)

nfeat(x)

nfeature(x)
```

Arguments

x	a **quanteda** 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

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

```
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

```
# 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)
```

---

ntoken *Count the number of tokens or types*

Description

Get the count of tokens (total features) or types (unique tokens).

Usage

```
ntoken(x, ...)

ntype(x, ...)
```

Arguments

x	a **quanteda** 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

```
# 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
ntoken(corpus_subset(data_corpus_inaugural, Year<1806), remove_punct = TRUE)
ntype(corpus_subset(data_corpus_inaugural, Year<1806), remove_punct = TRUE)
ntoken(dfm(corpus_subset(data_corpus_inaugural, Year<1800)))
ntype(dfm(corpus_subset(data_corpus_inaugural, Year<1800)))
```

---

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)

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

```
(opt <- quanteda_options())

quanteda_options(verbose = TRUE)
quanteda_options("verbose" = 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

```
## 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

Examples

```
## 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)
```

---

sparsity *Compute the sparsity of a document-feature matrix*

Description

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

Usage

```
sparsity(x)
```

Arguments

x	the document-feature matrix

Examples

```
inaug_dfm <- dfm(data_corpus_inaugural, verbose = FALSE)
sparsity(inaug_dfm)
sparsity(dfm_trim(inaug_dfm, min_termfreq = 5))
```

---

textmodel_affinity *Class affinity maximum likelihood text scaling model*

Description

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

Usage

```
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

Perry, Patrick O. and Kenneth Benoit. (2017) "Scaling Text with the Class Affinity Model". arXiv:1710.08963 [stat.ML].

See Also

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

Examples

```
(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

```
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 = 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

Nenadic, O. and Greenacre, M. (2007). Correspondence analysis in R, with two- and three-dimensional graphics: The ca package. *Journal of Statistical Software*, 20 (3), http://www.jstatsoft.org/v20/i03/.

See Also

coef.textmodel_lsa, ca

Examples

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

`textmodel_lsa` *Latent Semantic Analysis*

Description

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

Usage

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

Arguments

`x`	the dfm on which the model will be fit
`nd`	the number of dimensions to be included in output
`margin`	margin to be smoothed by the SVD

Details

svds in the **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

Rosario, Barbara. 2000. "Latent Semantic Indexing: An overview". *Technical report INFOSYS 240 Spring Paper, University of California, Berkeley.*

Deerwester, S., Dumais, S. T., Furnas, G. W., Landauer, T. K., & Harshman, R. 1990. "Indexing by latent semantic analysis". *Journal of the American society for information science* 41(6), 391.

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 = "b`

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`	$k \times J$; probability of the word given the class (empirical likelihood)
`Pc`	k-length named numeric vector of class prior probabilities
`PcGw`	$k \times J$; posterior class probability given the word
`Pw`	$J \times 1$; baseline probability of the word
`x`	the $I \times J$ training dfm `x`
`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

Manning, C. D., Raghavan, P., & Schütze, H. (2008). Introduction to Information Retrieval. Cambridge University Press. https://nlp.stanford.edu/IR-book/pdf/irbookonlinereading.pdf

Jurafsky, Daniel and James H. Martin. (2016) *Speech and Language Processing.* Draft of November 7, 2016. https://web.stanford.edu/~jurafsky/slp3/6.pdf

See Also

`predict.textmodel_nb`

Examples

```
## 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, ])
```

`textmodel_wordfish` *Wordfish text model*

Description

Estimate Slapin and Proksch's (2008) "wordfish" Poisson scaling model of one-dimensional document positions using conditional maximum likelihood.

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`	the dfm on which the model will be fit
`dir`	set global identification by specifying the indexes for a pair of documents such that $\hat{\theta}_{dir[1]} < \hat{\theta}_{dir[2]}$.
`priors`	prior precisions for the estimated parameters α_i, ψ_j, β_j, and θ_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

Jonathan Slapin and Sven-Oliver Proksch. 2008. "A Scaling Model for Estimating Time-Series Party Positions from Texts." *American Journal of Political Science* 52(3):705-772.

Lowe, Will and Kenneth Benoit. 2013. "Validating Estimates of Latent Traits from Textual Data Using Human Judgment as a Benchmark." *Political Analysis* 21(3), 298-313. http://doi.org/10.1093/pan/mpt002

See Also

`predict.textmodel_wordfish`

Examples

```
(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:
ie2010dwf <- dfm(data_corpus_irishbudget2010, verbose = FALSE)
(wf1 <- textmodel_wordfish(ie2010dfm, dir = c(6,5)))
(wf2a <- textmodel_wordfish(ie2010dfm, dir = c(6,5),
                            dispersion = "quasipoisson", dispersion_floor = 0))
(wf2b <- textmodel_wordfish(ie2010dfm, dir = c(6,5),
                            dispersion = "quasipoisson", dispersion_floor = .5))
plot(wf2a$phi, wf2b$phi, xlab = "Min underdispersion = 0", ylab = "Min underdispersion = .5",
     xlim = c(0, 1.0), ylim = c(0, 1.0))
plot(wf2a$phi, wf2b$phi, xlab = "Min underdispersion = 0", ylab = "Min underdispersion = .5",
     xlim = c(0, 1.0), ylim = c(0, 1.0), type = "n")
underdispersedTerms <- sample(which(wf2a$phi < 1.0), 5)
which(featnames(ie2010dfm) %in% names(topfeatures(ie2010dfm, 20)))
text(wf2a$phi, wf2b$phi, wf2a$features,
     cex = .8, xlim = c(0, 1.0), ylim = c(0, 1.0), col = "grey90")
text(wf2a$phi['underdispersedTerms'], wf2b$phi['underdispersedTerms'],
     wf2a$features['underdispersedTerms'],
     cex = .8, xlim = c(0, 1.0), ylim = c(0, 1.0), col = "black")
if (require(austin)) {
    wf_austin <- austin::wordfish(quanteda::as.wfm(ie2010dfm), dir = c(6,5))
    cor(wf1$theta, wf_austin$theta)
}
## End(Not run)
```

`textmodel_wordscores` *Wordscores text model*

Description

`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.

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.

Author(s)

Kenneth Benoit

References

Laver, Michael, Kenneth R Benoit, and John Garry. 2003. "Extracting Policy Positions From Political Texts Using Words as Data." *American Political Science Review* 97(02): 311-31

Beauchamp, N. 2012. "Using Text to Scale Legislatures with Uninformative Voting." New York University Mimeo.

Martin, L W, and G Vanberg. 2007. "A Robust Transformation Procedure for Interpreting Political Text." *Political Analysis* 16(1): 93-100.

See Also

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

Examples

```
(ws <- textmodel_wordscores(data_dfm_lbgexample, c(seq(-1.5, 1.5, .75), NA)))
summary(ws)
coef(ws)
predict(ws)
predict(ws, rescaling = "lbg")
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

```
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

```
# 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)
```

---

textplot_network *Plot a network of feature co-occurrences*

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 = "#4D4D4D", 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 highest frequency.
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) %>%
    tokens(remove_punct = TRUE) %>%
    tokens_tolower() %>%
    tokens_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

```
## 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
ca <- 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

```
textplot_wordcloud(x, min_size = 0.5, max_size = 4, min_count = 3,
  max_words = 500, color = "darkblue", font = NULL, adjust = 0,
  rotation = 0.1, random_order = FALSE, random_color = FALSE,
  ordered_color = FALSE, labelcolor = "gray20", labelsize = 1.5,
  labeloffset = 0, fixed_aspect = TRUE, ..., comparison = FALSE)
```

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`	ajust sizes of words by a constant. Useful for non-Engish 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 `compariosn=TRUE`.
`labelsize`	size of group labels. Only used when `compariosn=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 wordclound 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

```
# 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("#1F78B4", 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"))
```

---

textplot_xray *Plot the dispersion of key word(s)*

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

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

Arguments

...	any number of kwic class objects

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

```
## 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", "$1or", "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

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

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 =` 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 kth element of c is 1 if the kth word in z is equal to the kth 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 $c(x, z_r)$ across all expressions z_r in a corpus of text, and let n_i, for $i = 1, \ldots, M$, denote the number of the $c(x, z_r)$ 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.

λ: The K-way interaction parameter in the saturated loglinear model fitted to the n_i. It can be calculated as

$$\lambda = \sum_{i=1}^{M} (-1)^{K-b_i} * log n_i$$

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:

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

Value

`textstat_collocations` returns a data.frame of collocations and their scores and statistics. This consists of the collocations, their counts, length, and λ 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

References

Blaheta, D., & Johnson, M. (2001). Unsupervised learning of multi-word verbs. Presented at the ACLEACL Workshop on the Computational Extraction, Analysis and Exploitation of Collocations.

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\\-]{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_dist` *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_dist(x, selection = NULL, margin = c("documents", "features"),
  method = "euclidean", upper = FALSE, diag = FALSE, p = 2)

textstat_simil(x, selection = NULL, margin = c("documents", "features"),
  method = "correlation", upper = FALSE, diag = FALSE)
```

Arguments

`x`	a dfm object
`selection`	a valid index for document or feature names 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
`diag`	whether the diagonal of the distance matrix should be recorded
`p`	The power of the Minkowski distance.

Details

`textstat_dist` options are: `"euclidean"` (default), `"chisquared"`, `"chisquared2"`, `"hamming"`, `"kullback"`. `"manhattan"`, `"maximum"`, `"canberra"`, and `"minkowski"`.

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

Value

`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.

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")`.

Author(s)

Kenneth Benoit, Haiyan Wang

References

The "chisquared" metric is from Legendre, P., & Gallagher, E. D. (2001). "Ecologically meaningful transformations for ordination of species data". *Oecologia*, 129(2), 271–280. doi.org/10.1007/s004420100716

The "chisquared2" metric is the "Quadratic-Chi" measure from Pele, O., & Werman, M. (2010). "The Quadratic-Chi Histogram Distance Family". In *Computer Vision – ECCV 2010* (Vol. 6312, pp. 749–762). Berlin, Heidelberg: Springer, Berlin, Heidelberg. doi.org/10.1007/978-3-642-15552-9_54.

"hamming" is $\sum x \neq y$).

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

$$\sum P(x) * log(P(x)/p(y))$$

All other measures are described in the **proxy** package.

See Also

textstat_dist, as.list.dist, dist

Examples

```
# create a dfm from inaugural addresses from Reagan onwards
presDfm <- dfm(corpus_subset(data_corpus_inaugural, Year > 1990),
               remove = stopwords("english"), stem = TRUE, remove_punct = TRUE)

# distances for documents
(d1 <- textstat_dist(presDfm, margin = "documents"))
as.matrix(d1)

# distances for specific documents
textstat_dist(presDfm, "2017-Trump", margin = "documents")
textstat_dist(presDfm, "2005-Bush", margin = "documents", method = "jaccard")
(d2 <- textstat_dist(presDfm, c("2009-Obama" , "2013-Obama"), margin = "documents"))
as.list(d1)

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

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

# compute some term similarities
s2 <- textstat_simil(pres_dfm, c("fair", "health", "terror"), method = "cosine",
                     margin = "features")
head(as.matrix(s2), 10)
as.list(s2, n = 8)
```

`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(remove_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() +
    facet_wrap(~ group, scales = "free") +
    coord_flip() +
    scale_x_continuous(breaks = nrow(freq_weight):1,
                       labels = freq_weight$feature) +
    labs(x = NULL, y = "Relative frequency")
```

`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

```
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 $G2$ 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

Bondi, Marina, and Mike Scott, eds. 2010. *Keyness in Texts*. Amsterdam, Philadelphia: John Benjamins, 2010.

Stubbs, Michael. 2010. "Three Concepts of Keywords". In *Keyness in Texts*, Marina Bondi and Mike Scott, eds. pp21–42. Amsterdam, Philadelphia: John Benjamins.

Scott, M. & Tribble, C. 2006. *Textual Patterns: keyword and corpus analysis in language education*. Amsterdam: Benjamins, p. 55.

Dunning, Ted. 1993. "Accurate Methods for the Statistics of Surprise and Coincidence", *Computational Linguistics*, Vol 19, No. 1, pp. 61-74.

Examples

```
# 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 preseidents
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

```
textstat_lexdiv(x, measure = c("all", "TTR", "C", "R", "CTTR", "U", "S",
  "Maas"), log.base = 10, ...)
```

Arguments

x	an input object, such as a document-feature matrix object
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 formulae, N refers to the total number of tokens, and V to the number of types:

`"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 cited in Tweedie & Baayen, 1998) is calculated by:

$$K = 10^4 \times \frac{(\sum_{X=1}^{X} f_X X^2) - N}{N^2}$$

where N is the number of tokens, X is a vector with the frequencies of each type, and f_X is the frequencies for each X.

`"Maas"`: Maas' indices (a, $\log V_0$ & $\log {}_e V_0$):

$$a^2 = \frac{\log N - \log V}{\log N^2}$$

$$\log V_0 = \frac{\log V}{\sqrt{1 - \frac{\log V}{\log N}^2}}$$

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 **koRpus** package.

References

Covington, M.A. & McFall, J.D. (2010). Cutting the Gordian Knot: The Moving-Average Type-Token Ratio (MATTR). *Journal of Quantitative Linguistics*, 17(2), 94–100.

Maas, H.-D., (1972). \"Uber den Zusammenhang zwischen Wortschatzumfang und L\"ange eines Textes. *Zeitschrift f\"ur Literaturwissenschaft und Linguistik*, 2(8), 73–96.

McCarthy, P.M. & Jarvis, S. (2007). vocd: A theoretical and empirical evaluation. *Language Testing*, 24(4), 459–488.

McCarthy, P.M. & Jarvis, S. (2010). MTLD, vocd-D, and HD-D: A validation study of sophisticated approaches to lexical diversity assessment. *Behaviour Research Methods*, 42(2), 381–392.

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

Tweedie. F.J. & Baayen, R.H. (1998). How Variable May a Constant Be? Measures of Lexical Richness in Perspective. *Computers and the Humanities*, 32(5), 323–352.

Examples

```
mydfm <- dfm(corpus_subset(data_corpus_inaugural, Year > 1980), verbose = FALSE)
(result <- textstat_lexdiv(mydfm, c("CTTR", "TTR", "U")))
cor(textstat_lexdiv(mydfm, "all")[,-1])
```

`textstat_readability` *Calculate readability*

Description

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

Usage

```
textstat_readability(x, measure = c("all", "ARI", "ARI.simple", "Bormuth",
  "Bormuth.GP", "Coleman", "Coleman.C2", "Coleman.Liau", "Coleman.Liau.grade",
  "Coleman.Liau.short", "Dale.Chall", "Dale.Chall.old", "Dale.Chall.PSK",
  "Danielson.Bryan", "Danielson.Bryan.2", "Dickes.Steiwer", "DRP", "ELF",
  "Farr.Jenkins.Paterson", "Flesch", "Flesch.PSK", "Flesch.Kincaid", "FOG",
  "FOG.PSK", "FOG.NRI", "FORCAST", "FORCAST.RGL", "Fucks", "Linsear.Write",
  "LIW", "nWS", "nWS.2", "nWS.3", "nWS.4", "RIX", "Scrabble", "SMOG", "SMOG.C",
  "SMOG.simple",      "SMOG.de", "Spache", "Spache.old", "Strain",
 "Traenkle.Bailer", "Traenkle.Bailer.2", "Wheeler.Smith", "meanSentenceLength",
  "meanWordSyllables"), remove_hyphens = TRUE, min_sentence_length = 1,
  max_sentence_length = 10000, ...)
```

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`.
`...`	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("Readability zero one.  Ten, Eleven.", "The cat in a dilapidated tophat.")
textstat_readability(txt, "Flesch.Kincaid")
textstat_readability(txt, c("FOG", "FOG.PSK", "FOG.NRI"))
inaugReadability <- textstat_readability(data_corpus_inaugural, "all")
cor(inaugReadability[,-1])

textstat_readability(data_corpus_inaugural, measure = "Flesch.Kincaid")
inaugReadability <- textstat_readability(data_corpus_inaugural, "all")
cor(inaugReadability[,-1])
```

---

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, "\
	"fastestword" dumbest, but fastest, word tokenization method, calls stri_split_fixed(x, " ")
	"character" tokenization into individual characters
	"sentence" sentence segmenter, smart enough to handle some exceptions in English such as "Prof. Plum killed Mrs. Peacock." (but far from perfect).
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	remove separators and separator characters (spaces and variations of spaces, plus tab, newlines, and anything else in the Unicode "separator" category) when remove_punct=FALSE. 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). Note that if what = "word" and remove_punct = TRUE, then remove_separators has no effect. Use carefully.

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 and 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".
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.
...	additional arguments not used

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("Ha!", 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 lowecasing 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!
txt <- "Repo https://githib.com/kbenoit/quanteda, and www.stackoverflow.com."
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 = FALSE, what = "fasterword")


## MORE COMPARISONS
txt <- "#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://textasdata.com", remove_url = FALSE)
#tokens("great website http://textasdata.com", remove_url = TRUE)

txt <- c(text1="This is $10 in 999 different ways,\n up and down; left and right!",
       text2="@kenbenoit working: on #quanteda 2day\t4ever, http://textasdata.com?page=123.")
tokens(txt, verbose = TRUE)
tokens(txt, remove_numbers = TRUE, remove_punct = TRUE)
tokens(txt, remove_numbers = FALSE, remove_punct = TRUE)
tokens(txt, remove_numbers = TRUE, remove_punct = FALSE)
tokens(txt, remove_numbers = FALSE, remove_punct = FALSE)
tokens(txt, remove_numbers = FALSE, remove_punct = FALSE, remove_separators = FALSE)
tokens(txt, remove_numbers = TRUE, remove_punct = TRUE, remove_url = TRUE)

# character level
tokens("Great website: http://textasdata.com?page=123.", what = "character")
tokens("Great website: http://textasdata.com?page=123.", what = "character",
         remove_separators = FALSE)

# sentence level
tokens(c("Kurt Vongeut said; only assholes use semi-colons.",
           "Today is Thursday in Canberra:  It is yesterday in London.",
           "Today is Thursday in Canberra:  \nIt is yesterday in London.",
           "To be?  Or\nnot to be?"),
          what = "sentence")
tokens(data_corpus_inaugural[c(2,40)], what = "sentence")
```

```
# removing features (stopwords) from tokenized texts
txt <- char_tolower(c(mytext1 = "This is a short test sentence.",
                      mytext2 = "Short.",
                      mytext3 = "Short, shorter, and shortest."))
tokens(txt, remove_punct = TRUE)
tokens_remove(tokens(txt, remove_punct = TRUE), stopwords("english"))

# ngram tokenization
tokens(txt, remove_punct = TRUE, ngrams = 2)
tokens(txt, remove_punct = TRUE, ngrams = 2, skip = 1, concatenator = " ")
tokens(txt, remove_punct = TRUE, ngrams = 1:2)
# removing features from ngram tokens
tokens_remove(tokens(txt, remove_punct = TRUE, ngrams = 1:2), stopwords("english"))
```

`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 valuetype 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 valuetype = "regex"
(cw3 <- tokens_compound(mytoks, mydict1, valuetype = "regex"))

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

```
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('free*', 'libert*')))
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.

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(x, 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

Guthrie, D., B. Allison, W. Liu, and L. Guthrie. 2006. "A Closer Look at Skip-Gram Modelling."

Examples

```
# 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

```
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

Examples

```
toks <- tokens(data_corpus_irishbudget2010)

# lemmatization
infle <- c("foci", "focus", "focused", "focuses", "focusing", "focussed", "focusses")
lemma <- rep("focus", length(infle))
toks2 <- tokens_replace(toks, infle, lemma)
kwic(toks2, "focus*")

# stemming
type <- types(toks)
stem <- char_wordstem(type, "porter")
toks3 <- tokens_replace(toks, type, stem, case_insensitive = FALSE)
identical(toks3, tokens_wordstem(toks, "porter"))
```

---

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

```
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

```
## 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 reindex the types.

Usage

```
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

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

```
tokens_tortl(x)

char_tortl(x)
```

Arguments

x	the input object whose punctuation marks will be modified by the direction mark

tokens_wordstem *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

```
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

```
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

```
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

```
types(x)
```

Arguments

x	a tokens object

See Also

featnames

Examples

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

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