Package ‘quanteda’

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quanteda-package

An R package for the quantitative analysis of textual data

Description

Functions for creating and managing textual corpora, extracting features from textual data, and analyzing those features using quantitative methods.

Details

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. 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 very 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 Matrix package for sparse matrix objects, and computationally intensive processing (e.g. for tokens) handled in parallelized C++. 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.

Tools for working with dictionaries are one of quanteda’s principal strengths, and the package includes several core functions for preparing and applying dictionaries to texts, for example for lexicon-based sentiment analysis.

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 the quanteda.textmodels package’s functions for the "wordfish" and "Wordscores" models, or direct use with the ca package for correspondence analysis), or machine learning through a variety of other packages that take matrix or matrix-like inputs. quanteda includes functions for converting its core objects, but especially a dfm, into other formats so that these are easy to use with other analytic packages.

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;
- 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

https://github.com/quanteda/quanteda

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Coercion and checking methods for corpus objects

Description

Coercion functions to and from corpus objects, including conversion to a plain character object; and checks for whether an object is a corpus.

Usage

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

is.corpus(x)

as.corpus(x)

Arguments

x

object to be coerced or checked

use.names

logical; preserve (document) names if TRUE

... additional arguments used by specific methods

Value

as.character() returns the corpus as a plain character vector, with or without named elements.

is.corpus returns TRUE if the object is a corpus.

as.corpus() upgrades a corpus object to the newest format.

Note

as.character(x) where x is a corpus is equivalent to calling the deprecated texts(x).
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 and DocumentTermMatrix (from the tm package), 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, format = c("tidytext"), separator = " ", tolower = FALSE)

is.dictionary(x)
Arguments

- **x**: a dictionary-like object to be coerced or checked
- **format**: input format for the object to be coerced to a `dictionary`; current legal values are a data.frame with the fields `word` and `sentiment` (as per the `tidytext` package)
- **separator**: the character in between multi-word dictionary values. This defaults to " ".
- **tolower**: if TRUE, convert all dictionary values to lowercase

Value

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

`is.dictionary` returns TRUE if an object is a **quanteda dictionary**.

Examples

```r
## Not run:
data(sentiments, package = "tidytext")
as.dictionary(subset(sentiments, lexicon == "nrc"))
as.dictionary(subset(sentiments, lexicon == "bing"))
# to convert AFINN into polarities - adjust thresholds if desired
datafinn <- subset(sentiments, lexicon == "AFINN")
datafinn["sentiment"] <-
  with(datafinn,
    sentiment <- ifelse(score < 0, "negative",
      ifelse(score > 0, "positive", "netural"))
  )
with(datafinn, table(score, sentiment))
as.dictionary(datafinn)

dat <- data.frame(
  word = c("Great", "Horrible"),
  sentiment = c("positive", "negative")
)
as.dictionary(dat)
as.dictionary(dat, tolower = FALSE)

## 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.fcm

**Description**

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

**Usage**

```r
as.fcm(x)
```

**Arguments**

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

**Value**

as.fcm converts an input object into a fcm.

---

as.list.tokens

**Description**

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

**Usage**

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

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

is.tokens(x)

as.tokens(x, concatenator = "\_", ...)

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

x object to be coerced or checked

... additional arguments used by specific methods. For c.tokens, these are the tokens objects to be concatenated.

use.names logical; preserve names if TRUE. For as.character and unlist only.

concatenator character between multi-word expressions, default is the underscore character. See Details.

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

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.list returns a simple list 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.

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)
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

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

Arguments

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

Examples

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

as.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

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

Arguments

- `x`: a dictionary object

Value

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

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

## End(Not run)
```

### bootstrap_dfm

**Bootstrap a dfm**

Create an array of resampled dfms.

#### Usage

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

#### Arguments

- `x`: a character or corpus object
- `n`: number of resamples
- `...`: additional arguments passed to dfm()
- `verbose`: if TRUE print status messages

#### Details

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

#### Value

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

#### Author(s)

Kenneth Benoit
Examples

```r
# bootstrapping from the original text
set.seed(10)
txt <- c(textone = "This is a sentence. Another sentence. Yet another.",
        texttwo = "Premiere phrase. Deuxieme phrase."
).bootstrap_dfm(txt, n = 3, verbose = TRUE)
```

---

**char_select**

Select or remove elements from a character vector

**Description**

These functions select or discard elements from a character vector. For convenience, the functions `char_remove` and `char_keep` are defined as shortcuts for `char_select(x, pattern, selection = "remove")` and `char_select(x, pattern, selection = "keep")`, respectively.

These functions make it easy to change, for instance, stopwords based on pattern matching.

**Usage**

```r
char_select(
  x,
  pattern,
  selection = c("keep", "remove"),
  valuetype = c("glob", "fixed", "regex"),
  case_insensitive = TRUE
)
```

```r
char_remove(x, ...)
```

```r
char_keep(x, ...)
```

**Arguments**

- `x` an input character vector
- `pattern` a character vector, list of character vectors, dictionary, or collocations object. 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` logical; if TRUE, ignore case when matching a pattern or dictionary values
- `...` additional arguments passed by `char_remove` and `char_keep` to `char_select`. Cannot include selection.
Value

a modified character vector

Examples

# character selection
mykeywords <- c("natural", "national", "denatured", "other")
char_select(mykeywords, "nat\*", valuetype = "glob")
char_select(mykeywords, "nat", valuetype = "regex")
char_select(mykeywords, c("nature\*", "other"))
char_select(mykeywords, c("nature\*", "other"), selection = "remove")

# character removal
char_remove(letters[1:5], c("a", "c", "x"))
words <- c("any", "and", "Anna", "as", "announce", "but")
char_remove(words, "an\*")
char_remove(words, "an\*", case_insensitive = FALSE)
char_remove(words, "^\*n.*$", valuetype = "regex")

# remove some of the system stopwords
stopwords("en", source = "snowball")[1:6]
stopwords("en", source = "snowball")[1:6] %>%
  char_remove(c("me", "my\*"))

# character keep
char_keep(letters[1:5], c("a", "c", "x"))

---

char_tolower  

_Convert the case of character objects_

Description

char_tolower and char_toupper are replacements for base::tolower() and base::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)
Examples

```r
txt1 <- c(txt1 = "b A A", txt2 = "C C a b B")
char(tolower(txt1))
char(toupper(txt1))

# 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 quanteda objects to non-quanteda formats*

**Description**

Convert a quanteda **dfm** or **corpus** object to a format useable by other 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. For **corpus** objects, `convert` provides an easy way to make a corpus and its document variables into a data.frame.

**Usage**

```r
convert(x, to, ...)
```

### S3 method for class 'dfm'

```r
convert(  
  x,  
  to = c("lda", "tm", "stm", "austin", "topicmodels", "lsa", "matrix", "data.frame",
           "tripletlist"),  
  docvars = NULL,  
  omit_empty = TRUE,  
  docid_field = "doc_id",  
  ...  
)
```

### S3 method for class 'corpus'

```r
convert(x, to = c("data.frame", "json"), pretty = FALSE, ...)
```

**Arguments**

- `x` a **dfm** or **corpus** to be converted
- `to` target conversion format, one of:
  - "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. Note: The tm package version of as.TermDocumentMatrix() allows a weighting argument, which supplies a weighting function for TermDocumentMatrix(). Here the default is for term frequency weighting. If you want a different weighting, apply the weights after converting using one of the tm functions. For other available weighting functions from the tm package, see TermDocumentMatrix.

"stm" the format for the stm package

"austin" the wfm format from the austin package

"topicmodels" the "dm" format as used by the topicmodels package

"lsa" the "textmatrix" format as used by the lsa package

"data.frame" a data.frame of without row.names, in which documents are rows, and each feature is a variable (for a dfm), or each text and its document variables form a row (for a corpus)

"json" (corpus only) convert a corpus and its document variables into JSON format, using the format described in jsonlite::toJSON()

"tripletlist" a named "triplet" format list consisting of document, feature, and frequency

... unused directly
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. Only affects the "stm" format.

omit_empty logical; if TRUE, omit empty documents and features from the converted dfm. This is required for some formats (such as STM) that do not accept empty documents. Only used when to = "lda" or to = "topicmodels". For to = "stm" format, omit_empty is always TRUE.
docid_field character; the name of the column containing document names used when to = "data.frame". Unused for other conversions.

pretty adds indentation whitespace to JSON output. Can be TRUE/FALSE or a number specifying the number of spaces to indent. See prettify()

Value

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

Examples

```r
## convert a dfm
toks <- corpus_subset(data_corpus_inaugural, Year > 1970) %>%
tokens()
dfmat1 <- dfm(toks)

# austin's wfm format
identical(dim(dfmat1), dim(convert(dfmat1, to = "austin")))
```
# 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 text_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 meta information.
- a corpus object.
Usage

corpus(x, ...)

## S3 method for class 'corpus'
corpus(
  x,
  docnames = quanteda::docnames(x),
  docvars = quanteda::docvars(x),
  meta = quanteda::meta(x),
  ...
)

## S3 method for class 'character'
corpus(
  x,
  docnames = NULL,
  docvars = NULL,
  meta = list(),
  unique_docnames = TRUE,
  ...
)

## S3 method for class 'data.frame'
corpus(
  x,
  docid_field = "doc_id",
  text_field = "text",
  meta = list(),
  unique_docnames = TRUE,
  ...
)

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

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

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
meta

A named list that will be added to the corpus as corpus-level, user meta-data. This can later be accessed or updated using meta().

unique_docnames

logical; if TRUE, enforce strict uniqueness in docnames; otherwise, rename duplicated docnames using an added serial number, and treat them as segments of the same document.

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 and the $ operator for accessing or assigning docvars. For details, see [.corpus()]

Value

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

For quanteda >= 2.0, this is a specially classed character vector. It has many additional attributes but you should not access these attributes directly, especially if you are another package author. 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. Using the accessor and replacement functions ensures that future code to manipulate corpus objects will continue to work.

See Also

corpus, docvars(), meta(), as.character.corpus(), 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_group

Combine documents in corpus by a grouping variable

Description

Combine documents in a corpus object by a grouping variable, by concatenating their texts in the order of the documents within each grouping variable.

Usage

```r
corpus_group(x, groups = docid(x), fill = FALSE, concatenator = " ")
```

Arguments

- `x`: corpus object
groups grouping variable for sampling, equal in length to the number of documents. This will be evaluated in the docvars data.frame, so that docvars may be referred to by name without quoting. This also changes previous behaviours for groups. See news(Version >= "3.0", package = "quanteda") 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 object. This will result in a new "document" with empty content for levels not observed, but for which an empty document may be needed. If groups is a factor of dates, for instance, then fill = TRUE ensures that the new object will consist of one new "document" by date, regardless of whether any documents previously existed with that date. Has no effect if the groups variable(s) are not factors.

concatenator the concatenation character that will connect the grouped documents.

Value

a corpus object whose documents are equal to the unique group combinations, and whose texts are the concatenations of the texts by group. Document-level variables that have no variation within groups are saved in docvars. Document-level variables that are lists are dropped from grouping, even when these exhibit no variation within groups.

Examples

corp <- 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")))
corpus_group(corp, groups = grp)
corpus_group(corp, groups = c(1, 1, 2, 2))
corpus_group(corp, groups = factor(c(1, 1, 2, 2), levels = 1:3))

# with fill
corpus_group(corp, groups = factor(c(1, 1, 2, 2), levels = 1:3), fill = TRUE)

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

```r
# simple example
corp1 <- 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)))
summary(corp1)
summary(corpus_reshape(corp1, to = "sentences"))

# example with inaugural corpus speeches
(corp2 <- corpus_subset(data_corpus_inaugural, Year>2004))
corp2para <- corpus_reshape(corp2, to = "paragraphs")
corp2para
summary(corp2para, 50, showmeta = TRUE)
## Note that Bush 2005 is recorded as a single paragraph because that text
## used a single \n to mark the end of a paragraph.
```

---

**corpus_sample**

Randomly sample documents from a corpus

Description

Take a random sample of documents of the specified size from a corpus, with or without replacement, optionally by grouping variables or with probability weights.

Usage

```r
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; when used with by, the number to select from each group or a vector equal in length to the number of groups defining the samples to be chosen in each category of by. By defining a size larger than the number of documents, it is possible to oversample when replace = TRUE.
- **replace**: if TRUE, sample with replacement
- **prob**: a vector of probability weights for obtaining the elements of the vector being sampled. May not be applied when by is used.
- **by**: optional grouping variable for sampling. This will be evaluated in the docvars data.frame, so that docvars may be referred to by name without quoting. This also changes previous behaviours for by. See news(Version >= "2.9", package = "quanteda") for details.

Value

A corpus object (re)sampled on the documents, containing the document variables for the documents sampled.

Examples

```r
set.seed(123)
# sampling from a corpus
summary(corpus_sample(data_corpus_inaugural, size = 5))
summary(corpus_sample(data_corpus_inaugural, size = 10, replace = TRUE))

# sampling with by
corp <- data_corpus_inaugural
corp$century <- paste(floor(corp$Year / 100) + 1)
corp$century <- paste0(corp$century, ifelse(corp$century < 21, "th", "st"))
corpus_sample(corp, size = 2, by = century) %>% summary()
# needs drop = TRUE to avoid empty interactions

# oversampling
corpus_sample(corp, size = 5, replace = TRUE)
```

```r
# sampling sentences by document
corp <- corpus(c(one = "Sentence one. Sentence two. Third sentence.",
  two = "First sentence, doc2. Second sentence, doc2.")
  docvars = data.frame(var1 = c("a", "a"), var2 = c(1, 2)))
corpus_reshape(corp, to = "sentences") %>%
corpus_sample(replace = TRUE, by = docid(.))
```
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

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

```r
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, or collocations object. 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**: logical; if TRUE, ignore case when matching a pattern or dictionary values
- **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)
**corpus_segment**

- **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

```r
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
corp1 <- 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."))
corpseg1 <- corpus_segment(corp1, pattern = "##*")
cbind(corpseg1, docvars(corpseg1))

# segmenting a transcript based on speaker identifiers
corp2 <- corpus("Mr. Smith: Text.\nMrs. Jones: More text.\nMr. Smith: I’m speaking, again.")
corpseg2 <- corpus_segment(corp2, pattern = '\b[A-Z].+\s[A-Z][a-z]+:',
valuetype = "regex")
cbind(corpseg2, docvars(corpseg2))

# segmenting a corpus using crude end-of-sentence segmentation
corpseg3 <- corpus_segment(corp1, pattern = ".", valuetype = "fixed",
pattern_position = "after", extract_pattern = FALSE)
cbind(corpseg3, docvars(corpseg3))

## 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}\\n\\n", 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

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, drop_docid = TRUE, ...)

Arguments

x corpus object to be subsetted
subset logical expression indicating the documents to keep: missing values are taken as false
drop_docid if TRUE, docid for documents are removed as the result of subsetting.
... 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"))

corpus_trim

Remove sentences based on their token lengths or a pattern match

Description

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

Usage

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

Arguments

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

Value

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

Examples

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

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

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

---

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

Description

This is a long paragraph (2,914 characters) of text taken from a debate on Joe Higgins, delivered December 8, 2011.
**data_char_ukimmig2010**

**Usage**

data_char_sampletext

**Format**

character vector with one element

**Source**


**Examples**

tokens(data_char_sampletext, remove_punct = TRUE)

---

**data_char_ukimmig2010**  *Immigration-related sections of 2010 UK party manifestos*

**Description**

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

**Usage**

data_char_ukimmig2010

**Format**

A named character vector of plain ASCII texts

**Examples**

data_corpus_ukimmig2010 <-
corpus(data_char_ukimmig2010,
docvars = data.frame(party = names(data_char_ukimmig2010)))
summary(data_corpus_ukimmig2010, showmeta = TRUE)
**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)
- Party factor; name of the President’s political party

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

**Source**

**Examples**
```r
# some operations on the inaugural corpus
summary(data_corpus_inaugural)
head(docvars(data_corpus_inaugural), 10)
```
data_dfm_lbgexample

**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**


---

data_dictionary_LSD2015

**Description**

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

**Usage**

data_dictionary_LSD2015

**Lexicoder Sentiment Dictionary (2015)**
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 https://www.snsoroka.com/data-lexicoder/.

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


Examples

```r
# simple example
txt <- "This aggressive policy will not win friends."

tokens_lookup(tokens(txt), dictionary = data_dictionary_LSD2015, exclusive = FALSE)
## tokens from 1 document.
## text1 :
## [1] "This" "NEGATIVE" "policy" "will" "NEG_POSITIVE" "POSITIVE" "POSITIVE" "."
```
dfm

Create a document-feature matrix

Description

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

Usage

```r
dfm(x, tolower = TRUE, remove_padding = FALSE, verbose = quanteda_options("verbose"), ...)
```

Arguments

- **x**
  - a tokens or dfm object
- **tolower**
  - convert all features to lowercase
- **remove_padding**
  - logical: if TRUE, remove the "pads" left as empty tokens after calling `tokens()` or `tokens_remove()` with padding = TRUE
- **verbose**
  - display messages if TRUE
- ... not used directly

Value

- a dfm object
Changes in version 3

In quanteda v3, many convenience functions formerly available in dfm() were deprecated. Formerly, dfm() could be called directly on a character or corpus object, but we now steer users to tokenise their inputs first using tokens(). Other convenience arguments to dfm() were also removed, such as select, dictionary, thesaurus, and groups. All of these functions are available elsewhere, e.g. through dfm_group(). See news(Version >= "2.9", package = "quanteda") for details.

See Also
dfm_select(), dfm

Examples

```r
## for a corpus
toks <- data_corpus_inaugural %>%
corpus_subset(Year > 1980) %>%
tokens()
dfm(toks)

# removal options
toks <- tokens(c("a b c", "A B C D")) %>%
tokens_remove("b", padding = TRUE)
toks
dfm(toks)
dfm(toks) %>%
dfm_remove(pattern = "") # remove "pads"

# preserving case
dfm(toks, tolower = FALSE)
```

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)
dfm_compress

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.

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

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

# compress an fcm
fcmat1 <- 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(fcmat1)

txt <- c("The fox JUMPED over the dog.",
         "The dog jumped over the fox.")
toks <- tokens(txt, remove_punct = TRUE)
fcmat2 <- fcm(toks, context = "document")
colnames(fcmat2) <- rownames(fcmat2) <- tolower(colnames(fcmat2))
colnames(fcmat2)[5] <- rownames(fcmat2)[5] <- "fox"
fcmat2
fcm_compress(fcmat2)
dfm_group

Combine documents in a dfm by a grouping variable

Description

Combine documents in a dfm by a grouping variable, by summing the cell frequencies within group and creating new "documents" with the group labels.

Usage

dfm_group(x, groups = docid(x), fill = FALSE, force = FALSE)

Arguments

x

a dfm

groups

grouping variable for sampling, equal in length to the number of documents. This will be evaluated in the docvars data.frame, so that docvars may be referred to by name without quoting. This also changes previous behaviours for groups. See news(Version >= "3.0", package = "quanteda") 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 object. This will result in a new "document" with empty content for levels not observed, but for which an empty document may be needed. If groups is a factor of dates, for instance, then fill = TRUE ensures that the new object will consist of one new "document" by date, regardless of whether any documents previously existed with that date. Has no effect if the groups variable(s) are not factors.

force

logical; if TRUE, group by summing existing counts, even if the dfm has been weighted. This can result in invalid sums, such as adding log counts (when a dfm has been weighted by "logcount" for instance using dfm_weight()). Not needed when the term weight schemes "count" and "prop".

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. Document-level variables that are lists are dropped from grouping, even when these exhibit no variation within groups.

Examples

corp <- 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")))
dfm <- dfm(tokens(corp))
dfm_group(dfm, groups = grp)
dfm_group(dfm, groups = c(1, 1, 2, 2))

# with fill = TRUE
dfm_lookup

```r
dfm_group(dfmat, fill = TRUE,
          groups = factor(c("A", "A", "B", "C"), levels = LETTERS[1:4]))
```

### dfm_lookup

**Apply a dictionary to a dfm**

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

<table>
<thead>
<tr>
<th>Usage</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>dfm_lookup(</code></td>
</tr>
<tr>
<td>x, dictionary, levels = 1:5, exclusive = TRUE, valuetype = c(&quot;glob&quot;, &quot;regex&quot;, &quot;fixed&quot;), case_insensitive = TRUE, capkeys = !exclusive, nomatch = NULL, verbose = quanteda_options(&quot;verbose&quot;)</td>
</tr>
<tr>
<td>)</td>
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<table>
<thead>
<tr>
<th>Arguments</th>
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<tbody>
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<td>exclusive</td>
</tr>
<tr>
<td>valuetype</td>
</tr>
<tr>
<td>case_insensitive</td>
</tr>
<tr>
<td>capkeys</td>
</tr>
<tr>
<td>nomatch</td>
</tr>
<tr>
<td>verbose</td>
</tr>
</tbody>
</table>
Note

If using \texttt{dfm\_lookup} with dictionaries containing multi-word values, matches will only occur if the features themselves are multi-word or formed from n-grams. A better way to match dictionary values that include multi-word patterns is to apply \texttt{tokens\_lookup()} to the tokens, and then construct the dfm.

See Also

dfm\_replace

Examples

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

dfmat

# glob format
dfm\_lookup(dfmat, dict, valuetype = "glob")
dfm\_lookup(dfmat, dict, valuetype = "glob", case\_insensitive = FALSE)

# regex v. glob format: note that "united\_states" is a regex match for "tax*"
dfm\_lookup(dfmat, dict, valuetype = "glob")
dfm\_lookup(dfmat, dict, valuetype = "regex", case\_insensitive = TRUE)

# fixed format: no pattern matching
dfm\_lookup(dfmat, dict, valuetype = "fixed")
dfm\_lookup(dfmat, dict, valuetype = "fixed", case\_insensitive = FALSE)

# show unmatched tokens
dfm\_lookup(dfmat, dict, nomatch = ".\_UNMATCHED")
```

\textbf{dfm\_match}

\textit{Match the feature set of a dfm to given feature names}

Description

Match the feature set of a \texttt{dfm} to a specified vector of feature names. For existing features in \texttt{x} for which there is an exact match for an element of \texttt{features}, these will be included. Any features in \texttt{x} not \texttt{features} will be discarded, and any feature names specified in \texttt{features} but not found in \texttt{x} will be added with all zero counts.
Usage

dfm_match(x, features)

Arguments

x  a dfm
features  character; the feature names to be matched in the output dfm

Details

Selecting on another dfm’s featnames() 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().

Value

A dfm whose features are identical to those specified in features.

Note

Unlike dfm_select(), this function will add feature names not already present in x. It also provides only fixed, case-sensitive matches. For more flexible feature selection, see dfm_select().

See Also

dfm_select()

Examples

# matching a dfm to a feature vector
dfm_match(dfm(""), letters[1:5])
dfm_match(data_dfm_lbgexample, c("A", "B", "Z"))
dfm_match(data_dfm_lbgexample, c("B", "newfeat1", "A", "newfeat2"))

# matching one dfm to another
txt <- c("This is text one", "The second text", "This is text three")
(dfmat1 <- dfm(tokens(txt[1:2])))
(dfmat2 <- dfm(tokens(txt[2:3])))
(dfmat3 <- dfm_match(dfmat1, featnames(dfmat2)))
setequal(featnames(dfmat2), featnames(dfmat3))

---

dfm_replace

Replace features in dfm

Description

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

Usage

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

Arguments

x
  dfm whose features will be replaced

pattern
  a character vector. 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.

case_insensitive
  logical; if TRUE, ignore case when matching a pattern or dictionary values

verbose
  print status messages if TRUE

Examples

dfmat1 <- dfm(data_corpus_inaugural)

# lemmatization

taxwords <- c("tax", "taxing", "taxed", "taxed", "taxation")
lemma <- rep("TAX", length(taxwords))
featnames(dfm_select(dfmat1, pattern = taxwords))
dfmat2 <- dfm_replace(dfmat1, pattern = taxwords, replacement = lemma)
featnames(dfm_select(dfmat2, pattern = taxwords))

# stemming

feat <- featnames(dfmat1)
featstem <- char_wordstem(feat, "porter")
dfmat3 <- dfm_replace(dfmat1, pattern = feat, replacement = featstem, case_insensitive = FALSE)
identical(dfmat3, dfm_wordstem(dfmat1, "porter"))

dfm_sample

Randomly sample documents from a dfm

Description

Take a random sample of documents of the specified size from a dfm, with or without replacement,
optionally by grouping variables or with probability weights.

Usage

dfm_sample(x, size = NULL, replace = FALSE, prob = NULL, by = NULL)
**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.

**Arguments**

- **x**  
  the dfm object whose documents will be sampled

- **size**  
  a positive number, the number of documents to select; when used with by, the number to select from each group or a vector equal in length to the number of groups defining the samples to be chosen in each category of by. By defining a size larger than the number of documents, it is possible to oversample when replace = TRUE.

- **replace**  
  if TRUE, sample with replacement

- **prob**  
  a vector of probability weights for obtaining the elements of the vector being sampled. May not be applied when by is used.

- **by**  
  optional grouping variable for sampling. This will be evaluated in the docvars data.frame, so that docvars may be referred to by name without quoting. This also changes previous behaviours for by. See news(Version >= "2.9", package = "quanteda") for details.

**Value**

a dfm object (re)sampled on the documents, containing the document variables for the documents sampled.

**Examples**

```r
set.seed(10)
dfmat <- dfm(tokens(c("a b c d", "a a c c d d", "a b b c")))
dfmat
dfm_sample(dfmat)
dfm_sample(dfmat, replace = TRUE)
```

```r
# by groups
dfmat <- dfm(tokens(data_corpus_inaugural[50:58]))
dfm_sample(dfmat, by = Party, size = 2)
```
Usage

dfm_select(
  x,
  pattern = NULL,
  selection = c("keep", "remove"),
  valuetype = c("glob", "regex", "fixed"),
  case_insensitive = TRUE,
  min_nchar = NULL,
  max_nchar = NULL,
  padding = FALSE,
  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, ...)

fcm_keep(x, ...)

Arguments

x the dfm or fcm object whose features will be selected

pattern a character vector, list of character vectors, dictionary, or collocations object. 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 value-type for details.

case_insensitive logical; if TRUE, ignore case when matching a pattern or dictionary values

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

padding if TRUE, record the number of removed tokens in the first column.
**dfm_select**

- **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.

For compatibility with earlier versions, when `pattern` is a `dfm` object and `selection = "keep"`, then this will be equivalent to calling `dfm_match()`. In this case, the following settings are always used: `case_insensitive = FALSE`, and `valuetype = "fixed"`. This functionality is deprecated, however, and you should use `dfm_match()` instead.

**Note**

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

**See Also**

- `dfm_match()`

**Examples**

```r
dfmat <- tokens(c("My Christmas was ruined by your opposition tax plan.",
"Does the United_States or Sweden have more progressive taxation?"))

dfm(tolower = FALSE)
dict <- dictionary(list(countries = c("United_States", "Sweden", "France"),
wordsEndingInY = c("by", "my"),
notintext = "blahblah"))
dfm_select(dfmat, pattern = dict)
dfm_select(dfmat, pattern = dict, case_insensitive = FALSE)
dfm_select(dfmat, pattern = c("s$", ".y"), selection = "keep", valuetype = "regex")
dfm_select(dfmat, pattern = c("s$", ".y"), selection = "remove", valuetype = "regex")
dfm_select(dfmat, pattern = stopwords("english"), selection = "keep", valuetype = "fixed")
dfm_select(dfmat, pattern = stopwords("english"), selection = "remove", valuetype = "fixed")

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

dfmat <- dfm(tokens(c("This is a document with lots of stopwords.",
"No if, and, or but about it: lots of stopwords.")))
dfm

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

dfmat <- dfm(data_corpus_inaugural)
head(dfmat)
head(dfm_sort(dfmat))
head(dfm_sort(dfmat, decreasing = FALSE, "both"))
\texttt{dfm\_subset}

\begin{tabular}{ll}
\textbf{Extract a subset of a dfm} & \\
\end{tabular}

\textbf{Description}

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

\textbf{Usage}

\begin{verbatim}
dfm_subset(x, subset, drop_docid = TRUE, ...)
\end{verbatim}

\textbf{Arguments}

- \texttt{x} \hspace{1cm} dfm object to be subsetted
- \texttt{subset} \hspace{1cm} logical expression indicating the documents to keep: missing values are taken as false
- \texttt{drop_docid} \hspace{1cm} if TRUE, docid for documents are removed as the result of subsetting.
- \texttt{...} \hspace{1cm} not used

\textbf{Details}

To select or subset features, see \texttt{dfm\_select()} instead.

When \texttt{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 \texttt{dfm\_select()} where pattern is a dfm: that function matches features, while \texttt{dfm\_subset} will match documents.

\textbf{Value}

\texttt{dfm} object, with a subset of documents (and docvars) selected according to arguments

\textbf{See Also}

\texttt{subset.data.frame()}

\textbf{Examples}

\begin{verbatim}
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)))
dfm <- dfm(tokens(corp))
# selecting on a docvars condition
dfm_subset(dfm, grp > 1)
# selecting on a supplied vector
dfm_subset(dfm, c(TRUE, FALSE, TRUE, FALSE))
\end{verbatim}
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,
  force = FALSE,
  ...
)

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".
base: the base for the logarithms in the dfm_weight() and docfreq() calls; default is 10
force: logical; if TRUE, apply weighting scheme even if the dfm has been weighted before. This can result in invalid weights, such as as weighting by "prop" after applying "logcount", or after having grouped a dfm using dfm_group().
...: 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

Examples

dfmat1 <- as.dfm(data_dfm_lbgexample)
head(dfmat1[, 5:10])
head(dfm_tfidf(dfmat1)[, 5:10])
docfreq(dfmat1)[5:15]
head(dfm_weight(dfmat1)[, 5:10])

# replication of worked example from
# https://en.wikipedia.org/wiki/Tf-idf#Example_of_tf.80.93idf
dfmat2 <-
  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()
dfmat2
docfreq(dfmat2)
dfm_tfidf(dfmat2, scheme_tf = "prop") %>% round(digits = 2)

## Not run:
## comparison with tm
if (requireNamespace("tm")) {
  convert(dfmat2, to = "tm") %>% tm::weightTfIdf() %>% as.matrix()
  # same as:
  dfm_tfidf(dfmat2, 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).

**Details**

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

**Examples**

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

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

---

**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**

```r
dfm_trim(
x,
  min_termfreq = NULL,
  max_termfreq = NULL,
  termfreq_type = c("count", "prop", "rank", "quantile"),
  min_docfreq = NULL,
)```

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 interpreted. "count" sums the frequencies; "prop" divides the term frequencies by the total sum; "rank" is matched against the inverted ranking of features in terms of overall frequency, so that 1, 2, ... are the highest and second highest frequency features, and so on; "quantile" sets the cutoffs according to the quantiles (see `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 interpreted. "count" is the same as `[docfreq](x, scheme = "count"); "prop" divides the document frequencies by the total sum; "rank" is matched against the inverted ranking of document frequency, so that 1, 2, ... are the features with the highest and second highest document frequencies, and so on; "quantile" sets the cutoffs according to the quantiles (see `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

```
(dfmat <- dfm(data_corpus_inaugural[1:5]))

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

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

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

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

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

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

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

## End(Not run)

---

**dfm_weight**

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,
  smoothing = 0.5,
  force = FALSE
)
```
```r
dfm_smooth(x, smoothing = 1)
```

**Arguments**

- **x**: document-feature matrix created by `dfm`
- **scheme**: a label of the weight type:
  - **count** $t_{fij}$, 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 $t_{fij} / \sum_j t_{fij}$
  - **propmax** the proportion of the feature counts of the highest feature count in a document, $t_{fij} / \max_j t_{fij}$
  - **logcount** take the $1 + \log$ of each count, for the given base, or 0 if the count was zero: $1 + \log_{\text{base}}(t_{fij})$ if $t_{fij} > 0$, or 0 otherwise.
  - **boolean** recode all non-zero counts as 1
  - **augmented** equivalent to $k + (1 - k) \cdot \text{dfm\_weight}(x, "propmax")$
  - **logave** $(1 + \log$ of the counts$)/(1 + \log$ of the average count within document$)$, or
    $$\frac{1 + \log_{\text{base}} t_{fij}}{1 + \log_{\text{base}}(\sum_j t_{fij}/N_i)}$$
  - **logsmooth** log of the counts + smooth, or $t_{fij} + s$
- **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 for `dfm_smooth()` and 0.5 for `dfm_weight()`
- **force**: logical; if TRUE, apply weighting scheme even if the dfm has been weighted before. This can result in invalid weights, such as as weighting by "prop" after applying "logcount", or after having grouped a dfm using `dfm_group()`.

**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.
dictionary

Create a dictionary

Create a \texttt{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).
dictionary

Usage

dictionary(
  x,  
  file = NULL,  
  format = NULL,  
  separator = " ",  
  tolower = TRUE,  
  encoding = "utf-8"
)

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


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

See Also

as.dictionary(), as.list(), is.dictionary()

Examples

corp <- corpus_subset(data_corpus_inaugural, Year>1900)
dict <- dictionary(list(christmas = c("Christmas", "Santa", "holiday"),
opposition = c("Opposition", "reject", "notincorpus"),
taxing = "taxing",
taxation = "taxation",
taxregex = "tax*",
country = "america"))

head(dfm(tokens(corp), dictionary = dict))

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

# combine dictionaries
c(dict["christmas"], dict["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()))
dictlg <- dictionary(file = paste(td, "LaverGarry.cat", sep = "/"))
head(dfm(data_corpus_inaugural, dictionary = dictlg))

# import a LIWC formatted dictionary from http://www.moralfoundations.org
dictliwc <- dictionary(file = tf, format = "LIWC")
head(dfm(data_corpus_inaugural, dictionary = dictliwc))

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

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

**Usage**

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

**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
- `base`: the base with respect to which logarithms in the inverse document frequency weightings are computed; default is 10 (see Manning, Raghavan, and Schütze 2008, p123).
- `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
- `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.

**Value**

a numeric vector of document frequencies for each feature
References


Examples

```r
# replication of worked example from
dfmat2 <- 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()
dfmat2
docfreq(dfmat2)
docfreq(dfmat2, scheme = "inverse")
docfreq(dfmat2, scheme = "inverse", k = 1, smoothing = 1)
docfreq(dfmat2, scheme = "unary")
docfreq(dfmat2, scheme = "inversemax")
docfreq(dfmat2, scheme = "inverseprob")
```

---

doctime

*Get or set document names*

**Description**

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

**Usage**

```r
docnames(x)
docnames(x) <- value
docid(x)
segid(x)
```

**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. docnames can only be character, so any non-character value assigned to be a docname will be coerced to mode character.
docid returns an internal variable denoting the original "docname" from which a document came.
If an object has been reshaped (e.g. corpus_reshape() or segmented (e.g. corpus_segment()),
docid(x) returns the original docnames but segid(x) does the serial number of those segments within the original document.

Note

docid and segid are designed primarily for developers, not for end users. In most cases, you will want docnames instead. It is, however, the default for groups, so that documents that have been previously reshaped (e.g. corpus_reshape() or segmented (e.g. corpus_segment()) will be regrouped into their original docnames when groups = docid(x).

See Also

featnames()

Examples

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

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

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

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

corp <- corpus(c(textone = "This is a sentence. Another sentence. Yet another.",
texttwo = "Sentence 1. Sentence 2."))
corpsent <- corp %>%
    corpus_reshape(to = "sentences")
docnames(corpsent)

# docid
docid(corpsent)
docid(tokens(corpsent))
docid(dfm(tokens(corpsent)))

# segid
segid(corpsent)
docvars  

Get or set document-level variables

Description

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

Usage

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

## S3 method for class 'corpus'
x$name

## S3 replacement method for class 'corpus'
x$name <- value

## S3 method for class 'tokens'
x$name

## S3 replacement method for class 'tokens'
x$name <- value

## S3 method for class 'dfm'
x$name

## S3 replacement method for class 'dfm'
x$name <- 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` a vector of document variable values to be assigned to name
- `name` a literal character string specifying a single docvars name

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
Accessing or assigning docvars using the \$ operator

As of \texttt{quanteda} v2, it is possible to access and assign a docvar using the \$ operator. See Examples.

Note

Reassigning document variables for a \texttt{tokens} or \texttt{dfm} object is allowed, but discouraged. A better, more reproducible workflow is to create your docvars as desired in the \texttt{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 \texttt{tokens} or \texttt{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)
head(data_corpus_inaugural$President)

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

# accessing or assigning docvars for a corpus using "$"
data_corpus_inaugural$Year
data_corpus_inaugural$century <- floor(data_corpus_inaugural$Year / 100)
data_corpus_inaugural$century

# accessing or assigning docvars for tokens using "$"
toks <- tokens(corpus_subset(data_corpus_inaugural, Year <= 1805))
toks$Year
toks$Year <- 1991:1995
toks$Year
toks$nonexistent <- TRUE
docvars(toks)

# accessing or assigning docvars for a dfm using "$"
dfmat <- dfm(toks)
dfmat$Year
dfmat$Year <- 1991:1995
dfmat$Year
dfmat$nonexistent <- TRUE
docvars(dfmat)
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 = NULL, 
  ordered = FALSE, 
  tri = TRUE, 
  ... 
)

Arguments

x a 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 window
ordered if TRUE, count only the forward co-occurrences for each target token for bigram models, so that the i, j cell of the fcm is the number of times that token j occurs before the target token i within the window. Only makes sense for context = "window", and when ordered = TRUE, the argument tri has no effect.
tri if TRUE return only upper triangle (including diagonal). Ignored if ordered = TRUE.
... not used here
Details

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

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

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

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

is.fcm(x)
returns `TRUE` if and only if its x is an object of type `fcm`.

Author(s)

Kenneth Benoit (R), Haiyan Wang (R, C++), Kohei Watanabe (C++)

References


Examples

# see http://bit.ly/29b2zOA
toks1 <- tokens(c("A D A C E A D F E B A C E D"))
fcm(toks1, context = "window", window = 2)
fcm(toks1, context = "window", count = "weighted", window = 3)
fcm(toks1, context = "window", count = "weighted", window = 3,
weights = c(3, 2, 1), ordered = TRUE, tri = FALSE)

# with multiple documents
toks2 <- tokens(c("a a a b b c", "a a c e", "a c e f g"))
fcm(toks2, context = "document", count = "frequency")
fcm(toks2, context = "document", count = "boolean")
fcm(toks2, context = "window", window = 2)
txt3 <- c("The quick brown fox jumped over the lazy dog.",
           "The dog jumped and ate the fox.")
toks3 <- tokens(char_tolower(txt3), remove_punct = TRUE)
fcm(toks3, context = "document")
fcm(toks3, 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)

Kenneth Benoit

Examples

# with tri = FALSE
fcmat1 <- fcm(tokens(c("A X Y C B A", "X Y C A B B")), tri = FALSE)
rownames(fcmat1)[3] <- colnames(fcmat1)[3] <- "Z"
fcmat1
fcm_sort(fcmat1)

# with tri = TRUE
fcmat2 <- fcm(tokens(c("A X Y C B A", "X Y C A B B")), tri = TRUE)
rownames(fcmat2)[3] <- colnames(fcmat2)[3] <- "Z"
fcmat2
fcm_sort(fcmat2)
**featfreq**

*Compute the frequencies of features*

**Description**

For a **dfm** object, returns a frequency for each feature, computed across all documents in the dfm. This is equivalent to `colSums(x)`.

**Usage**

```r
featfreq(x)
```

**Arguments**

- `x` a dfm

**Value**

a (named) numeric vector of feature frequencies

**See Also**

`dfm_tfidf()`, `dfm_weight()`

**Examples**

```r
dfmat <- dfm(data_char_sampletext)
featfreq(dfmat)
```

---

**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**

```r
featnames(x)
```

**Arguments**

- `x` the dfm whose features will be extracted
Value

character vector of the feature labels

Examples

dfmat <- dfm(data_corpus_inaugural)

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

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

# contrast with descending total frequency order from topfeatures()
names(topfeatures(dfmat, 50))

index

Locate a pattern in a tokens object

Description

Locates a pattern within a tokens object, returning the index positions of the beginning and ending tokens in the pattern.

Usage

index(  
x,  
pattern,  
valuetype = c("glob", "regex", "fixed"),  
case_insensitive = TRUE  
)

is.index(x)

Arguments

x  
an input tokens object

pattern  
a character vector, list of character vectors, dictionary, or collocations object. 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  
logical; if TRUE, ignore case when matching a pattern or dictionary values
Value

a data.frame consisting of one row per pattern match, with columns for the document name, index positions from and to, and the pattern matched.

is.index returns TRUE if the object was created by index(); FALSE otherwise.

Examples

toks <- tokens(data_corpus_inaugural[1:8])
index(toks, pattern = "secure")
index(toks, pattern = c("secure", phrase("united states"))) %>% head()

is.collocations (Check if an object is collocations)

Description

Function to check if an object is a collocations object, created by quanteda.textstats::textstat_collocations().

Usage

is.collocations(x)

Arguments

x object to be checked

Value

TRUE if the object is of class collocations, FALSE otherwise

kwic (Locate keywords-in-context)

Description

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

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

```r
is.kwic(x)
```

```r
## S3 method for class 'kwic'
as.data.frame(x, ...)
```

Arguments

- `x` a character, corpus, or tokens object
- `pattern` a character vector, list of character vectors, dictionary, or collocations object. See pattern for details.
- `window` the number of context words to be displayed around the keyword
- `valuetype` the type of pattern matching: "glob" for "glob"-style wildcard expressions; "regex" for regular expressions; or "fixed" for exact matching. See valuetype for details.
- `separator` a character to separate words in the output
- `case_insensitive` logical; if TRUE, ignore case when matching a pattern or dictionary values
- `index` an index object to specify keywords
- `...` unused

Value

A kwic classed data.frame, with the document name (docname) and 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).

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.
See Also
  
  print-methods

Examples

# single token matching
	toks <- tokens(data_corpus_inaugural[1:8])
	kwic(toks, pattern = "secure\*", valuetype = "glob", window = 3)
	kwic(toks, pattern = "secur", valuetype = "regex", window = 3)
	kwic(toks, pattern = "security", valuetype = "fixed", window = 3)

# phrase matching
	kwic(toks, pattern = phrase("secur\* against"), window = 2)
	kwic(toks, pattern = phrase("war against"), valuetype = "regex", window = 2)

# use index
	idx <- index(toks, phrase("secur\* against"))
	kwic(toks, index = idx, window = 2)
	kw <- kwic(tokens(data_corpus_inaugural[1:20]), "provident\*")
	is.kwic(kw)
	is.kwic("Not a kwic")
	is.kwic(kw[, c("pre", "post")])

toks <- tokens(data_corpus_inaugural[1:8])
	kw <- kwic(toks, pattern = "secure\*", valuetype = "glob", window = 3)
	as.data.frame(kw)

meta

Get or set object metadata

Description

Get or set the object metadata in a corpus, tokens, dfm, or dictionary object. With the exception of
dictionaries, this will be corpus-level metadata.

Usage

meta(x, field = NULL, type = c("user", "object", "system", "all"))

meta(x, field = NULL) <- value

Arguments

x          an object for which the metadata will be read or set
field      metadata field name(s); if NULL (default), return all metadata names
type       "user" for user-provided corpus-level metadata; "system" for metadata set auto-
            matically when the corpus is created; or "all" for all metadata.
value      new value of the metadata field
Value

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

For `meta <-`, the corpus with the updated user-level metadata. Only user-level metadata may be assigned.

Examples

```r
meta(data_corpus_inaugural)
meta(data_corpus_inaugural, "source")
meta(data_corpus_inaugural, "citation") <- "Presidential Speeches Online Project (2014)."
meta(data_corpus_inaugural, "citation")
```

ndoc

**Count the number of documents or features**

Description

Get the number of documents or features in an object.

Usage

```r
ndoc(x)
nfeat(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()`.)

Value

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

See Also

`ntoken()`
Examples

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

# number of features
toks1 <- tokens(corpus_subset(data_corpus_inaugural, Year > 1980), remove_punct = FALSE)
toks2 <- tokens(corpus_subset(data_corpus_inaugural, Year > 1980), remove_punct = TRUE)
nfeat(dfm(toks1))
nfeat(dfm(toks2))
```

---

**nsentence**

*Count the number of sentences*

Description

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

Usage

```r
nsentence(x)
```

Arguments

- `x`: a character or corpus whose sentences will be counted

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

```r
# 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)
```
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)
nype(txt)
ntoken(char_tolower(txt)) # same
ntype(char_tolower(txt)) # fewer types
ntoken(char_tolower(txt), remove_punct = TRUE)
nype(char_tolower(txt), remove_punct = TRUE)

# with some real texts
**phrase**

Declare a pattern to be a sequence of separate patterns

### Description

Declares that a character expression consists of multiple patterns, separated by an element such as 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

```r
phrase(x, separator = " ")
as.phrase(x)
is.phrase(x)
```

### Arguments

- **x** character, dictionary, list, collocations, or tokens object; the compound patterns to be treated as a sequence separated by separator. For list, collocations, or tokens objects, use `as.phrase()`.
- **separator** character; the character in between the patterns. This defaults to " ". For `phrase()` only.

### Value

`phrase()` and `as.phrase()` return a specially classed list whose elements have been split into separate character (pattern) elements.

`is.phrase` returns TRUE if the object was created by `phrase()`, FALSE otherwise.

### See Also

`as.phrase()`
print-methods

Examples

# make phrases from characters
phrase(c("natural language processing"))
phrase(c("natural_language_processing", "text_analysis"), separator = ".")

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

# from a list
as.phrase(list(c("natural", "language", "processing")))

# from tokens
as.phrase(tokens("natural language processing"))

Description

Print method for quanteda objects. In each max_n* option, 0 shows none, and -1 shows all.

Usage

## S3 method for class 'corpus'
print(
x,
max_ndoc = quanteda_options("print_corpus_max_ndoc"),
max_nchar = quanteda_options("print_corpus_max_nchar"),
show_summary = quanteda_options("print_corpus_summary"),
...
)

## S4 method for signature 'dfm'
print(
x,
max_ndoc = quanteda_options("print_dfm_max_ndoc"),
max_nfeat = quanteda_options("print_dfm_max_nfeat"),
show_summary = quanteda_options("print_dfm_summary"),
...
)

## S4 method for signature 'dictionary2'
print(
x,
max_nkey = quanteda_options("print_dictionary_max_nkey"),
max_nval = quanteda_options("print_dictionary_max_nval"),
show_summary = quanteda_options("print_dictionary_summary"),
## S4 method for signature 'fcm'
print(
  x,
  max_nfeat = quanteda_options("print_dfm_max_nfeat"),
  show_summary = TRUE,
  ...
)

## S3 method for class 'kwic'
print(
  x,
  max_nrow = quanteda_options("print_kwic_max_nrow"),
  show_summary = quanteda_options("print_kwic_summary"),
  ...
)

## S3 method for class 'tokens'
print(
  x,
  max_ndoc = quanteda_options("print_tokens_max_ndoc"),
  max_ntoken = quanteda_options("print_tokens_max_ntoken"),
  show_summary = quanteda_options("print_tokens_summary"),
  ...
)

### Arguments

- **x** the object to be printed
- **max_ndoc** max number of documents to print; default is from the `print_*_max_ndoc` setting of `quanteda_options()`
- **max_nchar** max number of tokens to print; default is from the `print_corpus_max_nchar` setting of `quanteda_options()`
- **show_summary** print a brief summary indicating the number of documents and other characteristics of the object, such as docvars or sparsity.
- **...** not used
- **max_nfeat** max number of features to print; default is from the `print_dfm_max_nfeat` setting of `quanteda_options()`
- **max_nkey** max number of keys to print; default is from the `print_dictionary_max_max_nkey` setting of `quanteda_options()`
- **max_nval** max number of values to print; default is from the `print_dictionary_max_nval` setting of `quanteda_options()`
- **max_nrow** max number of documents to print; default is from the `print_kwic_max_nrow` setting of `quanteda_options()`
quanteda_options

max_n_token max number of tokens to print; default is from the \texttt{print_tokens\_max\_ntoken} setting of \texttt{quanteda\_options()}

See Also

\texttt{quanteda\_options()}

Examples

\begin{verbatim}
corp <- corpus(data_char\_ukimmig2010)
print(corp, max\_ndoc = 3, max\_nchar = 40)

toks <- tokens(corp)
print(toks, max\_ndoc = 3, max\_ntoken = 6)

dfm <- dfm(toks)
print(dfm, max\_ndoc = 3, max\_nfeat = 10)
\end{verbatim}

quanteda_options \hspace{1cm} \textit{Get or set package options for \texttt{quanteda}}

Description

Get or set global options affecting functions across \texttt{quanteda}.

Usage

\begin{verbatim}
quanteda_options(..., reset = \texttt{FALSE}, initialize = \texttt{FALSE})
\end{verbatim}

Arguments

\begin{verbatim}
... options to be set, as key-value pair, same as \texttt{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 \texttt{TRUE}, reset all \texttt{quanteda} options to their default values
initialize logical; if \texttt{TRUE}, reset only the \texttt{quanteda} options that are not already defined. Used for setting initial values when some have been defined previously, such as in \texttt{.Rprofile}.
\end{verbatim}

Details

Currently available options are:

\begin{verbatim}
verbose logical; if \texttt{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; defaults to \texttt{RcppParallel::defaultNumThreads()}
the number of threads can be changed only once in a session
\end{verbatim}
quanteda_options

print_dfm_max_ndoc, print_corpus_max_ndoc, print_tokens_max_ndoc integer; specify the number of documents to display when using the defaults for printing a dfm, corpus, or tokens object

print_dfm_max_nfeat, print_corpus_max_nchar, print_tokens_max_ntoken integer; specifies the number of features to display when printing a dfm, the number of characters to display when printing corpus documents, or the number of tokens to display when printing tokens objects

print_dfm_summary integer; specifies the number of documents to display when using the defaults for printing a dfm

print_dictionary_max_nkey, print_dictionary_max_nval the number of keys or values (respectively) to display when printing a dictionary

print_kwic_max_nrow the number of rows to display when printing a kwic object

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()

pattern_hashtag, pattern_username character; regex patterns for (social media) hashtags and usernames respectively, used to avoid segmenting these in the default internal "word" tokenizer

tokens_block_size integer; specifies the number of documents to be tokenized at a time in blocked tokenization. When the number is large, tokenization becomes faster but also memory-intensive.

tokens_locale character; specify locale in stringi boundary detection in tokenization and corpus reshaping. See stringi::stri_opts_brkiter().

tokens_tokenizer_word character; the current word tokenizer version used as a default for what = "word" in tokens(), one of "word1", "word2", "word3" (same as "word2"), or "word4".

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

---

**readtext-methods**  
*Extensions for readtext objects*

**Description**
These functions provide *quanteda* methods for *readtext* objects.

**Usage**

```r
## S3 method for class 'readtext'
docnames(x)

## S3 method for class 'readtext'
docvars(x, field = NULL)

## S3 method for class 'readtext'
ndoc(x)
```

**Arguments**

- `x` an object read by `readtext()` from the *readtext* package
- `field` string containing the document-level variable name

**Value**

docnames(x) returns a character vector of the document names from a readtext object
docvars(x, field = NULL) returns a data.frame of the document variables from a readtext object or a vector if field is a single value
ndoc(x) returns the number of documents from a readtext object
**spacyr-methods**  

**Extensions for and from spacy_parse objects**

**Description**

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

**Arguments**

- `x` an object returned by **spacy_parse**, or (for **spacy_parse**) a **corpus** object
- `...` not used for these functions

**Details**

**spacy_parse**(*x*, ...) and **spacy_tokenize**(*x*, ...) work directly on **quanteda** corpus objects.

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

nsentence(*x*) returns the number of sentences by document

**Examples**

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

corp <- corpus(c(doc1 = "And now, now, now for something completely different.",
               doc2 = "Jack and Jill are children."))
spacy_tokenize(corp)
(parsed <- spacy_parse(corp))

ntype(parsed)
ntoken(parsed)
ndoc(parsed)
docnames(parsed)

## 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**

```r
sparsity(x)
```

**Arguments**

- `x`: the document-feature matrix

**Examples**

```r
dfm <- dfm(data_corpus_inaugural)
sparsity(dfm)
sparsity(dfm_trim(dfm, min_termfreq = 5))
```

textmodels

*Models for scaling and classification of textual data*

**Description**

The `textmodel_*()` functions formerly in `quanteda` have now been moved to the `quanteda.textmodels` package.

**See Also**

`quanteda.textmodels::quanteda.textmodels-package`

textplots

*Plots for textual data*

**Description**

The `textplot_*()` functions formerly in `quanteda` have now been moved to the `quanteda.textplots` package.

**See Also**

`quanteda.textplots::quanteda.textplots-package`
textstats

Statistics for textual data

Description

The textstat_*() functions formerly in quanteda have now been moved to the **quanteda.textstats** package.

See Also

quanteda.textstats::quanteda.textstats-package

tokens

Construct a tokens object

Description

Construct a tokens object, either by importing a named list of characters from an external tokenizer, or by calling the internal **quanteda** tokenizer.

Usage

```r
tokens(
  x,
  what = "word",
  remove_punct = FALSE,
  remove_symbols = FALSE,
  remove_numbers = FALSE,
  remove_url = FALSE,
  remove_separators = TRUE,
  split_hyphens = FALSE,
  split_tags = FALSE,
  include_docvars = TRUE,
  padding = FALSE,
  verbose = quanteda_options("verbose"),
  ...
)
```

Arguments

- `x` the input object to the tokens constructor; a **tokens**, **corpus** or **character** object to tokenize.
- `what` character; which tokenizer to use. The default what = "word" is the version 2 **quanteda** tokenizer. Legacy tokenizers (version < 2) are also supported, including the default what = "word1". See the Details and quantedc Tokenizers below.
remove_punct logical; if TRUE remove all characters in the Unicode "Punctuation" [P] class, with exceptions for those used as prefixes for valid social media tags if preserve_tags = TRUE
remove_symbols logical; if TRUE remove all characters in the Unicode "Symbol" [S] class
remove_numbers logical; if TRUE remove tokens that consist only of numbers, but not words that start with digits, e.g. 2day
remove_url logical; if TRUE find and eliminate URLs beginning with http(s)
remove_separators logical; if TRUE remove separators and separator characters (Unicode "Separator" [Z] and "Control" [C] categories)
split_hyphens logical; if FALSE, do not split words that are connected by hyphenation and hyphenation-like characters in between words, e.g. "self-aware" becomes c("self", "-", "aware")
split_tags logical; if FALSE, do not split social media tags defined in quanteda_options(). The default patterns are pattern_hashtag = "#\w+#?" and pattern_username = "@[a-zA-Z0-9_]+".
include_docvars logical; if TRUE, pass docvars through to the tokens object. Does not apply when the input is a character data or a list of characters.
padding logical; 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.
verbose logical; if TRUE, print timing messages to the console
... used to pass arguments among the functions

Details
tokens() works on tokens class objects, which means that the removal rules can be applied post-tokenization, although it should be noted that it will not be possible to remove things that are not present. For instance, if the tokens object has already had punctuation removed, then tokens(x, remove_punct = TRUE) will have no additional effect.

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

Details
As of version 2, the choice of tokenizer is left more to the user, and tokens() is treated more as a constructor (from a named list) than a tokenizer. This allows users to use any other tokenizer that returns a named list, and to use this as an input to tokens(), with removal and splitting rules applied after this has been constructed (passed as arguments). These removal and splitting rules are conservative and will not remove or split anything, however, unless the user requests it.

You usually do not want to split hyphenated words or social media tags, but extra steps required to preserve such special tokens. If there are many random characters in your texts, you should split_hyphens = TRUE and split_tags = TRUE to avoid a slowdown in tokenization.
Using external tokenizers is best done by piping the output from these other tokenizers into the `tokens()` constructor, with additional removal and splitting options applied at the construction stage. These will only have an effect, however, if the tokens exist for which removal is specified at in the `tokens()` call. For instance, it is impossible to remove punctuation if the input list to `tokens()` already had its punctuation tokens removed at the external tokenization stage.

To construct a tokens object from a list with no additional processing, call `as.tokens()` instead of `tokens()`.

Recommended tokenizers are those from the `tokenizers` package, which are generally faster than the default (built-in) tokenizer but always splits infix hyphens, or `spacyr`. The default tokenizer in `quanteda` is very smart, however, and if you do not have special requirements, it works extremely well for most languages as well as text from social media (including hashtags and usernames).

**quanteda Tokenizers**

The default word tokenizer `what = "word"` splits tokens using `stri_split_boundaries(x, type = "word")` but by default preserves infix hyphens (e.g. "self-funding"), URLs, and social media "tag" characters (#hashtags and @usernames), and email addresses. The rules defining a valid "tag" can be found at https://www.hashtags.org/featured/what-characters-can-a-hashtag-include/ for hashtags and at https://help.twitter.com/en/managing-your-account/twitter-username-rules for usernames.

In versions < 2, the argument `remove_twitter` controlled whether social media tags were preserved or removed, even when `remove_punct = TRUE`. This argument is not longer functional in versions >= 2. If greater control over social media tags is desired, you should user an alternative tokenizer, including non-`quanteda` options.

For backward compatibility, the following older tokenizers are also supported through `what`:

- "word1" (legacy) implements similar behaviour to the version of `what = "word"` found in pre-version 2. (It preserves social media tags and infix hyphens, but splits URLs.) "word1" is also slower than "word".
- "fasterword" (legacy) splits on whitespace and control characters, using `stringi::stri_split_charclass(x, "[\p{Z}\p{C}]\+")`
- "fastestword" (legacy) splits on the space character, using `stringi::stri_split_fixed(x, "\")`
- "character" tokenization into individual characters
- "sentence" sentence segmenter based on `stri_split_boundaries`, but with additional rules to avoid splits on words like "Mr." that would otherwise incorrectly be detected as sentence boundaries.

For better sentence tokenization, consider using `spacyr`.

For forward compatibility including use of a more advanced tokenizer that will be used in major version 4, there is also a "word4" tokenizer that is even smarter than the default, which is also aliased as "word2" and "word3" (these are identical). See `tokenize_word4()` for full details.

**See Also**

`tokens_ngrams()`, `tokens_skipgrams()`, `as.list.tokens()`, `as.tokens()`
Examples

txt <- c(doc1 = "A sentence, showing how tokens() works.",
          doc2 = "@quantedainit and #textanalysis https://example.com?p=123.",
          doc3 = "Self-documenting code??",
          doc4 = "£1,000,000 for 50¢ is gr8 4ever \U0001f600")
tokens(txt)
tokens(txt, what = "word1")

# removing punctuation marks but keeping tags and URLs
tokens(txt[1:2], remove_punct = TRUE)

# splitting hyphenated words
tokens(txt[3])
tokens(txt[3], split_hyphens = TRUE)

# symbols and numbers
tokens(txt[4])
tokens(txt[4], remove_numbers = TRUE)
tokens(txt[4], remove_numbers = TRUE, remove_symbols = TRUE)

## Not run: # using other tokenizers
tokens(tokenizers::tokenize_words(txt[4]), remove_symbols = TRUE)
tokenizers::tokenize_words(txt, lowercase = FALSE, strip_punct = FALSE) %>%
tokens(remove_symbols = TRUE)
tokenizers::tokenize_characters(txt[3], strip_non_alphanum = FALSE) %>%
tokens(remove_punct = TRUE)
tokenizers::tokenize_sentences("The quick brown fox. It jumped over the lazy dog.") %>%
tokens()

## End(Not run)

tokens_chunk Segment tokens object by chunks of a given size

Description

Segment tokens into new documents of equally sized token lengths, with the possibility of overlapping the chunks.

Usage

tokens_chunk(x, size, overlap = 0, use_docvars = TRUE)

Arguments

x tokens object whose token elements will be segmented into chunks
size integer; the token length of the chunks
overlap integer: the number of tokens in a chunk to be taken from the last overlap tokens from the preceding chunk

use_docvars if TRUE, repeat the docvar values for each chunk; if FALSE, drop the docvars in the chunked tokens

Value

A tokens object whose documents have been split into chunks of length size.

See Also
tokens_segment()

Examples

```
txts <- c(doc1 = "Fellow citizens, I am again called upon by the voice of my country to execute the functions of its Chief Magistrate.",
          doc2 = "When the occasion proper for it shall arrive, I shall endeavor to express the high sense I entertain of this distinguished honor.")
toks <- tokens(txts)
tokens_chunk(toks, size = 5)
tokens_chunk(toks, size = 5, overlap = 4)
```

---

**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,
  valuetype = c("glob", "regex", "fixed"),
  concatenator = "_",
  window = 0L,
  case_insensitive = TRUE,
  join = TRUE
)
```
Arguments

- **x**
  - an input `tokens` object

- **pattern**
  - a character vector, list of character vectors, `dictionary`, or collocations object. 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.

- **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).

- **window**
  - integer; a vector of length 1 or 2 that specifies size of the window of tokens adjacent to `pattern` that will be compounded with matches to `pattern`. The window can be asymmetric if two elements are specified, with the first giving the window size before `pattern` and the second the window size after. If paddings (empty "" tokens) are found, window will be shrunk to exclude them.

- **case_insensitive**
  - logical; if `TRUE`, ignore case when matching a `pattern` or `dictionary` values

- **join**
  - logical; if `TRUE`, join overlapping compounds into a single compound; otherwise, form these separately. See examples.

Value

A `tokens` object in which the token sequences matching `pattern` have been replaced by new compounded "tokens" joined by the concatenator.

Note

Patterns to be compounded (naturally) consist of multi-word sequences, and how these are expected in `pattern` is very specific. If the elements to be compounded are supplied as space-delimited elements of a character vector, wrap the vector in `phrase()`. If the elements to be compounded are separate elements of a character vector, supply it as a list where each list element is the sequence of character elements.

See the examples below.

Examples

```r
txt <- "The United Kingdom is leaving the European Union."
toks <- tokens(txt, remove_punct = TRUE)

# character vector - not compounded
tokens_compound(toks, c("United", "Kingdom", "European", "Union"))

# elements separated by spaces - not compounded
tokens_compound(toks, c("United Kingdom", "European Union"))

# list of characters - is compounded
```
tokens_compound(toks, list(c("United", "Kingdom"), c("European", "Union")))

# elements separated by spaces, wrapped in phrase() - is compounded
tokens_compound(toks, phrase(c("United Kingdom", "European Union")))

# supplied as values in a dictionary (same as list) - is compounded
# (keys do not matter)
tokens_compound(toks, dictionary(list(key1 = "United Kingdom", key2 = "European Union")))

# pattern as dictionaries with glob matches
tokens_compound(toks, dictionary(list(key1 = c("U* K*"))), valuetype = "glob")

# note the differences caused by join = FALSE
compounds <- list(c("the", "European"), c("European", "Union"))
tokens_compound(toks, pattern = compounds, join = TRUE)
tokens_compound(toks, pattern = compounds, join = FALSE)

# use window to form ngrams
tokens_remove(toks, pattern = stopwords("en")) %>%
  tokens_compound(pattern = "leav*", join = FALSE, window = c(0, 3))

---

tokens_group

Combine documents in a tokens object by a grouping variable

Description

Combine documents in a tokens object by a grouping variable, by concatenating the tokens in the
order of the documents within each grouping variable.

Usage

tokens_group(x, groups = docid(x), fill = FALSE)

Arguments

x tokens object
groups grouping variable for sampling, equal in length to the number of documents. This will be evaluated in the docvars data.frame, so that docvars may be referred to by name without quoting. This also changes previous behaviours for groups. See news(Version >= "3.0", package = "quanteda") 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 object. This will result in a new "document" with empty content for levels not observed, but for which an empty document may be needed. If groups is a factor of dates, for instance, then fill = TRUE ensures that the new object will consist of one new "document" by date, regardless of whether any documents previously existed with that date. Has no effect if the groups variable(s) are not factors.
Value

A `tokens` object whose documents are equal to the unique group combinations, and whose tokens are the concatenations of the tokens by group. Document-level variables that have no variation within groups are saved in `docvars`. Document-level variables that are lists are dropped from grouping, even when these exhibit no variation within groups.

Examples

corp <- 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")))
toks <- tokens(corp)
tokens_group(toks, groups = grp)
tokens_group(toks, groups = c(1, 1, 2, 2))

# with fill
tokens_group(toks, groups = factor(c(1, 1, 2, 2), levels = 1:3))
tokens_group(toks, groups = factor(c(1, 1, 2, 2), levels = 1:3), fill = TRUE)

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,
  nested_scope = c("key", "dictionary"),
  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 logical; if TRUE, ignore case when matching a pattern or dictionary values

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.

nested_scope how to treat matches from different dictionary keys that are nested. When one value is nested within another, such as "a b" being nested within "a b c", then `tokens_lookup()` will match the longer. When `nested_scope = "key"`, this longer-match priority is applied only within the key, while "dictionary" applies it across keys, matching only the key with the longer pattern, not the matches nested within that longer pattern from other keys. See Details.

verbose print status messages if TRUE

Details

Dictionary values may consist of sequences, and there are different methods of counting key matches based on values that are nested or that overlap.

When two different keys in a dictionary are nested matches of one another, the `nested_scope` options provide the choice of matching each key's values independently (the "key") option, or just counting the longest match (the "dictionary" option). Values that are nested within the same key are always counted as a single match. See the last example below comparing the New York and New York Times for these two different behaviours.

Overlapping values, such as "a b" and "b a" are currently always considered as separate matches if they are in different keys, or as one match if the overlap is within the same key.

See Also

tokens_replace

Examples

toks1 <- tokens(data_corpus_inaugural)
dict1 <- dictionary(list(country = "united states",
    law=c("law*", "constitution"),
    freedom=c("free*", "libert*")))
dfm(tokens_lookup(toks1, dict1, valuetype = "glob", verbose = TRUE))
dfm(tokens_lookup(toks1, dict1, valuetype = "glob", verbose = TRUE, nomatch = "NONE"))

dict2 <- dictionary(list(country = "united states",
                       law = c("law", "constitution"),
                       freedom = c("freedom", "liberty")))
# dfm(applyDictionary(toks1, dict2, valuetype = "fixed"))
dfm(tokens_lookup(toks1, dict2, 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.")
toks2 <- tokens(txt)
dict3 <- 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(toks2, dict3, levels = 1)
tokens_lookup(toks2, dict3, levels = 2)
tokens_lookup(toks2, dict3, levels = 1:2)
tokens_lookup(toks2, dict3, levels = 3)
tokens_lookup(toks2, dict3, levels = c(1,3))
tokens_lookup(toks2, dict3, levels = c(2,3))

# show unmatched tokens
tokens_lookup(toks2, dict3, nomatch = "_UNMATCHED")

# nested matching differences
dict4 <- dictionary(list(paper = "New York Times", city = "New York"))
toks4 <- tokens("The New York Times is a New York paper.")
tokens_lookup(toks4, dict4, nested_scope = "key", exclusive = FALSE)
tokens_lookup(toks4, dict4, nested_scope = "dictionary", exclusive = FALSE)

tokens_ngrams

Create n-grams and skip-grams from tokens

Description

Create a set of n-grams (tokens in sequence) from already tokenized text objects, with an optional skip argument to form skip-grams. Both the n-gram 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 n-gram. 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 n-grams, 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 n-gram 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 skip-grams, 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 n-gram which is a superset of all n-grams and each (k − i) skip-gram until (k − i) == 0 (which includes 0 skip-grams).

Value

a tokens object consisting a list of character vectors of n-grams, 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.

References


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
cchar_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 tokens in a tokens object

Description
Substitute token types based on vectorized one-to-one matching. Since this function is created for
differentiation or user-defined stemming. It supports substitution of multi-word features by multi-
word features, but substitution is fastest when pattern and replacement are character vectors and
valuetype = "fixed" as the function only substitute types of tokens. Please use tokens_lookup() with
exclusive = FALSE to replace dictionary values.

Usage
tokens_replace(
  x,
  pattern,
  replacement,
  valuetype = "glob",
  case_insensitive = TRUE,
  verbose = quanteda_options("verbose")
)

Arguments

  x  
tokens object whose token elements will be replaced

  pattern  
a character vector or list of character vectors. See pattern for more details.

  replacement  
a character vector or (if pattern is a list) list of character vectors of the same
length as 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  
logical; if TRUE, ignore case when matching a pattern or dictionary values

  verbose  
print status messages if TRUE

See Also
tokens_lookup
Examples

toks1 <- tokens(data_corpus_inaugural, remove_punct = TRUE)

# lemmatization
taxwords <- c("tax", "taxing", "taxed", "taxed", "taxation")
lemma <- rep("TAX", length(taxwords))
toks2 <- tokens_replace(toks1, taxwords, lemma, valuetype = "fixed")
kwic(toks2, "TAX") %>%
tail(10)

# stemming
type <- types(toks1)
stem <- char_wordstem(type, "porter")
toks3 <- tokens_replace(toks1, type, stem, valuetype = "fixed", case_insensitive = FALSE)
identical(toks3, tokens_wordstem(toks1, "porter"))

# multi-multi substitution
toks4 <- tokens_replace(toks1, phrase(c("Supreme Court")),
                         phrase(c("Supreme Court of the United States")))
kwic(toks4, phrase(c("Supreme Court of the United States")))

tokens_sample

Randomly sample documents from a tokens object

Description

Take a random sample of documents of the specified size from a corpus, with or without replacement, optionally by grouping variables or with probability weights.

Usage

tokens_sample(x, size = NULL, replace = FALSE, prob = NULL, by = NULL)

Arguments

x a tokens object whose documents will be sampled

size a positive number, the number of documents to select; when used with by, the number to select from each group or a vector equal in length to the number of groups defining the samples to be chosen in each category of by. By defining a size larger than the number of documents, it is possible to oversample when replace = TRUE.

replace if TRUE, sample with replacement

prob a vector of probability weights for obtaining the elements of the vector being sampled. May not be applied when by is used.

by optional grouping variable for sampling. This will be evaluated in the docvars data.frame, so that docvars may be referred to by name without quoting. This also changes previous behaviours for by. See news(Version >= "2.9", package = "quanteda") for details.
Value

a tokens object (re)sampled on the documents, containing the document variables for the documents sampled.

See Also

sample

Examples

```r
set.seed(123)
toks <- tokens(data_corpus_inaugural[1:6])
toks
tokens_sample(toks)
tokens_sample(toks, replace = TRUE) %>% docnames()
tokens_sample(toks, size = 3, replace = TRUE) %>% docnames()

# sampling using by
docvars(toks)
tokens_sample(toks, size = 2, replace = TRUE, by = Party) %>% docnames()
```

tokens_select

Select or remove tokens from a tokens object

Description

These function select or discard tokens from a tokens object. 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. startpos and endpos determine the positions of tokens searched for pattern and areas affected are expanded by window.

Usage

```r
tokens_select(
  x,
  pattern,
  selection = c("keep", "remove"),
  valuetype = c("glob", "regex", "fixed"),
  case_insensitive = TRUE,
  padding = FALSE,
  window = 0,
  min_nchar = NULL,
  max_nchar = NULL,
  startpos = 1L,
```
endpos = -1L,
    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, or collocations object. 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 value-type for details.

case_insensitive logical; if TRUE, ignore case when matching a pattern or dictionary values

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

startpos, endpos integer; position of tokens in documents where pattern matching starts and ends, where 1 is the first token in a document. For negative indexes, counting starts at the ending token of the document, so that -1 denotes the last token in the document, -2 the second to last, etc. When the length of the vector is equal to ndoc, tokens in corresponding positions will be selected; when it is less than ndoc, values are repeated to make them equal in length.

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

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

A `tokens` object with tokens selected or removed based on their match to pattern.

Examples

```r
## tokens_select with simple examples
toks <- as.tokens(list(letters, LETTERS))
tokens_select(toks, c("b", "e", "f"), selection = "keep", padding = FALSE)
tokens_select(toks, c("b", "e", "f"), selection = "keep", padding = TRUE)
tokens_select(toks, c("b", "e", "f"), selection = "remove", padding = FALSE)
tokens_select(toks, c("b", "e", "f"), selection = "remove", padding = TRUE)

# how case_insensitive works
tokens_select(toks, c("b", "e", "f"), selection = "remove", case_insensitive = TRUE)
tokens_select(toks, c("b", "e", "f"), selection = "remove", case_insensitive = FALSE)

# use window
tokens_select(toks, c("b", "f"), selection = "keep", window = 1)
tokens_select(toks, c("b", "f"), selection = "remove", window = 1)
tokens_remove(toks, c("b", "f"), window = c(0, 1))
tokens_select(toks, pattern = c("e", "g"), window = c(1, 2))

# 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_split

**Split tokens by a separator pattern**

Description

Replaces tokens by multiple replacements consisting of elements split by a separator pattern, with
the option of retaining the separator. This function effectively reverses the operation of `tokens_compound()`.

Usage

```r
tokens_split(
  x,
  separator = " ",
  valuetype = c("fixed", "regex"),
  remove_separator = TRUE
)
```
Arguments

x  a tokens object
separator  a single-character pattern match by which tokens are separated
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.
remove_separator  if TRUE, remove separator from new tokens

Examples

# undo tokens_compound()
toks1 <- tokens("pork barrel is an idiomatic multi-word expression")
tokens_compound(toks1, phrase("pork barrel"))
tokens_compound(toks1, phrase("pork barrel")) %>%
tokens_split(separator = "_")

# similar to tokens(x, remove_hyphen = TRUE) but post-tokenization
toks2 <- tokens("UK-EU negotiation is not going anywhere as of 2018-12-24.")
tokens_split(toks2, separator = "-", remove_separator = FALSE)

tokens_subset  Extract a subset of a tokens

Description

Returns document subsets of a tokens that meet certain conditions, including direct logical opera-
tions 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, drop_docid = TRUE, ...)

Arguments

x  tokens object to be subsetted
subset  logical expression indicating the documents to keep: missing values are taken
as false
drop_docid  if TRUE, docid for documents are removed as the result of subsetting.
...  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))
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"),
  check_whitespace = TRUE
)

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)

check_whitespace logical; if TRUE, stop with a warning when trying to stem inputs containing whitespace

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

```r
# 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(tokens(txt)))
dfm_wordstem(origdfm)
```

---

### topfeatures

*Identify the most frequent features in a dfm*

**Description**

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

**Usage**

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

**Arguments**

- **x** the object whose features will be returned
- **n** how many top features should be returned
- **decreasing** If TRUE, return the n most frequent features; otherwise return the n least frequent features
- **scheme** one of count for total feature frequency (within group if applicable), or docfreq for the document frequencies of features
- **groups** grouping variable for sampling, equal in length to the number of documents. This will be evaluated in the docvars data.frame, so that docvars may be referred to by name without quoting. This also changes previous behaviours for groups. See news(Version >= "3.0", package = "quanteda") 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

defmat1 <- corpus_subset(data_corpus_inaugural, Year > 1980) %>%
  tokens(remove_punct = TRUE) %>%
  dfm()

defmat2 <- dfm_remove(defmat1, stopwords("en"))

# most frequent features
topfeatures(defmat1)
topfeatures(defmat2)

# least frequent features
topfeatures(defmat2, decreasing = FALSE)

# top features of individual documents
topfeatures(defmat2, n = 5, groups = docnames(defmat2))

# grouping by president last name
topfeatures(defmat2, n = 5, groups = President)

# features by document frequencies
tail(topfeatures(defmat1, 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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