Package ‘rsyntax’

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Description

Quotes can span across sentences, which makes it impossible to find them based on dependency tree queries. This function can be used as post-processing, AFTER using tqueries to find 'source' and 'quote' nodes, to add some of these quotes.

The quotes themselves are often easy to detect due to the use of quotation marks. There are two common ways of indicating the sources.

Firstly, the source might be used before the start of the quote (Steve said: "hey a quote!"). "I like quotes!"). Secondly, the source might be implied in the sentence where the quotes starts, or the sentence before that (Steve was mad. "What a stupid way of quoting me!").

In the first case, the source can be found with a tquery. If there is a source (source_val) in the quote_col that is linked to a part of the quote (quote_val), this function will add the rest of the quote.

In the second case, we can look for candidates near the beginning of the quote. The candidate criteria can be specified as tqueries

Usage

```r
add_span_quotes(
  tokens,
  text_col,
  quote_col = "quotes",
  source_val = "source",
  quote_val = "quote",
  tqueries = NULL,
  par_col = NULL,
  space_col = NULL,
  lag_sentences = 1,
  add_quote_symbols = NULL,
  quote_subset = NULL,
  copy = TRUE
)
```

Arguments

- `tokens` A tokenIndex with rsyntax annotations for 'sources' and 'quotes'
- `text_col` The column with the text (often 'token' or 'word')
- `quote_col` The column that contains the quote annotations
- `source_val` The value in quote_col that indicates the source
- `quote_val` The value in quote_col that indicates the quote
add_span_quotes

**tqueries**  A list of tqueries, that will be performed to find source candidates. The order of the queries determines which source candidates are preferred. It would make sense to use the same value as in source_val in the 'label' argument for the tquery.

**par_col**  If available in the parser output, the column with the paragraph id. We can assume that quotes do not span across paragraphs. By using this argument, quotes that are not properly closed (uneven number of quotes) will stop at the end of the paragraph.

**space_col**  If par_col is not used, paragraphs will be identified based on hard enters in the text_col. In some parsers, there is an additional "space" column that hold the whitespace and linebreaks, which can be included here.

**lag_sentences**  The max number of sentences looked backwards to find source candidates. Default is 1, which means the source candidates have to occur in the sentence where the quote begins (lag = 0) or the sentence before that (lag = 1)

**add_quote_symbols**  Optionally, add additional punctuation symbols for finding quotation marks. In some contexts and languages it makes sense to add single quotes, but in that case it is often necessary to also use the quote_subset argument. For instance, in Spacy (and probably other UD based annotations), single quotes in possessives (e.g., Bob's, scholars') have a PART POS tag, whereas quotation symbols have PUNCT, NOUN, VERB, or ADJ (for some reason).

**quote_subset**  Optionally, an expression to be evaluated on the columns of 'tokens' for selecting/deselecting tokens that can/cant be quotation marks. For example, pos != "PART" can be used for the example mentioned in add_quote_symbols.

**copy**  If TRUE, deep copy the data.table (use if output tokens do not overwrite input tokens)

### Value

the tokenIndex

### Examples

```r
## This function is best used after first annotating regular quotes
## Here we first apply 3 tqueries for annotating quotes in spacy tokens

tokens = tokens_spacy[doc_id == 'text6',]

direct = tquery(lemma = verbs, label='verb',
    children(req=FALSE, relation = c('npadvmod'), block=TRUE),
```

AND

Use AND search in tquery

Description
Use AND search in tquery

Usage
AND("")

Arguments
... name-value pairs for look-up terms. see ?query.
**Value**

A list, to be used as input to `tquery`

**Examples**

```r
tquery(AND(lemma = 'walk', POS='Noun'))  ## is also the default
```

---

**annotate**  
*Annotate a tokenlist based on rsyntax queries*

**Description**

This function has been renamed to `annotate_tqueries`.

**Usage**

```r
annotate(
  tokens,
  column,
  ...,  # Additional arguments
  block = NULL,
  fill = TRUE,
  overwrite = FALSE,
  block_fill = FALSE,
  copy = TRUE,
  verbose = FALSE
)
```

**Arguments**

- **tokens**: A tokenIndex data.table, or any data.frame coercible with `as_tokenindex`.
- **column**: The name of the column in which the annotations are added. The unique ids are added as `column_id`.
- **...**: One or multiple `tqueries`, or a list of queries, as created with `tquery`. Queries can be given a named by using a named argument, which will be used in the `annotation_id` to keep track of which query was used.
- **block**: Optionally, specify ids (doc_id - sentence - token_id triples) that are blocked from querying and filling (ignoring the id and recursive searches through the id).
- **fill**: Logical. If TRUE (default) also assign the fill nodes (as specified in the `tquery`). Otherwise these are ignored.
- **overwrite**: If TRUE, existing column will be overwritten. Otherwise (default), the existing annotations in the column will be blocked, and new annotations will be added. This is identical to using multiple queries.
### Annotate a tokenlist based on rsyntaxNodes

**Description**

Use rsyntaxNodes, as created with `tquery` and `apply_queries`, to annotate a tokenlist. Three columns will be added: a unique id for the query match, the labels assigned in the `tquery`, and a column with the fill level (0 is direct match, 1 is child of match, 2 is grandchild, etc.).

**Arguments**

- `block_fill`: If TRUE (and overwrite is FALSE), the existing fill nodes will also be blocked. In other words, the new annotations will only be added if the
- `copy`: If TRUE (default), the data.table is copied. Otherwise, it is changed by reference. Changing by reference is faster and more memory efficient, but is not predictable R style, so is optional.
- `verbose`: If TRUE, report progress (only usefull if multiple queries are given)

**Details**

Apply queries to extract syntax patterns, and add the results as two columns to a tokenlist. One column contains the ids for each hit. The other column contains the annotations. Only nodes that are given a name in the `tquery` (using the 'label' parameter) will be added as annotation.

Note that while queries only find 1 node for each labeld component of a pattern (e.g., quote queries have 1 node for "source" and 1 node for "quote"), all children of these nodes can be annotated by setting fill to TRUE. If a child has multiple ancestors, only the most direct ancestors are used (see documentation for the fill argument).

**Value**

The tokenIndex with the annotation columns

**Examples**

```r
## spacy tokens for: Mary loves John, and Mary was loved by John
tokens = tokens_spacy[tokens_spacy$doc_id == 'text3',]

## two simple example tqueries
passive = tquery(pos = "VERB*", label = "predicate",
    children(relation = c("agent"), label = "subject"))
active = tquery(pos = "VERB*", label = "predicate",
    children(relation = c("nsubj", "nsubjpass"), label = "subject"))

tokens = annotate_tqueries(tokens, "clause", pas=passive, act=active)
tokens
if (interactive()) plot_tree(tokens, annotation='clause')
```
annotate_tqueries
Annotate a tokenlist based on rsyntax queries

Description

Apply queries to extract syntax patterns, and add the results as three columns to a tokenlist. The first column contains the ids for each hit. The second column contains the annotation label. The third column contains the fill level (which you probably won’t use, but is important for some functionalities). Only nodes that are given a name in the tquery (using the 'label' parameter) will be added as annotation.

Note that while queries only find 1 node for each labeled component of a pattern (e.g., quote queries have 1 node for "source" and 1 node for "quote"), all children of these nodes can be annotated by setting fill to TRUE. If a child has multiple ancestors, only the most direct ancestors are used (see documentation for the fill argument).
**annotate_tqueries**

**Usage**

```r
annotate_tqueries(
  tokens,
  column,
  ...,  # One or multiple tqueries, or a list of queries, as created with tquery. Queries can be given a named by using a named argument, which will be used in the annotation_id to keep track of which query was used.
  block = NULL,
  fill = TRUE,
  overwrite = NA,
  block_fill = FALSE,
  copy = TRUE,
  verbose = FALSE
)
```

**Arguments**

- **tokens**: A tokenIndex data.table, or any data.frame coercible with `as_tokenindex`.
- **column**: The name of the column in which the annotations are added. The unique ids are added as column_id.
- **...**: One or multiple tqueries, or a list of queries, as created with tquery. Queries can be given a named by using a named argument, which will be used in the annotation_id to keep track of which query was used.
- **block**: Optionally, specify ids (doc_id - sentence - token_id triples) that are blocked from querying and filling (ignoring the id and recursive searches through the id).
- **fill**: Logical. If TRUE (default) also assign the fill nodes (as specified in the tquery). Otherwise these are ignored.
- **overwrite**: Applies if column already exists. If TRUE, existing column will be overwritten. If FALSE, the existing annotations in the column will be blocked, and new annotations will be added. This is identical to using multiple queries.
- **block_fill**: If TRUE (and overwrite is FALSE), the existing fill nodes will also be blocked. In other words, the new annotations will only be added if the
- **copy**: If TRUE (default), the data.table is copied. Otherwise, it is changed by reference. Changing by reference is faster and more memory efficient, but is not predictable R style, so is optional.
- **verbose**: If TRUE, report progress (only usefull if multiple queries are given)

**Value**

The tokenIndex data.table with the annotation columns added.

**Examples**

```r
## spacy tokens for: Mary loves John, and Mary was loved by John
tokens = tokens_spacy[tokens_spacy$doc_id == 'text3',]

## two simple example tqueries
passive = tquery(pos = "VERB*", label = "predicate",
```
apply_queries

apply_queries(tokens, ...) 

Description
Apply queries created with tquery

Usage
apply_queries(
  tokens,
  ...
) 

Arguments

- tokens: A tokenIndex data.table, or any data.frame coercible with as_tokenindex.
- ...: tqueries, as created with tquery. Can also be a list with tquery functions. It is recommended to use named arguments/lists, to name the tqueries.
- as_chain: If TRUE, Nodes that have already been assigned assigned earlier in the chain will be ignored (see 'block' argument).
- block: Optionally, specify ids (doc_id - sentence - token_id triples) where find_nodes will stop (ignoring the id and recursive searches through the id). Can also be a data.table returned by (a previous) apply_queries, in which case all ids are blocked.
- check: If TRUE, return a warning if nodes occur in multiple patterns, which could indicate that the find_nodes query is not specific enough.
- fill: If TRUE (default) the fill nodes are added. Otherwise these are ignored, even if the queries include fill()
- return_wide: If TRUE, return nodes in wide format.
- verbose: If TRUE, report progress (only useful if multiple queries are used)
**as_tokenindex**

**Value**

A data.table in which each row is a node for which all conditions are satisfied, and each column is one of the linked nodes (parents / children) with names as specified in the label argument.

**Examples**

```r
## spacy tokens for: Mary loves John, and Mary was loved by John
tokens = tokens_spacy[tokens_spacy$doc_id == 'text3',]

## two simple example tqueries
passive = tquery(pos = "VERB*", label = "predicate",
                 children(relation = c("agent"), label = "subject"))
active = tquery(pos = "VERB*", label = "predicate",
                children(relation = c("nsubj", "nsubjpass"), label = "subject"))

nodes = apply_queries(tokens, pas=passive, act=active)

nodes
```

---

**Prepare a tokenIndex**

**Description**

Creates a tokenIndex data.table. Accepts any data.frame given that the required columns (doc_id, sentence, token_id, parent, relation) are present. The names of these columns must be one of the values specified in the respective arguments.

The data in the data.frame will not be changed, with three exceptions. First, the column names will be changed if the default values are not used. Second, if a token has itself as its parent (which in some parsers is used to indicate the root), the parent is set to NA (as used in other parsers) to prevent infinite cycles. Third, the data will be sorted by doc_id, sentence, token_id.

**Usage**

```r
as_tokenindex(
  tokens,
  doc_id = c("doc_id", "document_id"),
  sentence = c("sentence", "sentence_id"),
  token_id = c("token_id"),
  parent = c("parent", "head_token_id"),
  relation = c("relation", "dep_rel"),
  paragraph = NULL
)
```

**Arguments**

- **tokens** A data.frame, data.table, or tokenindex.
- **doc_id** candidate names for the document id columns
<table>
<thead>
<tr>
<th><strong>sentence</strong></th>
<th>candidate names for sentence (id/index) column</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>token_id</strong></td>
<td>candidate names for the token id column. Has to be numeric (Some parsers return token_id’s as numbers with a prefix (t_1, w_1))</td>
</tr>
<tr>
<td><strong>parent</strong></td>
<td>candidate names for the parent id column. Has to be numeric</td>
</tr>
<tr>
<td><strong>relation</strong></td>
<td>candidate names for the relation column</td>
</tr>
<tr>
<td><strong>paragraph</strong></td>
<td>Optionally, the name of a column with paragraph ids. This is only necessary if sentences are numbered per paragraph, and therefore not unique within documents. If given, sentences are re-indexed to be unique within documents.</td>
</tr>
</tbody>
</table>

**Value**

a tokenIndex

**Examples**

as_tokenindex(tokens_corenlp)

---

**BREAK**  

*A special NOT condition if depth > 1*

---

**Description**

If depth > 1 in the children, parents or fill function, the children/parents will be retrieved recursively (i.e. children, children of children, etc.). If the look-up conditions (e.g., relation = 'nsubj') are not satisfied, a node will not be matched by the query, but the search will still continue for it’s parents/children. The special BREAK look-up function allows you to specify a condition for breaking the recursive loop (lending it’s name from the ‘break’ in a for loop). An example is that you might want to stop the recursive loop in a custom_fill() once it encounters a nested sentence, such as a relative clause: custom_fill(BREAK(relation = 'relcl')).

**Usage**

BREAK(...)

**Arguments**

...  
name-value pairs for look-up terms. see ?query.

**Value**

A list, to be used as input to tquery

**Examples**

tquery(NOT(POS=’Noun’))
Cast annotations to text

Description
Cast labeled tokens to sentences.

Usage
```r
cast_text(tokens, annotation, ..., text_col = "token", na.rm = T)
```

Arguments
- `tokens`: A tokenIndex
- `annotation`: The name of annotations (the "column" argument in annotate_tqueries)
- `...`: Optionally, group annotations together. Named arguments can be given where the name is the new group, and the value is a character vector with values in the annotation column. For example, `text = c('verb','predicate')` would group the 'verb' and 'predicate' nodes together under the name 'text'.
- `text_col`: The name of the column in tokens with the text. Usually this is "token", but some parsers use alternatives such as 'word'.
- `na.rm`: If true (default), drop tokens where annotation id is NA (i.e. tokens without labels)

Value
- a data.table

Examples
```r
tokens = tokens_spacy[tokens_spacy$doc_id == 'text3',]

## two simple example tqueries
passive = tquery(pos = "VERB*", label = "verb", fill=FALSE,
                children(relation = "agent",
                          children(label="subject")),
                children(relation = "nsubjpass", label="object"))
active = tquery(pos = "VERB*", label = "verb", fill=FALSE,
               children(relation = c("nsubj", "nsubjpass"), label = "subject"),
               children(relation = "dobj", label="object"))

tokens = annotate_tqueries(tokens, "clause", pas=passive, act=active, overwrite=T)
cast_text(tokens, 'clause')

## group annotations
cast_text(tokens, 'clause', text = c('verb','object'))
```
## use grouping to sort

```r
cast_text(tokens, 'clause', subject = 'subject',
        verb = 'verb', object = 'object')
```

---

**chop**  

**Chop of a branch of the tree**

---

### Description

Using the query language for tquery, chop of the branch down from the node that is found

### Usage

```r
chop(.tokens, ...)
```

### Arguments

- `.tokens`  
  A tokenIndex
- `...`  
  Arguments passed to tquery. For instance, relation = 'punct' cuts off all punctuation dependencies (in universal dependencies)

### Value

A tokenIndex with the rows of the nodes in the selected branches removed

### Examples

```r
spacy_conjunctions <- function(tokens) {
  no_fill = c('compound','case','relcl')
  tq = tquery(label='target', NOT(relation = 'conj'),
              rsyntax::fill(NOT(relation = no_fill), max_window = c(Inf,0)),
              children(relation = 'conj', label='origin',
                        rsyntax::fill(NOT(relation = no_fill), max_window=c(0,Inf))))
  tokens = climb_tree(tokens, tq)
  chop(tokens, relation = 'cc')
}

## spacy tokens for "Bob and John ate bread and drank wine"

tokens = tokens_spacy[tokens_spacy$doc_id == 'text5',]

tokens = spacy_conjunctions(tokens)
tokens

if (interactive()) plot_tree(tokens)
```
climb_tree

Have a node adopt its parent’s position

Description

given a tquery that identifies a node labeled "origin", that has a parent labeled "target", recursively have child adopt the parent’s position (parent and relation column) and adopt parents fill nodes. only_new restricts adding fill nodes to relations that child does not already have. This seems to be a good heuristic for dealing with argument drop

Usage

climb_tree(
    .tokens,
    tq,
    unpack = TRUE,
    isolate = TRUE,
    take_fill = TRUE,
    give_fill = TRUE,
    only_new = "relation",
    max_iter = 200
)

Arguments

.tokens A tokenIndex

tq A tquery. Needs to have a node labeled "origin" that has a parent labeled "target"

unpack If TRUE (default), create separate branches for the parent and the node that inherits the parent position

isolate If unpack is TRUE and isolate is TRUE (default is FALSE), isolate the new branch by recursively unpacking

take_fill If TRUE (default), give the node that will inherit the parent position a copy of the parent children (but only if it does not already have children with this relation; see only_new)

give_fill If TRUE (default), copy the children of the node that will inherit the parent position to the parent (but only if it does not already have children with this relation; see only_new)

only_new A character vector giving one or multiple column names that need to be unique for take_fill and give_fill

max_iter The climb tree function repeatedly resolves the first conjunction it encounters in a sentence. This can lead to many iterations for sentences with many (nested) conjunctions. It could be the case that in unforeseen cases or with certain parsers an infinite loop is reached, which is why we use a max_iter argument that breaks the loop and sends a warning if the max is reached.
copy_fill

Value

The reshaped tokenIndex

Examples

```r
spacy_conjunctions <- function(tokens) {
  no_fill = c('compound','case','relcl')
  tq = tquery(label='target', NOT(relation = 'conj'),
              rsyntax::fill(NOT(relation = no_fill), max_window = c(Inf,0)),
              children(relation = 'conj', label='origin',
                        rsyntax::fill(NOT(relation = no_fill), max_window=c(0,Inf))))
  tokens = climb_tree(tokens, tq)
  chop(tokens, relation = 'cc')
}

## spacy tokens for "Bob and John ate bread and drank wine"
tokens = tokens_spacy[tokens_spacy$doc_id == 'text5',]
tokens = spacy_conjunctions(tokens)
tokens
if (interactive()) plot_tree(tokens)
```

---

copy_fill  Copy nodes

Description

Copy nodes

Usage

```r
copy_fill(
  .tokens,
  from_node,
  to_node,
  subset = NULL,
  subset_fill = NULL,
  only_new = NULL
)
```

Arguments

- `.tokens` A tokenIndex in which nodes are selected with `select_nodes`.
- `from_node` The name of the node from which fill is copied
copy_nodes

Description

Copy nodes

Usage

```r
copy_nodes(
  .tokens,
  node,
  new,
  subset = NULL,
  keep_relation = TRUE,
  copy_fill = FALSE,
  subset_fill = NULL,
  only_new = NULL
)
```
Arguments

- `.tokens`: A tokenIndex in which nodes are selected with `select_nodes`.
- `node`: The name of the node that is to be copied.
- `new`: The name given to the copy.
- `subset`: A subset expression (that evaluates to a logical vector). The token column for each labeled node in the `tquery` can be referred to as `label$column`.
- `keep_relation`: If `FALSE`, remove relation (making node a root).
- `copy_fill`: If `TRUE`, also copy the fill.
- `subset_fill`: A subset on the fill nodes. Can only directly use token column. For example, use `pos == 'VERB'` to copy only verbs.
- `only_new`: If `TRUE`, direct fill children will only be copied to `to_node` if it does not already have nodes of this relation. This is a good heuristic for dealing with argument drop.

Value

A tokenIndex with a `.nodes` attribute

Examples

```r
tokens = tokens_spacy[tokens_spacy$doc_id == 'text1',]
tq = tquery(label='object', relation='dobj')
tokens2 = select_nodes(tokens, tq)
selected_nodes(tokens2)
copy_nodes(tokens2, 'object', 'new_object')
tokens3 = copy_nodes(tokens2, 'object', 'new_object', copy_fill=TRUE)
if (interactive()) plot_tree(tokens3, token, pos)
```

---

**custom_fill**

Specify custom fill behavior

Description

If a `tquery()`, `parents()` or `children()` function has set a label, all children of the matched node (that are not matched by another query) will also be given this label. This is called the 'fill' heuristic. The `custom_fill()` function can be used to give more specific conditions for which children need to be labeled.

The function can be used almost identically to the `children()` function. The specification of the look-up conditions works in the same way. **NOTE** that `custom_fill`, just like the `children()` function,
should be passed as an unnamed argument, and NOT to the 'fill' argument (which is the boolean argument for whether fill should be used)

For the custom_fill function, the special BREAK() look-up function is particularly powerful. custom_fill will recursively search for children, children of children, etc. The look-up conditions in custom_fill determine which of all these direct and indirect children to label. Often, however, you would want to the recursive loop to 'break' when certain conditions are met. For instance, to ignore children in a relative clause: custom_fill(BREAK(relation = 'relcl'))

Usage

custom_fill(  
  ...,  
  g_id = NULL,  
  depth = Inf,  
  connected = FALSE,  
  max_window = c(Inf, Inf),  
  min_window = c(0, 0)  
)

Arguments

... Accepts two types of arguments: name-value pairs for finding nodes (i.e. rows), and functions to look for parents/children of these nodes.
The name in the name-value pairs need to match a column in the data.table, and the value needs to be a vector of the same data type as the column. By default, search uses case sensitive matching, with the option of using common wildcards (* for any number of characters, and ? for a single character). Alternatively, flags can be used to to change this behavior to 'fixed' (__F), 'ignoring case' (__I) or 'regex' (__R). See details for more information.
If multiple name-value pairs are given, they are considered as AND statements, but see details for syntax on using OR statements, and combinations.
To look for parents and children of the nodes that are found, you can use the parents and children functions as (named or unnamed) arguments. These functions have the same query arguments as tquery, but with some additional arguments.
g_id Find nodes by global id, which is the combination of the doc_id, sentence and token_id. Passed as a data.frame or data.table with 3 columns: (1) doc_id, (2) sentence and (3) token_id.
depth A positive integer, determining how deep parents/children are sought. 1 means that only direct parents and children of the node are retrieved. 2 means children and grandchildren, etc. All parents/children must meet the filtering conditions (... or g_id)
connected Controls behavior if depth > 1 and filters are used. If FALSE, all parents/children to the given depth are retrieved, and then filtered. This way, grandchildren that satisfy the filter conditions are retrieved even if their parents do not satisfy the conditions. If TRUE, the filter is applied at each level of depth, so that only fully connected branches of nodes that satisfy the conditions are retrieved.
max_window  Set the max token distance of the children/parents to the node. Has to be either a numerical vector of length 1 for distance in both directions, or a vector of length 2, where the first value is the max distance to the left, and the second value the max distance to the right. Default is c(Inf, Inf) meaning that no max distance is used.

min_window  Like max_window, but for the min distance. Default is c(0,0) meaning that no min is used.

Value

Should not be used outside of tquery

Examples

tokens = tokens_spacy[token_spacy$doc_id == 'text4',]

## custom fill rule that ignores relative clauses
no_relcl_fill = custom_fill(BREAK(relation='relcl'))

## add custom fill as argument in children(). NOTE that it should be
## passed as an unnamed argument (and not to the fill boolean argument)
tq = tquery(label = 'verb', pos='VERB', fill=FALSE,
            children(label = 'subject', relation = 'nsubj', no_relcl_fill),
            children(label = 'object', relation = 'dobj', no_relcl_fill))

tokens = annotate_tqueries(tokens, "clause", tq)
tokens

dutch  

Dutch lemma

Description

Various categories of lemma, for use in syntax queries

Usage

data(dutch)

Format

list
### fill

*Specify custom fill behavior*

#### Description

This is soft deprecated, with the new preferred function being `custom_fill` to avoid namespace conflicts with `tidyr::fill()` and `data.table::fill()`

#### Usage

```r
call(fill(...))
```

#### Arguments

- `...` passes to `custom_fill`

#### Value

Should not be used outside of `tquery`

### get_branch_id

*Add the branch id as a column to the tokenindex*

#### Description

After splitting trees into branches

#### Usage

```r
call(get_branch_id(tokens))
```

#### Arguments

- `tokens` A tokenindex

#### Value

the tokenindex

#### Examples

```r
tokens = tokens_spacy[tokens_spacy$doc_id == 'text4',]
tokens = as_tokenindex(tokens)

tokens2 = isolate_branch(tokens, relation = 'relcl', copy_parent = TRUE)
get_branch_id(tokens2)
```
**get_long_ids**  
*Get ids in various forms to extract token_ids*

**Description**

Get ids in various forms to extract token_ids

**Usage**

```r
get_long_ids(..., select = NULL, with_fill = FALSE)
```

**Arguments**

- `...`: Either a data.table with the columns doc_id, sentence and token_id, or the output of `apply_queries`
- `select`: If not null, a character vector for selecting column names
- `with_fill`: If TRUE, include the ids of the fill nodes

**Value**

A data.table with the columns doc_id, sentence and token_id

---

**get_nodes**  
*Transform the nodes to long format and match with token data*

**Description**

Transform the nodes to long format and match with token data

**Usage**

```r
get_nodes(tokens, nodes, use = NULL, token_cols = c("token"))
```

**Arguments**

- `tokens`: A tokenIndex data.table, or any data.frame coercible with `as_tokenindex`
- `nodes`: A data.table, as created with `apply_queries`. Can be a list of multiple data.tables.
- `use`: Optionally, specify which columns from nodes to add. Other than convenient, this is slightly different from subsetting the columns in 'nodes' beforehand if fill is TRUE. When the children are collected, the ids from the not-used columns are still blocked (see 'block')
- `token_cols`: A character vector, specifying which columns from tokens to include in the output
isolate_branch

Value

A data.table with the nodes in long format, and the specified token_cols attached

Examples

```r
## spacy tokens for: Mary loves John, and Mary was loved by John
tokens = tokens_spacy[tokens_spacy$doc_id == 'text3',]

## two simple example tqueries
passive = tquery(pos = "VERB*", label = "predicate",
                children(relation = c("agent"), label = "subject"))
active = tquery(pos = "VERB*", label = "predicate",
                children(relation = c("nsubj", "nsubjpass"), label = "subject"))

nodes = apply_queries(tokens, pas=passive, act=active)
get_nodes(tokens, nodes)
```

isolate_branch

Isolate a branch in a dependency tree

Description

cuts of a branch at the nodes that match the lookup arguments (...). A "tree_parent" column is added to the tokenindex, that indicates for the new roots which node the parent was.

Usage

```r
isolate_branch(tokens, ..., copy_parent = TRUE, copy_parent_fill = TRUE)
```

Arguments

- `tokens`: A tokenindex
- `...`: lookup arguments to find the node to split. For example, isolate_branch(tokens, relation='relcl') isolates branches of which the top node (the new root) has the relation "relcl".
- `copy_parent`: If TRUE (default) copy the parent of the branch and include it in the isolated branch
- `copy_parent_fill`: If TRUE, also copy the parents fill nodes

Value

the tokenindex
mutate_nodes

Examples

tokens = tokens_spacy[tokens_spacy$doc_id == 'text4',]
tokens = as_tokenindex(tokens)

tokens2 = isolate_branch(tokens, relation = 'relcl', copy_parent = TRUE)
tokens2

if (interactive()) plot_tree(tokens2)

---

mutate_nodes

Mutate nodes

Description

Mutate nodes

Usage

mutate_nodes(.tokens, node, ..., subset = NULL)

Arguments

.tokens A tokenIndex in which nodes are selected with select_nodes.
.node The name of the node that is to be mutated
... named arguments. The name should be a column in tokens
subset A subset expression (that evaluates to a logical vector). The token column for each labeled node in the tquery can be referred to as label$column.

Value

A tokenIndex with a .nodes attribute

Examples

tokens = tokens_spacy[tokens_spacy$doc_id == 'text4',]

## use a tquery to label the nodes that you want to manipulate
tq = tquery(relation = "relcl", label = "relative_clause")

## apply query to select nodes
tokens2 = select_nodes(tokens, tq)

## as an example, we make the parent of the relative_clause
## nodes NA, effectively cutting of the relcl from the tree
tokens2 = mutate_nodes(tokens2, "relative_clause", parent=NA)

tokens2
nested_nodes

Search for parents or children in tquery

Description

Enables searching for parents or children. Should only be used inside of the tquery function, or within other children/parents functions. Look-up conditions are specified in the same way as in the tquery function.

Multiple children() or parents() functions can be nested side by side. This works as an AND condition: the node must have all these parents/children (unless the req [required] argument is set to FALSE).

The custom_fill() function is used to include the children of a 'labeled' node. It can only be nested in a query if the label argument is not NULL, and by default will include all children of the node that have not been assigned to another node. If two nodes have a shared child, the child will be assigned to the closest node.

Usage

children(
  ..., 
  g_id = NULL, 
  label = NA, 
  req = TRUE, 
  depth = 1, 
  connected = FALSE, 
  fill = TRUE, 
  block = FALSE, 
  max_window = c(Inf, Inf), 
  min_window = c(0, 0) 
)

not_children(
  ..., 
  g_id = NULL, 
  depth = 1, 
  connected = FALSE, 
  max_window = c(Inf, Inf), 
  min_window = c(0, 0) 
)

parents(
  ..., 
  g_id = NULL, 
  label = NA, 
  req = TRUE, 
  depth = 1, 
  connected = FALSE, 
  fill = TRUE, 
  block = FALSE, 
  max_window = c(Inf, Inf), 
  min_window = c(0, 0) 
)

}
connected = FALSE,
fill = TRUE,
block = FALSE,
max_window = c(Inf, Inf),
min_window = c(0, 0)
)

not_parents(
  ..., 
  g_id = NULL, 
  depth = 1, 
  connected = FALSE, 
  max_window = c(Inf, Inf), 
  min_window = c(0, 0)
)

Arguments

... Accepts two types of arguments: name-value pairs for finding nodes (i.e. rows), and functions to look for parents/children of these nodes.

The name in the name-value pairs need to match a column in the data.table, and the value needs to be a vector of the same data type as the column. By default, search uses case sensitive matching, with the option of using common wildcards (* for any number of characters, and ? for a single character). Alternatively, flags can be used to to change this behavior to 'fixed' (__F), 'ignoring case' (__I) or 'regex' (__R). See details for more information.

If multiple name-value pairs are given, they are considered as AND statements, but see details for syntax on using OR statements, and combinations.

To look for parents and children of the nodes that are found, you can use the parents and children functions as (named or unnamed) arguments. These functions have the same query arguments as tquery, but with some additional arguments.

g_id Find nodes by global id, which is the combination of the doc_id, sentence and token_id. Passed as a data.frame or data.table with 3 columns: (1) doc_id, (2) sentence and (3) token_id.

label A character vector, specifying the column name under which the selected tokens are returned. If NA, the column is not returned.

req Can be set to false to not make a node 'required'. This can be used to include optional nodes in queries. For instance, in a query for finding subject - verb - object triples, make the object optional.

depth A positive integer, determining how deep parents/children are sought. 1 means that only direct parents and children of the node are retrieved. 2 means children and grandchildren, etc. All parents/children must meet the filtering conditions (... or g_id)

connected Controls behavior if depth > 1 and filters are used. If FALSE, all parents/children to the given depth are retrieved, and then filtered. This way, grandchildren that satisfy the filter conditions are retrieved even if their parents do not satisfy the
Conditions. If TRUE, the filter is applied at each level of depth, so that only fully connected branches of nodes that satisfy the conditions are retrieved.

**fill**
Logical. If TRUE (default), the default custom_fill() will be used. To more specifically control fill, you can nest the custom_fill function (a special version of the children function).

**block**
Logical. If TRUE, the node will be blocked from being assigned (labeled). This is mainly useful if you have a node that you do not want to be assigned by fill, but also don’t want to 'label' it. Essentially, block is shorthand for using label and then removing the node afterwards. If block is TRUE, label has to be NA.

**max_window**
Set the max token distance of the children/parents to the node. Has to be either a numerical vector of length 1 for distance in both directions, or a vector of length 2, where the first value is the max distance to the left, and the second value the max distance to the right. Default is c(Inf, Inf) meaning that no max distance is used.

**min_window**
Like max_window, but for the min distance. Default is c(0,0) meaning that no min is used.

**Details**
Having nested queries can be confusing, so we tried to develop the find_nodes function and the accompanying functions in a way that clearly shows the different levels. As shown in the examples, the idea is that each line is a node, and to look for parents or children, we put them on the next line with indentation (in RStudio, it should automatically align correctly when you press enter inside of the children() or parents() functions).

There are several flags that can be used to change search condition. To specify flags, add a double underscore and the flag character to the name in the name value pairs (...). By adding the suffix __R, query terms are considered to be regular expressions, and the suffix __I uses case insensitive search (for normal or regex search). If the suffix __F is used, only exact matches are valid (case sensitive, and no wildcards). Multiple flags can be combined, such as lemma__RI, or lemma__IR (order of flags is irrelevant)

The not_children and not_parents functions will make the matched children/parents a NOT condition. Note that this is different from using the NOT() look-up function. NOT operates at the node level, so you specify that a node should NOT be matched if certain conditions are met. the not_parents and not_children functions operate at the pattern level, so you can specify that a pattern is invalid if these parents/children are matched.

Next to the OR, AND, and NOT functions, children/parents functions can have the special BREAK function for cases where depth > 1. If depth > 1 in the children, parents or fill function, the children/parents will be retrieved recursively (i.e. children, children of children, etc.). If the look-up conditions (e.g., relation = 'nsubj') are not satisfied, a node will not be matched by the query, but the search will still continue for it’s parents/children. The special BREAK look-up function allows you to specify a condition for breaking the recursive loop (lending it’s name from the 'break' in a for loop). An example is that you might want to stop the recursive loop in a custom_fill() once it encounters a nested sentence, such as a relative clause: custom_fill(BREAK(relation = 'relcl')).

**Value**
Should not be used outside of tquery
### NOT

*Use NOT search in tquery*

**Description**

Use NOT search in tquery

**Usage**

`NOT(...)`

**Arguments**

... name-value pairs for look-up terms. see ?query.

**Value**

A list, to be used as input to tquery

**Examples**

```
tquery(NOT(POS=’/quotesingle.Var Noun/quotesingle.Var))
```

### OR

*Use OR search in tquery*

**Description**

Use OR search in tquery

**Usage**

`OR(...)`

**Arguments**

... name-value pairs for look-up terms. see ?query.

**Value**

A list, to be used as input to tquery

**Examples**

```
tquery(OR(lemma = ’walk’, POS=’/quotesingle.Var Noun/quotesingle.Var))
```
plot_tree

Create an igraph tree from a sentence

Description

Create an igraph tree from a token_index (as_tokenindex) or a data.frame that can be coerced to a tokenindex.

By default, all columns in the data are included as labels. This can be changes by using the ... argument.

Usage

plot_tree(
  tokens,
  ...,  # Optionally, select which columns to include as labels and how to present them.
  sentence_i = 1,
  doc_id = NULL,
  sentence = NULL,
  annotation = NULL,
  only_annotation = FALSE,
  pdf_file = NULL,
  allign_text = TRUE,
  ignore_rel = NULL,
  all_lower = FALSE,
  all_abbrev = NULL,
  textsize = 1,
  spacing = 1,
  use_color = TRUE,
  max_curve = 0.3,
  palette = grDevices::terrain.colors,
  rel_on_edge = F,
  pdf_viewer = FALSE,
  viewer_mode = TRUE,
  viewer_size = c(100, 100)
)

Arguments

tokens  A tokenIndex data.table, or any data.frame coercible with as_tokenindex. Can also be a corpustools tCorpus.

...  Optionally, select which columns to include as labels and how to present them. Can be quoted or unquoted names and expressions, using columns in the tokenIndex. For example, plot_tree(tokens, token, pos) will use the $Token and $Pos columns in tokens. You can also use expressions for easy control of visualizations. For example: plot_tree(tokens, tolower(token), abbreviate(pos,1)). (note that abbreviate() is really useful here)
sentence_i  By default, plot_tree uses the first sentence (sentence_i = 1) in the data. sentence_i can be changed to select other sentences by position (the i-th unique sentence in the data). Note that sentence_i does not refer to the values in the sentence column (for this use the sentence argument together with doc_id).

doc_id  Optionally, the document id can be specified. If so, sentence_i refers to the i-th sentence within the given document.

sentence  Optionally, the sentence id can be specified (note that sentence_i refers to the position). If sentence is given, doc_id has to be given as well.

annotation  Optionally, a column with an rsyntax annotation, to add boxes around the annotated nodes.

only_annotation  If annotation is given, only.annotation = TRUE will print only the nodes with annotations.

pdf_file  Directly save the plot as a pdf file.

align_text  If TRUE (default) align text (the columns specified in ...) in a single horizontal line at the bottom, instead of following the different levels in the tree.

ignore_rel  Optionally, a character vector with relation names that will not be shown in the tree.

all_lower  If TRUE, make all text lowercase.

all_abbrev  If an integer, abbreviate all text, with the number being the target number of characters.

textsize  A number to manually change the textsize. The function tries to set a suitable textsize for the plotting device, but if this goes wrong and now everything is broken and sad, you can multiply the textsize with the given number.

spacing  A number for scaling the distance between words (between 0 and infinity).

use_color  If true, use colors.

max_curve  A number for controlling the allowed amount of curve in the edges.

palette  A function for creating a vector of n contiguous colors. See ?terrain.colors for standard functions and documentation.

rel_on_edge  If TRUE, print relation label on edge instead of above the node.

pdf_viewer  If TRUE, view the plot as a pdf. If no pdf_file is specified, the pdf will be saved to the temp folder.

viewer_mode  By default, the plot is saved as a PNG embedded in a HTML and opened in the viewer. This hack makes it independent of the size of the plotting device and enables scrolling. By setting viewer_mode to False, the current plotting device is used.

viewer_size  A vector of length 2, that multiplies the width (first value) and height (second value) of the viewer_mode PNG.

Value

plots a dependency tree.
Examples

tokens = tokens_spacy[tokens_spacy$doc_id == 'text3',]

if (interactive()) plot_tree(tokens, token, pos)

## plot with annotations

direct = tquery(label = 'verb', pos = 'VERB', fill=FALSE,
                children(label = 'subject', relation = 'nsubj'),
                children(label = 'object', relation = 'dobj'))
passive = tquery(label = 'verb', pos = 'VERB', fill=FALSE,
                 children(label = 'subject', relation = 'agent'),
                 children(label = 'object', relation = 'nsubjpass'))

if (interactive()) {
  tokens %>%
    annotate_tqueries('clause', pas=passive, dir=direct) %>%
    plot_tree(token, pos, annotation='clause')
}

print.tQuery

Description

S3 print for tQuery class

Usage

## S3 method for class 'tQuery'
print(x, ...)

Arguments

x a tQuery

... not used

Examples

q = tquery(label='quote',
            children(relation='nmod:according_to', label='source',
                     children(label='verb')))
q
quote_punctuation  \textit{Quote punctuation}

\textbf{Description}

Punctuation used in quotes, for use in syntax queries

\textbf{Usage}

\begin{verbatim}
data(quote_punctuation)
\end{verbatim}

\textbf{Format}

\begin{verbatim}
character()
\end{verbatim}

remove_fill  \textit{Remove fill}

\textbf{Description}

Like remove_nodes, but only removing the fill nodes

\textbf{Usage}

\begin{verbatim}
remove_fill(
  .tokens,
  node,
  rm_subset_fill = NULL,
  rm_subset = NULL,
  keep_shared = FALSE
)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{.tokens} A tokenIndex in which nodes are selected with \texttt{select_nodes}.
  \item \texttt{node} The name of the node that is to be mutated
  \item \texttt{rm_subset_fill} A subset on the fill nodes. Can only directly use token column. For example, use \texttt{pos == 'VERB'} to remove only verbs
  \item \texttt{rm_subset} A subset expression (that evaluates to a logical vector) to more specifically specify which nodes to remove. The token column for each labeled node in the tquery can be referred to as label$column.
  \item \texttt{keep_shared} If there is another node that has the same fill nodes, should the fill nodes that are shared also be removed?
\end{itemize}
**remove_nodes**

**Value**
A tokenIndex with a `.nodes` attribute

**Examples**
```
tokens = tokens_spacy[tokens_spacy$doc_id == 'text1',]
  
  ## use a tquery to label the nodes that you want to manipulate
  tq = tquery(pos = 'VERB',
               children(label = 'object', relation='dobj'))
  
  ## apply query to select nodes
  tokens2 = select_nodes(tokens, tq)
  remove_fill(tokens2, 'object')
```

---

**Description**
Remove nodes

**Usage**
```
remove_nodes(  
  .tokens,  
  node,  
  rm_subset = NULL,  
  with_fill = TRUE,  
  rm_subset_fill = NULL,  
  keep_shared = FALSE  
)
```

**Arguments**
- `.tokens` A tokenIndex in which nodes are selected with select_nodes.
- `node` The name of the node that is to be mutated
- `rm_subset` A subset expression (that evaluates to a logical vector) to more specifically specify which nodes to remove. The token column for each labeled node in the tquery can be referred to as label$column.
- `with_fill` If TRUE, also remove the fill nodes
- `rm_subset_fill` A subset on the fill nodes. Can only directly use token column. For example, use pos == 'VERB' to remove only verbs
- `keep_shared` If there is another node that has the same fill nodes, should the fill nodes that are shared also be removed?
Value
A tokenIndex with a .nodes attribute

Examples
```r
tokens = tokens_spacy[tokens_spacy$doc_id == 'text1',]

## use a tquery to label the nodes that you want to manipulate
tq = tquery(pos = 'VERB',
            children(label = 'object', relation='dobj'))

## apply query to select nodes
tokens2 = select_nodes(tokens, tq)
remove_nodes(tokens2, 'object')
remove_nodes(tokens2, 'object', with_fill=FALSE)
```

---

**reselect_nodes**  
*Within a chain of reshape operations, reapply the tquery*

Description
Within a chain of reshape operations, reapply the tquery

Usage
```r
reselect_nodes(.tokens)
```

Arguments
```
.tokens    A tokenIndex in which nodes are selected with select_nodes.
```

Value
A tokenIndex with a .nodes attribute

Examples
```r
tokens = tokens_spacy[tokens_spacy$doc_id == 'text4',]

## use a tquery to label the nodes that you want to manipulate
tq = tquery(relation = "relcl", label = "relative_clause")

## apply query to select nodes
tokens2 = select_nodes(tokens, tq)

## reuses the tq, that is stored in tokens2
## this makes it easy to make the selection anew after a transformation
tokens2 = reselect_nodes(tokens2)
```
rsyntax_threads

Get the number of threads to be used by rsyntax functions

Description

rsyntax relies heavily on the data.table package, which supports multithreading. By default, the number of threads set by data.table are used, as you can see with getDTthreads. With set_rsyntax_threads you can set the number of threads for rsyntax functions, without affecting the data.table settings.

Usage

rsyntax_threads()

Value

the setting for the number of threads used by rsyntax

Examples

rsyntax_threads()

selected_nodes

If select_nodes() is used, the selected nodes can be extracted with selected_nodes(). This is mainly for internal use, but it can also be useful for debugging, and to control loops of reshape operation (e.g. break if no selected nodes left)

Description

If select_nodes() is used, the selected nodes can be extracted with selected_nodes(). This is mainly for internal use, but it can also be useful for debugging, and to control loops of reshape operation (e.g. break if no selected nodes left)

Usage

selected_nodes(.tokens)

Arguments

.tokens A tokenIndex in which nodes are selected with select_nodes.

Value

A tokenIndex with a .nodes attribute
Examples

tokens = tokens_spacy[tokens_spacy$doc_id == 'text4',]

## use a tquery to label the nodes that you want to manipulate
qt = tquery(relation = "relcl", label = "relative_clause")

## apply query to select nodes
tokens2 = select_nodes(tokens, qt)

## Get selected nodes from tokenindex
selected_nodes(tokens2)

select_nodes

Apply tquery to initiate reshape operations

Description

Apply tquery to initiate reshape operations

Usage

select_nodes(
  tokens,
  tquery,
  fill = TRUE,
  fill_only_first = TRUE,
  .one_per_sentence = FALSE,
  .order = 1
)

Arguments

tokens A tokenIndex data.table, or any data.frame coercible with as_tokenindex.
tquery A tquery that selects and labels the nodes that are used in the reshape operations
fill Logical, should fill be used?
fill_only_first Logical, should a node only be filled once, with the nearest (first) labeled node?
.one_per_sentence If true, only one match per sentence is used, giving priority to patterns closest to the root (or farthest from the root if .order = -1). This is sometimes necessary to deal with recursion.
.order If .one_per_sentence is used, .order determines whether the patterns closest to (1) or farthest away (-1) are used.

Value

A tokenIndex with a .nodes attribute, that enables the use of reshape operations on the selected nodes
**set_rsyntax_threads**

Set number of threads to be used by rsyntax functions

**Description**

rsyntax relies heavily on the data.table package, which supports multithreading. By default, the number of threads set by data.table are used, as you can see with `getDTthreads`. Here you can set the number of threads for rsyntax functions, without affecting the data.table settings.

**Usage**

```r
set_rsyntax_threads(threads = NULL)
```

**Arguments**

- `threads` The number of threads to use. Cannot be higher than number of threads used by data.table, which you can change with `setDTthreads`. If left empty (NULL), all data.table threads are used

**Value**

Does not return a value. Sets the global `rsyntax_threads` option.

**Examples**

```r
tokens = tokens_spacy[tokens_spacy$doc_id == 'text4',]

## use a tquery to label the nodes that you want to manipulate
tq = tquery(relation = "relcl", label = "relative_clause")

## apply query to select nodes
tokens2 = select_nodes(tokens, tq)

## as an example, we make the parent of the relative_clause nodes NA, effectively cutting of the relcl from the tree
tokens2 = mutate_nodes(tokens2, "relative_clause", parent=NA)

tokens2

if (interactive()) plot_tree(tokens2)

## this is designed to work nicely with magrittr piping
if (interactive()) {
tokens %>%
  select_nodes(tq) %>%
  mutate_nodes("relative_clause", parent=NA) %>%
  plot_tree()
}
```
Examples

```r
current_threads = rsyntax_threads()
set_rsyntax_threads(2)

## undo change (necessary for CRAN checks)
set_rsyntax_threads(current_threads)
```

split_UD_conj

### Split conjunctions for dependency trees in Universal Dependencies

#### Description

Split conjunctions for dependency trees in Universal Dependencies

#### Usage

```r
split_UD_conj(
  tokens,
  conj_rel = "conj",
  cc_rel = c("cc", "cc:preconj"),
  unpack = T,
  no_fill = NULL,
  min_dist = 0,
  max_dist = Inf,
  right_fill_dist = T,
  compound_rel = c("compound*", "flat"),
  ...
)
```

#### Arguments

- **tokens**: a tokenIndex based on texts parsed with `spacy_parse` (with dependency=TRUE)
- **conj_rel**: The dependency relation for conjunctions. By default conj
- **cc_rel**: The dependency relation for the coordinating conjunction. By default cc. This will be removed.
- **unpack**: If TRUE (default), create separate branches for the parent and the node that inherits the parent position
- **no_fill**: Optionally, a character vector with relation types that will be excluded from fill
- **min_dist**: Optionally, a minimal distance between the conj node and its parent
- **max_dist**: Optionally, a maximum distance between the conj node and its parent
- **right_fill_dist**: Should fill to the right of the conjunction be used?
- **compound_rel**: The relation types indicating compounds
- **...**: specify conditions for the conjunction token. For instance, using ’pos = “VERB”‘ to only split VERB conjunctions. This is especially useful to use different no_fill conditions.
**subset_nodes**

**Subset a select_nodes selection**

**Value**

A tokenindex

**Examples**

```r
tokens = tokens_spacy[tokens_spacy$doc_id == 'text5',]

if (interactive()) {
  tokens %>%
    split_UD_conj() %>%
    plot_tree()
}
```

**Description**

Enables more control in reshape operations

**Usage**

```r
subset_nodes(.tokens, subset, copy = TRUE)
```

**Arguments**

- `.tokens` A tokenIndex in which nodes are selected with `select_nodes`
- `.subset` A subset expression (that evaluates to a logical vector). The token column for each labeled node in the tquery can be referred to as `label$column`
- `copy` If TRUE, make a deep copy of `.tokens`. Use if output does not overwrite `.tokens`

**Value**

A tokenIndex with a `nodes` attribute

**Examples**

```r
tokens = tokens_spacy[tokens_spacy$doc_id == 'text4',]

## use a tquery to label the nodes that you want to manipulate
tq = tquery(label='verb', children(relation='nsubj'))

## apply query to select nodes
tokens2 = select_nodes(tokens, tq)

selected_nodes(tokens2)$nodes
tokens2 = subset_nodes(tokens2, verb$relation == 'ROOT')
selected_nodes(tokens2)$nodes
```
**syntax_reader**  
Create a full text browser with highlighted rsyntax annotations

**Description**
Create a full text browser with highlighted rsyntax annotations

**Usage**
```r
syntax_reader(  
tokens,  
annotation,  
value = NULL,  
value2 = NULL,  
meta = NULL,  
token_col = "token",  
filename = NULL,  
view = TRUE,  
random_seed = NA,  
...)  
)
```

**Arguments**
- **tokens**: A tokenIndex
- **annotation**: The name of the column that contains the rsyntax annotation
- **value**: Optionally, a character vector with values in annotation. If used, only these values are fully colored, and the other (non NA) values only have border colors.
- **value2**: Optionally, a character vector with values in annotation other than those specified in `value`. If used, only these values have border colors.
- **meta**: Optionally, a data.frame with document meta data. Has to have a column named `doc_id` of which the values match with the `doc_id` column in `tokens`
- **token_col**: The name of the column in `tokens` with the token text
- **filename**: Optionally, a filename to directly save the file. If not specified, a temporary file is created
- **view**: If TRUE, the browser will immediately be viewed in the viewer panel
- **random_seed**: If a number is given, it is used as a seed to randomize the order of documents. This is useful for validations purposes, because the `doc_id` in the tokenindex is sorted.

... Arguments passed to `create_browser`

**Value**
The url for the file
Examples

tokens = tokens_spacy

## two simple example tqueries
passive = tquery(pos = "VERB*", label = "predicate",
  children(relation = c("agent"), label = "subject"))
active = tquery(pos = "VERB*", label = "predicate",
  children(relation = c("nsubj", "nsubjpass"), label = "subject"))

tokens = annotate_tqueries(tokens, 'clause', pas=passive, act=active)
syntax_reader(tokens, annotation = 'clause', value = 'subject')

tokens_corenlp   Example tokens for coreNLP English

description

Example tokens for coreNLP English

usage

data(tokens_corenlp)

format

data.frame

tokens_dutchclauses   Example tokens for Dutch clauses

description

Example tokens for Dutch clauses

usage

data(tokens_dutchclauses)

format

data.frame
```
tokens_dutchquotes       Example tokens for Dutch quotes

Description
Example tokens for Dutch quotes

Usage
data(tokens_dutchquotes)

Format
data.frame

tokens_spacy             Example tokens for spacy English

Description
Example tokens for spacy English

Usage
data(tokens_spacy)

Format
data.frame

tquery
Create a query for dependency based parse trees in a data.table (CoNLL-U or similar format).
```
**tquery**

**Description**

To find nodes you can use named arguments, where the names are column names (in the data.table on which the queries will be used) and the values are vectors with look-up values.

Children or parents of nodes can be queried by passing the children or parents function as (named or unnamed) arguments. These functions use the same query format as the tquery function, and children and parents can be nested recursively to find children of children etc.

The custom_fill() function (also see fill argument) can be nested to customize which children of a 'labeled' node need to be matched. It can only be nested in a query if the label argument is not NULL, and by default will include all children of the node that have not been assigned to another node. If two nodes have a shared child, the child will be assigned to the closest node.

Please look at the examples below for a recommended syntactic style for using the find_nodes function and these nested functions.

**Usage**

```r
tquery(..., g_id = NULL, label = NA, fill = TRUE, block = FALSE)
```

**Arguments**

- `...` Accepts two types of arguments: name-value pairs for finding nodes (i.e. rows), and functions to look for parents/children of these nodes.
- The name in the name-value pairs need to match a column in the data.table, and the value needs to be a vector of the same data type as the column. By default, search uses case sensitive matching, with the option of using common wildcards (* for any number of characters, and ? for a single character). Alternatively, flags can be used to to change this behavior to 'fixed' (__F), 'ignoring case' (__I) or 'regex' (__R). See details for more information.
- If multiple name-value pairs are given, they are considered as AND statements, but see details for syntax on using OR statements, and combinations.
- To look for parents and children of the nodes that are found, you can use the parents and children functions as (named or unnamed) arguments. These functions have the same query arguments as tquery, but with some additional arguments.
- `g_id` Find nodes by global id, which is the combination of the doc_id, sentence and token_id. Passed as a data.frame or data.table with 3 columns: (1) doc_id, (2) sentence and (3) token_id.
- `label` A character vector, specifying the column name under which the selected tokens are returned. If NA, the column is not returned.
- `fill` Logical. If TRUE (default), the default custom_fill() will be used. To more specifically control fill, you can nest the custom_fill function (a special version of the children function).
- `block` Logical. If TRUE, the node will be blocked from being assigned (labeled). This is mainly useful if you have a node that you do not want to be assigned by fill, but also don’t want to 'label' it. Essentially, block is shorthand for using label and then removing the node afterwards. If block is TRUE, label has to be NA.
Details

Multiple values in a name-value pair operate as OR conditions. For example, tquery(relation = c('nsubj','dobj')) means that the relation column should have the value 'nsubj' OR 'dobj'.

If multiple named arguments are given they operate as AND conditions. For example, tquery(relation = 'nsubj', pos = 'PROPN') means that the relation should be 'nsubj' AND the pos should be 'PROPN'.

This easily combines for the most common use case, which is to select on multiple conditions (relation AND pos), but allowing different (similar) values ('PROPN' OR 'NOUN'). For example: tquery(relation = 'nsubj', pos = c('PROPN','NOUN')) means that the node should have the 'nsubj' relation, but pos can be either 'PROPN' or 'NOUN'.

For more specific behavior, the AND(), OR() and NOT() functions can be used for boolean style conditions.

There are several flags that can be used to change search condition. To specify flags, add a double underscore and the flag character to the name in the name value pairs (...). By adding the suffix __R, query terms are considered to be regular expressions, and the suffix __I uses case insensitive search (for normal or regex search). If the suffix __F is used, only exact matches are valid (case sensitive, and no wildcards). Multiple flags can be combined, such as lemma__RI, or lemma_IR (order of flags is irrelevant).

Value

A tQuery object, that can be used with the apply_queries function.

Examples

```r
## it is convenient to first prepare vectors with relevant words/pos-tags/relations
.SAY_VERBS = c("tell", "show","say", "speak") ## etc.
.QUOTE_RELS = c("ccomp", "dep", "parataxis", "dobj", "nsubjpass", "advcl")
.SUBJECT_RELS = c("su", 'nsubj', 'agent', 'nmod:agent')

quotes_direct = tquery(lemma = .SAY_VERBS,
    children(label = 'source', p_rel = .SUBJECT_RELS),
    children(label = 'quote', p_rel = .QUOTE_RELS))
```

Description

Not strictly required. Only available for elegance and minor memory efficiency

Usage

```r
unselect_nodes(.tokens)
```
**unselect_nodes**

Arguments

- `.tokens` A tokenIndex in which nodes are selected with `select_nodes`.

Value

A tokenIndex (without a `.nodes` attribute)

Examples

```r
tokens = tokens_spacy[tokens_spacy$doc_id == 'text4',]

tq = tquery(relation = "relcl", label = "relative_clause")
tokens = select_nodes(tokens, tq)
selected_nodes(tokens)

tokens = unselect_nodes(tokens)

is.null(attr(tokens, '.nodes'))
```
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