

Package ‘nzilbb.labbcats’

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Title Accessing Data Stored in 'LaBB-CAT' Instances

Imports jsonlite, httr, stringr, utils, rstudioapi

Description 'LaBB-CAT' is a web-based language corpus management system developed by the New Zealand Institute of Language, Brain and Behaviour (NZILBB) - see <<https://labbcats.canterbury.ac.nz>>. This package defines functions for accessing corpus data in a 'LaBB-CAT' instance. You must have at least version 20190425.1121 of 'LaBB-CAT' to use this package.

For more information about 'LaBB-CAT', see Robert Fromont and Jennifer Hay (2008) <[doi:10.3366/E1749503208000142](https://doi.org/10.3366/E1749503208000142)> or Robert Fromont (2017) <[doi:10.1016/j.csl.2017.01.004](https://doi.org/10.1016/j.csl.2017.01.004)>.

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URL <https://github.com/nzilbb/labbcats-R>,
<https://labbcats.canterbury.ac.nz>

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countAnnotations	<i>Gets the number of annotations on the given layer of the given graph.</i>
------------------	--

Description

Returns the number of annotations on the given layer of the given graph (transcript).

Usage

```
countAnnotations(labbcac.url, id, layerId)
```

Arguments

labbcac.url	URL to the LaBB-CAT instance
id	A graph ID (i.e. transcript name)
layerId	A layer name

Value

The number of annotations on that layer

See Also

[getGraphIds](#) [getGraphIdsInCorpus](#) [getGraphIdsWithParticipant](#)

Examples

```
## Not run:
## define the LaBB-CAT URL
labbcats.url <- "https://labbcats.canterbury.ac.nz/demo/"

## Count the number of words in UC427_Viktoriapapp_A_ENG.eaf
token.count <- countAnnotations(labbcats.url, "UC427_Viktoriapapp_A_ENG.eaf", "orthography")

## End(Not run)
```

getAnchors	<i>Gets the given anchors in the given graph.</i>
------------	---

Description

Lists the given anchors in the given graph (transcript).

Usage

```
getAnchors(labbcats.url, id, anchorId)
```

Arguments

labbcats.url	URL to the LaBB-CAT instance
id	A graph ID (i.e. transcript name)
anchorId	A vector of anchor IDs (or a string representing one anchor ID)

Value

A named list of anchors, with members:

1. id The annotation's unique ID,
2. offset The offset from the beginning (in seconds if it's a transcript of a recording, or in characters if it's a text document)
3. confidence A rating from 0-100 of the confidence of the offset, e.g. 10: default value, 50: force-aligned, 100: manually aligned

See Also

[getAnnotations](#)

Examples

```
## Not run:
## define the LaBB-CAT URL
labbcats.url <- "https://labbcats.canterbury.ac.nz/demo/"

## Get the first 20 orthography tokens in UC427_ViktoriaPapp_A_ENG.eaf
orthography <- getAnnotations(labbcats.url, "UC427_ViktoriaPapp_A_ENG.eaf", "orthography", 20, 0)

## Get the start anchors for the above tokens
word.starts <- getAnchors(labbcats.url, "UC427_ViktoriaPapp_A_ENG.eaf", orthography$startId)

## End(Not run)
```

getAnnotationLabels	<i>Gets labels of annotations on a given layer, identified by given annotation IDs.</i>
---------------------	---

Description

Gets labels of annotations on a given layer, identified by given annotation IDs.

Usage

```
getAnnotationLabels(labbcats.url, id, layerId, count = 1,
  no.progress = FALSE)
```

Arguments

labbcats.url	URL to the LaBB-CAT instance
id	A vector of annotation IDs.
layerId	A layer name.
count	The number of annotations on the given layer to retrieve.
no.progress	Optionally suppress the progress bar when multiple fragments are specified - TRUE for no progress bar.

Value

A data frame of labels.

Examples

```
## Not run:
## define the LaBB-CAT URL
labbcats.url <- "https://labbcats.canterbury.ac.nz/demo/"

## Load some search results previously exported from LaBB-CAT
```

```

results <- read.csv("results.csv", header=T)

## Get the topic annotations for the matches
topics <- getAnnotationLabels(labbcat.url, results$MatchId, "topic")

## End(Not run)

```

getAnnotations *Gets the annotations on the given layer of the given graph.*

Description

Returns the annotations on the given layer of the given graph (transcript).

Usage

```

getAnnotations(labbcat.url, id, layerId, pageLength = NULL,
              pageNumber = NULL)

```

Arguments

labbcat.url	URL to the LaBB-CAT instance
id	A graph ID (i.e. transcript name)
layerId	A layer name
pageLength	The maximum number of annotations to return, or null to return all
pageNumber	The zero-based page number to return, or null to return the first page

Value

A named list of annotations, with members:

1. id The annotation's unique ID
2. layerId The name of the layer it comes from
3. label The value of the annotation
4. startId The ID of the start anchor,
5. endId The ID of the end anchor,
6. parentId The ID of the parent annotation,
7. ordinal The ordinal of the annotation among its peers,
8. confidence A rating from 0-100 of the confidence of the label e.g. 10: default value, 50: automatically generated, 100: manually annotated

See Also

[getGraphIds](#) [getGraphIdsInCorpus](#) [getGraphIdsWithParticipant](#) [countAnnotations](#)

Examples

```
## Not run:
## define the LaBB-CAT URL
labbcats.url <- "https://labbcats.canterbury.ac.nz/demo/"

## Get all the orthography tokens in UC427_ViktoriaPapp_A_ENG.eaf
orthography <- getAnnotations(labbcats.url, "UC427_ViktoriaPapp_A_ENG.eaf", "orthography")

## Get the first 20 orthography tokens in UC427_ViktoriaPapp_A_ENG.eaf
orthography <- getAnnotations(labbcats.url, "UC427_ViktoriaPapp_A_ENG.eaf", "orthography", 20, 0)

## End(Not run)
```

getAvailableMedia *List the media available for the given graph.*

Description

List the media available for the given graph.

Usage

```
getAvailableMedia(labbcats.url, id)
```

Arguments

labbcats.url	URL to the LaBB-CAT instance
id	A graph ID (i.e. transcript name)

Value

A named list of media files available for the given graph, with members:

1. trackSuffix The track suffix of the media
2. mimeType The MIME type of the file
3. url URL to the content of the file
4. name Name of the file

See Also

[getGraphIds](#)

Examples

```
## Not run:  
## define the LaBB-CAT URL  
labbcats.url <- "https://labbcats.canterbury.ac.nz/demo/"  
  
## List the media files available for BR2044_01ly0h1son.eaf  
media <- getAvailableMedia(labbcats.url, "BR2044_01ly0h1son.eaf")  
  
## End(Not run)
```

getCorpusIds	<i>Gets a list of corpus IDs.</i>
--------------	-----------------------------------

Description

Returns a list of corpora in the given 'LaBB-CAT' instance.

Usage

```
getCorpusIds(labbcats.url)
```

Arguments

labbcats.url URL to the LaBB-CAT instance

Value

A list of corpus IDs

Examples

```
## Not run:  
## List corpora  
corpora <- getCorpusIds("https://labbcats.canterbury.ac.nz/demo/")  
  
## End(Not run)
```

getDictionaries *List the dictionaries available.*

Description

List the dictionaries available.

Usage

```
getDictionaries(labbcat.url)
```

Arguments

labbcat.url URL to the LaBB-CAT instance

Value

A named list of layer manager IDs, each of which containing a list of dictionaries that the layer manager makes available.

See Also

[getDictionaryEntries](#)

Examples

```
## Not run:  
## List the dictionaries available  
dictionaries <- getDictionaries("https://labbcat.canterbury.ac.nz/demo/")  
  
## End(Not run)
```

getDictionaryEntries *Lookup entries in a dictionary.*

Description

Lookup entries in a dictionary.

Usage

```
getDictionaryEntries(labbcat.url, managerId, dictionaryId, keys)
```


Arguments

labbcats.url	URL to the LaBB-CAT instance
managerId	The layer manager ID of the dictionary, as returned by getDictionaries
dictionaryId	The ID of the dictionary, as returned by getDictionaries
keys	A list of entries to look up

Value

A data frame with the keys and their dictionary entries.

See Also

[getDictionaries](#)

Examples

```
## Not run:
## define the LaBB-CAT URL
labbcats.url <- "https://labbcats.canterbury.ac.nz/demo/"

keys <- c("the", "quick", "brown", "fox")

## get the pronunciations according to CELEX
entries <- getDictionaryEntries(labbcats.url, "CELEX-EN", "Phonology (wordform)", keys)

## End(Not run)
```

getGraphIds	<i>Gets a list of graph IDs.</i>
-------------	----------------------------------

Description

Returns a list of graph IDs (i.e. transcript names).

Usage

```
getGraphIds(labbcats.url)
```

Arguments

labbcats.url	URL to the LaBB-CAT instance
--------------	------------------------------

Value

A list of graph IDs

Examples

```
## Not run:  
## List all transcripts  
transcripts <- getGraphIds("https://labbcac.canterbury.ac.nz/demo/")  
  
## End(Not run)
```

`getGraphIdsInCorpus` *Gets a list of corpus IDs.*

Description

Returns a list of corpora in the given 'LaBB-CAT' instance.

Usage

```
getGraphIdsInCorpus(labbcac.url, id)
```

Arguments

<code>labbcac.url</code>	URL to the LaBB-CAT instance
<code>id</code>	The ID (name) of the corpus

Value

A list of corpus IDs

Examples

```
## Not run:  
## List transcripts in the QB corpus  
transcripts <- getGraphIdsInCorpus("https://labbcac.canterbury.ac.nz/demo/", "QB")  
  
## End(Not run)
```

`getGraphIdsWithParticipant`*Gets a list of IDs of graphs that include the given participant.*

Description

Returns a list of IDs of graphs (i.e. transcript names) that include the given participant.

Usage

```
getGraphIdsWithParticipant(labbcat.url, id)
```

Arguments

<code>labbcat.url</code>	URL to the LaBB-CAT instance
<code>id</code>	A participant ID

Value

A list of graph IDs

See Also

[getParticipantIds](#)

Examples

```
## Not run:
## define the LaBB-CAT URL
labbcat.url <- "https://labbcat.canterbury.ac.nz/demo/"

## List transcripts in which UC427_ViktoriaPapp_A_ENG speaks
transcripts <- getGraphIdsWithParticipant(labbcat.url, "UC427_ViktoriaPapp_A_ENG")

## End(Not run)
```

`getId`*Gets the store's ID.*

Description

The store's ID - i.e. the ID of the 'LaBB-CAT' instance.

Usage

```
getId(labbcat.url)
```

Arguments

labbcats.url URL to the LaBB-CAT instance

Value

The annotation store's ID

Examples

```
## Not run:
## Get ID of LaBB-CAT instance
instance.id <- getId("https://labbcats.canterbury.ac.nz/demo/")

## End(Not run)
```

getLayer	<i>Gets a layer definition.</i>
----------	---------------------------------

Description

Gets a layer definition.

Usage

```
getLayer(labbcats.url, id)
```

Arguments

labbcats.url URL to the LaBB-CAT instance
 id ID of the layer to get the definition for

Value

The definition of the given layer, with members:

1. id The layer's unique ID
2. parentId The layer's parent layer ID
3. description The description of the layer
4. alignment The layer's alignment - 0 for none, 1 for point alignment, 2 for interval alignment
5. peers Whether children have peers or not
6. peersOverlap Whether child peers can overlap or not
7. parentIncludes Whether the parent t-includes the child
8. saturated Whether children must temporally fill the entire parent duration (true) or not (false)
9. parentIncludes Whether the parent t-includes the child
10. type The type for labels on this layer
11. validLabels List of valid label values for this layer

See Also

[getLayerIds](#) [getLayers](#)

Examples

```
## Not run:  
## Get the definition of the orthography layer  
orthography.layer <- getLayer("https://labbcac.canterbury.ac.nz/demo/", "orthography")  
  
## End(Not run)
```

getLayerIds	<i>Gets a list of layer IDs.</i>
-------------	----------------------------------

Description

Layer IDs are annotation 'types'.

Usage

```
getLayerIds(labbcac.url)
```

Arguments

labbcac.url URL to the LaBB-CAT instance

Value

A list of layer IDs

Examples

```
## Not run:  
## Get names of all layers  
layer.ids <- getLayerIds("https://labbcac.canterbury.ac.nz/demo/")  
  
## End(Not run)
```

getLayers	<i>Gets a list of layer definitions.</i>
-----------	--

Description

Gets a list of layer definitions.

Usage

```
getLayers(labbcat.url)
```

Arguments

labbcat.url URL to the LaBB-CAT instance

Value

A list of layer definitions, with members:

1. id The layer's unique ID
2. parentId The layer's parent layer ID
3. description The description of the layer
4. alignment The layer's alignment - 0 for none, 1 for point alignment, 2 for interval alignment
5. peers Whether children have peers or not
6. peersOverlap Whether child peers can overlap or not
7. parentIncludes Whether the parent t-includes the child
8. saturated Whether children must temporally fill the entire parent duration (true) or not (false)
9. parentIncludes Whether the parent t-includes the child
10. type The type for labels on this layer
11. validLabels List of valid label values for this layer

See Also

[getLayerIds](#)

Examples

```
## Not run:  
## Get definitions of all layers  
layers <- getLayers("https://labbcat.canterbury.ac.nz/demo/")  
  
## End(Not run)
```

getMatchingGraphIds *Gets a list of IDs of graphs that match a particular pattern.*

Description

Gets a list of IDs of graphs (i.e. transcript names) that match a particular pattern.

Usage

```
getMatchingGraphIds(labbcat.url, expression, pageLength = NULL,  
  pageNumber = NULL, order = NULL)
```

Arguments

labbcat.url	URL to the LaBB-CAT instance
expression	An expression that determines which graphs match
pageLength	The maximum number of IDs to return, or null to return all
pageNumber	The zero-based page number to return, or null to return the first page
order	An expression that determines the order the graphs are listed in

Details

The results can be exhaustive, by omitting pageLength and pageNumber, or they can be a subset (a 'page') of results, by given pageLength and pageNumber values.

The order of the list can be specified. If omitted, the graphs are listed in ID order.

The expression language is currently not well defined, but expressions such as those in the examples can be used.

Value

A list of graph IDs (i.e. transcript names)

Examples

```
## Not run:  
## define the LaBB-CAT URL  
labbcat.url <- "https://labbcat.canterbury.ac.nz/demo/"  
  
## Get all transcripts whose names start with "BR"  
transcripts <- getMatchingGraphIds(labbcat.url, "id MATCHES 'BR.+')"  
  
## Get the first twenty transcripts in the "QB" corpus  
transcripts <- getMatchingGraphIds(  
  labbcat.url, "my('corpus').label = 'QB'", 20, 0)  
  
## Get the second transcript that has "QB247_Jacqui" as a speaker  
transcripts <- getMatchingGraphIds(  
  labbcat.url, "my('corpus').label = 'QB247_Jacqui'", 1, 1)
```

```
labbcats.url, "'QB247_Jacqui' IN labels('who')", 1, 1)

## Get all transcripts whose names start with "BR" and have "QB247_Jacqui" as a speaker,
## in word-count order
transcripts <- getMatchingGraphIds(
  labbcats.url, "my('corpus').label = 'QB' AND 'QB247_Jacqui' IN labels('who')", 1, 1,
  "my('transcript_word_count').label")

## End(Not run)
```

getMedia

Gets a given media track for a given graph.

Description

Gets a given media track for a given graph.

Usage

```
getMedia(labbcats.url, id, trackSuffix = "", mimeType = "audio/wav")
```

Arguments

labbcats.url	URL to the LaBB-CAT instance
id	A graph ID (i.e. transcript name)
trackSuffix	The track suffix of the media
mimeType	The MIME type of the media

Value

A URL to the given media for the given graph

See Also

[getGraphIds](#)

Examples

```
## Not run:
## define the LaBB-CAT URL
labbcats.url <- "https://labbcats.canterbury.ac.nz/demo/"

## Get URL for the WAV file for BR2044_OllyOhlson.eaf
media <- getMedia(labbcats.url, "BR2044_OllyOhlson.eaf")

## Get URL for the 'QuakeFace' video file for BR2044_OllyOhlson.eaf
media <- getMedia(labbcats.url, "BR2044_OllyOhlson.eaf", "_face", "video/mp4")
```



```
## End(Not run)
```

getMediaTracks	<i>List the predefined media tracks available for transcripts.</i>
----------------	--

Description

List the predefined media tracks available for transcripts.

Usage

```
getMediaTracks(labbcat.url)
```

Arguments

labbcat.url URL to the LaBB-CAT instance

Value

A list of media track definitions.

Examples

```
## Not run:  
## Get the media tracks configured in LaBB-CAT  
tracks <- getMediaTracks("https://labbcat.canterbury.ac.nz/demo/")  
  
## End(Not run)
```

getParticipantIds	<i>Gets a list of participant IDs.</i>
-------------------	--

Description

Returns a list of participant IDs.

Usage

```
getParticipantIds(labbcat.url)
```

Arguments

labbcat.url URL to the LaBB-CAT instance

Value

A list of participant IDs

Examples

```
## Not run:
## List all speakers
speakers <- getParticipantIds("https://labbcats.canterbury.ac.nz/demo/")

## End(Not run)
```

getSoundFragments *Gets sound fragments from 'LaBB-CAT'.*

Description

Gets sound fragments from 'LaBB-CAT'.

Usage

```
getSoundFragments(labbcats.url, id, start, end, sampleRate = NULL,
  no.progress = FALSE)
```

Arguments

labbcats.url	URL to the LaBB-CAT instance
id	The graph ID (transcript name) of the sound recording, or a vector of graph IDs.
start	The start time in seconds, or a vector of start times.
end	The end time in seconds, or a vector of end times.
sampleRate	Optional sample rate in Hz - if a positive integer, then the result is a mono file with the given sample rate.
no.progress	Optionally suppress the progress bar when multiple fragments are specified - TRUE for no progress bar.

Value

The name of the file, which is saved in the current directory, or a list of names of files, if multiple id's/start's/end's were specified

If a list of files is returned, they are in the order that they were returned by the server, which *should* be the order that they were specified in the id/start/end lists.

Examples

```
## Not run:
## define the LaBB-CAT URL
labbcats.url <- "https://labbcats.canterbury.ac.nz/demo/"

## Get the 5 seconds starting from 10s after the beginning of a recording
wav.file <- getSoundFragments(labbcats.url, "AP2505_Nelson.eaf", 10.0, 15.0)

## Get the 5 seconds starting from 10s as a mono 22kHz file
wav.file <- getSoundFragments(labbcats.url, "AP2505_Nelson.eaf", 10.0, 15.0, 22050)

## Load some search results previously exported from LaBB-CAT
results <- read.csv("results.csv", header=T)

## Get a list of fragments
wav.files <- getSoundFragments(labbcats.url, results$Transcript, results$Line, results$LineEnd)

## Get a list of fragments with no progress bar
wav.file <- getSoundFragments(
  labbcats.url, results$Transcript, results$Line, results$LineEnd, no.progress=TRUE)

## End(Not run)
```

labbcatsCredentials	<i>Sets the username and password that the package should use for connecting to a given LaBB-CAT server in future function calls.</i>
---------------------	---

Description

This step is optional, as all functions will prompt the user for the username and password if required. If the script is running in RStudio, then the RStudio password input dialog is used, hiding the credentials from view. Otherwise, the console is used, and credentials are visible.

Usage

```
labbcatsCredentials(labbcats.url, username, password)
```

Arguments

labbcats.url	URL to the LaBB-CAT instance
username	The LaBB-CAT username, if it is password-protected
password	The LaBB-CAT password, if it is password-protected

Details

The recommended approach is to *not* use labbcatsCredentials, to avoid saving user credentials in script files that may eventually become visible to other. Use labbcatsCredentials *only* in cases where the script execution is unsupervised.

Value

FALSE if the username/password are incorrect, NULL if they username/password are correct but the version of LaBB-CAT is incompatible with the package, and TRUE otherwise.

Examples

```
## Not run:
## define the LaBB-CAT URL
labbcats.url <- "https://labbcats.canterbury.ac.nz/demo/"

## specify the username/password in the script
## (only use labbcatsCredentials for scripts that must execute unsupervised!)
labbcatsCredentials(labbcats.url, "demo", "demo")

## End(Not run)
```

 nzilbb.labbcats

Accessing Data Stored in 'LaBB-CAT' Instances

Description

'LaBB-CAT' is a web-based language corpus management system developed by the New Zealand Institute of Language, Brain and Behaviour (NZILBB) - see <<https://labbcats.canterbury.ac.nz>>. This package defines functions for accessing corpus data in a 'LaBB-CAT' instance. You must have at least version 20190425.1121 of 'LaBB-CAT' to use this package. For more information about 'LaBB-CAT', see Robert Fromont and Jennifer Hay (2008) <[doi:10.3366/E1749503208000142](https://doi.org/10.3366/E1749503208000142)> or Robert Fromont (2017) <[doi:10.1016/j.csl.2017.01.004](https://doi.org/10.1016/j.csl.2017.01.004)>.

Details

Package: nzilbb.labbcats
 Version: 0.2-2
 Date: 2019-04-25
 Title: Accessing Data Stored in 'LaBB-CAT' Instances
 Authors@R: c(person("Robert", "Fromont", role = c("aut", "cre"), email = "robert.fromont@canterbury.ac.nz"))
 Imports: jsonlite, httr, stringr, utils, rstudioapi
 Description: 'LaBB-CAT' is a web-based language corpus management system developed by the New Zealand Institute of Language, Brain and Behaviour (NZILBB)
 License: GPL (>= 3)
 Copyright: New Zealand Institute of Language, Brain and Behaviour, University of Canterbury
 URL: <https://github.com/nzilbb/labbcats-R>, <https://labbcats.canterbury.ac.nz>
 RoxygenNote: 6.1.1
 Author: Robert Fromont [aut, cre]
 Maintainer: Robert Fromont <robert.fromont@canterbury.ac.nz>

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nzilbb.labbcats	Accessing Data Stored in 'LaBB-CAT' Instances

'LaBB-CAT' is a web-based language corpus management system and this package provides access to data stored in a 'LaBB-CAT' instance. You must have at least version 20190425.1121 of 'LaBB-CAT' to use this package.

Author(s)

NA

References

Robert Fromont and Jennifer Hay, "ONZE Miner: the development of a browser-based research tool", 2008 Robert Fromont, "Toward a format-neutral annotation store", 2017

Examples

Not run:

```
## define the LaBB-CAT URL
labbcats.url <- "https://labbcats.canterbury.ac.nz/demo/"

## Load some search results previously exported from LaBB-CAT
results <- read.csv("results.csv", header=T)

## Get the phonemic transcriptions for the matches
phonemes <- getAnnotationLabels(labbcats.url, results$MatchId, "phonemes")

## Get sound fragments for the matches
wav.files <- getSoundFragments(labbcats.url, results$Transcript, results$Line, results$LineEnd)

## End(Not run)
```

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