Package 'bioacoustica'

November 11, 2016

Type Package

Title Provides access to the BioAcoustica platform through R

Version 2.0

Date 2016-10-25

Description this package was designed to interface bioacoustica (http://bio.acousti.ca/).
In particular, it provides utilities to list and download available annotations.
In addition, it allows users to programatically upload their data.

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Depends R (>= 2.15.0),
MASS,
data.table,
RCurl,
xml2,
tuneR

LazyLoad TRUE

Collate 'get_annotations.R'
'utils.R'

URL https://github.com/BioAcoustica/bioacousticaR

RoxygenNote 5.0.1

Suggests testthat,
devtools

R topics documented:

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dowloadFilesForAnnotations

Retreive list of annotation files from a query

Description

This function uses a formated query (i.e. table) to retreive annotation raw data

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Usage

```
dowloadFilesForAnnotations(query, dst_dir, prefix = "annotation", force = F,
   ...)
```

Arguments

query	a data.table or data.frame (see details)
dst_dir	a directory to store the resulting data
prefix	a string to prepend to filenames
force	whether to downoad and overwrite pre-existing file
...	extra argument passed to link{getAnnotationFile}

Details

query must contain the columns id, start, end, file. They indicate, the annotation uid , the start and end of the wav file, and the url of the wav file, respactively. Typically, it will be obtained through [getAllAnnotationData](#).

Value

an inflated query with a extra columns mapping the path of the saved audio files

See Also

[getAllAnnotationData](#)

Examples

```
## Not run:
# we retreive all annotations from the database
all_annotations = getAllAnnotationData()
# we filter for only those made by one author before a certain date
query = all_annotations[author=="qgeissmann" & date < "2016-10-26"]
# we make one file for each annotation and save it in dst_dir
my_annotations <- dowloadFilesForAnnotations(query,
                                 dst_dir = "/tmp/my_annotation",
                                 verbose=T)

## End(Not run)
```

---

getAllAnnotationData   *Dowload a list of all annotations*

Description

Download the information corresponding to all available annotaions on bioacoustica

Usage

```
getAllAnnotationData(path = "/R/annotations")
```

Arguments

path	the view containing the annotations

Value

a data.table. The column id refers to the unique identifier of an annotation. start and end identify the section of this annotation and file maps the URL of the raw audio file. Other annotation data are available as extra columns.

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getAnnotationFile   *Fetch a portion of a remote wav file*

Description

This function can download only a portion of a wave file stored online and store it locally as a new wave file. It proceeds by dowloading metadata, uses them to locate the file chunk and reconstitute a file

Usage

```
getAnnotationFile(file, start, end, dst, force = F, first_chunk = 1024,
  verbose = F)
```

Arguments

file	the URL of a file
start	the start of the desired section, in second
end	the end of the desired section, in second
dst	a character vector indicating where to save the resulting file
force	whether to downoad and overwrite pre-existing file
first_chunk	the number of bytes downloaded at first in order to identify the file
verbose	weher to print extra information

Value

the path to resulting file

See Also

[dowloadFilesForAnnotations](), a wrapper around this function