

Package ‘bbsAssistant’

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Title Helper Functions for Obtaining Data and Information from the North American Breeding Bird Survey (BBS)

Version 1.0.0

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Description This package provides helper functions for downloading and manipulating North American Breeding Bird Survey (BBS) data and metadata from the U.S. Geological Survey. The functionality streamlines this the process by which these data are accessed, downloaded locally, and imported into R. Depends: R (>= 3.5.1).

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Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 6.1.1

Imports readr,
stringr,
dplyr,
xml2,
feather,
here,
glue,
rvest,
tidyr,
magrittr

Suggests testthat (>= 2.1.0),
ggplot2,
covr,
knitr,
usethis,
rmarkdown,
spelling

VignetteBuilder knitr

Language en-US

URL <https://github.com/TrashBirdEcology/bbsAssistant>

BugReports <https://github.com/TrashBirdEcology/bbsAssistant/issues>

R topics documented:

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|--------------------|------------------------------------------------------|
| export_bbsFeathers | <i>Save BBS dataframe as a feather file on disk.</i> |
|--------------------|------------------------------------------------------|

Description

Save the BBS data frame as a feather file to disk for easier import.

Usage

```
export_bbsFeathers(dataIn, newDir = here::here("bbsData/"), filename)
```

Arguments

| | |
|----------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| dataIn | Data to be saved to local disk (e.g., /bbsData/). This data frame is a product of merging route information and raw count data. Data frame should have at least the columns <code>dplyr::select(year, countrynum, statenum, route, bcr, latitude, longitude, aou, stoptotal)</code> . |
| newDir | Where to save the BBS data as feathers. If not specified will default to /bbsData/. |
| filename | Name of the new filename (e.g., 'arizona.zip'). This should be the same filename used to import the .zip from FTP (i.e, it should end with ".zip") This function will replace .zip with .feather |

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|----------------------|--------------------------------------------------------|
| get_analysis_results | <i>Get annual abundance indices from BBS analyses.</i> |
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Description

Downloads all species-regions annual abundances indices from various .csv files on the BBS analysis results page. See [results metadata](#) for analysis results and trend estimates.

Usage

```
get_analysis_results(url = NULL, analysis = "trend.ests")
```

Arguments

| | |
|----------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|
| url | Web link to the .csv file for annual abundance indices. Default = NULL. |
| analysis | Default = "trend.ests". Must be one of c("annual.ind.2016", "trend.ests", "core.trend.revised.2017", "core.2017", "expanded.2017", "core.twedt.revised.2017") |

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|-------------|-----------------------------------------------------------------------------------------|
| get_bbsData | <i>Download USGS Breeding Bird Survey data to file and import into the environment.</i> |
|-------------|-----------------------------------------------------------------------------------------|

Description

This function downloads a select subset or all the BBS data from the FTP server using the .txt file downloaded from get_regions() or using specified regions (e.g. Florida, Florida.zip). The data are saved to a temporary folder. This function was adapted from **oharar/rBBS** package. Note: this function requires an internet connection. If the bbs data are on file, please specify in the parameter file.

Usage

```
get_bbsData(file,
  dir = "ftp://ftpext.usgs.gov/pub/er/md/laurel/BBS/DataFiles/States/",
  year = NULL, aou = NULL, countrinum = NULL, states = NULL)
```

Arguments

| | |
|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|
| file | One file name including the .zip extension ("stateX.zip"). Preferably download a single state at a time, otherwise run time will take >1 minutes. |
| dir | URL to the StatesFiles. |
| year | Vector of years. Default = NULL (all years). |
| aou | Vector of AOU numeric codes. Default = NULL (all species). (For species list visit the BBS FTP site (ftpext.usgs.gov/pub/er/md/laurel/BBS/DataFiles/). |
| countrinum | Vector of country ID #'s. Default = NULL (all countryNums). |
| states | Vector of state names Default = NULL (all states). |

Value

If download successful, a dataframe with the results.

Examples

```
# download all species and years from Nebraska.
```

```
## Not run:
NE <- getDataBBS(file = "Nebrask.zip")
```

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

get_credibility_trends

Get data credibility and trends from the BBS analysis results

Description

The BBS provides regional and state-wide species population trend estimates. They also include a 'data credibility' rating (low, medium, or high deficiencies) for each species-region combination. This function uses web scraping to capture population trends and their credibility ratings.

Usage

```
get_credibility_trends(url = "https://www.mbr-pwrc.usgs.gov/cgi-bin/atlas15.pl?FLA&2&15&csrfmi
```

Arguments

| | |
|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------|
| url | Web address of the region or state for which species' population trends and credibility ratings are to be scraped. Default example is 'Kansas,USA'. |
|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------|

get_regions

Get the list of available data regions from the BBS website

Description

Read in list of regions (State/Prov/TerrName), from RegionCodes.txt, and then extract list of where the 10-stop data is kept. This function was adapted from the function **rBBS::GetRegions**.

Usage

```
get_regions(source = "ftp://ftpext.usgs.gov/pub/er/md/laurel/BBS/DataFiles/",
bbsDir = NULL)
```

Arguments

| | |
|--------|------------------------------------------------------------------------------------------------------------------------------------------|
| source | The website or location of the BBS data files. |
| bbsDir | The location of the local folder containing the bbs raw data. If this folder DNE, a new folder will be created in the working directory. |

| | |
|---------------|----------------------------------------------------|
| get_routeInfo | <i>Download route information from USGS server</i> |
|---------------|----------------------------------------------------|

Description

This function downloads information about route location from the BBS FTP server. This function was adapted from **oharar/rBBS** package.

Usage

```
get_routeInfo(routesFile = "routes.zip",
  routesDir = "ftp://ftpext.usgs.gov/pub/er/md/laurel/BBS/DataFiles/",
  RouteTypeID = 1, Stratum = NULL, BCR = NULL)
```

Arguments

| | |
|-------------|-------------------------------------------------------------------------------------------------------------|
| routesFile | Name of the route information file. Usually "routes.zip". |
| routesDir | Location of the routes.zip folder Should be in DatFiles folder (default). |
| RouteTypeID | One or more numbers indicating route substrate (1=roadside;2=water;3=off-road; Default = 1, roadside only). |
| Stratum | A vector of BBS physiographic stratum codes by which to filter the routes. |
| BCR | A vector of Bird Conservation Region codes where by which to filter the routes. |

Value

If download successful, a dataframe with the results.

Examples

```
# download BBS route data.
## Not run:
RouteInfo <- get_routeInfo()

## End(Not run)
```

| | |
|-----------------|-------------------------------|
| get_speciesList | <i>Download species names</i> |
|-----------------|-------------------------------|

Description

Read in list of species names, from SpeciesList.txt, and then extract list of where the data is kept. This function was borrowed from the function **rBBS::getSpNames()**.

Usage

```
get_speciesList(Dir = "ftp://ftpext.usgs.gov/pub/er/md/laurel/BBS/DataFiles/")
```

Arguments

Dir ftp URL for directory with data files

Value

A dataframe

| | |
|-----------|--------------------------------------------------------------------------------|
| get_unzip | <i>Downloads and unzips a zip archive to file from the USGS BBS FTP server</i> |
|-----------|--------------------------------------------------------------------------------|

Description

This function downloads the BBS data from the USGS FTP server to a temporary file, decompresses the .zip files, and imports the uncompressed .csv file into R. This function was adapted from the function `rBBS::GetUnzip()`.

Usage

```
get_unzip(ZipName, FileName)
```

Arguments

ZipName file to download
 FileName file to unzip to

Details

Used internally. If ZipName begins with 'http' or 'ftp', then download and unzip to Filename and return as a dataframe. Otherwise, unzip the file specified by ZipName and import into R as a dataframe.

Value

A dataframe

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|----------------|-------------------------------------------------------------------------------------------------------------------------------|
| import_bbsData | <i>A wrapper function for downloading raw data, filtering by species names/AOU codes, and merging with route information.</i> |
|----------------|-------------------------------------------------------------------------------------------------------------------------------|

Description

This function will import BBS data which has already been downloaded to file. Some parts of this function were borrowed from R package [oharar/rBBS](#).

Usage

```
import_bbsData(file, dir, year = NULL, aou = NULL, countrynum = NULL,
  states = NULL, routesFile = "routes.zip",
  routesDir = "ftp://ftpext.usgs.gov/pub/er/md/laurel/BBS/DataFiles/",
  RouteTypeID = 1, Stratum = NULL, BCR = NULL)
```

Arguments

| | |
|-------------|-------------------------------------------------------------------------------------------------------------|
| file | The name of the zipfile to be downloaded from dir |
| dir | http:// or ftp:/ link to bbs data location (here: state files) |
| year | Vector of years. Default = NULL (all years). |
| aou | Vector of AOU #s Default = NULL (all species). |
| countrynum | Vector of country ID #'s. Default = NULL (all countryNums). |
| states | Vector of state names Default = NULL (all states). |
| routesFile | Name of the route information file. Usually "routes.zip". |
| routesDir | Location of the routes.zip folder Should be in DatFiles folder (default). |
| RouteTypeID | One or more numbers indicating route substrate (1=roadside;2=water;3=off-road; Default = 1, roadside only). |
| Stratum | A vector of BBS physiographic stratum codes by which to filter the routes. |
| BCR | A vector of Bird Conservation Region codes where by which to filter the routes. |

| | |
|--------------------|-------------------------------------------|
| import_bbsFeathers | <i>Load the BBS data feathers into R.</i> |
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Description

This function loads .feather files into disk given a directory.

Usage

```
import_bbsFeathers(newDir, filename)
```

Arguments

| | |
|----------|--------------------------------------------------------------------------------------------------------------------------------|
| newDir | Where the BBS feathers are saved. |
| filename | Name of the feather filename (e.g., 'arizona.zip' or 'arizona'). This function will replace .zip with .feather when necessary. |

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| subset_speciesList | <i>Subset the BBS data by species, functional traits, and/or body mass. Default is null.</i> |
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Description

This function allows the user to subset the BBS data by specific species using AOU numbers.

Usage

```
subset_speciesList(myData, aou.ind = NULL, order.ind = NULL,
  fam.ind = NULL)
```

Arguments

| | |
|------------------------|---------------------------------------------------------------------------------------------------------------|
| <code>myData</code> | A data frame containing the BBS data. Must contain the column "aou". |
| <code>aou.ind</code> | Numeric or vector of numeric values of the AOU codes. These are the species you want to REMOVE from analysis. |
| <code>order.ind</code> | Character or vector of characters of taxonomic orders to remove |
| <code>fam.ind</code> | Character or vector of characters of taxonomic family to remove |

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