

Package ‘bbsAssistant’

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

Version 0.0.0.9000

Description Provides various helper functions for getting BBS data and metadata.

Depends R (>= 3.5.3)

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R topics documented:

| | |
|------------------------------|----------|
| export_bbsFeathers | 2 |
| funcMass | 2 |
| GetSpNames | 3 |
| get_bbsAous | 3 |
| get_bbsData | 4 |
| get_credTrends | 5 |
| get_regions | 5 |
| get_routeInfo | 6 |
| get_unzip | 6 |
| import_bbsData | 7 |
| import_bbsFeathers | 8 |
| subset_byAou | 8 |
| Index | 9 |

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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)
```

Arguments

| | |
|----------|---|
| dataIn | The BBS data to save. |
| newDir | Where to save the BBS data as feathers. |
| filename | Name of the new filename (e.g., 'arizona.zip'). This function will replace .zip with .feather |

| | |
|----------|--|
| funcMass | <i>Load functional trait and mass data</i> |
|----------|--|

Description

Load functional trait and mass data

Usage

```
funcMass(dataWD = paste0(getwd(), "/data"), fxn = TRUE, mass = TRUE)
```

Arguments

| | |
|--------|---|
| dataWD | Where the functional trait and mass dataframes are stored. |
| fxn | Logical. Retrieves functional trait data (reference). |
| mass | Logical. Retrieves body mass information (Dunning reference). |

| | |
|------------|-------------------------------|
| GetSpNames | <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

Usage

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

Arguments

| | |
|-----|---------------------------------------|
| Dir | ftp URL for directory with data files |
|-----|---------------------------------------|

Value

A dataframe

| | |
|-------------|--|
| get_bbsAous | <i>Import the species list used by the BBS from website or local disk.</i> |
|-------------|--|

Description

This function imports the species list (including AOU numbers) from their website. This list can be used to subset the species by name, AOU number, etc.

Usage

```
get_bbsAous(file = "ftp://ftpext.usgs.gov/pub/er/md/laurel/BBS/DataFiles/SpeciesList.txt",  
            skip = 7)
```

Arguments

| | |
|-----------|--|
| file | A character string for location for the species list (as .txt). |
| skipEmpty | Numeric, default = 7. The number of lines to skip. This may need to be updated if the file on webpage changes. |

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

Description

This function downloads a select or all the BBS data from the FTP server using the .txt file downloaded from get_regions(). 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, countrynum = 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 .) |
| countrynum | 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_credTrends

Get data credibility and trends from the BBS analysis

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_credTrends(url = "https://www.mbr-pwrc.usgs.gov/cgi-bin/atlas15.pl?KAN&2&15&csrfmiddlewaretoken=...")
```

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

Usage

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

| | |
|-------------|---|
| 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. |
| routeDir | Location of the routes.zip folder Should be in DatFiles folder (default). |
| routeFile | Name of the route information file. Usually "routes.zip". |

Value

If download successful, a dataframe with the results.

Examples

```
# download BBS route data.

## Not run:
RouteInfo <- get_routeInfo()

## End(Not run)
```

| | |
|-----------|--|
| get_unzip | <i>Downloads and unzips a zip archive to file.</i> |
|-----------|--|

Description

Downloads and unzips a zip archive to file.

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 Zipname and return as a data.frame.

Value

A dataframe

| | |
|----------------|---|
| 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 **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). |
| 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. |
| zipFileNames | One or more file names ("state.zip"), char vector. Preferably download a single state at a time, otherwise run time will take >1 minutes. |
| countryName | Vector of country names. Default = NULL (all countryNames). |
| regions | Vector of regionCodes. Default = NULL (all regions). |
| routeDir | Location of the routes.zip folder Should be in DatFiles folder (default). |
| routeFile | Name of the route information file. Usually "routes.zip". |

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

Description

Load the BBS data feathers into R.

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. |

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

Description

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

Usage

```
subset_byAou(myData, subset.by = NULL, aou.ind = NULL,
             order.ind = NULL, fam.ind = NULL)
```

Arguments

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

Index

`export_bbsFeathers`, [2](#)

`funcMass`, [2](#)

`get_bbsAous`, [3](#)

`get_bbsData`, [4](#)

`get_credTrends`, [5](#)

`get_regions`, [5](#)

`get_routeInfo`, [6](#)

`get_unzip`, [6](#)

`GetSpNames`, [3](#)

`import_bbsData`, [7](#)

`import_bbsFeathers`, [8](#)

`subset_byAou`, [8](#)