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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Encoding UTF-8

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Imports gdata,
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magrittr

Suggests testthat (>= 2.1.0),
ggplot2

R topics documented:

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export_bbsFeathers   *Save BBS dataframe as a feather file on disk.*

Description

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

Usage

```
export_bbsFeathers(dataIn, newDir = NULL, 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 dplyr::select(year, countrynum, statenum, route, bcr, latitude, longitude,aou, stoptotal).
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_bbsData   *Download USGS Breeding Bird Survey data to file and import into the environment.*

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, 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)
```

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get_credibility_trends

Scrape BBS data credibility scores and population trend estimates from BBS website

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Description

A function using web scraping tools to retrieve region-specific species trend estimates @sauer2017north and data credibility ratings. Current functionality does not include retrieving estimates per species, but rather per region.

Usage

```
get_credibility_trends(url = NULL)
```

Arguments

url   The url location of the web page to be scraped. Currently, you will have to specify this url. Default url is House Sparrows in Florida.

References

Regional Credibility Measures information can be found online at https://www.mbr-pwrc.usgs.gov/bbs/credhm09.html

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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/atlasa15.pl?KAN&2&15&csrfmiddleware
```

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'.

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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.

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get_routeInfo   *Download route information from USGS server*

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_speciesList   *Download species names*

Description

Read in list of species names, from SpeciesList.txt, and then extract list of where the data is kept

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

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get_unzip   *Downloads and unzips a zip archive to file.*

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 | *A wrapper function for downloading raw data, filtering by species names/AOU codes, and merging with route information.* |

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:// pr 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	*Load the BBS data feathers into R.*

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_speciesList	*Subset the BBS data by species, functional traits, and/or body mass. Default is null.*

Description

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

Usage

```
subset_speciesList(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

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