Package 'lifeR'

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Type Package			
Title Identify Sites for Your Bird List			
Version 1.0.3			
Description A suite of tools to use the 'eBird' database (https://ebird.org/home/) and APIs to compare users' species lists to recent observations and create a report of the top sites to visit to see new species.			
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RecentNearby Recent nearby eBird observations

Description

Recent nearby eBird observations

Usage

```
RecentNearby(
   key,
   lat = 32.241,
   lng = -110.938,
   dist = 50,
   back = 4,
   hotspot = TRUE,
   include_provisional = FALSE,
   max_tries = 5,
   timeout_sec = 30,
   verbose = TRUE
)
```

Arguments

key	Character eBird API key.	
lat	Numeric latitude; use negative values for southern latitudes (i.e. -46.86 , <i>not</i> $"46.86$ S).	
lng	Numeric longitude; use negative values for western longitudes (i.e72.08, not "72.08 W").	
dist	Numeric radius in kilometers of distance from geographic center point given by lat and lng from which to return recent observations.	
back	Integer number of days back to search for observations.	
hotspot	Logical indicating whether or not to restrict results to hotspot locations.	
include_provisional		
	Logical indicating whether or not to include observations which have not yet been reviewed.	
max_tries	Integer maximum number of query attempts to try.	
timeout_sec	Integer time to allow before query is aborted.	
verbose	Logical determining whether or not to print messages during queries.	

Details

The function uses the eBird API (see https://documenter.getpostman.com/view/664302/S1ENwy59/) to query recent sightings. Queries to the eBird API require a user key; more information on obtaining a key can be found at the eBird API documentation.

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Value

```
An object of class "recent_obs" with the following elements:
```

query_type The type of query performed.

query_parameters List of query parameters passed in request.

obs data frame of observations returned from query; if no observations are returned, obs is NULL. Columns include:

speciesCode The (usually) six-letter species code, see https://science.ebird.org/en/
use-ebird-data/the-ebird-taxonomy/

comName Species' common name.

sciName Species' scientific name.

locId eBird identifier of the location.

locName Name of the location.

obsDt Observation date as character string in the format "YYYY-MM-DD HH:MM".

howMany Number of individuals.

lat Decimal latitude.

Ing Decimal longitude.

obsValid Logical indicating if observation marked as valid.

obsReviewed Logical indicating if observation has been reviewed.

locationPrivate Logical indicating whether or not location is designated as private.

subId Checklist ID for this observation.

Examples

```
## Not run:
    # Read eBird key in from file
    key <- scan(file = "ebird-key.txt", what = "character")
    # Search for observations 5 km from lat/lng coordinates
    recent <- RecentNearby(key = key, lat = 32.28, lng = -111.02, dist = 5)
## End(Not run)</pre>
```

RecentNearbySpecies

Retrieve recent nearby observations of a species

Description

Retrieve recent nearby observations of a species

Usage

```
RecentNearbySpecies(
   key,
   species_code,
   lat = 32.241,
   lng = -110.938,
   dist = 50,
   back = 4,
   hotspot = TRUE,
   include_provisional = FALSE,
   max_tries = 5,
   timeout_sec = 30,
   verbose = TRUE
)
```

Arguments

key	Character eBird API key.	
species_code	Species code for species of interest; usually a six-character string such as "purmar" or "batpig". See https://science.ebird.org/en/use-ebird-data/the-ebird-taxonomy/ for more information.	
lat	Numeric decimal degree latitude; use negative values for southern latitudes (i.e. -46.86 , <i>not</i> " 46.86 S").	
lng	Numeric decimal degree longitude; use negative values for western longitudes (i.e. -72.08 , <i>not</i> " 72.08 W").	
dist	Numeric radius in kilometers of distance from geographic center point given by lat and lng from which to return recent observations of a species.	
back	Integer number of days back to search for observations.	
hotspot	Logical indicating whether or not to restrict results to hotspot locations.	
include_provisional		
	Logical indicating whether or not to include observations which have not yet been reviewed.	
max_tries	Integer maximum number of query attempts to try.	
timeout_sec	Integer time to allow before query is aborted.	
verbose	Logical determining whether or not to print messages during queries.	

Details

The function uses the eBird API (see https://documenter.getpostman.com/view/664302/S1ENwy59/) to query recent sightings of a species. Queries to the eBird API require a user key; you can request an eBird API key by logging into your eBird account and navigating to https://ebird.org/api/keygen/. See examples and vignette for using your eBird API key.

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Value

```
An object of class "recent_obs" with the following elements:
```

query_type The type of query performed.

query_parameters List of query parameters passed in request, including the species code.

obs Data frame of observations returned from query; if no observations are returned, obs is NULL. Columns include:

speciesCode The (usually) six-letter species code, see https://science.ebird.org/en/
use-ebird-data/the-ebird-taxonomy/

comName Species' common name.

sciName Species' scientific name.

locId eBird identifier of the location.

locName Name of the location.

obsDt Observation date as character string in the format "YYYY-MM-DD HH:MM".

howMany Number of individuals.

lat Decimal latitude.

Ing Decimal longitude.

obsValid Logical indicating if observation marked as valid.

obsReviewed Logical indicating if observation has been reviewed.

locationPrivate Logical indicating whether or not location is designated as private.

subId Checklist ID for this observation.

Examples

SitesReport

Create report for sites with most unseen species

Description

Create report for sites with most unseen species

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Usage

```
SitesReport(
  centers,
  ebird_key,
  species_seen,
  center_names = NULL,
  report_filename = "Goals-Report",
  report_dir = getwd(),
  report_format = c("html", "pdf"),
 max_sites = 5,
  dist = 50,
  back = 4,
  hotspot = TRUE,
  include_provisional = FALSE,
 max_tries = 5,
  timeout_sec = 30,
 messages = c("minimal", "none", "verbose"),
  drop_patterns = c("sp\\.", "\\/", "Domestic type", "hybrid"),
  include_maps = TRUE
)
```

Arguments

centers Numeric vector or matrix of latitude and longitude coordinates; vector should

be of length 2, e.g. c(latitude, longitude), while matrix should have two

columns (first column is latitude, second column is longitude).

ebird_key Character vector with eBird API key.

species_seen Character vector of species that have already been seen.

center_names Character vector of names to use for each pair of latitude and longitude coordi-

nates in centers.

report_filename

Name of output file without file extension (see report_format); e.g. if report_filename

is "sites-2021" and report_format is "html", the report will be saved to sites-

2021.html.

report_dir Destination folder for the output file; if NULL, report will be saved to working

directory.

report_format File format for report; takes one of two values: "html" or "pdf".

max_sites Maximum number of sites to return for each pair of coordinates defined in

centers; maximum is 12.

dist Numeric radius in kilometers of distance from each geographic center point de-

fined by coordinates in centers from which to return recent observations.

back Number of days back to search for observations.

hotspot Logical indicating whether or not to restrict results to hotspot locations.

include_provisional

Logical indicating whether not to include observations which have not yet been reviewed.

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max_tries Maximum number of query attempts to try (only for expert use). Integer time to allow before query is aborted (only for expert use). timeout_sec Character indicating the degree to which messages are printed during the report messages assembly process. Options are "minimal", "none", or "verbose". Character vector of patterns in species' names to exclude certain species from drop_patterns consideration, such as domesticated species, hybrids, and observations not identified to species level (e.g. "Toxostoma sp."). The function uses grep with fixed = FALSE to identify which species to exclude, hence the backslashes in the default values in drop_patterns. include_maps Logical vector indicating whether or not to draw maps of identified sites; should be length 1 or the number of centers (i.e. same length as centers if centers is a vector, same number of rows as centers if centers is a matrix).

Details

The function uses the eBird API (see https://documenter.getpostman.com/view/664302/S1ENwy59/) to build the report. Queries to the eBird API require a user key; you can request an eBird API key by logging into your eBird account and navigating to https://ebird.org/api/keygen/. See examples and vignette for using your eBird API key.

Value

Silently returns a list with two named elements:

results_list A list where each element is a list of the results of queries for a center. Each element is a list with two named elements:

center_info A list with latitude (lat), longitude (longitude), and name name of the geographic center.

results A tibble of observations from the top sites (with a maximum number of sites defined by max_sites).

report_details A list containing the settings used to build this report, such as days back and distances.

Examples

```
## Not run:
    # Read in data downloaded from eBird
    list_file <- system.file("extdata", "example-list.csv", package = "lifeR")
    user_list <- read.csv(file = list_file)
    # Only common names are required
    my_species <- user_list$Common.Name
    # Read in eBird API key from a text file
    key <- scan(file = "ebird-key.txt", what = "character")

# A single center requires vector of coordinates
    locs <- c(45, -109)
    SitesReport(centers = locs, ebird_key = key,
    species_seen = my_species)</pre>
```

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```
# For multiple centers, pass a matrix to centers argument
loc_mat <- matrix(data = c(33, -109, 39, -119.1), nrow = 2, byrow = TRUE)
loc_names <- c("Brushy Mountain", "Yerington")
SitesReport(centers = loc_mat, ebird_key = key,
species_seen = my_species, center_names = loc_names)
## End(Not run)</pre>
```

SplitNames

Split vector of names into two-column data frame

Description

Split vector of names into two-column data frame

Usage

```
SplitNames(x, delim = " - ")
```

Arguments

Vector of species names, in the format "Common Name - Scientific name".delimCharacter separator that delimits common from scientific names.

Details

Names from eBird are returned in a single column as: "Snow Goose - Anser caerulescens". This function provides a means of separating the common name ("Snow Goose") from the scientific name ("Anser caerulescens") into two separate columns.

Value

A data.frame of two columns, Common and Scientific.

Examples

```
# Read in data downloaded from eBird
user_file <- system.file("extdata", "example-list.csv", package = "lifeR")
user_list <- read.csv(file = user_file)
# Retrieve a two-column data frame with common names and scientific names
species_seen <- SplitNames(x = user_list$Species)
# If only common names are required, refer to \code{Common} column
species_seen <- SplitNames(x = user_list$Species)$Common</pre>
```

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