

Package ‘vectorsurvR’

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Type Package

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Description Allows registered 'VectorSurv' <<https://vectorsurv.org/>> users access to data through the 'VectorSurv API' <<https://api.vectorsurv.org/>>. Additionally provides functions for analysis and visualization.

License GPL-3

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Contents

getAbundance	2
getAbundanceAnomaly	3
getArthroCollections	4
getInfectionRate	5
getPools	6
getPoolsComparisionTable	7

getRegions	8
getSites	8
getSpatialFeatures	9
getSpeciesTable	9
getToken	10
getVectorIndex	11
plotInvasiveSums	12
plotVectorAbundance	13
processAbunAnom	15
sample_collections	15
sample_pools	16
sample_spatial	17
Index	18

getAbundance	<i>Calculate abundance</i>
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Description

Calculates abundance with option for filtering data and grouping results

Usage

```
getAbundance(  
  collections,  
  interval,  
  agency = NULL,  
  species = NULL,  
  trap = NULL,  
  sex = "female",  
  trapnight_min = 1,  
  trapnight_max = NULL,  
  separate_by = NULL  
)
```

Arguments

collections	Collections data retrieved from getArthroCollections()
interval	Calculation interval for abundance, accepts "CollectionDate", "Week", "Biweek", or "Month.
agency	An optional vector for filtering agency by character code
species	Character vector for filtering species. View species in your data ‘unique(data\$species_display_name)’. Defaults to all species if no selection
trap	Character vector for filtering trap type by acronym. View trap types in your data ‘unique(data\$trap_acronym)’. Defaults to all trap types

sex	Character vector for filtering sex type. View sex options <code>'unique(data\$sex_type')</code> . Defaults to "female".
trapnight_min	Minimum trap night restriction for calculation. Default is 1.
trapnight_max	Maximum trap night restriction for calculation. Default is no restriction.
separate_by	Separate/group the calculation by 'trap', 'species', 'agency', 'county', or 'spatial'. Default NULL does not separate.

Value

A dataframe of abundance calculations.

Examples

```
getAbundance(sample_collections,
              interval = 'Week',
              species = list('Cx pipiens'),
              trap = list('GRVD', 'C02'),
              sex = list("female"),
              trapnight_min = 1,
              trapnight_max = 5,
              separate_by = "species")
```

getAbundanceAnomaly	<i>Get Abundance Anomaly</i>
---------------------	------------------------------

Description

`'getAbundanceAnomaly(...)` 'requires at least five years prior to the `target_year` of arthro collections data to calculate for the specified parameters. The function uses the methods of the Gateway Abundance Anomaly calculator, and will not work if there is fewer than five years of data present.

Usage

```
getAbundanceAnomaly(
  collections,
  interval,
  target_year,
  agency = NULL,
  species = NULL,
  trap = NULL,
  sex = "female",
  trapnight_min = 1,
  trapnight_max = NULL,
  separate_by = NULL
)
```

Arguments

collections	Collections data retrieved from 'getArthroCollections()'
interval	Calculation interval for abundance, accepts "CollectionDate", "Biweek", "Week", and "Month"
target_year	Year to calculate analysis on. Collections data must have a year range of at least (target_year - 5, target_year)
agency	An optional vector for filtering agency by character code
species	Character vector for filtering species. View species in your data 'unique(data\$species_display_name)'. Defaults to all species if no selection
trap	Character vector for filtering trap type by acronym. View trap types in your data 'unique(data\$trap_acronym)'. Defaults to all trap types
sex	Character vector for filtering sex type. View sex options 'unique(data\$sex_type)'. Defaults to "female".
trapnight_min	Minimum trap night restriction for calculation. Default is 1.
trapnight_max	Maximum trap night restriction for calculation. Default is no restriction.
separate_by	Separate/group the calculation by 'trap', 'species', 'agency', 'county', or 'spatial'. Default NULL does not separate.

Value

Abundance anomaly calculation

Examples

```
getAbundanceAnomaly(sample_collections, "Biweek", target_year=2020, species="Cx pipiens")
```

getArthroCollections *Get arthropod collections data*

Description

'getArthroCollections()' obtains collections data on a year range [start_year, end_year] for authorized VectorSurv Gateway accounts.

Usage

```
getArthroCollections(
  token,
  start_year,
  end_year,
  arthropod,
  agency_ids = NULL,
  spatial_features = NULL,
  geocoded = TRUE
)
```

Arguments

token	A valid access token returned from 'getToken()'
start_year	Start year of data
end_year	End year of data
arthropod	Specify arthropod type from: 'mosquito', 'tick'
agency_ids	Filter on agency id, default to NULL for all available agencies, otherwise provide a vector of agency ids, such as 'agency_ids = c(55,56)'
spatial_features	Filter data by spatial feature
geocoded	Should city and county be calculated by collection long/lat instead of user input from site inform

Value

A dataframe of collections data

Examples

```
## Not run:
token = getToken()
collections = getArthroCollections(token, 2021, 2022, 'mosquito', c(55,56), TRUE)
## End(Not run)
```

getInfectionRate	<i>Calculate infection rate</i>
------------------	---------------------------------

Description

'getInfectionRate()' Calculates infection rate from pools data

Usage

```
getInfectionRate(
  pools,
  interval,
  target_disease,
  pt_estimate = "bc-mle",
  scale = 1000,
  agency = NULL,
  species = NULL,
  trap = NULL,
  sex = "female",
  separate_by = NULL
)
```

Arguments

pools	Pools data retrieved from 'getPools()'
interval	Calculation interval for infection rate, accepts "CollectionDate", "Biweek", "Week", and "Month"
target_disease	The disease to calculate infection rate for—i.e. "WNV". Disease acronyms are the accepted input. To see a list of disease acronyms, run 'unique(pools\$test_target_acronym)'
pt_estimate	The estimation type for infection rate. Options include: "mle", "bc-mle", "mir"
scale	Constant to multiply infection rate by
agency	An optional vector for filtering agency by character code
species	An optional vector for filtering species. Species_display_name is the accepted notation. To see a list of species present in your data run unique(collections\$species_display_name). If species is unspecified, the default NULL will return data for all species in data.
trap	An optional vector for filtering trap type by acronym. Trap_acronym is the accepted notation. Run unique(collections\$trap_acronym) to see trap types present in your data. If trap is unspecified, the default NULL will return data for all trap types.
sex	An optional vector for filtering sex type. Accepts 'male', 'female', or 'other'. If sex is unspecified, the default NULL will return data for female sex.
separate_by	Separate/group the calculation by 'trap', 'species' or 'agency'. Default NULL does not separate.

Value

Dataframe of infection rate calculation

getPools	<i>Get Pools data</i>
----------	-----------------------

Description

Retrieves VectorSurv pools data for desired year range

Usage

```
getPools(token, start_year, end_year, arthropod, agency_ids = NULL)
```

Arguments

token	access token retrieved from 'getToken()'
start_year	Beginning of year range
end_year	End of year range
arthropod	Specify arthropod type from: 'mosquito', 'tick', 'nontick'
agency_ids	Filter on agency id, default to NULL for all available agencies, otherwise provide a vector of agency ids

Value

Dataframe of pools data

Examples

```
## Not run:
token = getToken()
getPools(token, start_year = 2020, end_year = 2021, arthropod = 'tick', 55)
## End(Not run)
```

getPoolsComparisionTable

Get Pools Frequency Table

Description

‘getPoolsComparisionTable()’ produces a frequency table for positive, negative, and pending pools counts by year and species. The more years present in the data, the larger the table.

Usage

```
getPoolsComparisionTable(pools, interval, target_disease, separate_by = NULL)
```

Arguments

pools	Pools data retrieved from ‘getPools()’
interval	Calculation interval for comparison table, accepts “collection_date”, “Biweek”, “Week”, and “Month”
target_disease	The disease to calculate infection rate for—i.e. “WNV”. Disease acronyms are the accepted input. To see a list of disease acronyms, run ‘unique(pools\$target_acronym)’
separate_by	Separate/group the calculation by ‘trap’, ‘species’ or ‘agency’. Default NULL does not separate.

Value

Frequency table of for pools data

Examples

```
getPoolsComparisionTable(sample_pools,
                           interval = "Biweek",
                           target_disease = "WNV",
                           separate_by = "species")
```

getRegions	<i>Get region data</i>
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Description

‘getSites()’ obtains site data for authorized VectorSurv Gateway accounts.

Usage

getRegions(token)

Arguments

token A valid access token returned from ‘getToken()’

Value

A dataframe of region data, used internally to merge spatial information to collections

getSites	<i>Get sites data</i>
----------	-----------------------

Description

‘getSites()’ obtains site data for authorized VectorSurv Gateway accounts.

Usage

getSites(token, agency_ids = NULL)

Arguments

token A valid access token returned from ‘getToken()’
agency_ids Filter on agency id, default to NULL for all available agencies,otherwise provide a vector of agency ids, such as ‘agency_ids = c(55,56)’

Value

A dataframe of site data

Examples

```
## Not run:  
token = getToken()  
sites = getSites(token)  
## End(Not run)
```

getSpatialFeatures	<i>Get Spatial Features data</i>
--------------------	----------------------------------

Description

Retrieves VectorSurv spatial features data with optional agency filtering

Usage

```
getSpatialFeatures(token, agency_ids = NULL)
```

Arguments

token	Access token retrieved from 'getToken()'
agency_ids	Optional vector of agency IDs to filter by

Value

An sf object containing spatial features data

Examples

```
## Not run: token=getToken()  
spatial = getSpatialFeatures(token)  
## End(Not run)
```

getSpeciesTable	<i>Get Table For Species</i>
-----------------	------------------------------

Description

Allows users to create a custom table for vector species. The invasive species count, trap nights, and abundance are calculated by chosen groupings or time intervals. The table has output options based on document format.

Usage

```
getSpeciesTable(  
  token,  
  interval,  
  target_year,  
  cumulative = FALSE,  
  include_trap_nights = TRUE,  
  include_abundance = FALSE,  
  species = NULL,  
  trap = NULL,
```

```
sex = "female",
separate_by = NULL,
output_format = "auto",
caption = NULL,
agency_id = NULL
)
```

Arguments

token	Authentication token for API access, obtained from 'getToken()'
interval	Time interval for aggregation. One of: "CollectionDate", "Week", "Biweek", "Month"
target_year	The focal year to highlight in the plot (integer)
cumulative	T/F Adds columns for the cumulative sum count Default to FALSE
include_trap_nights	T/F Adds column for the tally of trap nights
include_abundance	T/F Adds column for abundance (non-cumulative only)
species	Character vector for filtering species. View species in your data 'unique(data\$species_display_name)'. Defaults to all species if no selection
trap	Character vector for filtering trap type by acronym. View trap types in your data 'unique(data\$trap_acronym)'. Defaults to all trap types
sex	Character vector for filtering sex type. View sex options 'unique(data\$sex_type)'. Defaults to "female".
separate_by	Adds a column from the data as a grouping variable. Accepts 'site', 'city', 'county', 'agency', 'trap', 'spatial'
output_format	Format to output table display. Accepts 'html', 'pdf', 'word' or 'auto'. Default auto returns the console format dataframe.
caption	Caption for table
agency_id	Agency identifier to filter data if applicable

Value

A table displaying invasive species interval or/and cumulative counts over time

getToken	<i>Get authentication token</i>
----------	---------------------------------

Description

getToken() returns a token needed to run getArthroCollections() and getPools(). Prints agencies associated with account credentials. The function prompts users for a VectorSurv account credentials.

Usage

```
getToken()
```

Value

User token

Examples

```
## Not run: token = getToken()
```

getVectorIndex	<i>Calculate vector index</i>
----------------	-------------------------------

Description

`'getVectorIndex()'` Calculates vector index from pools and collections data

Usage

```
getVectorIndex(
  collections,
  pools,
  interval,
  target_disease,
  pt_estimate = "bc-mle",
  scale = 1000,
  agency = NULL,
  species = NULL,
  trap = NULL,
  sex = NULL,
  trapnight_min = 1,
  trapnight_max = NULL,
  separate_by = NULL
)
```

Arguments

<code>collections</code>	Collections data retrieved from <code>'getArthroCollections()'</code>
<code>pools</code>	Pools data retrieved from <code>'getPools()'</code>
<code>interval</code>	Calculation interval for vector index, accepts "CollectionDate", "Biweek", "Week", and "Month"
<code>target_disease</code>	The disease to calculate infection rate for—i.e. "WNV". Disease acronyms are the accepted input. To see a list of disease acronyms, run <code>'unique(pools\$target_acronym)'</code>
<code>pt_estimate</code>	The estimation type for infection rate. Options include: "mle", "bc-mle", "mir"
<code>scale</code>	Constant to multiply infection rate, default is 1000

agency	Character vector for filtering agency by character code
species	Character vector for filtering species. View species in your data 'unique(data\$species_display_name)'. Defaults to all species if no selection
trap	Character vector for filtering trap type by acronym. View trap types in your data 'unique(data\$trap_acronym)'. Defaults to all trap types
sex	Character vector for filtering sex type. View sex options 'unique(data\$sex_type)'. Defaults to "female".
trapnight_min	Minimum trap night restriction for calculation. Default is 1.
trapnight_max	Maximum trap night restriction for calculation. Default is no restriction.
separate_by	Separate/group the calculation by 'trap', 'species' or 'agency'. Default NULL does not separate.

Value

Dataframe containing the vector index calculation

Examples

```
getVectorIndex(collections=sample_collections,
pools=sample_pools, interval="Month", target_disease = "WNV", pt_estimate="mle")
```

plotInvasiveSums	<i>Plot cumulative sum and interval sums of invasive species</i>
------------------	--

Description

This function graphs the cumulative sum of invasive mosquito specie(s) as a line chart over a selected interval. The bar chart shows the interval sum of invasive specie(s). For cumulative sum, a convex slope indicates increased rate of species trappings, concave a decrease in rate, and linear a constant rate.

Usage

```
plotInvasiveSums(
  token,
  interval,
  target_year,
  invasive_species,
  agency_ids = NULL
)
```

Arguments

token	A valid access token returned from 'getToken()'
interval	Calculation interval for abundance, accepts "CollectionDate", "Week", "Biweek", or "Month".
target_year	Year to plot
invasive_species	Names of invasive species to be plotted, multiple invasive species are entered in vector format i.e. 'invasive_species = c("Ae aegypti", "Ae albopictus")'
agency_ids	An optional vector for filtering agency by id

plotVectorAbundance	<i>Plot Vector Abundance Over Time with Comparison to Historical Averages</i>
---------------------	---

Description

This function creates a time series plot showing vector (mosquito) abundance over multiple years, highlighting a target year in red and optionally showing a historical average line. The plot helps visualize trends and anomalies in vector populations.

Usage

```
plotVectorAbundance(
  token,
  interval,
  target_year,
  start_year = NULL,
  end_year = NULL,
  species,
  trap,
  agency_ids = NULL,
  sex = "female",
  trapnight_min = 1,
  trapnight_max = NULL
)
```

Arguments

token	Authentication token for API access, typically obtained from 'getToken()'
interval	Time interval for aggregation. One of: "CollectionDate", "Week", "Biweek", "Month"
target_year	The focal year to highlight in the plot
start_year	Starting year for data retrieval. If NULL, defaults to 5 years before target_year
end_year	Ending year for data retrieval (integer). If NULL, defaults to target_year

species	Character vector for filtering species. View species in your data ‘unique(data\$species_display_name)’. Defaults to all species if no selection
trap	Character vector for filtering trap type by acronym. View trap types in your data ‘unique(data\$trap_acronym)’. Defaults to all trap types
agency_ids	Agency identifier to filter data if applicable
sex	Character vector for filtering sex type. View sex options ‘unique(data\$sex_type)’. Defaults to "female".
trapnight_min	Minimum number of trap nights to include (numeric). Defaults to 1
trapnight_max	Maximum number of trap nights to include (numeric). If NULL, uses maximum available

Value

A ggplot object showing vector abundance over time, with the target year highlighted in red and historical average shown in blue

Examples

```
## Not run:
# Basic usage with default parameters
token <- getToken()
plot <- plotVectorAbundance(
  token = token,
  interval = "Week",
  target_year = 2024,
  species = "Cx pipiens",
  trap = "C02"
)

# Compare multiple years with custom date range
plot <- plotVectorAbundance(
  token = token,
  interval = "Month",
  target_year = 2024,
  start_year = 2020,
  end_year = 2024,
  species = "Ae aegypti",
  trap = c("BG", "CDC"),
  sex = "female",
  trapnight_min = 3
)

## End(Not run)
```

processAbunAnom	<i>Process abundance anomaly</i>
-----------------	----------------------------------

Description

'processAbunAnom()' processes the output returned from 'getAbundanceAnomaly()' into a long form suitable for plotting using 'ggplot'

Usage

```
processAbunAnom(AbAnomOutput)
```

Arguments

AbAnomOutput output from 'getAbunAnom()'

Value

Abundance anomaly output processed into long form, used for plotting functions

sample_collections	<i>Sample Mosquito Collections Data</i>
--------------------	---

Description

Sample Mosquito Collections data imitates the essential components of real mosquito collections data

Usage

```
sample_collections
```

Format

A data frame with 5880 rows and 17 variables:

```
agency_code  character Four letter agency code
agency_id    interger Unique agency id number
county       character County which site resides
collection_id double Collection identification number
collection_date character The date the trap was picked up for collection
num_trap     integer The number of unique traps in operation at one site
site_code    integer Identifying code of site
surv_year    double Surveillance year of collection
```

trap_nights integer The number of nights a trap was in the field
 trap_problem_bit logical If there was an issue with the trap
 num_count integer Number of arthropods present in collection
 sex_type character Sex of collected arthropods
 species_display_name character Species name of collected arthropods
 trap_acronym character The acronym of the trap placed in the field
 collection_longitude numeric longitude of collection
 collection_latitude numeric latitude of collection
 spatial_feature character name of spatial feature to which data belongs
 multiple_features boolean T/F if the point is found within multiple selected spatial features

Source

<https://vectorsurv.org/>

sample_pools

Sample Pools Data

Description

Sample Pools data imitates the essential components of real mosquito pools data needed for calculations

Usage

sample_pools

Format

A data frame with 3500 rows and 15 variables:

agency_code character Four letter agency code
 agency_id integer Unique agency id number
 id integer Pool identification number
 surv_year integer Surveillance year of pool
 site_code integer Identifying code of site
 collection_date character The date the trap was picked up for collection
 sex_type integer Sex type of collected arthropods
 num_count integer Number of arthropods present in collection
 test_target_acronym character The disease being tested for in the pool
 test_method_name character Method used to test pool for disease
 test_status_name character Status of the tested disease, confirmed or negative

trap_acronym character The acronym of the trap placed in the field
species_display_name character Species name of collected arthropods
pool_longitude numeric longitude of pool
pool_latitude numeric latitude of pool

Source

<https://vectorsurv.org/>

sample_spatial	<i>Sample Spatial Data</i>
----------------	----------------------------

Description

Sample Spatial data imitates spatial feature data

Usage

sample_spatial

Format

A data frame with 3 rows and 5 variables:

agency character Agency name
agency_id interger Unique agency id number
id interger ID of spatial feature
name character Name of spatial feature
geometry multipolygon shape geometry spatial feature

Source

<https://vectorsurv.org/>

Index

- * **abundance**
 - getAbundanceAnomaly, 3
- * **authentication**
 - getToken, 10
- * **datasets**
 - sample_collections, 15
 - sample_pools, 16
 - sample_spatial, 17
- * **infection**
 - getInfectionRate, 5
- * **pools**
 - getInfectionRate, 5
 - getPools, 6
- * **rate**
 - getInfectionRate, 5

getAbundance, 2
getAbundanceAnomaly, 3
getArthroCollections, 4
getInfectionRate, 5
getPools, 6
getPoolsComparisionTable, 7
getRegions, 8
getSites, 8
getSpatialFeatures, 9
getSpeciesTable, 9
getToken, 10
getVectorIndex, 11

plotInvasiveSums, 12
plotVectorAbundance, 13
processAbunAnom, 15

sample_collections, 15
sample_pools, 16
sample_spatial, 17