

Package ‘vectorsurvR’

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Contents

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

getRegions	8
getSites	8
getSpatialFeatures	9
getToken	9
getVectorIndex	10
processAbunAnom	11
sample_collections	12
sample_pools	13
sample_spatial	14
Index	15

getAbundance	<i>Calculate abundance</i>
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Description

Calculates abundance

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, “Biweek”, “Week”, and “Month.
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 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.

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_feature'. Default NULL does not separate.

Value

A dataframe of abundance calculations.

Examples

```
getAbundance(sample_collections,
              interval = 'Week',
              species = list('Cx pipiens'),
              trap = list('GRVD', 'CQ2'),
              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 "collection_date", "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	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.
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_feature". 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
)
```

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

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,
```

```
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 “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\$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 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>
------------	------------------------

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)
```

Arguments

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

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)
```

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,
  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 <code>"collection_date"</code> , <code>"Biweek"</code> , <code>"Week"</code> , and <code>"Month"</code>
<code>target_disease</code>	The disease to calculate infection rate for—i.e. <code>"WNV"</code> . 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: <code>"mle"</code> , <code>"bc-mle"</code> , <code>"mir"</code>
<code>scale</code>	Constant to multiply infection rate, default is 1000
<code>agency</code>	An optional vector for filtering agency by character code
<code>species</code>	An optional vector for filtering species. <code>Species_display_name</code> is the accepted notation. To see a list of species present in your data run <code>unique(collections\$species_display_name)</code> . If species is unspecified, the default <code>NULL</code> will return data for all species in data.

trap	An optional vector for filtering trap type by acronym. Trap_acronym is the is the accepted notation. Run <code>unique(collections\$trap_acronym)</code> 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.
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")
```

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 2500 rows and 13 variables:

```
agency_code character Four letter agency code
agency_id   integer 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
```

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 2500 rows and 10 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>
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Description

Sample Spatial data imitates spatial feature data

Usage

```
sample_spatial
```

Format

A data frame with 3 rows and 4 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, 9
- * **datasets**
 - sample_collections, 12
 - sample_pools, 13
 - sample_spatial, 14
- * **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
getToken, 9
getVectorIndex, 10

processAbunAnom, 11

sample_collections, 12
sample_pools, 13
sample_spatial, 14