

Package ‘vectorsurvR’

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Type Package

Title Data Access and Analytical Tools for 'VectorSurv' Users

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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 |

| | |
|------------------------------|----|
| getToken | 8 |
| getVectorIndex | 8 |
| plotInfectionRate | 9 |
| processAbunAnom | 10 |
| sample_collections | 11 |
| sample_pools | 11 |

| | |
|--------------|-----------|
| Index | 13 |
|--------------|-----------|

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|--------------|----------------------|
| getAbundance | <i>Get abundance</i> |
|--------------|----------------------|

Description

Calculates abundance

Usage

```
getAbundance(
  collections,
  interval,
  species_list = NULL,
  trap_list = NULL,
  species_separate = FALSE
)
```

Arguments

| | |
|------------------|---|
| collections | Collections data retrieved from getArthroCollections() |
| interval | Calculation interval for abundance, accepts “collection_date”, “Biweek”, “Week”, and “Month. |
| species_list | Species filter for calculating abundance. 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_list | Trap filter for calculating abundance. Trap_acronym is the is the accepted notation. Run unique(collections\$trap_acronym) to see trap types present in your data. If trap_list is unspecified, the default NULL will return data for all trap types. |
| species_separate | Should the species in species_list have abundance calculated separately? Setting to FALSE calculates the combined abundance. The same result can be performed by calculating on one species at the time. |

Value

A dataframe of abundance values grouped by interval and filtered by parameters

Examples

```
getAbundance(sample_collections,
             interval = 'Week',
             species_list = list('Cx pipiens'),
             trap_list = list('GRVD', 'CO2'),
             species_separate = FALSE)
```

getAbundanceAnomaly *Get Abundance Anomaly*

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,
  species_list = NULL,
  trap_list = NULL,
  species_separate = FALSE
)
```

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) |
| species_list | Species filter for calculating abundance. 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_list | Trap filter for calculating abundance. Trap_acronym is the is the accepted notation. Run 'unique(collections\$trap_acronym)' to see trap types present in your data. If trap_list is unspecified, the default NULL will return data for all trap types |
| species_separate | Should the species in species_list have abundance calculated separately? Setting to FALSE calculates the combined abundance. The same result can be performed by calculating on one species at the time description |

Value

Abundance anomaly calculation

Examples

```
getAbundanceAnomaly(sample_collections,"Biweek",target_year=2020, species_list="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_id = 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_id | Filter on agency id, default to NULL for all available agencies, otherwise specify a single agency by code |

Value

A dataframe of collections data specific to users account

Examples

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

| | |
|------------------|---------------------------|
| getInfectionRate | <i>Get Infection Rate</i> |
|------------------|---------------------------|

Description

'getInfectionRate()' 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

```
getInfectionRate(
  pools,
  interval,
  target_disease,
  pt_estimate,
  scale = 1000,
  species_list = NULL,
  trap_list = 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\$target_acronym)' |
| pt_estimate | The estimation type for infection rate. Options include: "mle", "bc-mle", "mir" |
| scale | Constant to multiply infection rate by |
| species_list | Species filter for calculating infection rate species_display_name is the accepted notation. To see a list of species present in your data run 'unique(pools\$species_display_name)'. If species is unspecified, the default 'NULL' will return data for all species in data. |
| trap_list | Trap filter for calculating infection rate. Trap_acronym is the is the accepted notation. Run 'unique(pools\$trap_acronym)'. If trap_list is unspecified, the default 'NULL' will return data for all trap types. |

Value

Infection rate calculation

Examples

```
getInfectionRate(sample_pools,
                 interval = "Biweek",
                 target_disease = "WNV",
                 pt_estimate = "mle",
                 scale = 1000,
                 species_list = list("Cx pipiens"),
                 trap_list = list("C02"))
```

getPools

Get Pools data

Description

Retrieves VectorSurv pools data for desired year range

Usage

```
getPools(token, start_year, end_year, arthropod)
```

Arguments

| | |
|------------|--|
| token | access token retrived from 'getToken()' |
| start_year | Beginning of year range |
| end_year | End of year range |
| arthropod | Specify arthropod type from: 'mosquito', 'tick', 'nontick' |

Value

Dataframe of pools data

Examples

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

Arguments

| | |
|-------------------------------|--|
| <code>pools</code> | Pools data retrieved from <code>'getPools()'</code> |
| <code>interval</code> | Calculation interval for comparison table, accepts "collection_date", "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>species_separate</code> | Should the pools comparison be split by species of each pool. Default is FALSE |

Value

Frequency table of for pools data

Examples

```
getPoolsComparisionTable(sample_pools,  
  interval = "Biweek",  
  target_disease = "WNV",  
  species_separate = TRUE)
```

`getToken`*Get Token*

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`*Get Vector Index*

Description

`getVectorIndex()` 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

```
getVectorIndex(  
  collections,  
  pools,  
  interval,  
  target_disease,  
  pt_estimate,  
  scale = 1000,  
  species_list = NULL,  
  trap_list = NULL  
)
```


Arguments

| | |
|----------------|---|
| collections | Collections data retrieved from 'getArthroCollections()' |
| pools | Pools data retrieved from 'getPools()' |
| interval | Calculation interval for vector index, 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)' |
| pt_estimate | The estimation type for infection rate. Options include: "mle", "bc-"mle", "mir" |
| scale | Constant to multiply infection rate |
| species_list | Species filter for calculating abundance. Species_display_name is the accepted notation. To see a list of species present in your data run 'unique(pools\$species_display_name)'. If species is unspecified, the default 'NULL' will return data for all species in data. |
| trap_list | Trap filter for calculating abundance. Trap_acronym is the is the accepted notation. Run 'unique(pools\$trap_acronym)' to see trap types present in your data. If trap_list is unspecified, the default 'NULL' will return data for all trap types. |

Value

Vector index calculation

Examples

```
getVectorIndex(sample_collections, sample_pools, "Month", "WNV", "mle" )
```

plotInfectionRate *Plot Infection Rate*

Description

plotInfectionRate() plots the output returned from 'getInfectionRate()' with confidence intervals using ggplot

Usage

```
plotInfectionRate(InfRtOutput, year)
```

Arguments

| | |
|-------------|---|
| InfRtOutput | Output from returned 'getInfectionRate()' |
| year | Year to plot infection rate on |

Value

ggplot object

Examples

```
IR = getInfectionRate(sample_pools,
                      interval = "Week",
                      target_disease = "WNV",
                      pt_estimate = "mle", species_list = c("Cx pipiens"),
                      trap_list = c("C02", "GRVD") )
plotInfectionRate(InfRtOutput = IR, year = 2017)
```

processAbunAnom

process Abundance Anomaly

Description

‘processAbunAnom()’ processes the output returned from ‘getAbundanceAnomaly()’ into a long form suitable for plotting in ‘ggplot’

Usage

```
processAbunAnom(AbAnomOutput)
```

Arguments

AbAnomOutput output from ‘getAbunAnom()’

Value

Abundance anomaly output processed into long form

Examples

```
AbAnOut = getAbundanceAnomaly(sample_collections,
                              interval = "Biweek",
                              target_year = 2020,
                              species_list = c("Cx tarsalis", "Cx pipiens"),
                              species_separate = TRUE)
AbAnOut_L = processAbunAnom(AbAnOut)
```

| | |
|--------------------|--|
| sample_collections | <i>Sample Arthropod Collections Data</i> |
|--------------------|--|

Description

Sample Arthropod Collections data imitates the essential components of real collections data

Usage

sample_collections

Format

A data frame with 200 rows and 10 variables:

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
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

Source

<https://vectorsurv.org/>

| | |
|--------------|--------------------------|
| sample_pools | <i>Sample Pools Data</i> |
|--------------|--------------------------|

Description

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

Usage

sample_pools

Format

A data frame with 82644 rows and 10 variables:

pool_id integer Pool identification number
surv_year integer Surveillance year of pool
collection_date character The date the trap was picked up for collection
sex integer Sex of collected arthropods
num_count integer Number of arthropods present in collection
target_acronym character The disease being tested for in the pool
status_name character Status of the tested disease
trap_acronym character The acronym of the trap placed in the field
species_display_name character Species name of collected arthropods

Source

<https://vectorsurv.org/>

Index

- * **abundance**
 - getAbundanceAnomaly, 3
- * **authentication**
 - getToken, 8
- * **datasets**
 - sample_collections, 11
 - sample_pools, 11
- * **infection**
 - getInfectionRate, 5
- * **pools**
 - getInfectionRate, 5
 - getPools, 6
- * **rate**
 - getInfectionRate, 5

getAbundance, 2
getAbundanceAnomaly, 3
getArthroCollections, 4
getInfectionRate, 5
getPools, 6
getPoolsComparisionTable, 7
getToken, 8
getVectorIndex, 8

plotInfectionRate, 9
processAbunAnom, 10

sample_collections, 11
sample_pools, 11