Package ‘IxPopDyMod’

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Title Framework for Tick Population and Infection Modeling

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Description Code to specify, run, and then visualize and analyze the results of Ixodidae (hard-bodied ticks) population and infection dynamics models. Such models exist in the literature, but the source code to run them is not always available. ‘IxPopDyMod’ provides an easy way for these models to be written and shared.

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

URL https://github.com/dallenmidd/IxPopDyMod

Depends R (>= 3.2.4)

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config

Create a config object

Description

Make a config object from the input parameters, and ensure that the inputs meet the requirements for the model. The returned object is a complete description of a model run scenario.

Usage

```r
config(
  initial_population,
  transitions,
  parameters,
  predictors,
  steps,
  max_delay = 365L
)
```
Arguments

**initial_population**
Named numeric vector indicating starting population for each life stage. Life stages not specified are assumed to be 0.

**transitions**
A tibble in which each row corresponds to a transition between two tick life stages, or a transition from a tick life stage to mortality.

- **from** Tick life stage a transition is originating from, specified with a three character string. The final character specifies stage, with "e" = egg, "l" = larva, "n" = nymph, and "a" = adult. The middle character specifies infection, with "i" = infected, and "u" = uninfected. The first character is the current process or sub-stage, for example "q" = questing, "e" = engorged, and "r" = reproductive. We use "_" to indicate if any of these components is not relevant, for example "_" as the second character if we are ignoring infection.

- **to** Tick life stage a transition is going to. May be specified with the same three character format as the "from" field. Alternatively, may be the one of the strings "m" or "per_capita_m" to indicate mortality.

**transition_fun** A string; the name of the function to use to calculate the value of the transition. Must either be a function included in the package or a custom function that has been loaded into the workspace. Functions can take 0-2 predictors, and any number of parameters. Argument order matters - all transition functions must start with two predictor arguments (even if they are not used within the function), followed by any parameters. They must return a numeric vector. See constant_fun, expo_fun and infect_fun for examples for how to write custom functions.

**delay** If TRUE, transition is interpreted as a delay, if FALSE, transition is interpreted as a daily probability.

**pred1** Specifies the first predictor to use in a transition function. One of NA, a string identical to a value of the "pred" column in the predictors table, or a pattern that matches at least one life stage.

**pred2** Specifies the second predictor to use in a transition function. Format like pred1.

**parameters**
A tibble of parameters to use in the transitions described in the transitions table. Each row corresponds to a parameter value that may be used in one or more transitions. Parameter values will be used in transitions where the "from" and "to" fields of the two (parameters and transitions) tables match.

- **from** Used to identify the transitions that a parameter should be used for. Format like the "from" column in the transitions table, or a regex pattern that matches with one or more life stage strings.

- **to** Used to identify the transitions that a parameter should be used for. Format like the "to" column in the transitions table, or a regex pattern that matches with one or more life stage strings.

- **param_name** A string specifying the name of the argument in the function where you want to use a parameter.

**host_spp** Optional column, not needed for model configurations that do not dependent on host community. For a given row, NA if the parameter value
is not dependent on the host species. Otherwise, a string specifying the name of the host species that the parameter value pertains to.

**param_value** Numeric; the value of the parameter

**predictors** Optionally, a tibble of input data to be used as predictor values in transition functions, for example weather or host density.

**pred** String specifying the name of the predictor, e.g. "temp" or "host_den"

**pred_subcategory** This column allows specifying predictors for which there are multiple values for a given j_day. Predictor values are sorted by this column in the config set up. This ensures that when accessing a predictor with multiple values for the same j_day, we get a vector of predictor values ordered by this column. A typical use for this column is to specify the host density of each host species.

**j_day** Integer specifying the Julian day, or NA for predictors with constant value over time

**value** Numeric value of predictor

**steps** Numeric vector of length one indicating the duration to run the model over in days.

**max_delay** Numeric vector of length one. Determines the maximum number of days that a delayed transition can last.

### Details

The delay column affects how a transition row is used in the model. In all cases, a transition row is evaluated with any parameters and predictors, resulting in a transition value, t. If there is another row with the same "from", but either "m" or "per_capita_m" for the "to" stage, this row will be evaluated as well, resulting in a mortality transition value, m. Only delay transitions support "per_capita_m".

In non-delay transitions (where delay == FALSE), ticks can either advance to the "to" stage, die, or remain in the "from" stage. In this case, t is interpreted as the probability that a tick in the "from" stage will advance to the "to" stage at the next time step. The survival rate, or the probability that a tick will remain in the same "from" life stage, is calculated as 1 - (t + m).

In delay transitions (where delay == TRUE), ticks can either advance to the "to" stage, or die - there is no survival. In this case, t is used to determine the number of days until ticks in the "from" stage will emerge as ticks in the "to" stage. t will be vectorized over each day from the current time step to max_delay days ahead. The duration of the transition (in days) will be the index i of the first element in t where the cumulative sum of t[1:i] is greater than or equal to 1.

Delay transitions support two modes of mortality, "m" and "per_capita_m". For transitions to "m", the mortality value m is interpreted as a daily probability of mortality for each day in the delay transition. This differs from transitions to "per_capita_m", where m is the total probability of mortality over the entire duration of the delay transition.

### Value

A config object
Examples

# We rebuild an example config from its constituent parts. This is successful as expected, because we're just making a config that's identical to an example.
do.call(config, config_ex_1)

# If we modify the config to something unsuitable, the function will complain.
# For example, if we modify the egg to larvae transition to use a different function that requires an additional parameter.

## Not run:
# We define a super simple function that takes two parameters.
prod_fun <- function(x, y, a, b) a * b

my_config <- config_ex_1
my_config$transitions[1, 3] <- 'prod_fun'

# this will throw an error, because a parameter is missing
do.call(config, my_config)
# config() will report that parameter "b" is missing for the exponential function.

# Adding the parameter should fix the config
my_config$parameters[9,] <- list(from = '__e', to = '__l', param_name = 'b',
                                 param_value = 1)

# Now, this should run without issues
do.call(config, my_config)

## End(Not run)

---

config_ex_1

Simple model configuration example

Description

This model configuration uses only non-delay transitions, and no transitions depend on predictors (e.g. weather or host community). Parameter values are selected so that the population is stable over time.

Usage

config_ex_1

Format

A config
config_ex_2  
*Simple model configuration example using delays*

**Description**
This model configuration uses delay transitions for all transitions except the adult to eggs transition. As in config_ex_1, no transitions depend on predictors, and the population is stable over time.

**Usage**

```r
config_ex_2
```

**Format**
A config

---

constant_fun  
*Constant function*

**Description**
Constant function

**Usage**

```r
constant_fun(x, y, a)
```

**Arguments**

- **x**  
  Predictor 1 in transitions table. Not used in this function
- **y**  
  Predictor 2 in transitions table. Not used in this function
- **a**  
  Parameter a in parameters table.

**Value**
Numeric vector of length 1 equal to input parameter a

**Examples**

```r
constant_fun(NULL, NULL, 1)
```
**density_fun**  

*Density dependent mortality*

**Description**

Density dependent mortality

**Usage**

density_fun(x, y, a, b, c, pref)

**Arguments**

- **x**: Predictor 1 in transitions table. Numeric vector indicating host density for each of the host species. Length should be equal to the number of host species.
- **y**: Predictor 2 in transitions table. Number of feeding ticks in life stages specified by predictor 2.
- **a**: Parameter a in parameters table.
- **b**: Parameter b in parameters table.
- **c**: Parameter c in parameters table.
- **pref**: Parameters named pref in parameters table. Numeric vector of length equal to the number of host species. Values are the preference for ticks in a given transition for each host species.

**Value**

Numeric vector of length 1, indicating mortality rate

**Examples**

density_fun(c(10, 20), 100, .1, .3, .2, c(.5, .8))

---

**expo_fun**  

*Exponential function*

**Description**

Exponential function

**Usage**

expo_fun(x, y, a, b)
Arguments

\begin{itemize}
\item \texttt{x} \hspace{1cm} Predictor 1 in transitions table.
\item \texttt{y} \hspace{1cm} Predictor 2 in transitions table. Not used in this function.
\item \texttt{a} \hspace{1cm} Parameter \texttt{a} in parameters table.
\item \texttt{b} \hspace{1cm} Parameter \texttt{b} in parameters table.
\end{itemize}

Value

Numeric vector of length 1

Examples

\begin{itemize}
\item \texttt{expo_fun(.5, NULL, .1, .3)}
\end{itemize}

\begin{itemize}
\item \texttt{feed_fun(x, y, a, pref, q, tmin, tmax)}
\end{itemize}

Description

Probability of actively questing and then finding a host

Usage

\begin{itemize}
\item \texttt{feed_fun(x, y, a, pref, q, tmin, tmax)}
\end{itemize}

Arguments

\begin{itemize}
\item \texttt{x} \hspace{1cm} Predictor 1 in transitions table. Numeric vector indicating host density for each of the host species. Length should be equal to the number of host species.
\item \texttt{y} \hspace{1cm} Predictor 2 in transitions table. Numeric vector of length 1 indicating temperature.
\item \texttt{a} \hspace{1cm} Parameter \texttt{a} in parameters table.
\item \texttt{pref} \hspace{1cm} Parameters named \texttt{pref} in parameters table. Numeric vector of length equal to the number of host species. Values are the preference for ticks in a given transition for each host species.
\item \texttt{q} \hspace{1cm} Parameter \texttt{q} in parameters table. Used in Briere function.
\item \texttt{tmin} \hspace{1cm} Parameter \texttt{tmin} in parameters table. Indicates minimum temperature at which ticks actively quest.
\item \texttt{tmax} \hspace{1cm} Parameter \texttt{tmax} in parameters table. Indicates maximum temperature at which ticks actively quest.
\end{itemize}

Details

Product of binomial and Briere functions (prob of finding a host) \* (prob of active questing)
**find_n_feed**

**Value**

Numeric vector of length 1

**Examples**

```r
find_n_feed(10, 30, .001, .1, .5, 20, 40)
```

---

### find_n_feed

**Probability of finding a host and successfully feeding on it**

**Description**

Probability of finding a host and successfully feeding on it

**Usage**

```r
find_n_feed(x, y, a, pref, feed_success)
```

**Arguments**

- `x`: Predictor 1 in transitions table. Numeric vector indicating host density for each of the host species. Length should be equal to the number of host species.
- `y`: Predictor 2 in transitions table. Not used in this function.
- `a`: Parameter a in parameters table.
- `pref`: Parameters named pref in parameters table. Numeric vector of length equal to the number of host species. Values are the preference for ticks in a given transition for each host species.
- `feed_success`: Parameters named feed success in parameters table. Numeric vector of length equal to the number of host species. Values are the feeding success rate for ticks in a given transition while feeding on each host species.

**Value**

Numeric vector of length 1 indicating probability that ticks find any host and then successfully feed on that host.

**Examples**

```r
find_n_feed(10, NULL, .1, 1, .5)
```

```r
find_n_feed(runif(2) * 10, NULL, .1, runif(2), runif(2))
```
get_pred_from_table  Get a predictor from input data

Description
Get a predictor from input data

Usage
get_pred_from_table(time, pred, table)

Arguments
- time: Numeric vector of days to get data. Ignored if input is constant over time (as indicated by NA value in 'j_day' column)
- pred: string specifying the name of the predictor, e.g. "host_den"
- table: input predictors table

graph_lifecycle  Visualize transitions as a life cycle graph

Description
Visualize transitions as a life cycle graph

Usage
graph_lifecycle(transitions)

Arguments
- transitions: Tick transitions tibble

Details
This function could be used to visually confirm that a custom config has all the transitions intended

Value
None, plots a life cycle graph

Examples
graph_lifecycle(config_ex_1$transitions)
**graph_population_each_group**

*Graph population size of each life stage over time*

**Description**

Graph population size of each life stage over time

**Usage**

`graph_population_each_group(output)`

**Arguments**

- **output**  
  Model output; a tibble

**Value**

ggplot object

**Examples**

```r
out <- run(config_ex_1)
graph_population_each_group(out)
```

---

**graph_population_overall_trend**

*Graph overall trend in population*

**Description**

Graph overall trend in population

**Usage**

`graph_population_overall_trend(output)`

**Arguments**

- **output**  
  Model output; a tibble

**Details**

See roughly whether population is increasing or decreasing. Calculates and plots the rate of change in number of adult ticks between consecutive days.
Value

ggplot object

Examples

# Make a new config that results in a population where some ticks remain
# in their life stage for multiple days.
my_config <- config_ex_1
my_config$parameters$param_value <- c(0.5, 0, 0.01, 0.95, 0.1, 0.8, 900, 0)
out <- run(my_config)
graph_population_overall_trend(out)

growth_rate  Calculate multiplicative growth rate of population

Description

Calculate multiplicative growth rate of population

Usage

growth_rate(out)

Arguments

out  Model output data frame

Value

Numeric vector of length one representing growth rate

Examples

out <- run(config_ex_1)
growth_rate(out)
**host_example_config**  
*Configuration for showing how we can modify host community data*

**Description**  
Configuration for showing how we can modify host community data

**Usage**  
host_example_config

**Format**  
A config

---

**infect_example_config**  
*Configuration for showing infection dynamics*

**Description**  
Configuration for showing infection dynamics

**Usage**  
infect_example_config

**Format**  
A config

---

**infect_fun**  
*Probability that a feeding tick becomes engorged infected or uninfected*

**Description**  
Probability that a feeding tick becomes engorged infected or uninfected

**Usage**  
infect_fun(x, y, from_infected, to_infected, host_rc, pref)
Arguments

\( x \)
Predictor 1 in transitions table. Numeric vector indicating host density for each of the host species. Length should be equal to the number of host species.

\( y \)
Predictor 2 in transitions table. Not used in this function.

\( \text{from\_infected} \)
Parameter \( \text{from\_infected} \) in parameters table. Value should be 1 if transition is from an infected tick stage, 0 otherwise.

\( \text{to\_infected} \)
Parameter \( \text{to\_infected} \) in parameters table. Value should be 1 if transition is to an infected tick stage, 0 otherwise.

\( \text{host\_rc} \)
Parameters named \( \text{host\_rc} \) in parameters table. Numeric vector of length equal to the number of host species. Values are the host reservoir competence for each host species.

\( \text{pref} \)
Parameters named \( \text{pref} \) in parameters table. Numeric vector of length equal to the number of host species. Values are the preference for ticks in a given transition for each host species.

Details

Since density dependent mortality is subtracted later, in this function we assume that all feeding ticks feed successfully and become engorged.

Value

Numeric vector of length 1

Examples

infect_fun(10, NULL, 0, 0, .3, 1)
infect_fun(10, NULL, 0, 1, .3, 1)
infect_fun(10, NULL, 1, 1, .3, 1)

ogden2005

Configuration for Ixodes scapularis population dynamics model from Ogden et al. 2005

Description

This model configuration recreates the Ixodes scapularis (blacklegged tick) population dynamics model from Ogden et al. 2005. This is a relatively complete model of tick population dynamics, including the effects of both temperature and the host community on tick life-stage transitions. We include this configuration to show that our package can be used to recreate existing models.

Usage

ogden2005
ogden_feed_fun

Format

A config

**steps** Number of time steps to run the model. Here each step corresponds to one day.

**initial_population** Named vector of initial population size. Here the population starts with 10000 questing adults.

**transitions** A tibble giving the transitions between tick life stages.

**parameters** A tibble with the parameters to the life-stage transitions functions.

**predictors** A tibble with the average temperature for each day, and density of hosts over the model run. Here the host community is stable with 20 deer and 200 rodents.

**max_delay** The number of time units used for the delay functions.

See Also


Examples

data(ogden2005)
 ## Not run:
 output <- run(ogden2005)
 graph_population_each_group(output)

## End(Not run)

ogden_feed_fun

**Probability of actively questing times constant host finding probability**

Description

Probability of actively questing times constant host finding probability

Usage

ogden_feed_fun(x, y, a, q, tmin, tmax)

Arguments

- **x** Predictor 1 in transitions table. Numeric vector of length 1 indicating temperature.
- **y** Predictor 2 in transitions table. Not used in this function.
- **a** Parameter a in parameters table.
- **q** Parameter q in parameters table. Used in Briere function.
- **tmin** Parameter tmin in parameters table. Indicates minimum temperature at which ticks actively quest.
- **tmax** Parameter tmax in parameters table. Indicates maximum temperature at which ticks actively quest.
Details

(const prob of finding a host) * (prob of active questing)

Value

Numeric vector of length 1

See Also


Examples

ogden_feed_fun(30, NULL, .03, .01, 10, 35)

read_config

create a config object from a YAML file

Description

create a config object from a YAML file

Usage

read_config(file)

Arguments

file YAML file to read

Value

A config object

Examples

## Not run:
read_config('cfg.yml')

## End(Not run)
**run**

*Run the model*

---

**Description**

Run the model

**Usage**

```
run(cfg)
```

**Arguments**

- **cfg**
  - An `IxPopDyMod::config` object

**Value**

Data frame of population of ticks of each life stage each day

**Examples**

```
run(config_ex_1)
```

---

**run_all_configs**

*Run the model for each config*

---

**Description**

Simple convenience wrapper for calling run on each config in a list

**Usage**

```
run_all_configs(configs, parallel = FALSE)
```

**Arguments**

- **configs**
  - List of config objects
- **parallel**
  - Logical; if TRUE, run on all cores using parallel package.

**Value**

A list of data frame model outputs like those returned by `run()`
Examples

# run two example configs and save results

## Not run:
outputs <- run_all_configs(list(config_ex_1, config_ex_2))

## End(Not run)

snow_cover_fun  \textit{Mortality as a function of whether there is a snow on the ground}

Description

Mortality as a function of whether there is a snow on the ground

Usage

snow_cover_fun(x, y, no\_snow\_mort, snow\_mort)

Arguments

<table>
<thead>
<tr>
<th>x</th>
<th>amount of snow on ground</th>
</tr>
</thead>
<tbody>
<tr>
<td>y</td>
<td>not used in this transition function</td>
</tr>
<tr>
<td>no_snow_mort</td>
<td>mortality with no snow on the ground</td>
</tr>
<tr>
<td>snow_mort</td>
<td>mortality with snow on the ground</td>
</tr>
</tbody>
</table>

temp_example_config \textit{Configuration for showing how we can modify climate data}

Description

Configuration for showing how we can modify climate data

Usage

temp_example_config

Format

A \texttt{config}
vary_many_params

Generate copies of a config with all combinations of modified parameters

Description

Generate copies of a config with all combinations of modified parameters

Usage

vary_many_params(cfg, param_rows, values_list)

Arguments

- **cfg**: Base config to make modified copies of
- **param_rows**: Numeric vector indicating the rows in the parameters table where parameter values should be modified. Length must equal length of values_list
- **values_list**: List of numeric vectors. The values of a vector values_list[[i]] are the parameter values to use for the parameter identified by param_rows[[i]]

Value

A list of configs

Examples

```r
# create new configs with different values for the parameter determining
# mortality of eggs (which is found in row 2) and that determining
# mortality of larvae (which is found in row 4)
cfgs <- vary_many_params(config_ex_1,
                           param_rows = c(2, 4),
                           values_list = list(c(0, 0.1), c(.99, .98)))

# inspect parameter rows 2 and 4 in each of the new configs to verify that we
# have the new values
lapply(cfgs, function(cfg) cfg$params[c(2, 4), 'param_value'])
```
vparem

Generate copies of a config with a modified parameter

Description

Create copies of a config with a modified parameter. These new configs can be used to see how that parameter affects the model.

Usage

vparem(
  cfg,
  param_row = NA,
  to = NA,
  from = NA,
  param_name = NA,
  host_spp = NA,
  values
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cfg</td>
<td>Base config to make modified copies of</td>
</tr>
<tr>
<td>param_row</td>
<td>Row number of parameter to vary, if this is specified arguments from, to, param_name, and host_spp are unneeded</td>
</tr>
<tr>
<td>to</td>
<td>The to life stage of the parameter to change.</td>
</tr>
<tr>
<td>from</td>
<td>The from life stage from of the parameter to change. If this is given, to and param_name are also needed.</td>
</tr>
<tr>
<td>param_name</td>
<td>The name of the parameter to change.</td>
</tr>
<tr>
<td>host_spp</td>
<td>The host_spp identifying the parameter to change. Needed only if there are multiple rows in the parameter table with the same from, to and param_name, but different host_spp.</td>
</tr>
<tr>
<td>values</td>
<td>Numeric vector of values to use for parameter</td>
</tr>
</tbody>
</table>

Value

A list of configs

Examples

# create new configs with different values for the parameter determining # mortality of eggs (which is found in row 2)
cfgs <- vparem(config_ex_1, param_row = 2, values = c(0, 0.1, 0.2))

# inspect parameter row 2 in each of the new configs to verify that we have
winter_tick

# the new values
lapply(cfgs, function(cfg) cfg$parameters[[2, 'param_value']])

winter_tick  Configuration for winter tick population dynamics model

Description

This is a model configuration based on a literature search on the factors affect the winter tick life cycle. Many of the transitions and parameters in this configuration are drawn from Drew and Samuel (1986). We include this configuration to show that our package is flexible for modeling multiple tick species with different life histories.

Usage

winter_tick

Format

An object of class config of length 6.

See Also

Drew and Samuel (1986) doi: 10.1139/z86105
Drew and Samuel (1985) doi: 10.7589/0090355821.3.274

Examples

data(winter_tick)
## Not run:
output <- run(winter_tick)
graph_population_each_group(winter_tick)
## End(Not run)
**write_config**

Save a config object as files

**Description**

Write a config object as a YAML file, and write all dataframe components (transitions, parameters, predictors) as csv files. All paths must be explicitly specified as arguments. This function will not allow overwriting files.

**Usage**

```r
write_config(
  cfg, 
  config_path, 
  transitions_path, 
  parameters_path, 
  predictors_path
)
```

**Arguments**

- `cfg` A config object
- `config_path` Path to the output YAML config file
- `transitions_path` Path to output transitions csv
- `parameters_path` Path to output parameters csv
- `predictors_path` Path to output predictors csv

**Value**

None, writes config components to disk

**Examples**

```r
## Not run:
write_config(config_ex_1, 'cfg.yml', 'trans.csv', 'params.csv',
             'predictors.csv')

## End(Not run)
```
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