popdynmodel

An R package for modelling population dynamics and demography

October 3, 2023

Contents

1. Installation

`popdynmodel` depends on R $\geq$ 4.2.0 and requires installing and loading the following packages:

```
library(nimble)
library(MCMCvis)
library(rlang)
library(magrittr)
library(dplyr)
library(tidyr)
library(stringr)
library(tidyverse)
```

Then the files containing the package functions must be loaded:

```
source("Fonction_modelisation.R")
source("Fonction_modelisation_interne.R")
load("modfunparameters.rda")
```

2. Package content

riverfish

Description

This dataset gives the abundance and biomass of seven freshwater fish species on 85 sites sampled, from 2010 to 2022, by multiple-pass removal electrofishing. The sites are spread over six river-basins of metropolitan France.

Usage

```
data(riverfish)
```

Format

`riverfish` is a data frame with 14 variables:

`pop_id`	sampling site identifiers
`year`	sampling year
`taxa`	species common names
`family`	species family names
`gudgeon`	gudgeon guild: value is 1 if the species is a gudgeon and NA otherwise
`pass`	pass position in multiple-pass removal electrofishing
`headcount`	fishing catch size by species
`biomass`	fishing catch weight by species
`surface`	fishing surface
`fishing`	electrofishing protocol
`hydro_basin`	river-basin identifiers
`temperature`	water temperature per site and year
`depth`	fishing depth per site and year
`flow`	watercourse flow per site and year

Source

`riverfish` is based on data extracted from the national ASPE database managed by the French Biodiversity Agency (OFB).

get_ModParameters

Description

Gives the description of the parameters of modeling functions.

Usage

```
get_ModParameters(fun, parameter)
```

Arguments

`fun` [optional, character] name of the modelling function

`parameter` [optional, character] name(s) of the parameter(s)

Examples

```
# Get description about all parameters of mod_popoccup function
get_ModParameters(fun = "mod_popoccup")

# Get description about some parameters
get_ModParameters(parameter = "z")
get_ModParameters(parameter = c("z","N","B"))
```

mef_imputevalue

Description

Imputes missing values of a variable from observed values.

Usage

```
mef_imputevalue(df, var_id, var_tmp, var_imp)
```

Arguments

`df`	data frame
`var_id`	variable name with sampling location identifiers
`var_tmp`	variable name with continuous sampling times
`var_imp`	variable name with missing values to be imputed

Details

`mef_imputevalue` imputes missing values of a variable from observed values in order to get complete time series. At the location scale, the missing values are substituted by the previous time value or, failing that, by the following time value.

Value

`mef_imputevalue` returns the data frame `df` after imputing the missing values.

Examples

```
data(riverfish)
n <- sample(2010:2022, 4)
riverfish[n,"surface"] <- NA

# Imputation of surface missing values
df <- mef_imputevalue(riverfish, var_id=pop_id, var_tmp=year, var_imp=surface)
```

mef_convertquali

Description

Converts one or more quantitative variables into qualitative variables.

Usage

```
mef_convertquali(df, var_quali)
```

Arguments

`df`	data frame
`var_quali`	name(s) of qualitative variable(s) to convert

Details

`mef_convertquali` converts each quantitative variable by breaking it into multiple binary variables (one fewer than the number of modalities of qualitative variable).

Value

`mef_convertquali` returns the data frame `df` with the new binary variables.

Examples

```
data(riverfish)

# Conversion of variable flow
df <- mef_convertquali(riverfish, var_quali="flow")
```

mod_popoccup

Description

Fits Bayesian hierarchical occupancy model to presence-absence time series for estimating multi-taxa occurrence from colonisation and extinction probabilities. The modelling framework not accounts for taxa detection biases.

Usage

```
mod_popoccup(
    df,
    var_id,
    var_tmp,
    var_tax,
    var_cnt,
    var_reg = NULL,
    var_guild = NULL,
    period = NULL,
    timestep = 1,
    save_parameters = NULL
    n_chain = 3,
    n_iter = 10000,
    n_thin = n_iter / 100,
    n_burnin = n_iter / 4
)
```

Arguments

`df`	data.frame with variables used in the model
`var_id`	variable name with sampling location identifiers (must not contain missing values)
`var_tmp`	variable name with continuous sampling times (must be numeric without missing values)
`var_tax`	variable name with taxa identifiers (must not contain missing values)
`var_cnt`	variable name used to define presence/absence (must be numeric)
`var_reg`	[optional] variable(s) name(s) with regional identifiers
`var_guild`	[optional] variable(s) name(s) with taxa guilds identifiers
`period`	[optional] list with start and end times for estimating intermediate occupancy change rates (must be numeric)
`timestep`	[optional] interval between two consecutive times (must be numeric)

`save_parameters` [optional] character vector with the names of the parameters to save (by default, all model parametes are saved)

`n_chain` [optional] number of MCMC chains (must be numeric)

`n_iter` [optional] number of iterations per MCMC chain (must be numeric)

`n_thin` [optional] backup interval for MCMC samples (must be numeric)

`n_burnin` [optional] number of initial iterations to discard per Markov chain (must be numeric)

Details

`mod_popoccup` relies on Bayesian hierarchical state-space model that describes the occupancy dynamics of one or more taxa from presence-absence data. The successive occupancy states of locations defined by `var_id` depend on taxon- and location-specific probabilities of persistence and colonisation. Then, on a global scale (i.e. across all locations), the occupancy changes rates are estimated from the ratio of the number of occuped location from one time to the next and their geometric mean is used as average occupancy rate over the whole time period (c.f. section **??** for more details).

`var_reg` allows add the estimates of occupancy changes rates at intermediate spatial scales.

`var_guild` allows add the estimates of occupancy changes rates for guilds (geometric means of taxa occupancy rates).

`period` allows add the estimates of occupancy changes rates for intermediate time periods.

`timestep` allows account for regular gaps in time series (e.g. to estimate annual average occupancy rates from bi-annual monitoring).

The model is run using the `runMCMC` function of `nimble` package.

Value

`mod_popoccup` returns a list with the summaries of main statistics associated with the estimation of the requested parameters (`mcmc_summary`), the MCMC chains (`mcmc_chain`) and the list of parameters subscripts (`subscript`).

See Also

`mod_popoccupRS`, `modenv_popoccup` and `get_ModParametes`

Examples

```
## Not run:

data(riverfish)
df <- riverfish[riverfish$pass == 1,]

# Occupancy dynamics of taxa
mcmc.out <- mod_popoccup(df,
                         var_id = "pop_id",
                         var_tmp = "year",
                         var_tax = "taxa",
                         var_cnt = "headcount")

# Occupancy dynamics of taxa and families at basin level
mcmc.out <- mod_popoccup(df,
                         var_id = "pop_id",
                         var_tmp = "year",
                         var_tax = "taxa",
                         var_cnt = "headcount",
                         var_reg = "hydro_basin",
                         var_guild = "family")

# Occupancy dynamics with intermediate average occupancy rates every 6 years
mcmc.out <- mod_popoccup(df,
                         var_id = "pop_id",
                         var_tmp = "year",
                         var_tax = "taxa",
                         var_cnt = "headcount",
                         var_guild = "family",
                         period = list(c(2010,2016),c(2016,2022)),
                         save_parameters = "z_mulambda_gui")

## End(Not run)
```

modenv_popoccup

Description

Fits Bayesian hierarchical occupancy models to presence-absence time series for estimating multi-taxa occurrence from relationships with environmental covariates. The modelling framework not accounts for taxa detection biases.

Usage

```
modenv_popoccup(
    df,
    var_id,
    var_tmp,
    var_tax,
    var_cnt,
    var_envO = NULL,
    var_envP = NULL,
    var_envC = NULL,
    env_tmp = TRUE,
    var_reg = NULL,
    var_guild = NULL,
    period = NULL,
    timestep = 1,
    save_parameters = NULL,
    n_chain = 3,
    n_iter = 10000,
    n_thin = n_iter/100,
    n_burnin = n_iter/4
)
```

Arguments

`df` data.frame with variables used in the model

`var_id` variable name with sampling location identifiers (must not contain missing values)

`var_tmp` variable name with continuous sampling times (must be numeric without missing values)

`var_tax` variable name with taxa identifiers (must not contain missing values)

`var_cnt` variable name used to define presence/absence (must be numeric)

`var_envO` [optional] environmental covariate(s) name(s) related to occupancy probability (must be numeric without missing values)

`var_envP` [optional] environmental covariate(s) name(s) related to persistence probability (must be numeric without missing values) `var_envC` [optional] environmental covariate(s) name(s) related to colonisation probability (must be numeric without missing values)

`env_tmp` [optional] logical indicating whether the environmental covariates vary over time (`TRUE`) or only across locations (`FALSE`)

`var_reg` [optional] variable(s) name(s) with regional identifiers

`var_guild` [optional] variable(s) name(s) with taxa guilds identifiers

`period` [optional] list with start and end times for estimating intermediate occupancy change rates (must be numeric)

`timestep` [optional] interval between two consecutive times (must be numeric)

`save_parameters` [optional] character vector with the names of the parameters to save (by default, all model parametes are saved)

`n_chain` [optional] number of MCMC chains (must be numeric)

`n_iter` [optional] number of iterations per MCMC chain (must be numeric)

`n_thin` [optional] backup interval for MCMC samples (must be numeric)

`n_burnin` [optional] number of initial iterations to discard per Markov chain (must be numeric)

Details

`modenv_popoccup` relies on Bayesian hierarchical state-space models that describe the occupancy dynamics of one or more taxa from presence-absence data. The successive occupancy states of locations defined by `var_id` depend on taxon-specific responses to environmental covariates. Then, on a global scale (i.e. across all locations), the occupancy changes rates are estimated from the ratio of the number of occuped location from one time to the next and their geometric mean is used as average occupancy rate over the whole time period (c.f. section **??** for more details).

If `var_envO` is supplied, the occupancy states of the locations are modelled from the linear effect of environmental covariates on occupancy probabilities.

If `var_envP` and `var_envC` are supplied, the occupancy states of the locations are modelled from the linear effect of environmental covariates on persistence and colonisation probabilities.

If only `var_envP` is supplied, the occupancy states of the locations are modelled from the linear effect of environmental covariates on persistence probabilities and from taxon- and location-specific colonisation probabilities.

If only `var_envC` is supplied, the occupancy states of the locations are modelled from the linear effect of environmental covariates on colonisation probabilities and from taxon- and location-specific persistence probabilities.

`var_reg` allows add the estimates of occupancy changes rates at intermediate spatial scales.

`var_guild` allows add the estimates of occupancy changes rates for guilds (geometric means of taxa occupancy rates).

`period` allows add the estimates of occupancy changes rates for intermediate time periods.

`timestep` allows account for regular gaps in time series (e.g. to estimate annual average occupancy rates from bi-annual monitoring).

The models are run using the `runMCMC` function of `nimble` package.

Value

`modenv_popoccup` returns a list with the summaries of main statistics associated with the estimation of the requested parameters (`mcmc_summary`), the MCMC chains (`mcmc_chain`) and the list of parameters subscripts (`subscript`).

See Also

`modenv_popoccupRS`, `mod_popoccup` and `get_ModParametes`

Examples

```
## Not run:

data(riverfish)
df <- riverfish[riverfish$pass == 1,]

# Occupancy model with linear environmental effects on occupancy probability
mcmc.out <- modenv_popoccup(df,
                            var_id = "pop_id",
                            var_tmp = "year",
                            var_tax = "taxa",
                            var_cnt = "headcount",
                            var_envO = c("temperature","depth"))

# Occupancy model with linear environmental effects on persistence probability
mcmc.out <- modenv_popoccup(df,
                            var_id = "pop_id",
                            var_tmp = "year",
                            var_tax = "taxa",
                            var_cnt = "headcount",
                            var_envP = c("temperature","depth"))
```

```
# Occupancy model with linear environmental effects on colonisation probability
mcmc.out <- modenv_popoccup(df,
                            var_id = "pop_id",
                            var_tmp = "year",
                            var_tax = "taxa",
                            var_cnt = "headcount",
                            var_envC = c("temperature","depth"))

# Occupancy model with linear environmental effects on persistence
# and colonisation probabilities
mcmc.out <- modenv_popoccup(df,
                            var_id = "pop_id",
                            var_tmp = "year",
                            var_tax = "taxa",
                            var_cnt = "headcount",
                            var_envP = c("temperature","depth"),
                            var_envC = "temperature")

## End(Not run)
```

mod_popgrow

Description

Fits Bayesian hierarchical multi-taxa growth population models to abundance and/or biomass time series. The modelling framework not accounts for detection biases of taxa and individuals.

Usage

```
mod_popgrow(
   df,
   var_id,
   var_tmp,
   var_tax,
   var_cnt = NULL,
   var_wei = NULL,
   var_surf = NULL,
   var_reg = NULL,
   var_guild = NULL,
   period = NULL,
   timestep = 1,
   save_parameters = NULL,
   n_chain = 3,
   n_iter = 10000,
   n_thin = n_iter/100,
   n_burnin = n_iter/4
)
```

Arguments

`df` data.frame with variables used in the model

`var_id` variable name with sampling location identifiers (must not contain missing values)

`var_tmp` variable name with continuous sampling times (must be numeric without missing values)

`var_tax` variable name with taxa identifiers (must not contain missing values)

`var_cnt` [optional] variable name with taxa abundances (must be numeric)

`var_wei` [optional] variable name with taxa biomasses (must be numeric)

`var_surf` [optional] variable name with sampling surfaces, or other quantitative sampling efforts (must be numeric without missing values)

`var_reg` [optional] variable(s) name(s) with regional identifiers `var_guild` [optional] variable(s) name(s) with taxa guilds identifiers

`period` [optional] list with start and end times for estimating intermediate occupancy change rates (must be numeric)

`timestep` [optional] interval between two consecutive times (must be numeric)

`save_parameters` [optional] character vector with the names of the parameters to save (by default, all model parametes are saved)

`n_chain` [optional] number of MCMC chains (must be numeric)

`n_iter` [optional] number of iterations per MCMC chain (must be numeric)

`n_thin` [optional] backup interval for MCMC samples (must be numeric)

`n_burnin` [optional] number of initial iterations to discard per Markov chain (must be numeric)

Details

`mod_popgrow` relies on Bayesian hierarchical state-space models that include two or three main components. The first component describes the occupancy dynamics of taxa over time at locations defined by `var_id` from taxon- and location-specific probabilities of persistence and colonisation. Two other independent components describe the population growth of taxa on successively occupied locations, one based on abundance (if `var_cnt` is supplied) and other based on biomass (if `var_wei` is supplied). These two components are based on an autoregressive growth model. Then, at location and global scales (i.e. across all locations), the finite population growth rates are estimated as the changes in population size from one time to the next and their geometric means are used as average growth rates over the whole time period (c.f. section **??** for more details).

`var_surf` allows to account for variabilities in sampling effort from one time to the next.

`var_reg` allows add the estimates of growth rates at intermediate spatial scales.

`var_guild` allows add the estimates of guild growth rates at global and intermediate scales (geometric means of taxa growth rates).

`period` allows add the estimates of growth rates for intermediate time periods.

`timestep` allows to account for regular gaps in time series (e.g. to estimate annual average occupancy rates from bi-annual monitoring).

The models are run using the `runMCMC` function of `nimble` package.

Value

`mod_popgrow` returns a list with the summaries of main statistics associated with the estimation of the requested parameters (`mcmc_summary`), the MCMC chains (`mcmc_chain`) and the list of parameters subscripts (`subscript`).

See Also

`mod_popgrowRS`, `modenv_popgrow` and `get_ModParametes`

Examples

```
## Not run:

data(riverfish)
df <- riverfish[riverfish$pass == 1,]

# Population growth and abundance
mcmc.out <- mod_popgrow(df,
                        var_id = "pop_id",
                        var_tmp = "year",
                        var_tax = "taxa",
                        var_cnt = "headcount",
                        var_surf = "surface")

# Population growth and biomass
mcmc.out <- mod_popgrow(df,
                        var_id = "pop_id",
                        var_tmp = "year",
                        var_tax = "taxa",
                        var_wei = "biomass",
                        var_surf = "surface")

# Growth rates of families at location scale
df$id <- df$pop_id
mcmc.out <- mod_popgrow(df,
                        var_id = "pop_id",
                        var_tmp = "year",
                        var_tax = "taxa",
                        var_cnt = "headcount",
                        var_wei = "biomass",
                        var_surf = "surface",
                        var_reg = "id",
                        var_guild = "family")

## End(Not run)
```

modenv_popgrow

Description

Fits Bayesian hierarchical multi-taxa growth population models with environmental stochasticity to abundance and/or biomass time series. The modelling framework not accounts for detection biases of taxa and individuals.

Usage

```
modenv_popgrow(
   df,
   var_id,
   var_tmp,
   var_tax,
   var_env,
   var_cnt = NULL,
   var_wei = NULL,
   var_surf = NULL,
   var_reg = NULL,
   var_guild = NULL,
   period = NULL,
   timestep = 1,
   save_parameters = NULL,
   n_chain = 3,
   n_iter = 10000,
   n_thin = n_iter/100,
   n_burnin = n_iter/4
)
```

Arguments

`df`	data.frame with variables used in the model
`var_id`	variable name with sampling location identifiers (must not contain missing values)
`var_tmp`	variable name with continuous sampling times (must be numeric without missing values)
`var_tax`	variable name with taxa identifiers (must not contain missing values)
`var_env`	environmental covariate(s) name(s) whose values must be supplied by location and time (must be numeric without missing values)
`var_cnt`	[optional] variable name with taxa abundances (must be numeric)
`var_wei`	[optional] variable name with taxa biomasses (must be numeric)

`var_surf` [optional] variable name with sampling surfaces, or other quantitative sampling efforts (must be numeric without missing values)

`var_reg` [optional] variable(s) name(s) with regional identifiers

`var_guild` [optional] variable(s) name(s) with taxa guilds identifiers

`period` [optional] list with start and end times for estimating intermediate occupancy change rates (must be numeric)

`timestep` [optional] interval between two consecutive times (must be numeric)

`save_parameters` [optional] character vector with the names of the parameters to save (by default, all model parametes are saved)

`n_chain` [optional] number of MCMC chains (must be numeric)

`n_iter` [optional] number of iterations per MCMC chain (must be numeric)

`n_thin` [optional] backup interval for MCMC samples (must be numeric)

`n_burnin` [optional] number of initial iterations to discard per Markov chain (must be numeric)

Details

`modoenv_popgrow` relies on Bayesian hierarchical state-space models that include two or three main components. The first component describes the occupancy dynamics of taxa over time at locations defined by `var_id` from taxon- and location-specific probabilities of persistence and colonisation. Two other independent components describe the population growth of taxa on successively occupied locations, one based on abundance (if `var_cnt` is supplied) and other based on biomass (if `var_wei` is supplied). These two components are based on an autoregressive formulation in which growth rates are modelled as a linear function of environmental covariates. Then, at location and global scales (i.e. across all locations), the finite population growth rates are estimated as the changes in population size from one time to the next and their geometric means are used as average growth rates over the whole time period (c.f. section **??** for more details).

`var_surf` allows to account for variabilities in sampling effort from one time to the next.

`var_reg` allows add the estimates of growth rates at intermediate spatial scales.

`var_guild` allows add the estimates of guild growth rates at global and intermediate scales (geometric means of taxa growth rates).

`period` allows add the estimates of growth rates for intermediate time periods.

timestep allows to account for regular gaps in time series (e.g. to estimate annual average occupancy rates from bi-annual monitoring).

The models are run using the runMCMC function of nimble package.

Value

modenv_popgrow returns a list with the summaries of main statistics associated with the estimation of the requested parameters (mcmc_summary), the MCMC chains (mcmc_chain) and the list of parameters subscripts (subscript).

See Also

modenv_popgrowRS, mod_popgrow and get_ModParametes

Examples

```
## Not run:

data(riverfish)
df <- riverfish[riverfish$pass == 1,]

# Population growth and abundance
mcmc.out <- modenv_popgrow(df,
                           var_id = "pop_id",
                           var_tmp = "year",
                           var_tax = "taxa",
                           var_env = c("temperature","depth"),
                           var_cnt = "headcount",
                           var_surf = "surface")

# Population growth from abundance and biomass with intermediate growth rates
mcmc.out <- modenv_popgrow(df,
                           var_id = "pop_id",
                           var_tmp = "year",
                           var_tax = "taxa",
                           var_env = "depth",
                           var_cnt = "headcount",
                           var_wei = "biomass",
                           var_surf = "surface",
                           period = list(c(2010,2016),c(2016,2022)))

## End(Not run)
```

mod_popdyn

Description

Fits Bayesian hierarchical multi-taxa occupancy and growth models to abundance and/or biomass time series. The modelling framework not accounts for detection biases of taxa and individuals.

Usage

```
mod_popdyn(
   df,
   var_id,
   var_tmp,
   var_tax,
   var_cnt = NULL,
   var_wei = NULL,
   var_surf = NULL,
   var_reg = NULL,
   var_guild = NULL,
   period = NULL,
   timestep = 1,
   save_parameters = NULL,
   n_chain = 3,
   n_iter = 10000,
   n_thin = n_iter/100,
   n_burnin = n_iter/4
)
```

Arguments

`df` data.frame with variables used in the model

`var_id` variable name with sampling location identifiers (must not contain missing values)

`var_tmp` variable name with continuous sampling times (must be numeric without missing values)

`var_tax` variable name with taxa identifiers (must not contain missing values)

`var_cnt` [optional] variable name with taxa abundances (must be numeric)

`var_wei` [optional] variable name with taxa biomasses (must be numeric)

`var_surf` [optional] variable name with sampling surfaces, or other quantitative sampling efforts (must be numeric without missing values)

`var_reg` [optional] variable(s) name(s) with regional identifiers `var_guild` [optional] variable(s) name(s) with taxa guilds identifiers

`period` [optional] list with start and end times for estimating intermediate occupancy change rates (must be numeric)

`timestep` [optional] interval between two consecutive times (must be numeric)

`save_parameters` [optional] character vector with the names of the parameters to save (by default, all model parametes are saved)

`n_chain` [optional] number of MCMC chains (must be numeric)

`n_iter` [optional] number of iterations per MCMC chain (must be numeric)

`n_thin` [optional] backup interval for MCMC samples (must be numeric)

`n_burnin` [optional] number of initial iterations to discard per Markov chain (must be numeric)

Details

`mod_popdyn` relies on Bayesian hierarchical state-space models that include two or three main components. The first component describes the occupancy dynamics of taxa over time from presence-absence data (defined from abundances if `var_cnt` is supplied or, failing that, from biomasses). The successive occupancy states of locations defined by `var_id` depend on taxon- and location-specific probabilities of persistence and colonisation. Then, on a global scale (i.e. across all locations), the occupancy changes rates are estimated from the ratio of the number of occuped location from one time to the next and their geometric mean is used as average occupancy rate over the whole time period (c.f. section **??**).

The other two components describe the population growth of taxa on successively occupied locations, one based on abundance (if `var_cnt` is supplied) and other based on biomass (if `var_wei` is supplied). Then, at location and global scales, the finite population growth rates are estimated as the changes in population size from one time to the next and their geometric means are used as average growth rates over the whole time period (c.f. section **??**).

`var_surf` allows to account for variabilities in sampling effort over time in estimates of growth rates.

`var_reg` allows add the estimates of occupancy changes rates and growth rates at intermediate spatial levels.

`var_guild` allows add the estimates of occupancy changes rates and growth rates for guilds (geometric means of taxa rates).

`period` allows add the estimates of occupancy changes rates and growth rates for intermediate time periods.

timestep allows to account for regular gaps in time series (e.g. to estimate annual average occupancy rates from bi-annual monitoring).

The models are run using the runMCMC function of nimble package.

Value

mod_popdyn returns a list with the summaries of main statistics associated with the estimation of the requested parameters (mcmc_summary), the MCMC chains (mcmc_chain) and the list of parameters subscripts (subscript).

See Also

mod_popoccup, mod_popgrow, mod_popdynRS and get_ModParametes

Examples

```
## Not run:

data(riverfish)
df <- riverfish[riverfish$pass == 1,]

# Population dynamics from abundance
mcmc.out <- mod_popdyn(df,
                        var_id = "pop_id",
                        var_tmp = "year",
                        var_tax = "taxa",
                        var_cnt = "headcount",
                        var_surf = "surface")

# Population dynamics from biomass
mcmc.out <- mod_popdyn(df,
                       var_id = "pop_id",
                       var_tmp = "year",
                       var_tax = "taxa",
                       var_wei = "biomass",
                       var_surf = "surface")

# Occupancy change rates and growth rates for taxa families
mcmc.out <- mod_popdyn(df,
                       var_id = "pop_id",
                       var_tmp = "year",
                       var_tax = "taxa",
                       var_wei = "biomass",
                       var_surf = "surface",
                       var_guild = c("family","gudgeon"))

## End(Not run)
```

modenv_popdyn

Description

Fits Bayesian hierarchical multi-taxa occupancy and growth models with environmental stochasticity to abundance and/or biomass time series. The modelling framework not accounts for detection biases of taxa and individuals.

Usage

```
modenv_popgrow(
   df,
   var_id,
   var_tmp,
   var_tax,
   var_cnt = NULL,
   var_wei = NULL,
   var_env = NULL,
   var_envO = NULL,
   var_envP = NULL,
   var_envC = NULL,
   env_tmp = TRUE,
   var_surf = NULL,
   var_reg = NULL,
   var_guild = NULL,
   period = NULL,
   timestep = 1,
   save_parameters = NULL,
   n_chain = 3,
   n_iter = 10000,
   n_thin = n_iter/100,
   n_burnin = n_iter/4
)
```

Arguments

`df` data.frame with variables used in the model

`var_id` variable name with sampling location identifiers (must not contain missing values)

`var_tmp` variable name with continuous sampling times (must be numeric without missing values)

`var_tax` variable name with taxa identifiers (must not contain missing values)

`var_cnt` [optional] variable name with taxa abundances (must be numeric)

`var_wei` [optional] variable name with taxa biomasses (must be numeric) `var_env` [optional] environmental covariate(s) name(s) related to growth rates whose values must be supplied by location and time (must be numeric without missing values)

`var_envO` [optional] environmental covariate(s) name(s) related to occupancy probability (must be numeric without missing values)

`var_envP` [optional] environmental covariate(s) name(s) related to persistence probability (must be numeric without missing values)

`var_envC` [optional] environmental covariate(s) name(s) related to colonisation probability (must be numeric without missing values)

`env_tmp` [optional] logical indicating whether the environmental covariates related to occupancy model vary over time (`TRUE`) or only across locations (`FALSE`)

`var_surf` [optional] variable name with sampling surfaces, or other quantitative sampling efforts (must be numeric without missing values)

`var_reg` [optional] variable(s) name(s) with regional identifiers

`var_guild` [optional] variable(s) name(s) with taxa guilds identifiers

`period` [optional] list with start and end times for estimating intermediate occupancy change rates (must be numeric)

`timestep` [optional] interval between two consecutive times (must be numeric)

`save_parameters` [optional] character vector with the names of the parameters to save (by default, all model parametes are saved)

`n_chain` [optional] number of MCMC chains (must be numeric)

`n_iter` [optional] number of iterations per MCMC chain (must be numeric)

`n_thin` [optional] backup interval for MCMC samples (must be numeric)

`n_burnin` [optional] number of initial iterations to discard per Markov chain (must be numeric)

Details

`modoenv_popdyn` relies on Bayesian hierarchical state-space models that include two or three main components. The first component describes the occupancy dynamics of taxa from presence-absence data (defined from abundances if `var_cnt` is supplied or, failing that, from biomasses). If `var_envO`, `var_envP` or `var_envC` are supplied, the successive occupancy states of locations defined by `var_id` depend on taxon-specific responses to environmental covariates (c.f. `modenv_popoccup`). Otherwise the successive occupancy states of locations depend on taxon- and location-specific probabilities of persistence and colonisation. Then, on a global scale (i.e. across all locations), the occupancy changes rates are estimated from the ratio of the number of occuped locations from one time to the next and their geometric mean is used as average occupancy rate over the whole time period (c.f. section **??**).

Two other independent components describe the population growth of taxa on successively occupied locations, one based on abundance (if `var_cnt` is is supplied) and other based on biomass (if `var_wei` is supplied). These two components are based on an autoregressive growth formulation. If `var_env` is supplied the growth rates are modelled as a linear function of environmental covariates. Then, at location and global scales, the finite population growth rates are estimated as the changes in population size from one time to the next and their geometric means are used as average growth rates over the whole time period (c.f. section **??**).

`var_surf` allows to account for variabilities in sampling effort over time in estimates of growth rates.

`var_reg` allows add the estimates of occupancy changes rates and growth rates at intermediate spatial levels.

`var_guild` allows add the estimates of occupancy changes rates and growth rates for guilds (geometric means of taxa rates).

`period` allows add the estimates of occupancy changes rates and growth rates for intermediate time periods.

`timestep` allows to account for regular gaps in time series (e.g. to estimate annual average occupancy rates from bi-annual monitoring).

The models are run using the `runMCMC` function of `nimble` package.

Value

`modenv_popdyn` returns a list with the summaries of main statistics associated with the estimation of the requested parameters (`mcmc_summary`), the MCMC chains (`mcmc_chain`) and the list of parameters subscripts (`subscript`).

See Also

`modenv_popoccup`, `modenv_popgrow`, `modenv_popgdynRS` and `get_ModParametes`

Examples

```
## Not run:

data(riverfish)
df <- riverfish[riverfish$pass == 1,]
```

```
# Population dynamics with environmental effects on growth
mcmc.out <- modenv_popdyn(df,
                          var_id = "pop_id",
                          var_tmp = "year",
                          var_tax = "taxa",
                          var_cnt = "headcount",
                          var_env = c("temperature","depth"))

# Population dynamics with environmental effects on occupancy probability
mcmc.out <- modenv_popdyn(df,
                          var_id = "pop_id",
                          var_tmp = "year",
                          var_tax = "taxa",
                          var_cnt = "headcount",
                          var_envO = c("temperature","depth"))

# Population dynamics with environmental effects on growth and colonisation
# taking into account sampling effort effect
mcmc.out <- modenv_popdyn(df,
                          var_id = "pop_id",
                          var_tmp = "year",
                          var_tax = "taxa",
                          var_cnt = "headcount",
                          var_env = c("temperature","depth"),
                          var_envC = "temperature",
                          var_surf = "surface")

## End(Not run)
```