

Package: hmde (via r-universe)

December 10, 2024

Title Hierarchical Methods for Differential Equations

Version 0.1.0

Description Wrapper for Stan that offers a number of in-built models to implement a hierarchical Bayesian longitudinal model for repeat observation data. Model choice selects the differential equation that is fit to the observations. Single and multi-individual models are available.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Biarch true

Depends R (>= 3.5.0)

Imports methods, dplyr, ggplot2, purrr, Rcpp (>= 0.12.0), RcppParallel (>= 5.0.1), rlang, rstan (>= 2.18.1), rstantools (>= 2.3.1.1)

LinkingTo BH (>= 1.66.0), Rcpp (>= 0.12.0), RcppEigen (>= 0.3.3.3.0), RcppParallel (>= 5.0.1), rstan (>= 2.18.1), StanHeaders (>= 2.18.0)

SystemRequirements GNU make

Suggests knitr, rmarkdown, testthat (>= 3.0.0), withr, mnormt, here, patchwork, deSolve, cowplot

VignetteBuilder knitr

Config/testthat/edition 3

LazyData true

Config/pak/sysreqs make

Repository <https://traitecoevo.r-universe.dev>

RemoteUrl <https://github.com/traitecoevo/hmde>

RemoteRef HEAD

RemoteSha fed62c65a6fba6663c5aa58c71d8ffa16fc90478

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hmde-package *The 'hmde' package.*

Description

A package to implement a selection of hierarchical Bayesian longitudinal models for inverse Bayesian problems.

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References

Stan Development Team (NA). RStan: the R interface to Stan. R package version 2.26.23. <https://mc-stan.org>

hmde_assign_data	<i>Assign data to template for chosen model</i>
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Description

Assign data to template for chosen model

Usage

```
hmde_assign_data(model_template, data = NULL, ...)
```

Arguments

model_template	output from hmde_model
data	Input data tibble with columns including time, y_obs, obs_index, and additionally ind_id for multi-individual models
...	data-masking name-value pairs allowing specific input of elements

Value

updated named list with your data assigned to Stan model parameters

hmde_canham_de	<i>Differential equation for Canham growth single and multi- individual models</i>
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Description

Differential equation for Canham growth single and multi- individual models

Usage

```
hmde_canham_de(y = NULL, pars = NULL)
```

Arguments

y	input real
pars	list of parameters g_max, S_max, k

Value

value of differential equation at y

<code>hmde_const_de</code>	<i>Differential equation for constant growth single and multi- individual models</i>
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Description

Differential equation for constant growth single and multi- individual models

Usage

```
hmde_const_de(y = NULL, pars = NULL)
```

Arguments

<code>y</code>	input real
<code>pars</code>	list of parameter beta

Value

value of differential equation at y

<code>hmde_extract_estimates</code>	
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Extract samples and return measurement, individual, and population-level estimates

Description

Extract samples and return measurement, individual, and population-level estimates

Usage

```
hmde_extract_estimates(model = NULL, fit = NULL, input_measurement_data = NULL)
```

Arguments

<code>model</code>	model name character string
<code>fit</code>	fitted model Stan fit
<code>input_measurement_data</code>	data used to fit the model with ind_id, y_obs, time, obs_index tibble

Value

named list with data frames for measurement, individual, population-level, and error parameter estimates

`hmde_linear_de`

Differential equation for linear growth single individual model

Description

Differential equation for linear growth single individual model

Usage

```
hmde_linear_de(y = NULL, pars = NULL)
```

Arguments

y	input real
pars	list of parameters beta_0, beta_1

Value

value of differential equation at y

`hmde_model`

Select data configuration template for hmde supported model

Description

Select data configuration template for hmde supported model

Usage

```
hmde_model(model = NULL)
```

Arguments

model	model name character string
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Value

named list that matches Stan model parameters

`hmde_model_des` *Function to select DE given model name*

Description

Function to select DE given model name

Usage

```
hmde_model_des(model = NULL)
```

Arguments

model	character string model name
-------	-----------------------------

Value

DE function corresponding to specific model

`hmde_model_names` *Returns names of available models.*

Description

Returns names of available models.

Usage

```
hmde_model_names()
```

Value

vector of character strings for model names.

<code>hmde_model_pars</code>	<i>Show parameter list for hmde supported model</i>
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Description

Show parameter list for hmde supported model

Usage

```
hmde_model_pars(model = NULL)
```

Arguments

<code>model</code>	model name character string
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Value

named list that matches Stan model parameters

<code>hmde_plot_de_pieces</code>	<i>Plot pieces of chosen differential equation model for each individual. Structured to take the individual data tibble that is built by the hmde_extract_estimates function using the ind_par_name_mean estimates. Function piece will go from the first fitted size to the last. Accepted ggplot arguments will change the axis labels, title, line colour, alpha</i>
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Description

Plot pieces of chosen differential equation model for each individual. Structured to take the individual data tibble that is built by the hmde_extract_estimates function using the ind_par_name_mean estimates. Function piece will go from the first fitted size to the last. Accepted ggplot arguments will change the axis labels, title, line colour, alpha

Usage

```
hmde_plot_de_pieces(
  model = NULL,
  individual_data = NULL,
  measurement_data = NULL,
  xlab = "Y(t)",
  ylab = "f",
  title = NULL,
  colour = "#006600",
  alpha = 0.4
)
```

Arguments

<code>model</code>	model name character string
<code>individual_data</code>	tibble with estimated DE parameters
<code>measurement_data</code>	tibble with estimated measurements
<code>xlab</code>	character string for replacement x axis label
<code>ylab</code>	character string for replacement y axis label
<code>title</code>	character string for replacement plot title
<code>colour</code>	character string for replacement line colour
<code>alpha</code>	real number for replacement alpha value

Value

ggplot object

hmde_plot_obs_est_inds

Plot estimated and observed values over time for a chosen number of individuals based on posterior estimates. Structured to take in the measurement_data tibble constructed by the hmde_extract_estimates function.

Description

Plot estimated and observed values over time for a chosen number of individuals based on posterior estimates. Structured to take in the measurement_data tibble constructed by the hmde_extract_estimates function.

Usage

```
hmde_plot_obs_est_inds(
  ind_id_vec = NULL,
  n_ind_to_plot = NULL,
  measurement_data = NULL,
  xlab = "Time",
  ylab = "Y(t)",
  title = NULL
)
```

Arguments

ind_id_vec	vector with list of ind_id values
n_ind_to_plot	integer giving number of individuals to plot if not specified
measurement_data	tibble with estimated measurements
xlab	character string for replacement x axis label
ylab	character string for replacement y axis label
title	character string for replacement plot title

Value

ggplot object

hmde_run

Run chosen pre-built model in Stan

Description

Run chosen pre-built model in Stan

Usage

```
hmde_run(model_template, ...)
```

Arguments

model_template	model template generated by hmde_model and updated by hmde_assign_data
...	additional arguments passed to rstan::sampling

Value

Stanfit model output

hmde_vb_de*Differential equation for von Bertalanffy growth single and multi- individual models***Description**

Differential equation for von Bertalanffy growth single and multi- individual models

Usage

```
hmde_vb_de(y = NULL, pars = NULL)
```

Arguments

y	input real
pars	list of parameters Y_max, growth_rate

Value

value of differential equation at y

Lizard_Size_Data*Skink size data - Lampropholis delicata***Description**

A subset of data from Kar, Nakagawa, and Noble (2024), used to model growth behaviour in a skink species. Observations are of the length from the tip of the nose to the start of the cloaca. Data was prepared by taking a simple random sample with replacement of 50 individual IDs among individuals with at least 5 observations each. Data was then transformed to conform to the needs of a model data set in the package.

Usage

```
Lizard_Size_Data
```

Format**Lizard_Size_Data:**

A data frame with 336 rows and 4 columns:

ind_id ID number for individual

time Days since first observation.

y_obs Individual size in mm.

obs_index Index of observations for individual

Source

<https://osf.io/hjkxd/>

Tree_Size_Data

Garcinia recondita - Barro Colorado Island data

Description

A subset of data from the Barro Colorado Island long term forest plot managed by the Smithsonian Tropical Research Institute (Condit et al. 2019). Data was prepared by taking a simple random sample without replacement of 30 individual IDs from *Garcinia recondita*. The sampling frame was restricted to individuals with 6 observations since 1990, and a difference between observed first and last sizes of more than 3cm in order to avoid identifiability issues. Data was then transformed and renamed to match the required structure to act as demonstration for the package.

Usage

Tree_Size_Data

Format

Tree_Size_Data:

A data frame with 300 rows and 4 columns:

ind_id ID number for individual

time Years since first observation.

y_obs Individual diameter at breast height (DBH) in centimetres.

obs_index Index of observations for individual

Source

<https://doi.org/10.15146/5xcp-0d46>

References

<https://doi.org/10.1002/ecy.4140>

Tree_Size_Ests

Garcinia recondita model estimates - Barro Colorado Island data

Description

Estimated sizes, individual growth parameters, and population-level hyper-parameters for *Garcinia recondita* fit with a Canham growth function hierarchical model. The data used to fit the model is the Tree_Size_Data object.

Usage

Tree_Size_Ests

Format

Tree_Size_Ests:

A list with 4 elements:

measurement_data A tibble with 5 columns that gives information on size observations and estimates.

individual_data A tibble with 13 columns that gives posterior estimates for individual growth parameters.

error_data A tibble with 5 columns that gives posterior estimates of the error parameter.

population_data A tibble with 5 columns that gives posterior estimates for population-level hyper-parameters.

Trout_Size_Data

SUSTAIN Salmo trutta data

Description

A subset of data from the SUSTAIN trout capture-recapture data set from Moe et al. (2020). Observations are of total body length in centimetres. Data prepared by taking a stratified sample of individual IDs based on the number of observations per individual: 25 individuals with 2 observations, 15 with 3, 10 with 4. Within the groups a simple random sample without replacement was used. Data was then transformed and renamed to match the required structure to act as demonstration for the package.

Usage

Trout_Size_Data

Format

Trout_Size_Data:

A data frame with 135 rows and 4 columns:

ind_id ID number for individual

time Years since first capture and tagging of individual.

y_obs Individual length in centimetres.

obs_index Index of observations for individual

Source

<https://doi.org/10.3897/BDJ.8.e52157>

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