

# Package ‘hmde’

July 4, 2025

**Title** Hierarchical Methods for Differential Equations

**Version** 1.2.1

**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. O'Brien et al. (2024) <[doi:10.1111/2041-210X.14463](https://doi.org/10.1111/2041-210X.14463)>.

**License** GPL (>= 3)

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**Biarch** true

**Depends** R (>= 4.1.0)

**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, mixtools, MASS

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**LazyData** true

**URL** <https://traitecoevo.github.io/hmde/>

**BugReports** <https://github.com/traitecoevo/hmde/issues>

**NeedsCompilation** yes

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**Repository** CRAN

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hmde-package	<i>The 'hmde' package.</i>
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Description

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

Author(s)

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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>

**See Also**

Useful links:

- <https://traitecoevo.github.io/hmde/>
- Report bugs at <https://github.com/traitecoevo/hmde/issues>

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hmde_affine_de	<i>Differential equation for affine growth single individual model</i>
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**Description**

Differential equation for affine growth single individual model

**Usage**

```
hmde_affine_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_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

**Examples**

```
# basic usage of hmde_assign_data
hmde_model("constant_single_ind") |> hmde_assign_data(Trout_Size_Data)
```

---

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

---

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

---

**Description**

Differential equation for constant growth single and multi- individual models

**Usage**

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

**Arguments**

y	input real
pars	list of parameter beta

**Value**

value of differential equation at y

---

hmde_extract_estimates	<i>Extract samples and return measurement, individual, and population-level estimates</i>
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**Description**

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

**Usage**

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

**Arguments**

fit	fitted model Stan fit
input_measurement_data	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

**Examples**

```
# basic usage of hmde_extract_estimates
hmde_model("constant_single_ind") |>
  hmde_assign_data(Trout_Size_Data)|>
  hmde_run(chains = 1, iter = 1000,
           verbose = FALSE, show_messages = FALSE) |>
  hmde_extract_estimates(Trout_Size_Data)
```

---

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

**Value**

named list that matches Stan model parameters

**Examples**

```
# basic usage of hmde_model
hmde_model("constant_single_ind")
```

---

hmde\_model\_des

*Function to select DE given model name*


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**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

**Examples**

```
# basic usage of hmde_model_des
hmde_model_des("constant_single_ind")
```

---

hmde_model_names	<i>Returns names of available models.</i>
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**Description**

Returns names of available models.

**Usage**

```
hmde_model_names()
```

**Value**

vector of character strings for model names.

**Examples**

```
# basic usage of hmde_model_names
hmde_model_names()
```

---

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

---

**Description**

Show parameter list for hmde supported model

**Usage**

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

**Arguments**

model                      model name character string

**Value**

named list that matches Stan model parameters

**Examples**

```
# basic usage of hmde_model_pars
hmde_model_pars("constant_single_ind")
```

---

hmde_plot_de_pieces	<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(
  estimate_list = NULL,
  xlab = "Y(t)",
  ylab = "f",
  title = NULL,
  colour = "#006600",
  alpha = 0.4
)
```

**Arguments**

estimate_list	list output from hmde_extract_estimates
xlab	character string for replacement x axis label
ylab	character string for replacement y axis label
title	character string for replacement plot title
colour	character string for replacement line colour
alpha	real number for replacement alpha value



**Value**

ggplot object

**Examples**

```
# basic usage of hmde_plot_de_pieces
hmde_plot_de_pieces(estimate_list = Tree_Size_Ests)
```

---

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

**Arguments**

estimate_list	list output of hmde_extract_estimates
measurement_data	tibble with estimated measurements
ind_id_vec	vector with list of ind_id values
n_ind_to_plot	integer giving number of individuals to plot if not specified
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

**Examples**

```
# basic usage of hmde_plot_obs_est_inds
hmde_plot_obs_est_inds(estimate_list = Tree_Size_Ests,
                      n_ind_to_plot = 5)
```

---

hmde_run	<i>Run chosen pre-built model in Stan</i>
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**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

**Examples**

```
# basic usage of hmde_run
hmde_model("constant_single_ind") |>
  hmde_assign_data(Trout_Size_Data)|>
  hmde_run(chains = 1, iter = 1000,
          verbose = FALSE, show_messages = FALSE)
```

---

hmde_vb_de	<i>Differential equation for von Bertalanffy growth single and multi- individual models</i>
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---

**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

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Lizard_Size_Data	<i>Skink size data - Lampropholis delicata</i>
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**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**

[doi:10.15146/5xcp0d46](https://doi.org/10.15146/5xcp0d46)

**References**

[doi:10.1002/ecy.4140](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 5 elements:

**model** A character string giving the model name - Canham with multiple individuals.

**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.

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Trout\_Size\_Data

*SUSTAIN Salmo trutta* data

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### 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**

[doi:10.3897/BDJ.8.e52157](https://doi.org/10.3897/BDJ.8.e52157)

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