

Package ‘BayesianDEB’

May 6, 2026

Title Bayesian Dynamic Energy Budget Modelling

Version 0.1.4

Description Provides a Bayesian framework for Dynamic Energy Budget (DEB) modelling via 'Stan'. Implements the standard DEB model of Kooijman (2010, <[doi:10.1017/CBO9780511805400](https://doi.org/10.1017/CBO9780511805400)>) as a state-space model with Hamiltonian Monte Carlo inference (Carpenter et al., 2017, <[doi:10.18637/jss.v076.i01](https://doi.org/10.18637/jss.v076.i01)>). Includes individual-level growth models, growth-reproduction models, hierarchical multi-individual models with partial pooling, and toxicokinetic-toxicodynamic (TKTD) models for ecotoxicology following the DEBtox framework (Jager et al., 2006, <[doi:10.1007/s10646-006-0060-x](https://doi.org/10.1007/s10646-006-0060-x)>). Supports prior specification from biological knowledge, convergence diagnostics (Vehtari et al., 2021, <[doi:10.1214/20-BA1221](https://doi.org/10.1214/20-BA1221)>), posterior predictive checks, derived quantity estimation, and visualisation via 'ggplot2'.

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URL <https://github.com/sciom/BayesianDEB>

BugReports <https://github.com/sciom/BayesianDEB/issues>

Encoding UTF-8

RoxygenNote 7.3.3

SystemRequirements CmdStan
(<https://mc-stan.org/users/interfaces/cmdstan>)

Depends R (>= 4.1.0)

Imports posterior (>= 1.5.0), rlang (>= 1.1.0), cli (>= 3.6.0),
ggplot2 (>= 3.4.0), bayesplot (>= 1.10.0), deSolve (>= 1.40),
stats, utils

Suggests cmdstanr (>= 0.8.0), testthat (>= 3.0.0), loo (>= 2.6.0),
digest, dplyr (>= 1.1.0), tidyr (>= 1.3.0), knitr, rmarkdown,
withr

Additional_repositories <https://stan-dev.r-universe.dev>

Config/testthat/edition 3

VignetteBuilder knitr

LazyData true

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-04-21 19:42:25 UTC

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arrhenius *Arrhenius Temperature Correction*

Description

Computes the temperature correction factor for DEB rate parameters based on the Arrhenius relationship (Kooijman, 2010, Eq. 1.2). In DEB theory all rate parameters (e.g., $\{p_{Am}\}$, $[p_M]$, v) scale with temperature by the same factor:

Usage

```
arrhenius(temp, T_ref = 293.15, T_A = 8000)
```

Arguments

temp	Body (or ambient) temperature in Kelvin. Renamed from T in version 0.1.4 to avoid shadowing R's built-in T symbol (= TRUE); pass positionally or use temp = ... explicitly.
T_ref	Reference temperature in Kelvin (default 293.15 K = 20 °C).
T_A	Arrhenius temperature in Kelvin (default 8000 K).

Details

$$c_T = \exp\left(\frac{T_A}{T_{\text{ref}}} - \frac{T_A}{T}\right)$$

where T and T_{ref} are in Kelvin and T_A is the Arrhenius temperature (a species-specific constant, typically 6000–12000 K for ectotherms; Kooijman, 2010, Table 8.1). At $T = T_{\text{ref}}$, the factor is exactly 1.

Value

Numeric correction factor (dimensionless, > 0).

References

Kooijman, S.A.L.M. (2010). *Dynamic Energy Budget Theory for Metabolic Organisation*. 3rd edition. Cambridge University Press, Eq. 1.2. doi:10.1017/CBO9780511805400

Examples

```
# Correction at 25 C relative to 20 C reference
arrhenius(298.15, T_ref = 293.15, T_A = 8000) # ~ 1.74

# No correction at reference temperature
arrhenius(293.15) # exactly 1
```

bdeb_data

*Prepare Data for BDEB Models***Description**

Converts long-format data frames into the structured list required by the BayesianDEB Stan programs. Growth observations are matched to the DEB state variable $L = V^{1/3}$ (structural length); reproduction records are interval counts of offspring over $[t_{\text{start}}, t_{\text{end}}]$. The function validates column names, rejects negative times/lengths, sorts by individual and time, and (for hierarchical models) pads ragged observation vectors into matrices with NaN fill, as required by Stan's fixed-size array declarations.

Usage

```
bdeb_data(growth = NULL, reproduction = NULL, concentration = NULL, f_food = 1)
```

Arguments

growth	A data frame with columns: id, time (days), length (structural length in cm, i.e., $L = V^{1/3}$). If your data are physical (observed) lengths , multiply by the shape coefficient: $L = \delta_M \times L_w$. See the package vignette for guidance on δ_M .
reproduction	A data frame with columns: id, t_start, t_end, count (number of offspring in the interval). For cumulative counts use <code>repro_to_intervals()</code> first.
concentration	Optional named numeric vector or data frame mapping individual/group id to external toxicant concentration C_w (for DEBtox models; see <code>bdeb_tox()</code>).
f_food	Scaled functional response $f \in [0, 1]$, the ratio of actual to maximum ingestion rate (Kooijman, 2010, Eq. 2.3). Default 1 (ad libitum feeding).

Value

A bdeb_data object (S3 list) ready for `bdeb_model()`.

References

Kooijman, S.A.L.M. (2010). *Dynamic Energy Budget Theory for Metabolic Organisation*. 3rd edition. Cambridge University Press. doi:10.1017/CBO9780511805400

Examples

```
# Simple growth data
df <- data.frame(
  id = rep(1, 10),
  time = seq(0, 45, by = 5),
  length = c(0.1, 0.15, 0.22, 0.30, 0.38, 0.44, 0.49, 0.52, 0.54, 0.55)
)
dat <- bdeb_data(growth = df)
```

bdeb_derived

*Compute Derived Biological Quantities from the Posterior***Description**

Transforms the raw DEB parameter draws into biologically interpretable quantities, automatically propagating parameter uncertainty. All formulas follow Kooijman (2010, Ch. 3, Table 3.1) strictly.

Usage

```
bdeb_derived(fit, quantities = c("L_inf", "k_M", "growth_rate"), f = 1)
```

Arguments

fit	A <code>bdeb_fit()</code> object.
quantities	Character vector of quantities to compute. One or more of "L_m", "L_inf", "k_M", "growth_rate", "g".
f	Scaled functional response $f \in (0, 1]$ for computing food-dependent quantities ("L_inf", "growth_rate"). Default 1 (ad libitum).

Value

A `posterior::draws_df` with one column per requested quantity and one row per posterior draw.

DEB length terminology

DEB theory distinguishes several length measures. This function returns **structural length** $L = V^{1/3}$, which is the cube root of structural volume. Structural length is *not* the same as **physical (observed) length** L_w , which relates to L via the shape coefficient: $L_w = L/\delta_M$. The shape coefficient δ_M is species-specific (typically 0.1–0.5) and is not estimated by this package. If your data are physical lengths, you should either (a) convert to structural length before fitting, or (b) divide `L_inf` by your species' δ_M to obtain the physical asymptotic length.

Available quantities

"L_m" Maximum structural length at $f = 1$ (Kooijman, 2010, Table 3.1):

$$L_m = \kappa \{p_{Am}\} / [p_M]$$

This is a **species-level constant** independent of food. Units: cm.

"L_inf" Ultimate structural length at food level f (Kooijman, 2010, Eq. 3.4):

$$L_i = f \cdot L_m = f \kappa \{p_{Am}\} / [p_M]$$

The asymptotic length when $dV/dt = 0$ at constant food. Depends on f . Units: cm. Dimensional check: $(-)(-)(\text{J d}^{-1}\text{cm}^{-2})/(\text{J d}^{-1}\text{cm}^{-3}) = \text{cm}$.

"k_M" Somatic maintenance rate constant:

$$k_M = [p_M]/[E_G]$$

Units: d⁻¹.

"growth_rate" Von Bertalanffy growth rate (Kooijman, 2010, Eq. 3.23):

$$\dot{r}_B = \frac{k_M g}{3(f + g)}$$

where $g = [E_G] v / (\kappa \{p_{Am}\})$ is the energy investment ratio. Depends on f . Units: d⁻¹.

"g" Energy investment ratio (Kooijman, 2010, Table 3.1):

$$g = [E_G] v / (\kappa \{p_{Am}\})$$

Dimensionless. Large g means growth is expensive relative to reserve turnover.

Reference example

For *Eisenia fetida* with AmP parameters $\{p_{Am}\} = 5.0$, $[p_M] = 0.5$, $\kappa = 0.75$: $L_m = 0.75 \times 5.0/0.5 = 7.5$ cm (structural). With $\delta_M \approx 0.24$, the physical maximum length would be $L_m/\delta_M \approx 31$ mm, consistent with observations.

References

- Kooijman, S.A.L.M. (2010). *Dynamic Energy Budget Theory for Metabolic Organisation*. 3rd edition. Cambridge University Press. doi:10.1017/CBO9780511805400
- Marques, G.M., Augustine, S., Lika, K., Pecquerie, L., Domingos, T. and Kooijman, S.A.L.M. (2018). The AmP project: comparing species on the basis of dynamic energy budget parameters. *PLOS Computational Biology*, 14(5), e1006100. doi:10.1371/journal.pcbi.1006100

bdeb_diagnose

MCMC Convergence Diagnostics

Description

Reports a comprehensive set of NUTS/HMC diagnostics following the recommendations of Vehtari et al. (2021):

Divergent transitions Indicate that the numerical leapfrog integrator encountered regions of high curvature. Even a single divergence can bias the posterior. Remedy: increase `adapt_delta`.

Treedepth saturation The NUTS trajectory hit the maximum allowed tree depth, meaning it could not find a U-turn. Remedy: increase `max_treedepth`.

E-BFMI Energy Bayesian Fraction of Missing Information. Values below 0.3 indicate that the momentum resampling is inefficient (Betancourt, 2016).

\hat{R} Split- \hat{R} convergence diagnostic. Values > 1.01 indicate incomplete mixing across chains.

Bulk and tail ESS Effective sample size for the bulk and tails of the posterior. Values below 400 suggest that posterior summaries may be unreliable.

Usage

```
bdeb_diagnose(fit, pars = NULL, verbose = TRUE)
```

Arguments

fit	A <code>bdeb_fit()</code> object.
pars	Character vector of parameter names to report. Default: all model parameters (excluding generated quantities such as <code>log_lik</code> , <code>L_rep</code> , and <code>lp__</code>).
verbose	Logical; if TRUE (default) the diagnostic messages and parameter summary table are printed via <code>cli</code> functions and <code>message()</code> . All output is suppressible with <code>suppressMessages()</code> . Set to FALSE for a silent run (the invisible return value is unchanged).

Value

Invisibly returns a list with components `n_divergent`, `n_max_treedepth`, `ebfmi`, and `summary` (a `posterior::summarise_draws()` tibble).

References

Vehtari, A., Gelman, A., Simpson, D., Carpenter, B. and Bürkner, P.-C. (2021). Rank-normalization, folding, and localization: an improved \hat{R} for assessing convergence of MCMC. *Bayesian Analysis*, 16(2), 667–718. doi:10.1214/20BA1221

Betancourt, M. (2016). Diagnosing biased inference with divergences. Stan case study. https://mc-stan.org/users/documentation/case-studies/divergences_and_bias.html

bdeb_ec50

Extract EC50 and NEC from a DEBtox Fit

Description

Extracts the full posterior distribution of the EC_{50} and the NEC (no-effect concentration, z_w) from a fitted DEBtox model. Both quantities are computed analytically in the Stan generated quantities block, avoiding the need for post-hoc root finding. At toxicokinetic steady state the stress factor equals $s = b_w(C_w - z_w)$ for $C_w > z_w$, so setting $s = 0.5$ yields

Usage

```
bdeb_ec50(fit, prob = 0.9, verbose = TRUE)
```

Arguments

fit	A <code>bdeb_fit()</code> object from a DEBtox model.
prob	Credible interval probability. Default 0.90.
verbose	Logical; if TRUE (default) the summary table is printed via <code>cli::cli_verbatic()</code> / <code>message()</code> and can be silenced with <code>suppressMessages()</code> . Set to FALSE for a silent run; the invisible return value is identical.

Details

$$EC_{50} = z_w + \frac{0.5}{b_w}.$$

The NEC is the threshold concentration below which no effect occurs; it corresponds directly to the parameter z_w in the damage model of Kooijman & Bedaux (1996).

Value

A named list with:

- draws: posterior draws of EC50
- summary: mean, median, sd, lower, upper
- NEC: posterior summary of the no-effect concentration

References

Kooijman, S.A.L.M. and Bedaux, J.J.M. (1996). *The Analysis of Aquatic Toxicity Data*. VU University Press, Amsterdam.

bdeb_fit

Fit a BDEB Model via Hamiltonian Monte Carlo

Description

Compiles the bundled Stan program via **cmdstanr** (which handles caching internally based on the Stan source hash) and runs the No-U-Turn Sampler (NUTS; Hoffman & Gelman, 2014). The Stan ODE system is solved at each leapfrog step using the BDF stiff solver (`ode_bdf`) with absolute and relative tolerances of 10^{-6} .

Usage

```
bdeb_fit(
  model,
  chains = 4,
  iter_warmup = 1000,
  iter_sampling = 1000,
  adapt_delta = 0.8,
  max_treedepth = 10,
  seed = NULL,
  parallel_chains = NULL,
  threads_per_chain = NULL,
  refresh = 200,
  ...
)
```

Arguments

model	A <code>bdeb_model()</code> object.
chains	Number of independent MCMC chains. Default 4 (the minimum recommended by Vehtari et al., 2021, for reliable \hat{R}).
iter_warmup	Number of warmup (adaptation) iterations per chain. Default 1000. Stan uses dual-averaging to tune the step size and diagonal mass matrix during warmup.
iter_sampling	Number of post-warmup sampling iterations per chain. Default 1000 (yielding 4000 total draws with 4 chains).
adapt_delta	Target Metropolis acceptance probability for NUTS. Default 0.8. Increase toward 1.0 to reduce divergences at the cost of smaller step sizes and longer runtime.
max_treedepth	Maximum binary-tree depth for NUTS. Default 10 (i.e., up to $2^{10} = 1024$ leapfrog steps per transition).
seed	Integer random seed for full reproducibility.
parallel_chains	Number of chains to run in parallel. Default $\min(\text{chains}, \text{detectCores}() - 1)$.
threads_per_chain	Number of threads per chain for within-chain parallelism via Stan's <code>reduce_sum</code> . Default NULL (no threading; the model runs sequentially within each chain). Set to e.g. 4 for the "hierarchical" or "debtax" models to distribute per-individual / per-group ODE solves across threads. When threading is active, adjust <code>parallel_chains</code> so that <code>chains * threads_per_chain</code> does not exceed available cores. Has no effect on "individual" or "growth_repro" models (single ODE solve, nothing to distribute).
refresh	How often to print sampling progress (iterations). Default 200. Set to 0 for silent operation.
...	Additional arguments forwarded to <code>CmdStanModel\$sample()</code> .

Details

Tuning guidance. If `bdeb_diagnose()` reports divergent transitions, increase `adapt_delta` toward 1.0 (e.g., 0.95 or 0.99). This reduces the step size, trading speed for geometric fidelity of the sampler. If the maximum treedepth is frequently saturated, increase `max_treedepth` (e.g., 12 or 15). For hierarchical models, starting values can matter; the non-centred parameterisation used in `bdeb_hierarchical_growth.stan` should suffice in most cases.

Value

A `bdeb_fit` object containing the `CmdStanMCMC` result, the model specification, and sampling metadata.

References

Hoffman, M.D. and Gelman, A. (2014). The No-U-Turn Sampler: adaptively setting path lengths in Hamiltonian Monte Carlo. *Journal of Machine Learning Research*, 15(47), 1593–1623.

Vehtari, A., Gelman, A., Simpson, D., Carpenter, B. and Bürkner, P.-C. (2021). Rank-normalization, folding, and localization: an improved \hat{R} for assessing convergence of MCMC. *Bayesian Analysis*, 16(2), 667–718. doi:10.1214/20BA1221

Examples

```
# \dontrun{ } because bdeb_fit() requires the external CmdStan toolchain
# (not on CRAN) and a single fit takes > 30 seconds (Stan compilation
# + MCMC). Users can run this manually after `cmdstanr::install_cmdstan()`.
## Not run:
data(eisenia_growth)
dat <- bdeb_data(growth = eisenia_growth[eisenia_growth$id == 1, ])
mod <- bdeb_model(dat, type = "individual")
fit <- bdeb_fit(mod, chains = 2, iter_sampling = 500)

## End(Not run)
```

bdeb_loo

LOO Cross-Validation for Model Comparison

Description

Computes approximate leave-one-out cross-validation (LOO-CV) using Pareto-smoothed importance sampling (PSIS; Vehtari et al., 2017). Requires that the Stan model includes a `log_lik` array in the generated quantities block.

Usage

```
bdeb_loo(fit, endpoint = c("all", "growth", "reproduction"), ...)
```

Arguments

<code>fit</code>	A <code>bdeb_fit()</code> object.
<code>endpoint</code>	Which log-likelihood to use for "growth_repro" models: "all" (default, concatenates growth + reproduction), "growth", or "reproduction". Ignored for "individual" models.
<code>...</code>	Additional arguments passed to <code>loo::loo()</code> .

Details

Currently supported for "individual" and "growth_repro" models only. The "hierarchical" and "debttox" models do not store per-observation `log_lik` in generated quantities: "hierarchical" computes the likelihood inside `reduce_sum` (no access to individual contributions outside the function); "debttox" uses the same `reduce_sum` approach and its generated quantities block only computes EC50/NEC. Adding per-group `log_lik` to DEBtox is planned for a future version. An informative error is raised for unsupported types.

Value

A loo object (see [loo::loo\(\)](#)).

Conditional independence assumption

For "growth_repro" models with endpoint = "all", growth and reproduction observations are concatenated and each treated as an independent data point. This is valid because the two endpoints are **conditionally independent given the latent DEB process** (growth observations depend only on $V(t)$, reproduction counts depend only on ΔE_R ; given the ODE solution, they share no additional error). Use endpoint = "growth" or endpoint = "reproduction" to compute LOO for a single endpoint.

References

Vehtari, A., Gelman, A. and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*, 27(5), 1413–1432. doi:10.1007/s1122201696964

bdeb_model

Specify a BDEB Model

Description

Creates a model specification that binds together the prepared data, the DEB process model (encoded as a pre-written Stan program), the prior distributions, and the observation model. Internally it calls the appropriate `build_stan_data_*`() function to assemble the list of named values that Stan expects. The Stan program is *not* compiled at this stage — compilation and sampling happen in `bdeb_fit()`.

Usage

```
bdeb_model(
  data,
  type = c("individual", "growth_repro", "hierarchical", "debttox"),
  priors = list(),
  observation = list(),
  temperature = NULL
)
```

Arguments

data	A <code>bdeb_data()</code> object.
type	Model type: "individual", "growth_repro", "hierarchical", or "debttox".
priors	Named list of <code>bdeb_prior</code> objects (see <code>prior_lognormal()</code> , <code>prior_beta()</code> , etc.). Entries not supplied are filled from <code>prior_default()</code> .

observation	Named list of observation model specs for each endpoint. Default: <code>list(growth = obs_normal(), reproduction = obs_negbinom())</code> .
temperature	Optional list with components <code>T_obs</code> (observation temperature in Kelvin), <code>T_ref</code> (reference temperature in K), and <code>T_A</code> (Arrhenius temperature in K). If provided, the correction factor $c_T = \exp(T_A/T_{\text{ref}} - T_A/T_{\text{obs}})$ (see <code>arrhenius()</code>) is applied inside the Stan ODE to all rate parameters: $\{p_{Am}\}$, $[p_M]$, v , k_J (<code>growth_repro</code>), k_d (<code>debtox</code>). Parameters that are not rates (κ , $[E_G]$, z_w , b_w) are not corrected. The posterior gives estimates at T_{ref} , making results comparable across experiments at different temperatures. The correction is global (single temperature for the entire experiment). If NULL (default), no correction is applied ($c_T = 1$). The field was renamed from <code>T</code> to <code>T_obs</code> in version 0.1.4 to avoid shadowing R's built-in <code>T</code> symbol.

Details

The four model types correspond to increasingly complex DEB formulations:

"individual" Standard 2-state DEB (reserve E , structure V), Kooijman (2010, Ch. 2). The ODE is solved with Stan's `ode_bdf` (stiff BDF solver) at tolerances 10^{-6} .

"growth_repro" 3-state model adding the reproduction buffer E_R . Offspring counts are modelled as $R_i \sim \text{NegBin}(k_R \Delta E_R, \phi)$, where $\Delta E_R = E_R(t_{\text{end}}) - E_R(t_{\text{start}})$.

"hierarchical" 2-state model with a lognormal random effect on $\{p_{Am}\}$: $\log p_{Am,j} = \mu + \sigma z_j$, $z_j \sim N(0, 1)$ (non-centred). Shared parameters $[p_M]$, κ , v , $[E_G]$ are estimated from all individuals jointly (partial pooling; Gelman & Hill, 2006). Initial structural length $L_{0,j}$ varies per individual; initial reserve density E_0 is shared (assumes organisms start with the same reserve state, which is typical for lab-reared cohorts).

"debtox" 4-state TKTD model following Jager et al. (2006). Adds scaled damage D_w with $dD_w/dt = k_d(\max(C_w - z_w, 0) - D_w)$. The EC_{50} is computed analytically as $z_w + 0.5/b_w$.

Value

A `bdeb_model` object (S3 list).

References

- Kooijman, S.A.L.M. (2010). *Dynamic Energy Budget Theory for Metabolic Organisation*. 3rd edition. Cambridge University Press. doi:10.1017/CBO9780511805400
- Gelman, A. and Hill, J. (2006). *Data Analysis Using Regression and Multilevel/Hierarchical Models*. Cambridge University Press.
- Jager, T., Heugens, E.H.W. and Kooijman, S.A.L.M. (2006). Making sense of ecotoxicological test results: towards application of process-based models. *Ecotoxicology*, 15(3), 305–314. doi:10.1007/s106460060060x

bdeb_plots	<i>Plot Methods for BDEB Objects</i>
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Description

Visualisation methods for BDEB fits, posterior predictive checks, and derived quantities using `ggplot2`. All plots return `ggplot2` objects that can be further customised.

bdeb_ppc	<i>Posterior Predictive Checks for BDEB Models</i>
----------	--

Description

Extracts replicated data y^{rep} generated in the Stan generated quantities block and pairs them with the observed data y . Following Gelman et al. (2013, Ch. 6), posterior predictive checks (PPCs) answer: "could the observed data plausibly have been generated by the fitted model?" If the replicated data envelopes consistently miss systematic features of y , the model is mis-specified.

Usage

```
bdeb_ppc(fit, type = c("growth", "reproduction", "all"))
```

Arguments

<code>fit</code>	A <code>bdeb_fit()</code> object.
<code>type</code>	Which endpoint to check: "growth", "reproduction", or "all". Default "growth".

Details

For growth endpoints, the replicated lengths L_i^{rep} are drawn as $L_i^{\text{rep}} \sim N(\hat{L}_i, \sigma_L)$ in the Stan program. For reproduction, $R_i^{\text{rep}} \sim \text{NegBin}(k_R \Delta E_R, \phi)$.

Value

A `bdeb_ppc` object containing observed data (`L_obs` or `R_obs`), a matrix of replicated data (`L_rep` or `R_rep`), and metadata for `plot.bdeb_ppc()`.

Supported models

- "individual" Full PPC with `L_rep` and `L_obs`.
- "growth_repro" Growth PPC via `L_rep`; reproduction PPC via `R_rep`.
- "hierarchical" Not available. The Stan model uses `reduce_sum` and does not generate `L_rep`. Use `bdeb_diagnose()` and trace plots for model checking.
- "debtox" Not available for the same reason. Use `plot_dose_response()` for visual model checking.

References

Gelman, A., Carlin, J.B., Stern, H.S., Dunson, D.B., Vehtari, A. and Rubin, D.B. (2013). *Bayesian Data Analysis*. 3rd edition. Chapman & Hall/CRC. (Chapter 6: Model checking.)

bdeb_prior_predictive *Prior Predictive Check*

Description

Simulates growth trajectories by sampling parameters from the prior distributions and forward-integrating the DEB ODE in R (Euler method). This is the prior analogue of `bdeb_ppc()` and answers: "what range of data does the model predict *before seeing any data*?" Following Gabry et al. (2019), if the prior predictive distribution covers biologically implausible values, the priors should be tightened.

Usage

```
bdeb_prior_predictive(model, n_draws = 500, dt = 0.5, seed = NULL)
```

Arguments

model	A <code>bdeb_model()</code> object.
n_draws	Number of prior draws. Default 500.
dt	Euler step size (days). Default 0.5.
seed	Integer seed for reproducibility. Default NULL.

Details

Does **not** require CmdStan — all sampling and simulation is done in R using Euler integration (step size `dt`). This is an **approximate visualisation tool**, not exact Stan inference. The ODE trajectories may differ slightly from the BDF solver used during fitting.

Value

A list with class "bdeb_prior_predictive" containing:

- t Time vector.
- L Matrix of simulated trajectories (draws x time points).
- L_inf Vector of prior-predictive ultimate lengths.
- priors Named list of prior objects used.

References

Gabry, J., Simpson, D., Vehtari, A., Betancourt, M. and Gelman, A. (2019). Visualization in Bayesian workflow. *Journal of the Royal Statistical Society: Series A*, 182(2), 389–402. doi:10.1111/rssa.12378

Examples

```
dat <- bdeb_data(growth = data.frame(id = 1, time = 0:10,
  length = seq(0.1, 0.5, length.out = 11)))
mod <- bdeb_model(dat, type = "individual")
pp <- bdeb_prior_predictive(mod, n_draws = 100, seed = 1)
plot(pp, n_draws = 30)
```

bdeb_session_info *Reproducibility Report*

Description

Prints a concise summary of the software environment used for a BayesianDEB analysis. Useful for supplementary materials in publications or for diagnosing cross-machine discrepancies.

Usage

```
bdeb_session_info(fit = NULL)
```

Arguments

`fit` Optional `bdeb_fit()` object. If provided, includes model-specific details (type, chains, iterations, `adapt_delta`, `seed`).

Value

Invisibly returns a named list with all reported information.

Examples

```
bdeb_session_info()
```

bdeb_summary *Posterior Summary for BDEB Parameters*

Description

Returns a tidy summary table of posterior draws for model parameters and optionally derived quantities.

Usage

```
bdeb_summary(fit, pars = NULL, prob = 0.9, ...)
```

Arguments

fit	A <code>bdeb_fit()</code> object.
pars	Character vector of parameter names. Default: all model parameters.
prob	Probability for credible intervals. Default 0.90 (5th/95th percentiles).
...	Ignored.

Value

A `posterior::draws_summary` data frame.

bdeb_tox	<i>DEBtox Model Specification</i>
----------	-----------------------------------

Description

Convenience wrapper for `bdeb_model()` that sets `type = "debtox"` and provides a `stress` argument to select the physiological mode of action (PMoA) of the toxicant. The underlying TKTD framework follows Jager et al. (2006) and the GUTS-RED-SD simplification of Jager & Zimmer (2012):

Usage

```
bdeb_tox(
  data,
  stress = c("assimilation", "maintenance", "growth_cost"),
  priors = list(),
  ...
)
```

Arguments

data	A <code>bdeb_data()</code> object with concentration specified.
stress	Physiological mode of action. Currently only "assimilation" is implemented.
priors	Named list of priors. Missing entries filled from <code>prior_default("debtox")</code> . The toxicological parameters k_d , z_w , b_w default to weakly informative log-normal priors.
...	Additional arguments passed to <code>bdeb_model()</code> .

Details

Toxicokinetics. Scaled internal damage D_w tracks the external concentration with first-order kinetics:

$$\frac{dD_w}{dt} = k_d(\max(C_w - z_w, 0) - D_w)$$

where k_d is the dominant rate constant, z_w is the NEC (no-effect concentration), and C_w is the external concentration.

Stress on assimilation. The assimilation flux is reduced by a factor $\max(1 - b_w D_w, 0)$, where b_w is the effect intensity. At steady state ($D_w = C_w - z_w$), the EC_{50} for $50\% z_w + 0.5/b_w$.

Value

A `bdeb_model` object of type "debtox".

Note

Lifecycle: beta. Stress on assimilation is implemented and tested; "maintenance" and "growth_cost" modes are planned.

Important limitation: the DEBtox model fits **one ODE per concentration group**, not per individual. If your data contain multiple individuals per concentration, they are automatically aggregated to group means per time point (with a warning). This is appropriate for group-level summary data but does not capture within-group individual variation. A hierarchical DEBtox extension is planned for a future version.

References

- Jager, T., Heugens, E.H.W. and Kooijman, S.A.L.M. (2006). Making sense of ecotoxicological test results: towards application of process-based models. *Ecotoxicology*, 15(3), 305–314. doi:[10.1007/s106460060060x](https://doi.org/10.1007/s106460060060x)
- Jager, T. and Zimmer, E.I. (2012). Simplified Dynamic Energy Budget model for analysing ecotoxicity data. *Ecological Modelling*, 225, 74–81. doi:[10.1016/j.ecolmodel.2011.11.012](https://doi.org/10.1016/j.ecolmodel.2011.11.012)

Examples

```
# R-side specification only (no Stan sampling)
data(debtox_growth)
# one replicate per concentration avoids aggregation warning
dt <- debtox_growth[debtox_growth$id %in% c(1, 11, 21, 31), ]
dat <- bdeb_data(growth = dt, concentration = c(0, 20, 80, 200))
mod <- bdeb_tox(dat, stress = "assimilation")
```

`coef.bdeb_fit`
Extract Point Estimates from a BDEB Fit

Description

Returns posterior medians of all model parameters as a named numeric vector, consistent with the S3 `coef()` convention.

Usage

```
## S3 method for class 'bdeb_fit'
coef(object, type = c("median", "mean"), ...)
```

Arguments

<code>object</code>	A <code>bdeb_fit()</code> object.
<code>type</code>	One of "median" (default) or "mean".
<code>...</code>	Ignored.

Value

Named numeric vector of point estimates.

debtox_growth	<i>Simulated DEBtox Growth Data</i>
---------------	-------------------------------------

Description

Simulated growth data under toxicant exposure for 4 concentration groups (0, 20, 80, 200 arbitrary units) with 10 individuals per group measured weekly over 6 weeks. Designed for fitting the DEBtox (TKTD) model in `bdeb_tox()`. The toxicant acts through stress on assimilation: the effective assimilation rate is reduced by a factor $\max(1 - b_w \max(C_w - z_w, 0), 0)$ following the DEBtox framework of Jager et al. (2006).

Usage

```
debtox_growth
```

Format

A data frame with 280 rows and 4 columns:

id Individual identifier (integer, 1–40)

concentration External toxicant concentration (arbitrary units)

time Observation time in days (0, 7, 14, ..., 42)

length Structural length in cm (with measurement error)

Source

Simulated with NEC $z_w = 15$, effect intensity $b_w = 0.003$, and base DEB parameters identical to [eisenia_growth](#).

References

Jager, T., Heugens, E.H.W. and Kooijman, S.A.L.M. (2006). Making sense of ecotoxicological test results: towards application of process-based models. *Ecotoxicology*, 15(3), 305–314. doi:[10.1007/s106460060060x](https://doi.org/10.1007/s106460060060x)

Examples

```
data(debtox_growth)
head(debtox_growth)
```

 debtox_simulate *Simulate DEBtox Growth Under Toxicant Exposure*

Description

Forward-integrates the 4-state DEBtox ODE (E , V , E_R , D_w) with stress on assimilation. Standalone simulator independent of Stan.

Usage

```
debtox_simulate(
  t_max,
  p_Am,
  p_M,
  kappa,
  v,
  E_G,
  E0,
  L0,
  k_d,
  z_w,
  b_w,
  C_w,
  f = 1,
  dt = 0.5
)
```

Arguments

t_max	End time (days).
p_Am	Surface-area-specific assimilation rate $\{p_{Am}\}$ ($\text{J d}^{-1} \text{cm}^{-2}$).
p_M	Volume-specific somatic maintenance $[p_M]$ ($\text{J d}^{-1} \text{cm}^{-3}$).
kappa	Allocation fraction to soma.
v	Energy conductance (cm d^{-1}).
E_G	Specific cost of structure (J cm^{-3}).
E0	Initial reserve density (J cm^{-3}).
L0	Initial structural length (cm).
k_d	Damage recovery rate (d^{-1}).
z_w	No-effect concentration (NEC).
b_w	Effect intensity.
C_w	External toxicant concentration.
f	Scaled functional response $f \in [0, 1]$. Default 1.
dt	Integration step size (days). Default 0.5.

Value

Data frame with columns time, E, V, L, R (reproduction buffer), Dw (scaled damage).

Examples

```
traj <- debtox_simulate(t_max = 42, p_Am = 5, p_M = 0.5,
  kappa = 0.75, v = 0.2, E_G = 400, E0 = 1, L0 = 0.1,
  k_d = 0.3, z_w = 15, b_w = 0.003, C_w = 80)
plot(traj$time, traj$L, type = "l")
```

deb_fluxes

*Compute DEB Energy Fluxes***Description**

Given current state (E, V) and the core DEB parameters, computes all standard energy fluxes defined by the κ -rule (Kooijman, 2010, Eqs. 2.3–2.12):

Usage

```
deb_fluxes(E, V, f, p_Am, p_M, kappa, v, E_G, k_J = 0, E_Hp = 0)
```

Arguments

E	Reserve energy (J).
V	Structural volume (cm^3).
f	Scaled functional response $f \in [0, 1]$.
p_Am	Surface-area-specific maximum assimilation rate $\{p_{Am}\}$ ($\text{J d}^{-1} \text{cm}^{-2}$).
p_M	Volume-specific somatic maintenance rate $[p_M]$ ($\text{J d}^{-1} \text{cm}^{-3}$).
kappa	Allocation fraction to soma $\kappa \in (0, 1)$.
v	Energy conductance (cm d^{-1}).
E_G	Specific cost of structure $[E_G]$ (J cm^{-3}).
k_J	Maturity maintenance rate coefficient k_J (d^{-1}). Default 0.
E_Hp	Maturity at puberty E_H^p (J). Default 0.

Details

- \dot{p}_A Assimilation: $f\{p_{Am}\}L^2$.
- \dot{p}_C Mobilisation: $E v L / (E + [E_G]V)$.
- \dot{p}_M Somatic maintenance: $[p_M]V$.
- \dot{p}_G Growth: $\max(\kappa\dot{p}_C - \dot{p}_M, 0)$.
- \dot{p}_J Maturity maintenance: $k_J E_H^p$.
- \dot{p}_R Reproduction: $\max((1 - \kappa)\dot{p}_C - \dot{p}_J, 0)$.

Value

Named list with fluxes p_A , p_C , p_M , p_G , p_J , p_R , structural length L ($V^{1/3}$), and scaled reserve density e ($E/([E_m]V + 10^{-12})$). The 10^{-12} stabilisation prevents division by zero when $V = 0$; in that edge case e returns a small finite number rather than Inf or NA.

References

Kooijman, S.A.L.M. (2010). *Dynamic Energy Budget Theory for Metabolic Organisation*. 3rd edition. Cambridge University Press, Ch. 2. doi:10.1017/CBO9780511805400

deb_simulate	<i>Simulate DEB Growth Trajectory</i>
--------------	---------------------------------------

Description

Forward-integrates the standard 2-state DEB ODE (reserve E , structure V) using Euler's method. This is a standalone simulator independent of Stan — useful for exploring parameter space, generating synthetic data, teaching, and prior predictive checks.

Usage

```
deb_simulate(t_max, p_Am, p_M, kappa, v, E_G, E0, L0, f = 1, dt = 0.5)
```

Arguments

t_max	End time (days).
p_Am	Surface-area-specific assimilation rate $\{p_{Am}\}$ ($J d^{-1} cm^{-2}$).
p_M	Volume-specific somatic maintenance $[p_M]$ ($J d^{-1} cm^{-3}$).
kappa	Allocation fraction to soma.
v	Energy conductance ($cm d^{-1}$).
E_G	Specific cost of structure ($J cm^{-3}$).
E0	Initial reserve density ($J cm^{-3}$).
L0	Initial structural length (cm).
f	Scaled functional response $f \in [0, 1]$. Default 1.
dt	Integration step size (days). Default 0.5.

Value

Data frame with columns time, E (reserve), V (volume), L (structural length).

Numerical note

This uses the LSODA solver from **deSolve**, which automatically switches between stiff (BDF) and non-stiff (Adams) methods. This matches the BDF solver used in the Stan models, ensuring numerical consistency between R-side simulation and Stan-side inference. The dt parameter controls output resolution, not integration accuracy (governed by $rtol/atol = 1e-6$).

Examples

```
# Simulate E. fetida growth for 84 days
traj <- deb_simulate(t_max = 84, p_Am = 5, p_M = 0.5,
  kappa = 0.75, v = 0.2, E_G = 400, E0 = 1, L0 = 0.1)
plot(traj$time, traj$L, type = "l", xlab = "Days", ylab = "L (cm)")
```

eisenia_cd

Eisenia andrei Cadmium Toxicity Data (Van Gestel 1991)

Description

Real experimental growth data for *Eisenia andrei* exposed to cadmium in natural soil at 23 °C from Van Gestel et al. (1991), obtained via the EGrowth database (Mathieu, 2018). Five concentration groups (0, 10, 32, 100, 320 mg Cd/kg) with 7 time points each over 85 days. Group-mean body mass was converted to structural length via $L = (W/d_V)^{1/3}$ with $d_V = 1.05 \text{ g cm}^{-3}$.

Usage

```
eisenia_cd
```

Format

A data frame with 35 rows and 4 columns:

id Concentration group identifier (1–5)

time Time in days (0–85)

length Structural length in cm

concentration Cadmium concentration (mg Cd/kg soil)

Source

EGrowth database, curve IDs gr0119–gr0123. <https://github.com/JeromeMathieuEcology/EGrowth>

References

Van Gestel, C.A.M., Van Dis, W.A., Dirven-Van Breemen, E.M., Sparenburg, P.M. and Baerselman, R. (1991). Influence of cadmium, copper, and pentachlorophenol on growth and sexual development of *Eisenia andrei* (Oligochaeta; Annelida). *Biology and Fertility of Soils*, 12, 117–121. doi:10.1007/BF00341486

Examples

```
data(eisenia_cd)
plot(eisenia_cd$time, eisenia_cd$length,
  col = as.factor(eisenia_cd$concentration),
  xlab = "Days", ylab = "Structural length (cm)")
```

`eisenia_growth`*Simulated Eisenia fetida Growth Data*

Description

Simulated growth dataset for 21 individuals of the earthworm *Eisenia fetida* measured weekly over 12 weeks under controlled laboratory conditions (20 °C, ad libitum feeding), following a standard OECD 222 test protocol design. DEB parameters are based on the *E. fetida* entry in the Add-my-Pet collection (AmP; Marques et al., 2018). Individual variation in $\{p_{Am}\}$ was drawn from a lognormal distribution with CV $\approx 10\%$. Gaussian measurement error $\sigma_L = 0.015$ cm was added to the structural length.

Usage

`eisenia_growth`

Format

A data frame with 273 rows and 3 columns:

id Individual identifier (integer, 1–21)

time Observation time in days (0, 7, 14, ..., 84)

length Structural length in cm ($= V^{1/3}$), with measurement error

Source

Simulated from the standard DEB model (Kooijman, 2010, Eqs. 2.4–2.6) with parameters: $\{p_{Am}\} = 5.0$ J/d/cm², $[p_M] = 0.5$ J/d/cm³, $\kappa = 0.75$, $v = 0.2$ cm/d, $[E_G] = 400$ J/cm³. Individual variation: $\{p_{Am}\}_j \sim \text{LogNormal}(\log 5.0, 0.1)$, $L_{0,j} \sim \text{LogNormal}(\log 0.1, 0.05)$. Observation error: $\sigma_L = 0.015$ cm.

References

Kooijman, S.A.L.M. (2010). *Dynamic Energy Budget Theory for Metabolic Organisation*. 3rd edition. Cambridge University Press. doi:10.1017/CBO9780511805400

Marques, G.M., Augustine, S., Lika, K., Pecquerie, L., Domingos, T. and Kooijman, S.A.L.M. (2018). The AmP project: comparing species on the basis of dynamic energy budget parameters. *PLOS Computational Biology*, 14(5), e1006100. doi:10.1371/journal.pcbi.1006100

OECD (2016). Test No. 222: Earthworm Reproduction Test (*Eisenia fetida* / *Eisenia andrei*). OECD Guidelines for the Testing of Chemicals.

Examples

```
data(eisenia_growth)
head(eisenia_growth)
```

eisenia_neuhauser *Eisenia fetida* Growth Data (Neuhauser 1980)

Description

Real experimental growth data for *Eisenia fetida* on activated sludge at 25 °C from Neuhauser, Hartenstein & Kaplan (1980), obtained via the EGrowth database (Mathieu, 2018). The dataset comprises 37 group-mean body mass measurements (20 worms per replicate) over 250 days, from hatchling (~8 mg) to adult (~2350 mg). Wet mass was converted to structural length via $L = (W/d_V)^{1/3}$ with tissue density $d_V = 1.05 \text{ g cm}^{-3}$.

Usage

eisenia_neuhauser

Format

A data frame with 37 rows and 3 columns:

- id** Individual/group identifier (always 1)
- time** Time in days since start (1–250)
- length** Structural length in cm (0.20–1.31)

Source

EGrowth database, curve ID gr0226. <https://github.com/JeromeMathieuEcology/EGrowth>

References

- Neuhauser, E.F., Hartenstein, R. and Kaplan, D.L. (1980). Growth of the earthworm *Eisenia foetida* in relation to population density and food rationing. *Oikos*, 35, 93–98. doi:10.2307/3544730
- Mathieu, J. (2018). EGrowth: a global database on intraspecific body growth variability in earthworm. *Soil Biology and Biochemistry*, 122, 71–80. doi:10.1016/j.soilbio.2018.04.004

Examples

```
data(eisenia_neuhauser)
plot(eisenia_neuhauser$time, eisenia_neuhauser$length,
     xlab = "Days", ylab = "Structural length (cm)")
```

`folsomia_repro`*Simulated Folsomia candida Reproduction Data*

Description

Simulated 28-day reproduction dataset for the springtail *Folsomia candida* exposed to 5 cadmium concentrations (0, 10, 50, 100, 500 mg Cd/kg dry soil) with 6 replicates per concentration. The experimental design follows ISO 11267 (springtail reproduction test). Toxicant effects were simulated using a simple NEC-based model: expected offspring = $120 \times \max(1 - b_w \max(C - z_w, 0), 0)$, with Poisson sampling around the expected value.

Usage

`folsomia_repro`

Format

A data frame with 30 rows and 5 columns:

id Replicate identifier (integer, 1–30)

concentration Cadmium concentration in mg/kg dry soil

t_start Start of observation interval (day 0)

t_end End of observation interval (day 28)

count Number of juveniles produced in the interval

Source

Simulated with NEC $z_w = 30$ mg/kg, effect intensity $b_w = 0.005$ (mg/kg)⁻¹, and control offspring count ≈ 120 .

References

ISO 11267 (2014). *Soil quality — Inhibition of reproduction of Collembola (Folsomia candida) by soil contaminants.*

Examples

```
data(folsomia_repro)
head(folsomia_repro)
```

observation_models *Observation Model Specifications*

Description

Observation Model Specifications

Usage

```
obs_normal()
obs_lognormal()
obs_student_t(nu = 5)
obs_poisson()
obs_negbinom()
```

Arguments

nu Degrees of freedom. Default 5.

Value

A bdeb_obs object (list with class "bdeb_obs").

Functions

- `obs_normal()`: Gaussian observation error (default for growth)
- `obs_lognormal()`: Log-normal observation error (multiplicative)
- `obs_student_t()`: Student-t observation error (robust to outliers)
- `obs_poisson()`: Poisson observations (for count data)
- `obs_negbinom()`: Negative binomial observations (overdispersed counts)

Examples

```
obs_normal()
obs_lognormal()
obs_negbinom()
```

`plot.bdeb_fit`*Plot a BDEB Fit*

Description

Plot a BDEB Fit

Usage

```
## S3 method for class 'bdeb_fit'
plot(
  x,
  type = c("trace", "posterior", "pairs", "trajectory", "prior_posterior"),
  pars = NULL,
  n_draws = 100,
  seed = NULL,
  ...
)
```

Arguments

<code>x</code>	A <code>bdeb_fit()</code> object.
<code>type</code>	Type of plot. One of: <ul style="list-style-type: none">"trace": MCMC trace plots"posterior": marginal posterior densities"pairs": bivariate posterior scatter plots"trajectory": predicted trajectories with data overlay"prior_posterior": prior (red) vs posterior (blue) densities
<code>pars</code>	Character vector of parameters to plot. Default: core DEB parameters.
<code>n_draws</code>	Number of posterior draws for trajectory plots. Default 100.
<code>seed</code>	Integer seed for reproducible draw selection in trajectory plots. Default NULL (no seed).
<code>...</code>	Additional arguments passed to bayesplot functions.

Value

A `ggplot2` object.

plot.bdeb_ppc	<i>Plot Posterior Predictive Checks</i>
---------------	---

Description

Plot Posterior Predictive Checks

Usage

```
## S3 method for class 'bdeb_ppc'
plot(x, n_draws = 50, ...)
```

Arguments

x	A <code>bdeb_ppc()</code> object.
n_draws	Number of replicated trajectories to show. Default 50.
...	Ignored.

Value

A ggplot2 object.

plot_dose_response	<i>Plot DEBtox Dose-Response</i>
--------------------	----------------------------------

Description

Produces a dose-response curve by **forward-simulating** the full 4-state DEBtox ODE from the posterior in R (Euler integration). For each posterior draw, the ODE is solved at every concentration in a fine grid from 0 to $1.2 \times \max(C_w)$. The y-axis shows the predicted final structural length relative to the control ($C = 0$) at the same draw, so that each curve propagates the full parameter uncertainty through the dynamic model.

Usage

```
plot_dose_response(
  fit,
  endpoint = "growth",
  n_draws = 100,
  n_conc = 50,
  dt = 1,
  t_end = NULL,
  seed = NULL
)
```

Arguments

fit	A <code>bdeb_fit()</code> object from a DEBtox model.
endpoint	Which endpoint to plot. Currently only "growth".
n_draws	Number of posterior draws to use. Default 100.
n_conc	Number of concentration points in the continuous grid. Default 50.
dt	Euler integration step size (days). Default 1.0. Smaller values are more accurate but slower. The Stan model uses BDF with adaptive stepping; this is an approximation for visualisation.
t_end	End time for the simulation (days). Default NULL (uses the last observation time from the fitted data).
seed	Integer seed for reproducible draw selection. Default NULL.

Details

This is a **visualisation tool**, not exact Stan inference. The R-side Euler integrator (step size `dt`) is an approximation of the BDF solver used during fitting. For quantitative results, use `bdeb_ec50()` which extracts the analytically computed EC_{50} and NEC directly from the Stan posterior.

Performance note. Each draw requires `n_conc` ODE integrations, so `n_draws * n_conc` total. With default settings (100 draws, 50 concentrations) this takes a few seconds. Reduce `n_draws` for faster interactive use.

Value

A `ggplot2` object.

predict.bdeb_fit *Predict from a BDEB Fit*

Description

When `newdata = NULL`, extracts the fitted trajectories (`L_hat`) from the Stan posterior (exact). When `newdata` is provided, performs **R-side forward simulation** (Euler integration) from the posterior draws under new environmental conditions or extended time horizons. The Euler integrator is an **approximation** — for quantitative results at the original data conditions, prefer `newdata = NULL`.

Usage

```
## S3 method for class 'bdeb_fit'
predict(object, newdata = NULL, n_draws = 200, dt = 0.5, seed = NULL, ...)

bdeb_predict(fit, newdata = NULL, n_draws = 200, dt = 0.5, seed = NULL)
```

Arguments

object	A <code>bdeb_fit()</code> object.
newdata	Optional named list with new conditions. Supported fields: <code>t_predict</code> Numeric vector of prediction time points (days). Required when <code>newdata</code> is not NULL. <code>f_food</code> Scaled functional response (default: value from the fitted model). <code>concentration</code> External toxicant concentration (scalar; only for "debtox" models; default 0).
n_draws	Number of posterior draws to use. Default 200.
dt	Euler step size for forward simulation (days). Default 0.5.
seed	Integer seed for reproducible draw selection. Default NULL (no seed).
...	Ignored.
fit	A <code>bdeb_fit()</code> object.

Value

A `bdeb_prediction` object with components `t` (time vector), `L_hat` (matrix: draws x time points), `n_draws`, `model_type`.

priors

Prior Distribution Specifications for BDEB Models

Description

Constructor functions for prior distribution objects used in `bdeb_model()`. Each returns a lightweight `bdeb_prior` S3 object that encodes the distribution family and its hyperparameters. The prior is evaluated inside the Stan model block; hyperparameters are passed as data so that changing priors does not require recompilation.

Usage

```
prior_lognormal(mu = 0, sigma = 1)
```

```
prior_normal(mu = 0, sigma = 1)
```

```
prior_beta(a = 2, b = 2)
```

```
prior_halfnormal(sigma = 1)
```

```
prior_halfcauchy(sigma = 1)
```

```
prior_exponential(rate = 1)
```

Arguments

mu	Mean.
sigma	Scale of the half-Cauchy.
a	Shape parameter alpha.
b	Shape parameter beta.
rate	Rate parameter (1/mean).

Details

The choice of prior family follows the recommendations for DEB parameters in Hackenberger (2025, Ch. 6) and general guidelines from Gelman et al. (2013, Sec. 2.9):

- Positive rate parameters ($\{p_{Am}\}$, $[p_M]$, v , $[E_G]$) — log-normal, because the log-transform maps the strictly positive domain to the real line.
- Allocation fraction $\kappa \in (0, 1)$ — Beta, the natural conjugate for bounded parameters.
- Observation-error standard deviations — half-normal (or half-Cauchy for heavier tails), which place zero mass on negative values (Gelman, 2006).
- Hierarchical standard deviations — exponential, following the advice of Betancourt & Girolami (2015) for non-centred parameterisations.

Value

A `bdeb_prior` object (list with class "bdeb_prior").

Functions

- `prior_lognormal()`: Log-normal prior (for positive parameters: `p_Am`, `p_M`, `v`, `E_G`, etc.)
- `prior_normal()`: Normal prior (for unconstrained parameters)
- `prior_beta()`: Beta prior (for (0,1)-constrained parameters: `kappa`)
- `prior_halfnormal()`: Half-normal prior (for scale parameters: `sigma_L`, etc.)
- `prior_halfcauchy()`: Half-Cauchy prior (for scale parameters, heavier tails)
- `prior_exponential()`: Exponential prior (for variance components in hierarchical models)

References

- Gelman, A. (2006). Prior distributions for variance parameters in hierarchical models. *Bayesian Analysis*, 1(3), 515–534. doi:10.1214/06BA117A
- Gelman, A., Carlin, J.B., Stern, H.S., Dunson, D.B., Vehtari, A. and Rubin, D.B. (2013). *Bayesian Data Analysis*. 3rd edition. Chapman & Hall/CRC.

Examples

```
# Log-normal prior on assimilation rate: median ~ exp(1.5) ~ 4.5
prior_lognormal(mu = 1.5, sigma = 0.5)

# Beta(2,2) prior on kappa - symmetric, favouring 0.5
prior_beta(a = 2, b = 2)
```

prior_default *Default Priors for DEB Parameters*

Description

Returns a named list of weakly informative priors for standard DEB parameters. The defaults are calibrated against the parameter ranges observed in the Add-my-Pet (AmP) collection (Marques et al., 2018) for standard ecotoxicological test species. All positive rate parameters use log-normal priors whose 95% are roughly one order of magnitude around typical values; κ uses Beta(2, 2) which is symmetric on (0, 1) with prior mean 0.5.

Usage

```
prior_default(type = c("individual", "growth_repro", "hierarchical", "debtox"))
```

Arguments

type One of "individual", "growth_repro", "hierarchical", "debtox".

Value

Named list of bdeb_prior objects.

References

Marques, G.M., Augustine, S., Lika, K., Pecquerie, L., Domingos, T. and Kooijman, S.A.L.M. (2018). The AmP project: comparing species on the basis of dynamic energy budget parameters. *PLOS Computational Biology*, 14(5), e1006100. doi:10.1371/journal.pcbi.1006100

Examples

```
prior_default("individual")
```

prior_species *Species-Specific Priors from the AmP Collection*

Description

Returns priors calibrated to a specific species using parameter estimates from the Add-my-Pet (AmP) collection (Marques et al., 2018). The log-normal priors are centred on the AmP point estimate (log scale) with a moderate spread ($\sigma = 0.3$) that places 95% value.

Usage

```
prior_species(
  species,
  type = c("individual", "growth_repro", "hierarchical", "debtox")
)
```

Arguments

species	Character string: species name with underscore separator (e.g., "Eisenia_fetida"). Case-insensitive.
type	Model type for filling model-specific defaults.

Details

Currently supported species (more will be added):

Eisenia_fetida Compost earthworm; AmP entry Eisenia_fetida.

Eisenia_andrei Sibling species of *E. fetida*; shares similar DEB parameters.

Folsomia_candida Springtail; standard ISO reproduction test species.

Daphnia_magna Water flea; classic aquatic ecotox model.

Lumbricus_rubellus Field earthworm; common biomonitoring species.

Value

Named list of bdeb_prior objects, suitable for the priors argument of `bdeb_model()` or `bdeb_tox()`.

References

Marques, G.M., Augustine, S., Lika, K., Pecquerie, L., Domingos, T. and Kooijman, S.A.L.M. (2018). The AmP project: comparing species on the basis of dynamic energy budget parameters. *PLOS Computational Biology*, 14(5), e1006100. doi:10.1371/journal.pcbi.1006100

Examples

```
# Use AmP-calibrated priors for E. fetida
prior_species("Eisenia_fetida")

# Combine with model specification (R-side, no Stan sampling)
data(eisenia_growth)
dat <- bdeb_data(growth = eisenia_growth[eisenia_growth$id == 1, ])
mod <- bdeb_model(dat, type = "individual",
  priors = prior_species("Eisenia_fetida"))
```

repro_to_intervals *Convert Cumulative Reproduction to Intervals*

Description

Many ecotoxicological protocols (e.g., ISO 11267 for *Folsomia candida*, OECD 222 for *Eisenia fetida*) report cumulative offspring counts at successive observation times. The DEB reproduction buffer model, however, requires interval counts $\Delta R = R(t_{\text{end}}) - R(t_{\text{start}})$ so that the negative-binomial likelihood can be applied to each counting period. This function computes the first-difference per individual.

Usage

```
repro_to_intervals(df)
```

Arguments

`df` Data frame with columns: `id`, `time`, `cumulative`.

Value

Data frame with columns: `id`, `t_start`, `t_end`, `count`.

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