Package: trps (via r-universe)

March 15, 2025

Type Package

Title Bayesian trophic position models using stan

Version 0.1.0

Description Bayesian trophic position models using stan by leveraging 'brms' for stable isotope data. Trophic position models are derived by using equations from Post (2002) <doi:10.1890/0012-9658(2002)083[0703:USITET]2.0.CO;2>, and Huevel et al. (2024) <doi:10.1139/cjfas-2024-0028>.

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Encoding UTF-8

LazyData true

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Roxygen list(markdown = TRUE)

Depends R (>= 3.5)

URL `https://benjaminhlina.github.io/trps/`, `https://github.com/benjaminhlina/trps`

BugReports `https://github.com/benjaminhlina/trps/issues`

VignetteBuilder knitr

Config/pak/sysreqs make libicu-dev

Repository https://benjaminhlina.r-universe.dev

RemoteUrl https://github.com/benjaminhlina/trps

RemoteRef HEAD

RemoteSha d145b9de918418c98850a690d1b0f36804c9461e

Contents

`add_alpha` *Calculate and add α*

Description

Calculate α for a two source trophic position model using equations from Post 2002.

Usage

```
add_alpha(data, abs = FALSE)
```

Arguments

`data`	`data.frame` of stable isotope samples with mean values for two baselines. For aquatic ecosystems, baseline one needs to come from a benthic source and baseline two needs to come from a pelagic source. Baseline δ^{13}C columns need to be named `c1` and `c2`, with the consumer's δ^{13}C column named `d13c`.
`abs`	logical that controls whether the absolute value is taken for the numerator and denominator. Default is `FALSE` meaning that the absolute value is not taken.

Details

$$\alpha = (\delta^{13}C_c - \delta^{13}C_2)/(\delta^{13}C_1 - \delta^{13}C_2)$$

where $\delta^{13}C_c$ is the isotopic value for consumer, $\delta^{13}C_1$ is the mean isotopic value for baseline 1 and $\delta^{13}C_2$ is the mean isotopic value for baseline 2.

Value

a `data.frame` that has `alpha`, `min_alpha`, and `max_alpha` added.

Examples

```
combined_iso |>
  add_alpha()
```

`baseline_1_iso` *Stable isotope data for amphipods (baseline 1)*

Description

Stable isotope data (δ^{13}C and δ^{15}N) for amphipods collected from an ecoregion in Lake Ontario.

Usage

```
baseline_1_iso
```

Format

`data.frame` containing 14 rows and 5 variables

common_name name of the spcies (i.e., Amphipoda)

ecoregion ecoregion where samples were collected

d13c_b1 observed values for δ^{13}C

d15n_b1 observed values for δ^{15}N

`baseline_2_iso` *Stable isotope data for dreissenids (baseline 2)*

Description

Stable isotope data (δ^{13}C and δ^{15}N) for dreissenid collected from an ecoregion in Lake Ontario.

Usage

```
baseline_2_iso
```

Format

`data.frame` containing 12 rows and 5 variables

common_name name of the spcies (i.e., Dreissenids)

ecoregion ecoregion where samples were collected

d13c_b2 observed values for δ^{13}C

d15n_b2 observed values for δ^{15}N

`combined_iso` *Stable isotope data for lake trout, amphipods (benthic baseline; baseline 1) and dreissenids (pelagic baseline; baseline 2),*

Description

Stable isotope data (δ^{13}C and δ^{15}N) for lake trout collected from two ecoregions in Lake Ontario. Values of δ^{13}C and δ^{15}N for a benthic baseline (amphipods; baseline 1; `d13c_b1` and `d15n_b1`) and pelagic baseline (dreissenids; baseline 2; `d13c_b2` and `d15n_b2`) with the means for each baseline calculated (`c1`, `n1`, `c2`, and `n2`).

Usage

```
combined_iso
```

Format

`data.frame` containing 117 rows and 13 variables

id row id number

common_name name of the spcies (i.e., Lake Trout)

ecoregion ecoregion where samples were collected

d13c observed values for δ^{13}C of consumer

d15n observed values for δ^{15}N of consumer

d13c_b1 observed values for δ^{13}C of baseline 1

d15n_b1 observed values for δ^{15}N of baseline 1

d13c_b2 observed values for δ^{13}C of baseline 2

d15n_b2 observed values for δ^{15}N of baseline 2

c1 mean values for δ^{13}C of baseline 1

n1 mean values for δ^{15}N of baseline 1

c2 mean values for δ^{13}C of baseline 2

n2 mean values for δ^{15}N of baseline 2

`consumer_iso` *Stable isotope data for lake trout (consumer)*

Description

Stable isotope data (δ^{13}C and δ^{15}N) for lake trout collected from an ecoregion in Lake Ontario.

Usage

```
consumer_iso
```

Format

`data.frame` containing 30 rows and 6 variables

common_name name of the spcies (i.e., Lake Trout)

ecoregion ecoregion where samples were collected

d13c observed values for δ^{13}C

d15n observed values for δ^{15}N

`one_source_model` *Bayesian model - One Source Trophic Position*

Description

Estimate trophic position using a one source model derived from Post 2002 using a Bayesian framework.

Usage

```
one_source_model(bp = FALSE)
```

Arguments

`bp`	logical value that controls whether informed priors are supplied to the model for δ^{15}N baseline. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for δ^{15}N baseline (`n1`).

Details

$$\delta^{15}N = \delta^{15}N_1 + \Delta N \times (tp - \lambda_1)$$

δ^{15}N are values from the consumer, $\delta^{15}N_1$ is mean δ^{15}N values of baseline 1, ΔN is the trophic discrimination factor for N (i.e., `dn` mean of `3.4`), tp is trophic position, and λ_1 is the trophic level of baselines which are often a primary consumer (e.g., `2`).

The data supplied to `brms()` needs to have the following variables `d15n`, `n1`, and `l1` (λ) which is usually `2`.

Value

returns model structure for one source model to be used in a `brms()` call.

See Also

`brms::brms()`

Examples

```
one_source_model()
```

`one_source_priors` *Bayesian priors - One Source Trophic Position*

Description

Create priors for one source trophic position model derived from Post 2002.

Usage

```
one_source_priors(bp = FALSE)
```

Arguments

`bp`	logical value that controls whether informed priors are supplied to the model for δ^{15}N baseline. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for δ^{15}N baseline (`n1`).

Value

returns priors for one source model to be used in a `brms()` call.

See Also

`brms::brms()`

Examples

```
one_source_priors()
```

`one_source_priors_params` *Adjust Bayesian priors - One Source Trophic Position*

Description

Adjust priors for one source trophic position model derived from Post 2002.

Usage

```
one_source_priors_params(
  n1 = NULL,
  n1_sigma = NULL,
  dn = NULL,
  dn_sigma = NULL,
  tp_lb = NULL,
  tp_ub = NULL,
  sigma_lb = NULL,
  sigma_ub = NULL,
  bp = FALSE
)
```

Arguments

`n1`	mean (μ) prior for the mean δ^{15}N baseline. Defaults to `9`.
`n1_sigma`	variance (σ) for the mean δ^{15}N baseline. Defaults to `1`.
`dn`	mean (μ) prior value for ΔN. Defaults to `3.4`.
`dn_sigma`	variance (σ) for δ^{15}N. Defaults to `0.25`.
`tp_lb`	lower bound prior for trophic position. Defaults to `2`.
`tp_ub`	upper bound prior for trophic position. Defaults to `10`.
`sigma_lb`	lower bound prior for σ. Defaults to `0`.
`sigma_ub`	upper bound prior for σ. Defaults to `10`.
`bp`	logical value that controls whether informed priors are supplied to the model for δ^{15}N baseline. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for δ^{15}N baseline (`n1`).

Details

$$\delta^{15}N = \delta^{15}N_1 + \delta N \times (tp - \lambda_1)$$

This function allows the user to adjust the priors for the following variables in the equation above:

- The mean (`n1`; μ) and variance (`n1_sigma`; σ) for the mean δ^{15}N for a given baseline ($\delta^{15}N_1$). This prior assumes a normal distribution.

- The mean (`dn`; μ) and variance (`dn_sigma`; σ) of ΔN (i.e, trophic enrichment factor). This prior assumes a normal distribution.
- The lower (`tp_lb`) and upper (`tp_ub`) bounds for trophic position. This prior assumes a uniform distribution.
- The lower (`sigma_lb`) and upper (`sigma_ub`) bounds for variance (σ). This prior assumes a uniform distribution.

Value

`stanvars` object to be used with `brms()` call.

See Also

`one_source_priors()`, `one_source_model()`, and `brms::brms()`

Examples

```
one_source_priors_params()
```

`two_source_model` *Bayesian model - Two Source Trophic Position*

Description

Trophic position using a two source model derived from Post 2002 using a Bayesian framework.

Usage

```
two_source_model(bp = FALSE, lambda = NULL)
```

Arguments

`bp`	logical value that controls whether informed priors are supplied to the model for both δ^{15}N and δ^{15}C baselines. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for both δ^{15}N and δ^{15}C baseline (`c1`, `c2`, `n1`, and `n2`).
`lambda`	numerical value, `1` or `2`, that controls whether one or two λs are used. See details for equations and when to use `1` or `2`. Defaults to `1`.

Details

We will use the following equations from Post 2002:

1. $$\delta^{13}C_c = \alpha \times (\delta^{13}C_1 - \delta^{13}C_2) + \delta^{13}C_2$$
2. $$\delta^{15}N = \Delta N \times (tp - \lambda_1) + n_1 \times \alpha + n_2 \times (1 - \alpha)$$

3. $$\delta^{15}N = \Delta N \times (tp - (\lambda_1 \times \alpha + \lambda_2 \times (1 - \alpha))) + n_1 \times \alpha + n_2 \times (1 - \alpha)$$

For equation 1)

where $\delta^{13}C_c$ is the isotopic value for consumer, α is the ratio between baselines and consumer $\delta^{13}C$, $\delta^{13}C_1$ is the mean isotopic value for baseline 1, and $\delta^{13}C_2$ is the mean isotopic value for baseline 2

For equation 2) and 3)

δ^{15}N are values from the consumer, n_1 is δ^{15}N values of baseline 1, n_2 is δ^{15}N values of baseline 2, ΔN is the trophic discrimination factor for N (i.e., mean of `3.4`), tp is trophic position, and λ_1 and/or λ_2 are the trophic levels of baselines which are often a primary consumer (e.g., `2` or `2.5`).

The data supplied to `brms()` when using baselines at the same trophic level (`lambda` argument set to `1`) needs to have the following variables, `d15n`, `c1`, `c2`, `n1`, `n2`, `l1` (λ_1) which is usually `2`. If using baselines at different trophic levels (`lambda` argument set to `2`) the data frame needs to have `l1` and `l2` with a numerical value for each trophic level (e.g.,2 and `2.5`; λ_1 and λ_2).

Value

returns model structure for two source model to be used in a `brms()` call.

See Also

`brms::brms()`

Examples

```
two_source_model()
```

`two_source_model_ar` *Bayesian model - Two Source Trophic Position with α_r*

Description

Estimate trophic position using a two source model with α_r derived from Post 2002 and Heuvel et al. 2024 using a Bayesian framework.

Usage

```
two_source_model_ar(bp = FALSE, lambda = NULL)
```

Arguments

`bp`	logical value that controls whether informed priors are supplied to the model for both δ^{15}N baselines. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for both δ^{15}N baseline (`n1` and `n2`).
`lambda`	numerical value, `1` or `2`, that controls whether one or two lambdas are used. See details for equations and when to use `1` or `2`. Defaults to `1`.

Details

We will use the following equations derived from Post 2002 and Heuvel et al. 2024:

1. $$\alpha = (\delta^{13}C_c - \delta^{13}C_2)/(\delta^{13}C_1 - \delta^{13}C_2)$$
2. $$\alpha = \alpha_r \times (\alpha_{max} - \alpha_{min}) + \alpha_{min}$$
3. $$\delta^{15}N = \Delta N \times (tp - \lambda_1) + n_1 \times \alpha_r + n_2 \times (1 - \alpha_r)$$
4. $$\delta^{15}N = \Delta N \times (tp - (\lambda_1 \times \alpha_r + \lambda_2 \times (1 - \alpha_r))) + n_1 \times \alpha_r + n_2 \times (1 - \alpha_r)$$

For equation 1)

This equation is a carbon source mixing model with $\delta^{13}C_c$ is the isotopic value for consumer, $\delta^{13}C_1$ is the mean isotopic value for baseline 1 and $\delta^{13}C_2$ is the mean isotopic value for baseline 2. This equation is added to the data frame using `add_alpha()`.

For equation 2)

α is being corrected using equations in Heuvel et al. 2024 with α_r being the corrected value (bound by 0 and 1), α_{min} is the minimum α value calculated using `add_alpha()` and α_{max} being the maximum α value calculated using `add_alpha()`.

For equation 3) and 4)

δ^{15}N are values from the consumer, n_1 is δ^{15}N values of baseline 1, n_2 is δ^{15}N values of baseline 2, ΔN is the trophic discrimination factor for N (i.e., mean of `3.4`), tp is trophic position, and λ_1 and/or λ_2 are the trophic levels of baselines which are often a primary consumer (e.g., `2` or `2.5`).

The data supplied to `brms()` when using baselines at the same trophic level (`lambda` argument set to `1`) needs to have the following variables, `d15n`, `n1`, `n2`, `l1` (λ_1) which is usually `2`. If using baselines at different trophic levels (`lambda` argument set to `2`) the data frame needs to have `l1` and `l2` with a numerical value for each trophic level (e.g., `2` and `2.5`; λ_1 and λ_2).

Value

returns model structure for two source model to be used in a `brms()` call.

See Also

`brms::brms()`

Examples

```
two_source_model_ar()
```

`two_source_model_arc` *Bayesian model - Two Source Trophic Position with α_r and carbon mixing model*

Description

Estimate trophic position using a two source model with α_r derived from Post 2002 and Heuvel et al. 2024 using a Bayesian framework.

Usage

```
two_source_model_arc(bp = FALSE, lambda = NULL)
```

Arguments

`bp`	logical value that controls whether informed priors are supplied to the model for both δ^{15}N and δ^{15}C baselines. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for both δ^{15}N and δ^{15}C baseline (`c1`, `c2`, `n1`, and `n2`).
`lambda`	numerical value, `1` or `2`, that controls whether one or two lambdas are used. See details for equations and when to use `1` or `2`. Defaults to `1`.

Details

We will use the following equations derived from Post 2002 and Heuvel et al. 2024:

1. $$\alpha = (\delta^{13}C_c - \delta^{13}C_2)/(\delta^{13}C_1 - \delta^{13}C_2)$$

2. $$\alpha = \alpha_r \times (\alpha_{max} - \alpha_{min}) + \alpha_{min}$$

3. $$\delta^{13}C = c_1 \times \alpha_c + c_2 \times (1 - \alpha_c)$$

4. $$\delta^{15}N = \Delta N \times (tp - \lambda_1) + n_1 \times \alpha_c + n_2 \times (1 - \alpha_c)$$

5. $$\delta^{15}N = \Delta N \times (tp - (\lambda_1 \times \alpha_c + \lambda_2 \times (1 - \alpha_c))) + n_1 \times \alpha_c + n_2 \times (1 - \alpha_c)$$

For equation 1)

This equation is a carbon source mixing model with $\delta^{13}C_c$ is the isotopic value for consumer, $\delta^{13}C_1$ is the mean isotopic value for baseline 1 and $\delta^{13}C_2$ is the mean isotopic value for baseline 2.

For equation 2)

α is being corrected using equations in Heuvel et al. 2024. with α_r being the corrected value (bound by 0 and 1), α_{min} is the minimum α value calculated using `add_alpha()` and α_{max} being the maximum α value calculated using `add_alpha()`.

For equation 3)

This equation is a carbon source mixing model with δ^{13}C being estimated using `c_1`, `c_2` and α_c calculated in equation 1.

For equation 4) and 5)

δ^{15}N are values from the consumer, n_1 is δ^{15}N values of baseline 1, n_2 is δ^{15}N values of baseline 2, ΔN is the trophic discrimination factor for N (i.e., mean of `3.4`), tp is trophic position, and λ_1 and/or λ_2 are the trophic levels of baselines which are often a primary consumer (e.g., `2` or `2.5`).

The data supplied to `brms()` when using baselines at the same trophic level (`lambda` argument set to `1`) needs to have the following variables, `d15n`, `n1`, `n2`, `l1` (λ_1) which is usually `2`. If using baselines at different trophic levels (`lambda` argument set to `2`) the data frame needs to have `l1` and `l2` with a numerical value for each trophic level (e.g., `2` and `2.5`; λ_1 and λ_2).

Value

returns model structure for two source model to be used in a `brms()` call.

See Also

`brms::brms()`

Examples

```
two_source_model_arc()
```

`two_source_priors` *Bayesian priors - Two Source Trophic Position*

Description

Create priors for two source trophic position model derived from Post 2002.

Usage

```
two_source_priors(bp = FALSE)
```

Arguments

`bp`	logical value that controls whether informed priors are supplied to the model for both δ^{15}N and δ^{15}C baselines. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for both δ^{15}N and δ^{15}C baseline (`c1`, `c2`, `n1`, and `n2`).

Value

returns priors for two source model to be used in a `brms()` call.

See Also

`two_source_model()` and `brms::brms()`

Examples

```
two_source_priors()
```

`two_source_priors_ar` *Bayesian priors - Two Source Trophic Position with α_r*

Description

Create priors for trophic position using a two source model with α_r derived from Post 2002 and Heuvel et al. 2024.

Usage

```
two_source_priors_ar(bp = FALSE)
```

Arguments

`bp`	logical value that controls whether informed priors are supplied to the model for δ^{15}N baselines. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for both δ^{15}N baseline (`n1`, and `n2`).

Value

returns priors for two source model to be used in a `brms()` call.

See Also

`brms::brms()`

Examples

```
two_source_priors_ar()
```

`two_source_priors_arc` *Bayesian priors - Two Source Trophic Position with α_r and carbon mixing model*

Description

Create priors for trophic position using a two source model with α_r derived from Post 2002 and Heuvel et al. 2024.

Usage

```
two_source_priors_arc(bp = FALSE)
```

Arguments

`bp`	logical value that controls whether informed priors are supplied to the model for both δ^{15}N and δ^{15}C baselines. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for both δ^{15}N and δ^{15}C baseline (`c1`, `c2`, `n1`, and `n2`).

Value

returns priors for two source model to be used in a `brms()` call.

See Also

`brms::brms()`

Examples

```
two_source_priors_arc()
```

`two_source_priors_params` *Adjust Bayesian priors - Two Source Trophic Position*

Description

Adjust priors for two source trophic position model derived from Post 2002.

Usage

```
two_source_priors_params(
  a = NULL,
  b = NULL,
  c1 = NULL,
  c1_sigma = NULL,
  c2 = NULL,
  c2_sigma = NULL,
  n1 = NULL,
  n1_sigma = NULL,
  n2 = NULL,
  n2_sigma = NULL,
  dn = NULL,
  dn_sigma = NULL,
  tp_lb = NULL,
  tp_ub = NULL,
  sigma_lb = NULL,
  sigma_ub = NULL,
  bp = FALSE
)
```

Arguments

`a`	(α) exponent of the random variable for beta distribution. Defaults to `1`. See beta distribution for more information.
`b`	(β) shape parameter for beta distribution. Defaults to `1`. See beta distribution for more information.
`c1`	mean (μ) prior for the mean of the first δ^{13}C baseline. Defaults to `-21`.
`c1_sigma`	variance (σ)for the mean of the first δ^{13}C baseline. Defaults to `1`.
`c2`	mean (μ) prior for or the mean of the second δ^{13}C baseline. Defaults to `-26`.
`c2_sigma`	variance (σ)for the mean of the first δ^{13}C baseline. Defaults to `1`.
`n1`	mean (μ) prior for the mean of the first δ^{15}N baseline. Defaults to `8`.
`n1_sigma`	variance (σ)for the mean of the first δ^{15}N baseline. Defaults to `1`.
`n2`	mean (μ) prior for or the mean of the second δ^{15}N baseline. Defaults to `9.5`.
`n2_sigma`	variance (σ) for the mean of the second δ^{15}N baseline. Defaults to `1`.
`dn`	mean (μ) prior value for ΔN. Defaults to `3.4`.
`dn_sigma`	variance (σ) for δ^{15}N. Defaults to `0.5`.
`tp_lb`	lower bound for priors for trophic position. Defaults to `2`.
`tp_ub`	upper bound for priors for trophic position. Defaults to `10`.
`sigma_lb`	lower bound for priors for σ. Defaults to `0`.
`sigma_ub`	upper bound for priors for σ. Defaults to `10`.
`bp`	logical value that controls whether informed priors are supplied to the model for both δ^{15}N and δ^{15}C baselines. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for both δ^{15}N and δ^{15}C baseline (`c1`, `c2`, `n1`, and `n2`).

Details

We will use the following equations from Post 2002:

1. $$\delta^{13}C_c = \alpha * (\delta^{13}C_1 - \delta^{13}C_2) + \delta^{13}C_2$$
2. $$\delta^{15}N = \Delta N \times (tp - \lambda_1) + n_1 \times \alpha + n_2 \times (1 - \alpha)$$
3. $$\delta^{15}N = \Delta N \times (tp - (\lambda_1 \times \alpha + \lambda_2 \times (1 - \alpha))) + n_1 \times \alpha + n_2 \times (1 - \alpha)$$

- The random exponent (α; `a`) and shape parameters (β; `b`) for α. This prior assumes a beta distribution.
- The mean (`c1`; μ) and variance (`c1_sigma`; σ) of the mean for the first $\delta^{13}C$ for a given baseline. This prior assumes a normal distributions.
- The mean (`c2`;μ) and variance (`c2_sigma`; σ) of the mean for the second $\delta^{13}C$ for a given baseline. This prior assumes a normal distributions.
- The mean (`n1`; μ) and variance (`n1_sigma`; σ) of the mean for the first $\delta^{15}N$ for a given baseline. This prior assumes a normal distributions.
- The mean (`n2`;μ) and variance (`n2_sigma`; σ) of the mean for the second δ^{15}N for a given baseline. This prior assumes a normal distributions.
- The mean (`dn`; μ) and variance (`dn_sigma`; σ) of ΔN (i.e, trophic enrichment factor). This prior assumes a normal distributions.
- The lower (`tp_lb`) and upper (`tp_ub`) bounds for priors for trophic position. This prior assumes a uniform distributions.
- The lower (`sigma_lb`) and upper (`sigma_ub`) bounds for variance (σ). This prior assumes a uniform distributions.

Value

`stanvars` object to be used with `brms()` call.

See Also

`two_source_priors()`, `two_source_model()`, and `brms::brms()`

Examples

```
two_source_priors_params()
```

`two_source_priors_params_ar`

Adjust Bayesian priors - Two Source Trophic Position with α_r

---

Description

Create priors for trophic position using a two source model with α_r derived from Post 2002 and Heuvel et al. 2024.

Usage

```
two_source_priors_params_ar(
  a = NULL,
  b = NULL,
  n1 = NULL,
  n1_sigma = NULL,
  n2 = NULL,
  n2_sigma = NULL,
  dn = NULL,
  dn_sigma = NULL,
  tp_lb = NULL,
  tp_ub = NULL,
  sigma_lb = NULL,
  sigma_ub = NULL,
  bp = FALSE
)
```

Arguments

`a`	(α) exponent of the random variable for beta distribution. Defaults to `1`. See beta distribution for more information.
`b`	(β) shape parameter for beta distribution. Defaults to `1`. See beta distribution for more information.
`n1`	mean (μ) prior for first δ^{15}N baseline. Defaults to `8.0`.
`n1_sigma`	variance (σ)for first δ^{15}N baseline. Defaults to `1`.
`n2`	mean (μ) prior for second δ^{15}N baseline. Defaults to `9.5`.
`n2_sigma`	variance (σ) for second δ^{15}N baseline. Defaults to `1`.
`dn`	mean (μ) prior value for ΔN. Defaults to `3.4`.
`dn_sigma`	variance (σ) for δ^{15}N. Defaults to `0.5`.
`tp_lb`	lower bound for priors for trophic position. Defaults to `2`.
`tp_ub`	upper bound for priors for trophic position. Defaults to `10`.
`sigma_lb`	lower bound for priors for σ. Defaults to `0`.
`sigma_ub`	upper bound for priors for σ. Defaults to `10`.

`bp`	logical value that controls whether informed baseline priors are supplied to the model for δ^{15}N baselines. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for both δ^{15}N baseline (`n1` and `n2`)

Details

We will use the following equations derived from Post 2002 and Heuvel et al. 2024:

1. $$\alpha = (\delta^{13}C_c - \delta^{13}C_2)/(\delta^{13}C_1 - \delta^{13}C_2)$$
2. $$\alpha = \alpha_r \times (\alpha_{max} - \alpha_{min}) + \alpha_{min}$$
3. $$\delta^{15}N = \Delta N \times (tp - \lambda_1) + n_1 \times \alpha_r + n_2 \times (1 - \alpha_r)$$
4. $$\delta^{15}N = \Delta N \times (tp - (\lambda_1 \times \alpha_r + \lambda_2 \times (1 - \alpha_r))) + n_1 \times \alpha_r + n_2 \times (1 - \alpha_r)$$

For equation 1)

This equation is a carbon source mixing model with $\delta^{13}C_c$ is the isotopic value for consumer, $\delta^{13}C_1$ is the mean isotopic value for baseline 1 and $\delta^{13}C_2$ is the mean isotopic value for baseline 2. This equation is added to the data frame using `add_alpha()`.

For equation 2)

α is being corrected using equations in Heuvel et al. 2024 with α_r being the corrected value (bound by 0 and 1), α_{min} is the minimum α value calculated using `add_alpha()` and α_{max} being the maximum α value calculated using `add_alpha()`.

For equation 3) and 4)

δ^{15}N are values from the consumer, n_1 is δ^{15}N values of baseline 1, n_2 is δ^{15}N values of baseline 2, ΔN is the trophic discrimination factor for N (i.e., mean of `3.4`), tp is trophic position, and λ_1 and/or λ_2 are the trophic levels of baselines which are often a primary consumer (e.g., `2` or `2.5`).

This function allows the user to adjust the priors for the following variables in the equation above:

- The random exponent (α; `a`) and shape parameters (β; `b`) for α_r. This prior assumes a beta distribution.
- The mean (`n2`;μ) and variance (`n2_sigma`; σ) of the second δ^{15}N for a given baseline. This prior assumes a normal distributions.
- The mean (`c1`;μ) and variance (`c1_sigma`; σ) of the second δ^{13}C for a given baseline. This prior assumes a normal distributions.
- The mean (`c2`;μ) and variance (`c2_sigma`; σ) of the second δ^{13}C for a given baseline. This prior assumes a normal distributions.
- The mean (`dn`; μ) and variance (`dn_sigma`; σ) of ΔN (i.e, trophic enrichment factor). This prior assumes a normal distributions.
- The lower (`tp_lb`) and upper (`tp_ub`) bounds for priors for trophic position. This prior assumes a uniform distributions.
- The lower (`sigma_lb`) and upper (`sigma_ub`) bounds for variance (σ). This prior assumes a uniform distributions.

Value

`stanvars` object to be used with `brms()` call.

See Also

`two_source_priors_ar()`, `two_source_model_ar()`, and `brms::brms()`

Examples

```
two_source_priors_params_ar()
```

`two_source_priors_params_arc`

Adjust Bayesian priors - Two Source Trophic Position with α_r and carbon mixing model

Description

Adjust priors for trophic position using a two source model with α_r derived from Post 2002 and Heuvel et al. 2024

Usage

```
two_source_priors_params_arc(
  a = NULL,
  b = NULL,
  n1 = NULL,
  n1_sigma = NULL,
  n2 = NULL,
  n2_sigma = NULL,
  c1 = NULL,
  c1_sigma = NULL,
  c2 = NULL,
  c2_sigma = NULL,
  dn = NULL,
  dn_sigma = NULL,
  tp_lb = NULL,
  tp_ub = NULL,
  sigma_lb = NULL,
  sigma_ub = NULL,
  bp = FALSE
)
```

Arguments

`a`	(α) exponent of the random variable for beta distribution. Defaults to `1`. See beta distribution for more information.
`b`	(β) shape parameter for beta distribution. Defaults to `1`. See beta distribution for more information.
`n1`	mean (μ) prior for first δ^{15}N baseline. Defaults to `8.0`.
`n1_sigma`	variance (σ)for first δ^{15}N baseline. Defaults to `1`.
`n2`	mean (μ) prior for second δ^{15}N baseline. Defaults to `9.5`.
`n2_sigma`	variance (σ) for second δ^{15}N baseline. Defaults to `1`.
`c1`	mean (μ) prior for first δ^{13}C baseline. Defaults to `-21`.
`c1_sigma`	variance (σ)for first δ^{13}C baseline. Defaults to `1`.
`c2`	mean (μ) prior for second δ^{13}C baseline. Defaults to `-26`.
`c2_sigma`	variance (σ) for second δ^{13}C baseline. Defaults to `1`.
`dn`	mean (μ) prior value for ΔN. Defaults to `3.4`.
`dn_sigma`	variance (σ) for δ^{15}N. Defaults to `0.25`.
`tp_lb`	lower bound for priors for trophic position. Defaults to `2`.
`tp_ub`	upper bound for priors for trophic position. Defaults to `10`.
`sigma_lb`	lower bound for priors for σ. Defaults to `0`.
`sigma_ub`	upper bound for priors for σ. Defaults to `10`.
`bp`	logical value that controls whether informed baseline priors are supplied to the model for δ^{15}N baselines. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for both δ^{15}N baseline (`n1` and `n2`)

Details

We will use the following equations derived from Post 2002 and Heuvel et al. 2024:

1. $$\alpha = (\delta^{13}C_c - \delta^{13}C_2)/(\delta^{13}C_1 - \delta^{13}C_2)$$

2. $$\alpha = \alpha_r \times (\alpha_{max} - \alpha_{min}) + \alpha_{min}$$

3. $$\delta^{13}C = c_1 \times \alpha_r + c_2 \times (1 - \alpha_r)$$

4. $$\delta^{15}N = \Delta N \times (tp - \lambda_1) + n_1 \times \alpha_r + n_2 \times (1 - \alpha_r)$$

5. $$\delta^{15}N = \Delta N \times (tp - (\lambda_1 \times \alpha_r + \lambda_2 \times (1 - \alpha_r))) + n_1 \times \alpha_r + n_2 \times (1 - \alpha_r)$$

For equation 1)

This equation is a carbon source mixing model with $\delta^{13}C_c$ is the isotopic value for consumer, $\delta^{13}C_1$ is the mean isotopic value for baseline 1 and $\delta^{13}C_2$ is the mean isotopic value for baseline 2.

For equation 2)

α is being corrected using equations in Heuvel et al. 2024. with α_r being the corrected value (bound by 0 and 1), α_{min} is the minimum α value calculated using `add_alpha()` and α_{max} being the maximum α value calculated using `add_alpha()`.

For equation 3)

This equation is a carbon source mixing model with δ^{13}C being estimated using `c_1`, `c_2` and α_r calculated in equation 1.

For equation 4) and 5)

δ^{15}N are values from the consumer, n_1 is δ^{15}N values of baseline 1, n_2 is δ^{15}N values of baseline 2, ΔN is the trophic discrimination factor for N (i.e., mean of `3.4`), tp is trophic position, and λ_1 and/or λ_2 are the trophic levels of baselines which are often a primary consumer (e.g., `2` or `2.5`).

This function allows the user to adjust the priors for the following variables in the equation above:

- The random exponent (α; `a`) and shape parameters (β; `b`) for α_r. This prior assumes a beta distribution.
- The mean (`n2`;μ) and variance (`n2_sigma`; σ) of the second δ^{15}N for a given baseline. This prior assumes a normal distributions.
- The mean (`c1`;μ) and variance (`c1_sigma`; σ) of the second δ^{13}C for a given baseline. This prior assumes a normal distributions.
- The mean (`c2`;μ) and variance (`c2_sigma`; σ) of the second δ^{13}C for a given baseline. This prior assumes a normal distributions.
- The mean (`dn`; μ) and variance (`dn_sigma`; σ) of ΔN (i.e, trophic enrichment factor). This prior assumes a normal distributions.
- The lower (`tp_lb`) and upper (`tp_ub`) bounds for priors for trophic position. This prior assumes a uniform distributions.
- The lower (`sigma_lb`) and upper (`sigma_ub`) bounds for variance (σ). This prior assumes a uniform distributions.

Value

`stanvars` object to be used with `brms()` call.

See Also

`two_source_priors_arc()`, `two_source_model_arc()`, and `brms::brms()`

Examples

```
two_source_priors_params_ar()
```

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