

Package ‘trps’

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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](https://doi.org/10.1890/0012-9658(2002)083[0703:USITET]2.0.CO;2)>, Vander Zanden and Vadeboncoeur (2002) <[doi:10.1890/0012-9658\(2002\)083\[2152:FAIOBA\]2.0.CO;2](https://doi.org/10.1890/0012-9658(2002)083[2152:FAIOBA]2.0.CO;2)>, and Heuvel et al. (2024) <[doi:10.1139/cjfas-2024-0028](https://doi.org/10.1139/cjfas-2024-0028)>.

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URL <https://benjaminhlina.github.io/trps/>,
<https://github.com/benjaminhlina/trps>

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VignetteBuilder knitr

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add_alpha	<i>Calculate and add α</i>
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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 $\delta^{13}\text{C}$ columns need to be named c1 and c2, with the consumer's $\delta^{13}\text{C}$ 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	<i>Stable isotope data for amphipods (baseline 1)</i>
----------------	---

Description

Stable isotope data ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) 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 species (i.e., Amphipoda)

ecoregion ecoregion where samples were collected

d13c_b1 observed values for $\delta^{13}\text{C}$

d15n_b1 observed values for $\delta^{15}\text{N}$

baseline_2_iso	<i>Stable isotope data for dreissenids (baseline 2)</i>
----------------	---

Description

Stable isotope data ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) 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 species (i.e., Dreissenids)

ecoregion ecoregion where samples were collected

d13c_b2 observed values for $\delta^{13}\text{C}$

d15n_b2 observed values for $\delta^{15}\text{N}$

combined_iso	<i>Stable isotope data for lake trout, amphipods (benthic baseline; baseline 1) and dreissenids (pelagic baseline; baseline 2),</i>
--------------	---

Description

Stable isotope data ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) for lake trout collected from two ecoregions in Lake Ontario. Values of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ 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 species (i.e., Lake Trout)

ecoregion ecoregion where samples were collected

d13c observed values for $\delta^{13}\text{C}$ of consumer

d15n observed values for $\delta^{15}\text{N}$ of consumer

d13c_b1 observed values for $\delta^{13}\text{C}$ of baseline 1

d15n_b1 observed values for $\delta^{15}\text{N}$ of baseline 1

d13c_b2 observed values for $\delta^{13}\text{C}$ of baseline 2

d15n_b2 observed values for $\delta^{15}\text{N}$ of baseline 2

c1 mean values for $\delta^{13}\text{C}$ of baseline 1

n1 mean values for $\delta^{15}\text{N}$ of baseline 1

c2 mean values for $\delta^{13}\text{C}$ of baseline 2

n2 mean values for $\delta^{15}\text{N}$ of baseline 2

consumer_iso	<i>Stable isotope data for lake trout (consumer)</i>
--------------	--

Description

Stable isotope data ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) 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 species (i.e., Lake Trout)

ecoregion ecoregion where samples were collected

d13c observed values for $\delta^{13}\text{C}$

d15n observed values for $\delta^{15}\text{N}$

one_source_model	<i>Bayesian model - One Source Trophic Position</i>
------------------	---

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 $\delta^{15}\text{N}$ baseline. Default is FALSE meaning the model will use uninformed priors, however, the supplied data.frame needs values for $\delta^{15}\text{N}$ baseline (n1).

Details

$$\delta^{15}\text{N} = \delta^{15}\text{N}_1 + \Delta\text{N} \times (tp - \lambda_1)$$

$\delta^{15}\text{N}$ are values from the consumer, $\delta^{15}\text{N}_1$ is mean $\delta^{15}\text{N}$ 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 $\delta^{15}\text{N}$ baseline. Default is `FALSE` meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for $\delta^{15}\text{N}$ 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 $\delta^{15}\text{N}$ baseline. Defaults to 9.
n1_sigma	variance (σ) for the mean $\delta^{15}\text{N}$ baseline. Defaults to 1.
dn	mean (μ) prior value for ΔN . Defaults to 3.4.
dn_sigma	variance (σ) for $\delta^{15}\text{N}$. 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 $\delta^{15}\text{N}$ baseline. Default is FALSE meaning the model will use uninformed priors, however, the supplied data.frame needs values for $\delta^{15}\text{N}$ 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 $\delta^{15}\text{N}$ 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	<i>Bayesian model - Two Source Trophic Position</i>
------------------	---

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 $\delta^{15}\text{N}$ and $\delta^{15}\text{C}$ baselines. Default is FALSE meaning the model will use uninformed priors, however, the supplied data.frame needs values for both $\delta^{15}\text{N}$ and $\delta^{15}\text{C}$ baseline (c1, c2, n1, and n2). |
| lambda | numerical value, 1 or 2, that controls whether one or two λ s 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)

$\delta^{15}N$ are values from the consumer, n_1 is $\delta^{15}N$ values of baseline 1, n_2 is $\delta^{15}N$ 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. \(2024\)](#) [doi:10.1139/cjfas20240028](https://doi.org/10.1139/cjfas20240028) using a Bayesian framework.

Usage

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

Arguments

<code>bp</code>	logical value that controls whether informed priors are supplied to the model for both $\delta^{15}N$ baselines. Default is <code>FALSE</code> meaning the model will use uninformed priors, however, the supplied data.frame needs values for both $\delta^{15}N$ baseline (<code>n1</code> and <code>n2</code>).
<code>lambda</code>	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) [doi:10.1139/cjfas20240028](https://doi.org/10.1139/cjfas20240028):

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) [doi:10.1139/cjfas20240028](https://doi.org/10.1139/cjfas20240028) 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)

$\delta^{15}N$ are values from the consumer, n_1 is $\delta^{15}N$ values of baseline 1, n_2 is $\delta^{15}N$ 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) [doi:10.1139/cjfas20240028](#) 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 $\delta^{15}\text{N}$ and $\delta^{15}\text{C}$ baselines. Default is FALSE meaning the model will use uninformed priors, however, the supplied data.frame needs values for both $\delta^{15}\text{N}$ and $\delta^{15}\text{C}$ 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) [doi:10.1139/cjfas20240028](#):

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) [doi:10.1139/cjfas20240028](https://doi.org/10.1139/cjfas20240028). 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 $\delta^{13}\text{C}$ being estimated using `c_1`, `c_2` and α_c calculated in equation 1.

For equation 4) and 5)

$\delta^{15}\text{N}$ are values from the consumer, n_1 is $\delta^{15}\text{N}$ values of baseline 1, n_2 is $\delta^{15}\text{N}$ 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 $\delta^{15}\text{N}$ and $\delta^{15}\text{C}$ baselines. Default is FALSE meaning the model will use uninformed priors, however, the supplied data frame needs values for both $\delta^{15}\text{N}$ and $\delta^{15}\text{C}$ 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. \(2024\)](#) [doi:10.1139/cjfas20240028](https://doi.org/10.1139/cjfas20240028).

Usage

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

Arguments

`bp` logical value that controls whether informed priors are supplied to the model for $\delta^{15}\text{N}$ baselines. Default is FALSE meaning the model will use uninformed priors, however, the supplied `data.frame` needs values for both $\delta^{15}\text{N}$ 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) [doi:10.1139/cjfas20240028](https://doi.org/10.1139/cjfas20240028).

Usage

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

Arguments

bp logical value that controls whether informed priors are supplied to the model for both $\delta^{15}\text{N}$ and $\delta^{15}\text{C}$ baselines. Default is FALSE meaning the model will use uninformed priors, however, the supplied data.frame needs values for both $\delta^{15}\text{N}$ and $\delta^{15}\text{C}$ 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 $\delta^{13}\text{C}$ baseline. Defaults to -21.
c1_sigma	variance (σ) for the mean of the first $\delta^{13}\text{C}$ baseline. Defaults to 1.
c2	mean (μ) prior for or the mean of the second $\delta^{13}\text{C}$ baseline. Defaults to -26.
c2_sigma	variance (σ) for the mean of the first $\delta^{13}\text{C}$ baseline. Defaults to 1.
n1	mean (μ) prior for the mean of the first $\delta^{15}\text{N}$ baseline. Defaults to 8.
n1_sigma	variance (σ) for the mean of the first $\delta^{15}\text{N}$ baseline. Defaults to 1.
n2	mean (μ) prior for or the mean of the second $\delta^{15}\text{N}$ baseline. Defaults to 9.5.
n2_sigma	variance (σ) for the mean of the second $\delta^{15}\text{N}$ baseline. Defaults to 1.
dn	mean (μ) prior value for ΔN . Defaults to 3.4.
dn_sigma	variance (σ) for $\delta^{15}\text{N}$. 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 priors are supplied to the model for both $\delta^{15}\text{N}$ and $\delta^{15}\text{C}$ baselines. Default is FALSE meaning the model will use uninformed priors, however, the supplied data. <code>f</code> frame needs values for both $\delta^{15}\text{N}$ and $\delta^{15}\text{C}$ 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 $\delta^{15}N$ 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. \(2024\) doi:10.1139/cjfas20240028](#).

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 $\delta^{15}\text{N}$ baseline. Defaults to 8.0.
n1_sigma	variance (σ) for first $\delta^{15}\text{N}$ baseline. Defaults to 1.
n2	mean (μ) prior for second $\delta^{15}\text{N}$ baseline. Defaults to 9.5.
n2_sigma	variance (σ) for second $\delta^{15}\text{N}$ baseline. Defaults to 1.
dn	mean (μ) prior value for ΔN . Defaults to 3.4.
dn_sigma	variance (σ) for $\delta^{15}\text{N}$. 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 $\delta^{15}\text{N}$ baselines. Default is FALSE meaning the model will use uninformed priors, however, the supplied data.frame needs values for both $\delta^{15}\text{N}$ baseline (n1 and n2)

Details

We will use the following equations derived from Post 2002 and Heuvel et al. (2024 doi:10.1139/cjfas20240028):

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) doi:10.1139/cjfas20240028 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)

$\delta^{15}\text{N}$ are values from the consumer, n_1 is $\delta^{15}\text{N}$ values of baseline 1, n_2 is $\delta^{15}\text{N}$ 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 ($n2;\mu$) and variance ($n2_sigma$; σ) of the second $\delta^{15}\text{N}$ for a given baseline. This prior assumes a normal distributions.
- The mean ($c1;\mu$) and variance ($c1_sigma$; σ) of the second $\delta^{13}\text{C}$ for a given baseline. This prior assumes a normal distributions.
- The mean ($c2;\mu$) and variance ($c2_sigma$; σ) of the second $\delta^{13}\text{C}$ 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_arc()
```

```
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. \(2024\) doi:10.1139/cjfas20240028](#)

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 $\delta^{15}\text{N}$ baseline. Defaults to 8.0.
n1_sigma	variance (σ) for first $\delta^{15}\text{N}$ baseline. Defaults to 1.
n2	mean (μ) prior for second $\delta^{15}\text{N}$ baseline. Defaults to 9.5.
n2_sigma	variance (σ) for second $\delta^{15}\text{N}$ baseline. Defaults to 1.
c1	mean (μ) prior for first $\delta^{13}\text{C}$ baseline. Defaults to -21.
c1_sigma	variance (σ) for first $\delta^{13}\text{C}$ baseline. Defaults to 1.
c2	mean (μ) prior for second $\delta^{13}\text{C}$ baseline. Defaults to -26.
c2_sigma	variance (σ) for second $\delta^{13}\text{C}$ baseline. Defaults to 1.
dn	mean (μ) prior value for ΔN . Defaults to 3.4.
dn_sigma	variance (σ) for $\delta^{15}\text{N}$. 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 $\delta^{15}\text{N}$ baselines. Default is FALSE meaning the model will use uninformed priors, however, the supplied data.frame needs values for both $\delta^{15}\text{N}$ baseline (n1 and n2)

Details

We will use the following equations derived from Post 2002 and Heuvel et al. (2024) doi:10.1139/cjfas20240028:

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) [doi:10.1139/cjfas20240028](https://doi.org/10.1139/cjfas20240028). 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 $\delta^{13}C$ being estimated using `c_1`, `c_2` and α_r calculated in equation 1.

For equation 4) and 5)

$\delta^{15}N$ are values from the consumer, n_1 is $\delta^{15}N$ values of baseline 1, n_2 is $\delta^{15}N$ 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 $\delta^{15}N$ for a given baseline. This prior assumes a normal distributions.
- The mean (`c1`; μ) and variance (`c1_sigma`; σ) of the second $\delta^{13}C$ for a given baseline. This prior assumes a normal distributions.
- The mean (`c2`; μ) and variance (`c2_sigma`; σ) of the second $\delta^{13}C$ 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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