Package ‘tidyttmoment’

May 8, 2026

Title Functional Trait Moment Calculation

Version 0.0.5

Depends R (>= 4.1.0)

Description Calculates the community four 'moments' (mean, variance, skewness, and kurtosis) of a given trait based on the moments described in Wieczynski et al. (2019) <doi:10.1073/pnas.1813723116>. These functional metrics are extremely useful in characterizing the distribution of traits in a plant community. It also provides tidyverse-friendly wrappers to seamlessly calculate advanced functional diversity indices (e.g., FDis, Rao's Q) using 'fundiversity' (Grenie et al. 2023 <doi:10.1111/ecog.06585>) and functional rarity indices using 'funrar' (Grenie et al. 2017 <doi:10.1111/ddi.12629>). Evaluating these community-weighted moments and diversity metrics allows researchers to evaluate shifts in optimal phenotypes and understand ecological filtering with exactness.

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Suggests covr, testthat (>= 3.1.5)

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.3.3

URL `https://github.com/PaulESantos/tidyttmoment`, `https://paulesantos.github.io/tidyttmoment/`

BugReports `https://github.com/PaulESantos/tidyttmoment/issues`

Imports cli, dplyr, lifecycle, tidyr, fundiversity, funrar, rlang, tibble

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-03-23 17:20:02 UTC

Contents

`tidy_calc_diversity` *Calculate functional diversity indices from tidy data*

Description

[Experimental]

Wraps the `fundiversity` package to calculate functional diversity indices (FRic, FDiv, FEve, FDis, Rao's Q) directly from a tidy long-format data frame. Automatically handles parallelization if a `future::plan()` is set.

Usage

```
tidy_calc_diversity(
  df,
  comm_names,
  sp_names,
  trait_names,
  trait_value,
  weight,
  index = c("FRic", "FDiv", "FEve", "FDis", "RaoQ")
)
```

Arguments

`df`	A data frame containing the trait and community data.
`comm_names`	Unquoted column name containing the community names/IDs.
`sp_names`	Unquoted column name containing the species names/IDs.
`trait_names`	Unquoted column name containing the trait IDs.
`trait_value`	Unquoted column name containing the actual trait values.
`weight`	Unquoted column name containing the variable used to weight the trait values (e.g. abundance).
`index`	Character vector of indices to compute. Options are "FRic", "FDiv", "FEve", "FDis", "RaoQ". Default is to compute all.

Value

A tibble with community coordinates and the selected functional diversity indices.

`tidy_calc_moment` *Calculate community weighted mean, variance, skewness, and kurtosis*

Description

[Experimental]

Calculates the community weighted mean, variance, skewness, and excess kurtosis of a given trait based on the moments described in Wieczynski et al. (2019).

Usage

```
tidy_calc_moment(df, trait_names, comm_names, trait_value, weight)
```

Arguments

`df`	A data frame containing the trait and community data.
`trait_names`	Unquoted column name containing the trait IDs.
`comm_names`	Unquoted column name containing the community names/IDs.
`trait_value`	Unquoted column name containing the actual trait values.
`weight`	Unquoted column name containing the variable used to weight the trait values (e.g. abundance).

Value

Returns a tibble with the columns comm, trait, cwm (mean), cwv (variance), cws (skewness), and cwk (excess kurtosis).

References

Enquist, B. J., Norberg, J., Bonser, S. P., Violle, C., Webb, C. T., Henderson, A., ... & Savage, V. M. (2015). Scaling from traits to ecosystems. *Advances in Ecological Research*, 52, 249-318.

Metcalfe, R. J., Ozturk, M., & Pouteau, R. (2020). Using functional traits to model annual plant community dynamics. *Ecology*.

Šímová, I., Violle, C., Kraft, N. J., Storch, D., Svenning, J. C., Gallagher, R. V., ... & Enquist, B. J. (2018). Spatial patterns and climate relationships of major plant traits in the New World differ between woody and herbaceous species. *Global Ecology and Biogeography*, 27(8), 895-916.

Wieczynski, D. J., Boyle, B., Buzzard, V., Duran, S. M., Henderson, A. N., Hulshof, C. M., ... & Savage, V. M. (2019). Climate shapes and shifts functional biodiversity in forests worldwide. *Proceedings of the National Academy of Sciences*, 116(2), 587-592.

Examples

```
df <- data.frame(trait = c("height", "height", "weight", "weight"),
                 trait_value = c(5, 10, 15, 12),
                 abundancia = c(1, 2, 1, 3),
                 comm = c("A", "A", "B", "B"))
tidy_calc_moment(df,
trait_names = trait,
comm_names = comm,
trait_value = trait_value,
weight = abundancia)
```

`tidy_calc_rarity` *Calculate functional rarity indices from tidy data*

Description

[Experimental]

Wraps the `funrar` package to calculate functional rarity indices (Distinctiveness and Uniqueness) directly from a tidy long-format data frame.

Usage

```
tidy_calc_rarity(df, comm_names, sp_names, trait_names, trait_value, weight)
```

Arguments

`df`	A data frame containing the trait and community data.
`comm_names`	Unquoted column name containing the community names/IDs.
`sp_names`	Unquoted column name containing the species names/IDs.
`trait_names`	Unquoted column name containing the trait IDs.
`trait_value`	Unquoted column name containing the actual trait values.
`weight`	Unquoted column name containing the variable used to weight the trait values (e.g. abundance).

Value

A list of tibbles containing distinctiveness and uniqueness metrics.

`tidy_to_matrices` *Convert tidy long data to community and trait matrices*

Description

[Experimental]

Helper function to pivot a tidy long-format data frame into a site-by-species abundance matrix and a species-by-trait matrix, which are required for indices like functional diversity and rarity.

Usage

```
tidy_to_matrices(df, comm_names, sp_names, trait_names, trait_value, weight)
```

Arguments

`df`	A data frame containing the trait and community data.
`comm_names`	Unquoted column name containing the community names/IDs.
`sp_names`	Unquoted column name containing the species names/IDs.
`trait_names`	Unquoted column name containing the trait IDs.
`trait_value`	Unquoted column name containing the actual trait values.
`weight`	Unquoted column name containing the variable used to weight (e.g., abundance).

Value

A list containing `site_species` (a site by species matrix) and `species_traits` (a species by trait matrix).

Examples

```
df <- data.frame(
  comm = c("A", "A", "B", "B"),
  species = c("sp1", "sp2", "sp1", "sp3"),
  trait = c("height", "height", "height", "height"),
  trait_value = c(5, 10, 5, 15),
  abundance = c(1, 2, 1, 3)
)
tidy_to_matrices(df, comm, species, trait, trait_value, abundance)
```

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