

# Package ‘BioTImEr’

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**Type** Package

**Title** Tools to Use and Explore the 'BioTIME' Database

**Version** 0.2.4

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**License** MIT + file LICENSE

**URL** <https://github.com/bioTIMEHub/BioTImEr>

**BugReports** <https://github.com/bioTIMEHub/BioTImEr/issues>

**Description** The 'BioTIME' database was first published in 2018 and inspired ideas, questions, project and research article. To make it even more accessible, an R package was created.

The 'BioTImEr' package provides tools designed to interact with the 'BioTIME' database. The functions provided include the 'BioTIME' recommended methods for preparing (gridding and rarefaction) time series data, a selection of standard biodiversity metrics (including species richness, numerical abundance and exponential Shannon) alongside examples on how to display change over time. It also includes a sample subset of both the query and meta data, the full versions of which are freely available on the 'BioTIME' website <<https://biotime.st-andrews.ac.uk/home.php>>.

**Depends** R (>= 4.3.0)

**Imports** dplyr, tidyr, ggplot2, vegan, dggridR (>= 3.1.0), checkmate

**Suggests** maps, knitr, rmarkdown, formatR, testthat (>= 3.0.0), vdiffR

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**VignetteBuilder** knitr

**NeedsCompilation** no

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BTsubset_data	<i>BioTIME subset</i>
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Description

A subset of data from BioTIME temporal surveys.

**Usage**

BTsubset\_data

**Format**

## 'BTsubset\_data' A data frame with 81,084 rows and 17 columns:

**ID\_ALL\_RAW\_DATA** Unique BioTIME identifier for record**ABUNDANCE** Double representing the abundance for the record (see metadata for details of ABUNDANCE\_TYPE)**BIOMASS** Double representing the biomass for the record (see metadata for details of BIOMASS\_TYPE)**ID\_SPECIES** Unique identifier linking to the species table**SAMPLE\_DESC** Concatenation of variables comprising unique sampling event**LATITUDE** Latitude of record**LONGITUDE** Longitude of record**DEPTH** Depth or elevation of record if available**DAY** Numerical day of record**MONTH** Numerical value of month for record, i.e. January=1**YEAR** Year of record**STUDY\_ID** BioTIME study unique identifier**newID** Validated species identifier key**valid\_name** Highest taxonomic resolution of individual, preferred is genus and species**resolution** Level of resolution, i.e. 'species' represented by genus and species**taxon** Higher level taxonomic grouping, i.e. Fish**Source**<<https://biotime.st-andrews.ac.uk/download.php>>

BTsubset\_meta

*BioTIME subset metadata***Description**

A subset of the metadata from BioTIME

**Usage**

BTsubset\_meta

**Format**

## 'BTsubset\_meta' A data frame with 12 rows and 25 columns:

**STUDY\_ID** BioTIME study unique identifier  
**REALM** Realm of study location, i.e. Marine  
**CLIMATE** Climate of study location, i.e. Temperate  
**HABITAT** Habitat of study location, i.e. Rivers  
**PROTECTED\_AREA** Binary variable indicating if the study is within a protected area  
**BIOME\_MAP** Biome of study location (taken from the WWF biomes, i.e. Temperate broadleaf and mixed forests)  
**TAXA** High level taxonomic identity of study species, i.e. Fish  
**ORGANISMS** More detailed information on taxonomy, i.e. woody plants  
**TITLE** Title of study as identified in original source  
**AB\_BIO** A, B or AB to designate abundance only, biomass only or both  
**DATA\_POINTS** Number of unique data points in study, e.g. 10 data points spanning 15 years = 10  
**START\_YEAR** First year of study  
**END\_YEAR** Last year of study  
**CENT\_LAT** Central latitude taken from the convex hull around all study coordinates  
**CENT\_LONG** Central longitude taken from the convex hull around all study coordinates  
**NUMBER\_OF\_SPECIES** Number of distinct species in study  
**NUMBER\_OF\_SAMPLES** Number of distinct samples in study  
**NUMBER\_LAT\_LONG** Number of distinct geographic coordinates in study  
**TOTAL** Total number of records in study  
**GRAIN\_SIZE\_TEXT** Grain size described in text, i.e. size of forest plots  
**AREA\_SQ\_KM** Total area of study in km<sup>2</sup>  
**DATE\_STUDY\_ADDED** Date that the study was added to the database  
**ABUNDANCE\_TYPE** Type of abundance, i.e. count  
**BIOMASS\_TYPE** Type of biomass, i.e. weight  
**SAMPLE\_DESC** Concatenation of descriptors comprising the unique sampling event

**Source**

<<https://biotime.st-andrews.ac.uk/download.php>>

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getAlphaMetrics	<i>Alpha diversity metrics</i>
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## Description

Calculates a set of standard alpha diversity metrics

## Usage

```
getAlphaMetrics(x, measure)
```

## Arguments

x	(data.frame) BioTIME data table in the format of the output of the <a href="#">gridding</a> function and/or <a href="#">resampling</a> function.
measure	(character) chosen currency defined by a single column name.

## Details

The function `getAlphaMetrics` computes nine alpha diversity metrics for a given community data frame, where `measure` is a character input specifying the abundance or biomass field used for the calculations. For each row of the data frame with data, `getAlphaMetrics` calculates the following metrics:

- Species richness (S) as the total number of species in each year with currency > 0.
- Numerical abundance (N) as the total currency (sum) in each year (either total abundance or total biomass).
- Maximum Numerical abundance (maxN) as the highest currency value reported in each year.
- Shannon or Shannon–Weaver index is calculated as  $\sum_i p_i \log_b p_i$ , where  $p_i$  is the proportional abundance of species  $i$  and  $b$  is the base of the logarithm (natural logarithms), while exponential Shannon is given by  $\exp(\text{Shannon})$ .
- Simpson's index is calculated as  $1 - \sum p_i^2$ , while Inverse Simpson as  $1 / \sum p_i^2$ .
- McNaughton's Dominance is calculated as the sum of the  $p_i$  of the two most abundant species.
- Probability of intraspecific encounter or PIE is calculated as  $\left(\frac{N}{N-1}\right) \left(1 - \sum_{i=1}^S \pi_i^2\right)$ .

Note that the input data frame needs to be in the format of the output of the [gridding](#) function and/or [resampling](#) functions, which includes keeping the default BioTIME data column names. If such columns are not found an error is issued and the computations are halted.

## Value

Returns a data frame with results for species richness (S), numerical abundance (N), maximum numerical abundance (maxN), Shannon Index (Shannon), Exponential Shannon (expShannon), Simpson's Index (Simpson), Inverse Simpson (InvSimpson), Probability of intraspecific encounter (PIE) and McNaughton's Dominance (DomMc) for each year and assemblageID.

## Examples

```
x <- data.frame(
  resamp = 1L,
  YEAR = rep(rep(2010:2015, each = 4), times = 4),
  Species = c(replicate(n = 8L, sample(letters, 24L, replace = FALSE))),
  ABUNDANCE = rpois(24 * 8, 10),
  assemblageID = rep(LETTERS[1L:8L], each = 24)
)
res <- getAlphaMetrics(x, measure = "ABUNDANCE")
```

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getBetaMetrics	<i>Beta diversity metrics</i>
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## Description

Calculates a set of standard beta diversity metrics

## Usage

```
getBetaMetrics(x, measure)
```

## Arguments

x	(data.frame) BioTIME data table in the format of the output of the <a href="#">gridding</a> function and/or <a href="#">resampling</a> functions.
measure	(character) chosen currency defined by a single column name.

## Details

The function `getBetaMetrics` computes three beta diversity metrics for a given community data frame, where `measure` is a character input specifying the abundance or biomass field used for the calculations. `getBetaMetrics` calls the [vegdist](#) function which calculates for each row the following metrics: Jaccard dissimilarity (`method = "jaccard"`), Morisita-Horn dissimilarity (`method = "horn"`) and Bray-Curtis dissimilarity (`method = "bray"`). Here, the dissimilarity metrics are calculated against the baseline year of each assemblage time series i.e. the first year of each time series. Note that the input data frame needs to be in the format of the output of the [gridding](#) and/or [resampling](#) functions, which includes keeping the default BioTIME data column names. If such columns are not found an error is issued and the computations are halted.

## Value

Returns a `data.frame` with results for Jaccard dissimilarity (`JaccardDiss`), Morisita-Horn dissimilarity (`MorisitaHornDiss`), and Bray-Curtis dissimilarity (`BrayCurtisDiss`) for each year and assemblageID.

**Examples**

```
x <- data.frame(
  resamp = 1L,
  YEAR = rep(rep(2010:2015, each = 4), times = 4),
  Species = c(replicate(
    n = 8L,
    sample(letters, 24L, replace = FALSE))),
  ABUNDANCE = rpois(24 * 8, 10),
  assemblageID = rep(LETTERS[1L:8L], each = 24)
)

res <- getBetaMetrics(x, measure = "ABUNDANCE")
```

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getLinearRegressions    *Get Linear Regressions BioTIME*

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**Description**

Fits linear regression models to [getAlphaMetrics](#) or [getBetaMetrics](#) outputs

**Usage**

```
getLinearRegressions(x, divType, pThreshold = 0.05)
```

**Arguments**

x	( <code>'data.frame'</code> ) BioTIME data table in the format of the output of <a href="#">getAlphaMetrics</a> or <a href="#">getBetaMetrics</a> functions
divType	( <code>'character'</code> ) string specifying the nature of the metrics in the data; either <code>'divType = "alpha"'</code> or <code>'divType = "beta"'</code> are supported
pThreshold	( <code>'numeric'</code> ) P-value threshold for statistical significance

**Details**

The function `'getLinearRegressions'` fits simple linear regression models (see [lm](#) for details) for a given output (`'data'`) of either [getAlphaMetrics](#) or [getBetaMetrics](#) function. `'divType'` needs to be specified in agreement with x. The typical model has the form `'metric ~ year'`. Note that assemblages with less than 3 time points and/or single species time series are removed.

**Value**

Returns a single long `'data.frame'` with results of linear regressions (slope, p-value, significance, intercept) for each `'assemblageID'`.

## Examples

```
library(BioTImEr)
x <- data.frame(
  resamp = 1L,
  YEAR = rep(rep(2010:2015, each = 4), times = 4),
  Species = c(replicate(n = 8L * 6L, sample(letters[1L:10L], 4L, replace = FALSE))),
  ABUNDANCE = rpois(24 * 8, 10),
  assemblageID = rep(LETTERS[1L:8L], each = 24)
)
alpham <- getAlphaMetrics(x, "ABUNDANCE")
getLinearRegressions(x = alpham, divType = "alpha", pThreshold = 0.01)
betam <- getBetaMetrics(x = x, "ABUNDANCE")
getLinearRegressions(x = betam, divType = "beta")
```

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gridding

gridding *BioTIME* data

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## Description

grids BioTIME data into a discrete global grid based on the location of the samples (latitude/longitude).

## Usage

```
gridding(meta, btf, res = 12, resByData = FALSE)
```

## Arguments

meta	(data.frame) BioTIME metadata.
btf	(data.frame) BioTIME data.
res	(integer) cell resolution. Must be in the range [0,30]. Larger values represent finer resolutions. Default: 12 (~96 sq km). Passed to <a href="#">dgconstruct</a> .
resByData	(logical) FALSE by default. If TRUE, the function <a href="#">dg_closest_res_to_area</a> is called to adapt 'res' to the data extent.

## Details

Each BioTIME study contains distinct samples which were collected with a consistent methodology over time, and each with unique coordinates and date. These samples can be fixed plots (i.e. SL or 'single-location' studies where measures are taken from a set of specific georeferenced sites at any given time) or wide-ranging surveys, transects, tows, and so on (i.e. ML or 'multi-location' studies where measures are taken from multiple sampling locations over large extents that may or may not align from year to year, see [runResampling](#)). [gridding](#) is a function designed to deal with the issue of varying spatial extent between studies by using a global grid of hexagonal cells derived from [dgconstruct](#) and assigning the individual samples to the cells across the grid based on its latitude and longitude. Specifically, each sample is assigned a different combination of study ID and grid cell resulting in a unique identifier for each assemblage time series within each cell (assemblageID).

This allows for the integrity of each study and each sample to be maintained, while large extent studies are split into local time series at the grid cell level. By default meta represents a long form data frame containing the data information for BioTIME studies and btf is a data frame containing long form data from a main BioTIME query (see Example). `res` defines the global grid cell resolution, thus determining the size of the cells (see `vignette("dggridR")`). `res = 12` was found to be the most appropriate value when working on the whole BioTIME database (corresponding to ~96 km<sup>2</sup> cell area), but the user can define their own grid resolution (e.g. `res = 14`, or when `resbyData = TRUE` allow the function to find the best `res` based on the average study extent).

### Value

Returns a 'data.frame', with selected columns from the btf and meta data frames, an extra integer column called 'cell' and two character columns called 'StudyMethod' and 'assemblageID' (concatenation of study\_ID and cell).

### Examples

```
library(BioTIMEr)
gridded_data <- gridding(BTsubset_meta, BTsubset_data)
```

---

resampling

*Rarefy BioTIME data to an equal number of samples per year*

---

### Description

Takes the output of `gridding` and applies sample-based rarefaction to standardise the number of samples per year within each cell-level time series (i.e. assemblageID).

### Usage

```
resampling(x, measure, resamps = 1L, conservative = FALSE)
```

### Arguments

<code>x</code>	(data.frame) BioTIME gridded data to be resampled (in the format of the output of the <code>gridding</code> function).
<code>measure</code>	(character) currency to be retained during the sample-based rarefaction. Can be either defined by a single column name or a vector of two or more column names.
<code>resamps</code>	(integer) number of repetitions. Default is 1.
<code>conservative</code>	(logical). FALSE by default. If TRUE, whenever a NA is found in the measure field(s), the whole sample is removed instead of the missing observations only.

## Details

Sample-based rarefaction prevents temporal variation in sampling effort from affecting diversity estimates (see Gotelli N.J., Colwell R.K. 2001 Quantifying biodiversity: procedures and pitfalls in the measurement and comparison of species richness. Ecology Letters 4(4), 379-391) by selecting an equal number of samples across all years in a time series. `resampling` counts the number of unique samples taken in each year (sampling effort), identifies the minimum number of samples across all years, and then uses this minimum to randomly resample each year down to that number. Thus, standardising the sampling effort between years, standard biodiversity metrics can be calculated based on an equal number of samples (e.g. using `getAlphaMetrics`, `getAlphaMetrics`). `measure` is a character input specifying the chosen currency to be used during the sample-based rarefaction. It can be a single column name or a vector of two or more column names - e.g. for BioTIME, `measure="ABUNDANCE"`, `measure="BIOMASS"` or `measure = c("ABUNDANCE", "BIOMASS")`.

By default, any observations with NA within the currency field(s) are removed. You can choose to remove the full sample where such observations are present by setting `conservative` to `TRUE`. `resamps` can be used to define multiple iterations, effectively creating multiple alternative datasets as in each iteration different samples will be randomly selected for the years where number of samples > minimum. Note that the function always returns a single data frame, i.e. if `resamps > 1`, the returned data frame is the result of individual data frames concatenated together, one from each iteration identified by a numerical unique identifier `1:resamps`.

## Value

Returns a single long form data.frame containing the total currency or currencies of interest (sum) for each species in each year within each rarefied time series (i.e. `assemblageID`). An extra integer column called `resamp` indicates the specific iteration.

## Examples

```
library(BioTIMEr)
set.seed(42)
x <- gridding(BTsubset_meta, BTsubset_data)
resampling(x, measure = "BIOMASS")
resampling(x, measure = "ABUNDANCE")
resampling(x, measure = c("ABUNDANCE", "BIOMASS"))
```

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scale_color_biotime	<i>Scale construction for ggplot use</i>
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## Description

Scale construction for ggplot use

Scale construction for filling in ggplot

**Usage**

```
scale_color_biotime(palette = "realms", discrete = TRUE, reverse = FALSE, ...)
```

```
scale_colour_biotime(palette = "realms", discrete = TRUE, reverse = FALSE, ...)
```

```
scale_fill_biotime(palette = "realms", discrete = TRUE, reverse = FALSE, ...)
```

**Arguments**

palette	One of: 'realms', 'gradient', 'cool', 'warm', default to 'realms'.
discrete	See Details. default to 'FALSE'
reverse	Default to 'FALSE'
...	Passed to <a href="#">discrete_scale</a> or <a href="#">scale_color_gradient</a>

**Details**

USAGE NOTE: Remember to change these arguments when plotting colours continuously.

**Value**

If discrete is TRUE, the function returns a colour palette produced by [discrete\\_scale](#) and if discrete is FALSE, the function returns a colour palette produced by [scale\\_color\\_gradient](#).

If discrete is TRUE, the function returns a colour palette produced by [discrete\\_scale](#) and if discrete is FALSE, the function returns a colour palette produced by [scale\\_color\\_gradient](#).

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