# Package: BioFTF (via r-universe)

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**Type** Package

**Title** Biodiversity Assessment Using Hill-Number Functional Tools

**Version** 3.0.0

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**Description** Tools for biodiversity assessment through Hill-number diversity profiles treated as functions of the order q. The package computes the profiles of Hill (1973) <doi:10.2307/1934352>, their analytical first and second derivatives, curvature, radius of curvature, arc length, cumulative integral functions, profile areas, area-based rankings and relative changes over time, together with static and interactive three-dimensional biodiversity surfaces. The functional approach follows Di Battista, Fortuna and Maturo (2017) <doi:10.1016/j.ecolind.2016.10.032>, Maturo and Di Battista (2018) <doi:10.1016/j.ecolind.2017.08.016> and Maturo (2018) <doi:10.1016/j.ecolind.2018.03.013>.

**License** GPL (>= 2)

**Depends** R (>= 3.6.0)

**Imports** graphics, grDevices

**Suggests** plotly, knitr, rmarkdown, testthat (>= 3.0.0)

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`BioFTF-package` *Biodiversity Assessment Using Hill-Number Functional Tools*

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## Description

Hill-number diversity profiles are treated as functions of the order $q$ and summarised through functional tools: derivatives, curvature, radius of curvature, arc length, cumulative integral functions, areas, rankings, and biodiversity surfaces over time.

## Details

Rows of the input matrix are communities, sites, or time points. Columns are species. Absolute and relative non-negative abundances are both accepted, because every row is rescaled to sum to one.

The main functions are `hill_profile` for the profiles, `hill_derivative`, `hill_curvature`, `hill_area`, `hill_cum`, `hill_arc` and `hill_ranking` for the functional tools, and `hill_surface_plot` and `hill_surface_compare` for static or rotatable three-dimensional surfaces.

Versions 1.x of the package computed the same functional tools on the Patil-Taillie beta profile. The relation between the two profiles is given in `hill_profile`. The function names of versions 1.x are still available but deprecated; see `BioFTF-deprecated`.

## Author(s)

Fabrizio Maturo, Francesca Fortuna, Tonio Di Battista.

## References

Di Battista, T., Fortuna, F. and Maturo, F. (2017). BioFTF: An R package for biodiversity assessment with the functional data analysis approach. *Ecological Indicators*, 73, 726–732. doi:10.1016/j.ecolind.2016.10.032

Maturo, F. and Di Battista, T. (2018). A functional approach to Hill's numbers for assessing changes in species variety of ecological communities over time. *Ecological Indicators*, 84, 70–81. doi:10.1016/j.ecolind.2017.08.016

Maturo, F. (2018). Unsupervised classification of ecological communities ranked according to their biodiversity patterns via a functional principal component decomposition of Hill's numbers integral functions. *Ecological Indicators*, 90, 305–315. doi:10.1016/j.ecolind.2018.03.013

Hill, M. O. (1973). Diversity and evenness: a unifying notation and its consequences. *Ecology*, 54(2), 427–432. doi:10.2307/1934352

Patil, G. P. and Taillie, C. (1982). Diversity as a concept and its measurement. *Journal of the American Statistical Association*, 77(379), 548–561. doi:10.1080/01621459.1982.10477845

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`datirel` *Data Summaries and Wrappers*

---

## Description

Relative abundances, species summaries, a wrapper that returns all the functional tools, and a wrapper that saves the profile plots to a PDF file.

## Usage

```
datirel(x)
summary_species(x)
summary_species_relative(x)
alltools(x, from = 0, to = 2, n = 101)
export_plots(x, file, from = 0, to = 2, n = 101)
```

## Arguments

| | |
|---|---|
| `x` | A numeric matrix or data frame of non-negative abundances. Rows are communities, sites, or time points; columns are species. |
| `from`, `to` | Finite lower and upper endpoints of the grid of orders. |
| `n` | Number of equally spaced orders. |
| `file` | Path of the PDF file to create. |

## Value

`datirel` returns the matrix of relative abundances. `summary_species` returns a data frame with richness, total abundance, and smallest and largest abundance of each community, zeros included; `summary_species_relative` returns the same summaries for relative abundances. `alltools` returns a list with the relative abundances, the species summary, and the output of `hill_profile`, `hill_first_derivative`, `hill_second_derivative`, `hill_curvature`, `hill_radius`, `hill_area`, `hill_cum`, `hill_arc`, and `hill_ranking`. `export_plots` writes one page for each of profile, first derivative, second derivative, curvature, radius of curvature, and cumulative integral function, and invisibly returns `file`.

## Examples

```
x <- matrix(c(3, 5, 5, 2, 1,
              2, 6, 8, 5, 1,
              7, 3, 2, 1, 0),
            nrow = 3, byrow = TRUE)
datirel(x)
summary_species(x)
summary_species_relative(x)
```

```
res <- alltools(x, from = 0, to = 5, n = 251)
names(res)
res$ranking

out <- file.path(tempdir(), "BioFTF-plots.pdf")
export_plots(x, file = out)
unlink(out)
```

---

hill_derivative *Functional Tools Derived from Hill-Number Profiles*

---

## Description

Derivatives, curvature, radius of curvature, cumulative integral functions, areas, arc lengths, rankings, and changes between consecutive rows, all computed from Hill-number profiles.

## Usage

```
hill_derivative(x, order = 1, from = 0, to = 2, n = 101,
                domain = NULL, allow_negative = FALSE)
hill_first_derivative(x, from = 0, to = 2, n = 101,
                      domain = NULL, allow_negative = FALSE)
hill_second_derivative(x, from = 0, to = 2, n = 101,
                       domain = NULL, allow_negative = FALSE)
hill_curvature(x, from = 0, to = 2, n = 101,
               domain = NULL, allow_negative = FALSE)
hill_radius(x, from = 0, to = 2, n = 101,
            domain = NULL, allow_negative = FALSE)
hill_area(x, from = 0, to = 2, n = 101, domain = NULL,
          baseline = 0, allow_negative = FALSE)
hill_cum(x, from = 0, to = 2, n = 101, domain = NULL,
         baseline = 0, allow_negative = FALSE)
hill_arc(x, from = 0, to = 2, n = 101,
         domain = NULL, allow_negative = FALSE)
hill_ranking(x, from = 0, to = 2, n = 101, domain = NULL,
             baseline = 0, allow_negative = FALSE)
hill_total_change(x, from = 0, to = 2, n = 101, domain = NULL,
                  baseline = 0, allow_negative = FALSE)
hill_derivative_plot(x, order = 1, from = 0, to = 2, n = 101,
                     domain = NULL, allow_negative = FALSE,
                     legend = "bottomright", ...)
hill_curvature_plot(x, from = 0, to = 2, n = 101,
                    domain = NULL, allow_negative = FALSE,
                    legend = "topright", ...)
hill_radius_plot(x, from = 0, to = 2, n = 101,
                 domain = NULL, allow_negative = FALSE,
                 legend = "topleft", ...)
```

```
hill_cum_plot(x, from = 0, to = 2, n = 101, domain = NULL,
              baseline = 0, allow_negative = FALSE,
              legend = "topleft", ...)
```

## Arguments

| | |
|---|---|
| `x` | A numeric matrix or data frame of non-negative abundances. Rows are communities, sites, or time points; columns are species. |
| `order` | Derivative order, 1 or 2. |
| `from`, `to` | Finite lower and upper endpoints of the grid of orders. |
| `n` | Number of equally spaced orders used when `domain = NULL`. |
| `domain` | Optional numeric vector of finite orders. Areas, cumulative integrals, and arc lengths require at least two strictly increasing values. |
| `baseline` | Constant subtracted from the profile before integration. With `baseline = 1`, the smallest value a Hill number can take, the area of a community with a single species is zero. |
| `allow_negative` | Logical. If `FALSE` (default), negative orders raise an error. See `hill_profile`. |
| `legend` | Position of the legend, as accepted by `legend`, or `NULL` for no legend. |
| `...` | Further arguments passed to `matplot`. `hill_radius_plot` uses a logarithmic vertical axis. |

## Details

*Derivatives.* First and second derivatives are analytical. Writing $L(q) = \log \sum_i p_i^q$ and $g(q) = L(q)/(1-q)$, the Hill number is $D = \exp(g)$, so that $D' = Dg'$ and $D'' = D(g'^2 + g'')$. The derivatives of $L$ are the mean and the variance of $\log p_i$ under the weights $p_i^q / \sum_j p_j^q$. Near $q = 1$, where the closed form is numerically unstable, a Taylor expansion is used. The derivatives therefore do not depend on the spacing of the grid.

*Curvature and radius.* The curvature is $|D''|/(1 + D'^2)^{3/2}$ and the radius of curvature is its reciprocal. Where the curvature is numerically zero (below $10^{-8}$), as for a community whose species are equally abundant or far along the flat tail of a profile, the radius is returned as `NA`.

*Area and cumulative integral.* `hill_cum` returns $\int_{q_1}^{q} (D(u) - b)\, du$, with $b$ the baseline, at each order of the grid, and `hill_area` its value at the last order. Both use the trapezoidal rule, whose error decreases with the square of the grid spacing. With the default `n = 101` the relative error of the area is of order $10^{-4}$ on $[0, 2]$ and grows with wider domains, so `n` should be increased together with `to`.

*Arc length.* `hill_arc` returns the length of the polygonal line through the profile. It is bounded below by `to - from`, attained by a flat profile. The arc length depends on the units of both axes.

*Ranking.* `hill_ranking` reports the Hill numbers of order 0, 1, and 2 together with area and arc length. `area_rank` is 1 for the largest area. `arc_rank` is 1 for the shortest arc, that is, for the flattest profile; it orders communities by how little the profile changes along the domain and is not a ranking by diversity. A larger area does not imply that one profile lies above the other at every order: when two profiles cross, the communities are not ordered in an intrinsic sense and the area ranking depends on the chosen domain. As `to` increases, the area is progressively dominated by $D(\infty) = 1/\max_i p_i$.

*Change.* `hill_total_change` compares the area of each row with the area of the previous one, which is meaningful when rows are ordered, for instance in time.

## Value

hill_derivative, hill_first_derivative, hill_second_derivative, hill_curvature, hill_radius, and hill_cum return matrices with orders in rows and communities in columns; the exact orders are stored in the attribute "q". hill_area and hill_arc return one-column data frames with one row per community. hill_ranking returns a data frame with columns richness, shannon, simpson, hill_area, area_rank, arc_length, and arc_rank. hill_total_change returns a data frame with columns from, to, area_from, area_to, absolute_change, and relative_change. Plot functions return the plotted matrix invisibly.

## References

Di Battista, T., Fortuna, F. and Maturo, F. (2017). BioFTF: An R package for biodiversity assessment with the functional data analysis approach. *Ecological Indicators*, 73, 726–732. doi:10.1016/j.ecolind.2016.10.032

Maturo, F. and Di Battista, T. (2018). A functional approach to Hill's numbers for assessing changes in species variety of ecological communities over time. *Ecological Indicators*, 84, 70–81. doi:10.1016/j.ecolind.2017.08.016

Maturo, F. (2018). Unsupervised classification of ecological communities ranked according to their biodiversity patterns via a functional principal component decomposition of Hill's numbers integral functions. *Ecological Indicators*, 90, 305–315. doi:10.1016/j.ecolind.2018.03.013

## See Also

hill_profile, hill_surface_plot.

## Examples

```
x <- matrix(c(54, 20, 17,  6,  3,
              25, 25, 25, 25,  0,
              35, 35, 30,  0,  0),
            nrow = 3, byrow = TRUE)
rownames(x) <- c("A", "B", "C")

## Derivatives at selected orders.
hill_first_derivative(x, domain = c(0, 0.5, 1, 2))
hill_second_derivative(x, domain = c(0, 0.5, 1, 2))
head(hill_curvature(x))

## Area, cumulative integral function, arc length, and ranking on [0, 2].
hill_area(x)
tail(hill_cum(x))
hill_arc(x)
hill_ranking(x)

## Area above the minimum value of a Hill number on a wider domain.
hill_area(x, from = 0, to = 10, n = 1001, baseline = 1)

## Plots.
hill_derivative_plot(x, order = 1)
hill_curvature_plot(x)
```

```
hill_cum_plot(x, from = 0, to = 10, n = 501)

## Change in area between consecutive surveys.
surveys <- matrix(c(40, 30, 15, 10,  5,
                    35, 30, 18, 12,  5,
                    30, 28, 20, 15,  7,
                    25, 25, 22, 18, 10,
                    20, 24, 24, 20, 12,
                    15, 22, 25, 22, 16),
                  nrow = 6, byrow = TRUE)
rownames(surveys) <- 2018:2023
hill_total_change(surveys)
```

---

`hill_profile` *Hill-Number Diversity Profiles*

---

## Description

Compute and plot Hill-number diversity profiles for ecological communities, sites, or time points.

## Usage

```
hill_profile(x, from = 0, to = 2, n = 101, domain = NULL,
             allow_negative = FALSE)
hill(x, from = 0, to = 2, n = 101, domain = NULL,
     allow_negative = FALSE)
hill_profile_plot(x, from = 0, to = 2, n = 101, domain = NULL,
                  allow_negative = FALSE, legend = "topright", ...)
hill_plot(x, from = 0, to = 2, n = 101, domain = NULL,
          allow_negative = FALSE, legend = "topright", ...)
```

## Arguments

| | |
|---|---|
| `x` | A numeric matrix or data frame of non-negative abundances. Rows are communities, sites, or time points; columns are species. A numeric vector is treated as a single community. |
| `from`, `to` | Finite lower and upper endpoints of the grid of orders. The default is $0 \leq q \leq 2$. Larger upper endpoints, such as 10, 20, or 100, extend the profile towards the dominance end. |
| `n` | Number of equally spaced orders between `from` and `to`, used when `domain = NULL`. |
| `domain` | Optional numeric vector of orders at which the profile is evaluated. When supplied, `from`, `to` and `n` are ignored. It may contain a single order and may contain `Inf`. |
| `allow_negative` | Logical. If `FALSE` (default), negative orders raise an error. See Details. |
| `legend` | Position of the legend, as accepted by `legend`, or `NULL` for no legend. |
| `...` | Further arguments passed to `matplot`. |

## Details

For relative abundances $p_1, \ldots, p_S$, the Hill number of order $q$ is

$$D(q) = \left( \sum_{i:p_i>0} p_i^q \right)^{1/(1-q)}, \qquad q \neq 1,$$

with $D(1) = \exp(-\sum_i p_i \log p_i)$ defined by continuity. $D(0)$ is species richness, $D(1)$ is the exponential of Shannon entropy, $D(2)$ is the inverse Simpson concentration, and $D(\infty) = 1/\max_i p_i$ is the reciprocal of the Berger-Parker dominance. $D(q)$ is expressed in effective numbers of species and is non-increasing in $q$; it is constant only when all the species present are equally abundant.

*Range of the order.* Most of the variation of the profile lies between $q = 0$ and $q = 2$, which is the default. Increasing `to` adds the part of the curve that converges to $D(\infty)$; the limit itself is obtained with `domain = Inf`.

*Negative orders.* For $q < 0$ the Hill number is larger than species richness, so it can no longer be read as an effective number of species out of the $S$ observed, and it is driven by the smallest positive abundances: $D(-\infty) = 1/\min_i p_i$. These are the abundances most affected by sampling error, and the value changes abruptly when a rare species goes undetected. Negative orders are therefore rejected unless `allow_negative = TRUE`.

*Relation with the Patil-Taillie profile.* Versions 1.x of the package used the beta profile of Patil and Taillie (1982),

$$\Delta(\beta) = \frac{1 - \sum_i p_i^{\beta+1}}{\beta}, \qquad -1 \leq \beta \leq 1,$$

which equals $S - 1$ at $\beta = -1$, Shannon entropy as $\beta \to 0$, and the Gini-Simpson index at $\beta = 1$. With $q = \beta + 1$ the two profiles are linked by

$$\Delta(\beta) = \frac{1 - D(q)^{-\beta}}{\beta},$$

so the interval $[-1, 1]$ for $\beta$ corresponds to $[0, 2]$ for $q$. The two profiles induce the same ordering of communities at each order, but they are measured on different scales: the beta profile is an entropy, whereas the Hill number is its numbers equivalent. Derivatives, curvature, arc length, and areas are not invariant to this transformation, so functional tools computed on the two profiles differ and may rank communities differently.

## Value

`hill_profile` and `hill` return a matrix with orders in rows and communities in columns. The exact orders are stored in the attribute `"q"`. Plot functions return the profile invisibly.

## References

Hill, M. O. (1973). Diversity and evenness: a unifying notation and its consequences. *Ecology*, 54(2), 427–432. doi:10.2307/1934352

Patil, G. P. and Taillie, C. (1982). Diversity as a concept and its measurement. *Journal of the American Statistical Association*, 77(379), 548–561. doi:10.1080/01621459.1982.10477845

Di Battista, T., Fortuna, F. and Maturo, F. (2017). BioFTF: An R package for biodiversity assessment with the functional data analysis approach. *Ecological Indicators*, 73, 726–732. doi:10.1016/j.ecolind.2016.10.032

Maturo, F. and Di Battista, T. (2018). A functional approach to Hill's numbers for assessing changes in species variety of ecological communities over time. *Ecological Indicators*, 84, 70–81. doi:10.1016/j.ecolind.2017.08.016

Maturo, F. (2018). Unsupervised classification of ecological communities ranked according to their biodiversity patterns via a functional principal component decomposition of Hill's numbers integral functions. *Ecological Indicators*, 90, 305–315. doi:10.1016/j.ecolind.2018.03.013

## See Also

hill_derivative, hill_area, hill_surface_plot.

## Examples

```
x <- matrix(c(54, 20, 17,  6,  3,
              25, 25, 25, 25,  0,
              35, 35, 30,  0,  0,
              70, 10, 10,  5,  5),
            nrow = 4, byrow = TRUE)
rownames(x) <- c("A", "B", "C", "D")

## Default grid: 101 orders between 0 and 2.
p <- hill_profile(x)
head(p)

## Selected orders, including the limit for q tending to infinity.
hill_profile(x, domain = c(0, 1, 2, 5, 10, 100, Inf))

## A wider domain.
hill_profile_plot(x, from = 0, to = 10, n = 201)

## Negative orders exceed species richness.
hill_profile(x, domain = c(-1, 0), allow_negative = TRUE)
```

---

# hill_surface *Hill-Number Biodiversity Surfaces*

---

## Description

Compute, plot, and compare surfaces obtained by placing the Hill-number profiles of ordered rows side by side. Plots are either rotatable or static.

## Usage

```
hill_surface(x, from = 0, to = 2, n = 101, domain = NULL,
             time = NULL, allow_negative = FALSE)
hill_surface_plot(x, from = 0, to = 2, n = 101, domain = NULL,
                  time = NULL, plot = c("interactive", "static"),
                  allow_negative = FALSE,
                  xlab = "Order q", ylab = "Time",
                  zlab = "Hill number",
                  main = "Hill-number surface",
                  theta = 40, phi = 25, ...)
hill_surface_compare(x, y, from = 0, to = 2, n = 101,
                     domain = NULL, time = NULL,
                     labels = c("Surface 1", "Surface 2"),
                     plot = c("interactive", "static"),
                     mode = c("overlay", "difference"),
                     allow_negative = FALSE,
                     main = "Comparison of Hill-number surfaces",
                     theta = 40, phi = 25, ...)
```

## Arguments

| | |
|---|---|
| `x`, `y` | Numeric abundance matrices or data frames with at least two rows. Rows are ordered time points or sites along a gradient; columns are species. `x` and `y` must have the same number of rows; the species may differ. |
| `from`, `to` | Finite lower and upper endpoints of the grid of orders. |
| `n` | Number of equally spaced orders used when `domain = NULL`. |
| `domain` | Optional vector of finite, strictly increasing orders. |
| `time` | Optional numeric vector of strictly increasing values, one for each row. If `NULL`, row names are used when they can be read as increasing numbers, for example years; otherwise rows are numbered from 1. |
| `plot` | `"interactive"` (default) returns a **plotly** surface that can be rotated and zoomed in the viewer or in a browser. `"static"` draws a perspective plot on the current graphics device. |
| `allow_negative` | Logical. If `FALSE` (default), negative orders raise an error. See `hill_profile`. |
| `xlab`, `ylab`, `zlab`, `main` | Axis labels and title. |
| `theta`, `phi` | Viewing angles of the static plot, as in `persp`. |
| `labels` | Names of the two surfaces. |
| `mode` | `"overlay"` shows the two surfaces together (interactive) or side by side on a common vertical scale (static). `"difference"` shows the pointwise difference `y` minus `x`. |
| `...` | Further arguments passed to `plot_ly` for interactive plots or to `persp` for static plots. |

## Details

The surface has the order $q$ on one horizontal axis, time on the other, and the Hill number on the vertical axis. Profiles are observed only at the rows of the data: between two consecutive rows the surface is a linear interpolation drawn for display, not an estimate of diversity at intermediate times.

Interactive plots require the suggested package **plotly**. In the static plot the colour of each facet follows the height of the surface, and lines mark the observed profiles and a subset of the orders.

## Value

`hill_surface` returns a list with components `q` (orders), `time`, and `z`, a matrix of Hill numbers with orders in rows and time points in columns. With `plot = "interactive"`, `hill_surface_plot` and `hill_surface_compare` return a **plotly** object. With `plot = "static"`, `hill_surface_plot` invisibly returns the surface, and `hill_surface_compare` invisibly returns a list with the two surfaces and their difference.

## References

Maturo, F. and Di Battista, T. (2018). A functional approach to Hill's numbers for assessing changes in species variety of ecological communities over time. *Ecological Indicators*, 84, 70–81. doi:10.1016/j.ecolind.2017.08.016

## See Also

`hill_profile`, `hill_total_change`.

## Examples

```
years <- 2018:2027
x <- matrix(c(40, 35, 15,  5,  5,  0,
              38, 34, 16,  6,  4,  2,
              35, 30, 18,  8,  5,  4,
              30, 28, 20, 10,  7,  5,
              25, 26, 21, 12,  9,  7,
              20, 24, 22, 14, 11,  9,
              16, 21, 23, 16, 13, 11,
              12, 18, 24, 18, 15, 13,
               9, 15, 24, 20, 17, 15,
               6, 12, 23, 22, 19, 18),
            nrow = length(years), byrow = TRUE)
rownames(x) <- years

## A second set of surveys on the same years.
y <- x
y[, 1] <- x[, 1] + 15
y[, 6] <- x[, 6] + 4

## Surface between q = 0 and q = 10.
s <- hill_surface(x, from = 0, to = 10, n = 121)
str(s)
```

```
## Static figures.
hill_surface_plot(x, from = 0, to = 10, n = 121, plot = "static")
hill_surface_plot(x, from = 0, to = 10, n = 121, plot = "static",
                  theta = 130, phi = 20,
                  main = "Hill-number surface, 2018-2027")
hill_surface_compare(x, y, from = 0, to = 10, n = 121,
                     labels = c("Area 1", "Area 2"), plot = "static")
hill_surface_compare(x, y, from = 0, to = 10, n = 121,
                     labels = c("Area 1", "Area 2"), plot = "static",
                     mode = "difference")

## Rotatable figures.
if (interactive() && requireNamespace("plotly", quietly = TRUE)) {
  hill_surface_plot(x, from = 0, to = 10, n = 121)
  hill_surface_compare(x, y, from = 0, to = 10, n = 121,
                       labels = c("Area 1", "Area 2"))
  hill_surface_compare(x, y, from = 0, to = 10, n = 121,
                       labels = c("Area 1", "Area 2"),
                       mode = "difference")
}
```

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