

# Package ‘BioFTF’

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**Title** Biodiversity Assessment Using Functional Tools

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**Depends** R (>= 3.1.0)

**Suggests** MASS

**Description** The main drawback of the most common biodiversity indices is that different measures may lead to different rankings among communities. This instrument overcomes this limit using some functional tools with the diversity profiles. In particular, the derivatives, the curvature, the radius of curvature, the arc length, and the surface area are proposed. The goal of this method is to interpret in detail the diversity profiles and obtain an ordering between different ecological communities on the basis of diversity. In contrast to the typical indices of diversity, the proposed method is able to capture the multidimensional aspect of biodiversity, because it takes into account both the evenness and the richness of the species present in an ecological community.

**License** GPL (>= 2)

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**BugReports** f.maturo@unich.it

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alltools	<i>Apply the whole analysis to the dataset.</i>
----------	---

---

## Description

This function provides the derivatives, the curvature, the radius of curvature and the arc length of diversity profiles. Moreover, it computes the surface area under the beta profile and ranks the communities.

## Usage

```
alltools(x,n)
```

## Arguments

- |   |   |
|---|---|
| x | A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.  |
| n | The number of points of the domain $[-1,1]$ that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval $[3,10000]$ because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is $n=20$ . |

## Author(s)

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**Source**

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PARAMETRIC FUNCTIONAL ANALYSIS OF VARIANCE FOR FISH BIODIVERSITY ASSESSMENT - T. Di Battista, F. Fortuna, F. Mauro - Journal of Environmental Informatics. Special issue of Marine and Freshwater Environmental Engineering and Management, Journal of Environmental Informatics. In press.

**Examples**

```
#example 1
x=matrix(c(3,5,5,2,1,2,6,8,5,1),2,5)
x
alltools(x,20)
```

#Some examples expressed by relative abundance:

```
#example 2
x=matrix(c(0.3,0.5,0.1,0.05,0.05,0.25,0.25,0.25,0.25,0,0.35,0.3,0.35,0,0),3,5)
x
alltools(x,20)
```

```
#example 3
x=matrix(runif(1000),10,100)
#let's consider some missing species
x[1,1:20]=0
x[2,1:40]=0
x[3,1:60]=0
x[4,1:19]=0
x
alltools(x,20)
```

```
#example 4
x=matrix(runif(100),20,5)
x[1,1:2]=0
x[2,1:3]=0
x
alltools(x,20)
```

```
#example 5
a=c(0.35,0.35,0.27,0.01,0.02)
b=c(0.54,0.20,0.17,0.06,0.03)
c=c(0.35,0.35,0.30,0,0)
d=c(0.51,0.31,0.07,0.10,0.01)
e=c(0.40,0.20,0.10,0.30,0)
x=matrix(rbind(a,b,c,d,e),5,5)
x
alltools(x,20)
```

---

 arc

---

*Compute the arc length of beta profile for each community.*


---

### Description

This function provides the arc length of beta profile for each community. The arc length is a useful tool to establish a ranking among communities with intersecting profiles and the same number of species. It represents the length of a curve if it were rectified; it is a scalar measure extremely high in case of maximum dominance, whereas it decreases in case of high evenness. Unlike the classical indices, it considers each point of the domain corresponding to a different biodiversity value. For this reason, the arc length provides a ranking rule for communities with intersecting profiles, making possible to order them without the use of graphs. This is not possible with the classical indices.

### Usage

arc(x,n)

### Arguments

- |   |  |
|---|--|
| x | A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.   |
| n | The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is n=20. |

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**Examples**

```
x=matrix(c(0.3,0.5,0.1,0.05,0.05,0.25,0.25,0.25,0.25,0,0.35,0.3,0.35,0,0),3,5)
arc(x,20)
```

---

 area

---

*Compute the area under the beta profile for each community.*


---

**Description**

This function provides the area under the beta profile for each community. In an ecological framework, the area under the profiles can be used to assess biodiversity because it can rank communities, even if they have different number of species. Indeed, in a case of maximum dominance, the area is extremely low; while in a case of evenness, it increase. The main advantage of using area is that the ordering among communities can be investigated without the analysis of a graph. It provides a scalar measure of biodiversity considering the whole domain. This is not possible with the classical indices.

**Usage**

```
area(x,n)
```

**Arguments**

- |   |  |
|---|--|
| x | A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.   |
| n | The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is n=20. |

**Examples**

```
x=matrix(c(0.3,0.5,0.1,0.05,0.05,0.25,0.25,0.25,0.25,0,0.35,0.3,0.35,0,0),3,5)
area(x,20)
```

---

beta	<i>Compute the values of beta profile for each community in every part of the beta domain.</i>
------	--

---

### Description

The matrix obtained with "beta" contains the values of diversity measures computed for each community by column and for each point of the domain. This matrix provides the values of diversity profile; it displays a complete picture of diversity. Indeed, the most frequently used indices of biodiversity are special cases of this function.

### Usage

beta(x,n)

### Arguments

- |   |  |
|---|--|
| x | A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.   |
| n | The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is n=20. |

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## Examples

```
x=matrix(c(0.3,0.5,0.1,0.05,0.05,0.25,0.25,0.25,0.25,0,0.35,0.3,0.35,0,0),3,5)
beta(x,20)
```

---

betaprime

*Compute the values of the first derivative of beta profile for each community in every part of the beta domain.*

---

## Description

This function provides the values of the first derivative of beta profile. This is an essential component of functional data analysis (Ramsay and Silverman, 2005), and in an ecological framework, is useful for highlighting the characteristics of the profiles and explaining some of the variation from curve to curve. For "beta" close to -1, high absolute values for the first derivative correspond to a strong decrease of the profile; thus, a sudden decrease suggests the presence of few prevalent species in a community (dominance). On the contrary, low absolute values indicate that living organisms tend to be equally distributed among the species (evenness).

## Usage

```
betaprime(x,n)
```

## Arguments

- x            A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.
- n            The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is n=20.

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**Examples**

```
a=c(0.35,0.35,0.27,0.01,0.02)
b=c(0.54,0.20,0.17,0.06,0.03)
c=c(0.35,0.35,0.30,0,0)
d=c(0.51,0.31,0.07,0.10,0.01)
e=c(0.40,0.20,0.10,0.30,0)
x=matrix(rbind(a,b,c,d,e),5,5)
x
betaprime(x,20)
```

---

betaprime\_plot

*Plot the first derivative of the beta profile for each community.*


---

**Description**

This function provides the plot of the first derivative of the beta profile. The domain "beta" represents the sensibility to changes in the presence of rare species. This is an essential component of functional data analysis (Ramsay and Silverman, 2005), and in an ecological framework, is useful for highlighting the characteristics of the profiles and explaining some of the variation from curve to curve. For "beta" close to -1, high absolute values for the first derivative correspond to a strong decrease of the profile; thus, a sudden decrease suggests the presence of few prevalent species in a community (dominance). On the contrary, low absolute values indicate that living organisms tend to be equally distributed among the species (evenness).

**Usage**

```
betaprime_plot(x,n)
```

**Arguments**

x                    A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.



n The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is n=20.

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### Examples

```
a=c(0.35,0.35,0.27,0.01,0.02)
b=c(0.54,0.20,0.17,0.06,0.03)
c=c(0.35,0.35,0.30,0,0)
d=c(0.51,0.31,0.07,0.10,0.01)
e=c(0.40,0.20,0.10,0.30,0)
x=matrix(rbind(a,b,c,d,e),5,5)
x
betaprime_plot(x,20)
```

---

betasecond

*Compute the values of the second derivative of beta profile for each community in every part of the beta domain.*

---

### Description

This function provides the values of the second derivative of the beta profile. The second derivative represents the deceleration of the profile for any given value of "beta". For "beta" close to -1, high values of the second derivative denote high dominance because the profile tends to be extremely curved when some prevalent species are present in a community. For the interval [0,1] the second derivative tends always towards zero.

**Usage**

```
betasecond(x, n)
```

**Arguments**

- |   |  |
|---|--|
| x | A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.   |
| n | The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is n=20. |

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**Examples**

```
a=c(0.35,0.35,0.27,0.01,0.02)
b=c(0.54,0.20,0.17,0.06,0.03)
c=c(0.35,0.35,0.30,0,0)
d=c(0.51,0.31,0.07,0.10,0.01)
e=c(0.40,0.20,0.10,0.30,0)
x=matrix(rbind(a,b,c,d,e),5,5)
x
betasecond(x,20)
```

---

betasecond\_plot      *Plot the second derivative of the beta profile for each community.*

---

## Description

This function provides the plot of the second derivative of the beta profile. The domain "beta" represents the sensibility to changes in the presence of rare species. The second derivative represents the deceleration of the profile for any given value of "beta". For "beta" close to -1, high values of the second derivative denote high dominance because the profile tends to be extremely curved when some prevalent species are present in a community. For the interval [0,1] the second derivative tends always towards zero.

## Usage

```
betasecond_plot(x,n)
```

## Arguments

- x      A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.
- n      The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is n=20.

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**Examples**

```

a=c(0.35,0.35,0.27,0.01,0.02)
b=c(0.54,0.20,0.17,0.06,0.03)
c=c(0.35,0.35,0.30,0,0)
d=c(0.51,0.31,0.07,0.10,0.01)
e=c(0.40,0.20,0.10,0.30,0)
x=matrix(rbind(a,b,c,d,e),5,5)
x
betasecond_plot(x,20)

```

---

beta\_plot

*Plot the beta profile for each community.*


---

**Description**

This function provides a plot of the diversity profiles of the considered communities. The domain "beta" represents the sensibility to changes in the presence of rare species. It is a decreasing and concave upward curve showing different values of biodiversity for each value of beta. The most frequently used indices of biodiversity are special cases of this function. The diversity profile displays a complete picture of biodiversity. Its plot allows the analyst to rank different communities when the curves do not intersect. Indeed, the higher curve highlights biological populations with higher diversity and vice versa. The function tends towards a straight line, decreasing for beta values in the range -1 to 1. The profile tends to be more curved if there is a prevalence of few species over the others.

**Usage**

```
beta_plot(x,n)
```

**Arguments**

x	A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.
n	The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is n=20.

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**Examples**

```
a=c(0.35,0.35,0.27,0.01,0.02)
b=c(0.54,0.20,0.17,0.06,0.03)
c=c(0.35,0.35,0.30,0,0)
d=c(0.51,0.31,0.07,0.10,0.01)
e=c(0.40,0.20,0.10,0.30,0)
x=matrix(rbind(a,b,c,d,e),5,5)
x
beta_plot(x,20)
```

---

curvature

*Compute the values of the curvature of the beta profile function for each community in every part of the beta domain.*

---

**Description**

This function provides the values of the curvature of the beta profile for each part of the domain. The curvature reflects the community composition; in particular, if we consider communities with different numbers of species, the curvature is a good indicator of the lack of balance among species. Great levels of curvature highlights high imbalance among different species and vice-versa.

**Usage**

```
curvature(x,n)
```

**Arguments**

- x A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.
- n The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a

value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is  $n=20$ .

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### Examples

```
x=matrix(c(0.3,0.5,0.1,0.05,0.05,0.25,0.25,0.25,0.25,0,0.35,0.3,0.35,0,0),3,5)
curvature(x,20)
```

---

curvature\_plot

*Plot the curvature of the beta profiles for each community.*

---

### Description

This function provides a plot of the curvature functions of the diversity profiles for the considered communities. The domain "beta" represents the sensibility to changes in the presence of rare species. The graph of the curvature reflects the community composition; in particular, if we consider communities with different numbers of species, the curvature is a good indicator of the lack of balance among species. Great levels of curvature highlights high imbalance among different species and vice-versa.

### Usage

```
curvature_plot(x,n)
```

### Arguments

**x** A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.

n The number of points of the domain  $[-1,1]$  that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval  $[3,10000]$  because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is  $n=20$ .

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### Examples

```
x=matrix(c(0.3,0.5,0.1,0.05,0.05,0.25,0.25,0.25,0.25,0,0.35,0.3,0.35,0,0),3,5)
curvature_plot(x,20)
```

---

datirel

*Create a matrix with the relative frequencies for each community.*

---

### Description

Create a matrix with the relative frequencies for each community.

### Usage

```
datirel(x)
```

### Arguments

x A data matrix with the absolute abundance of the species.

**Examples**

```
x=matrix(c(3,5,5,2,1,2,6,8,5,1),2,5)
x
datirel(x)
```

---

export_plots	<i>Export the figures of beta profiles, derivatives, radius of curvature and curvature in a pdf file.</i>
--------------	---

---

**Description**

This function creates a pdf file with the figures of beta profiles, derivatives, radius of curvature and curvature according to the biodiversity computed using the functional tools.

**Usage**

```
export_plots(x,n)
```

**Arguments**

x	A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.
n	The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is n=20.

**Author(s)**

Fabrizio Mauro, Francesca Fortuna, Tonio Di Battista

**Source**

ENVIRONMENTAL MONITORING THROUGH FUNCTIONAL BIODIVERSITY TOOLS - T. Di Battista, F. Fortuna, F. Mauro - Ecological Indicators (2016) 60, 237-247 - online (2015). DOI: 10.1016/j.ecolind.2015.05.056.

PARAMETRIC FUNCTIONAL ANALYSIS OF VARIANCE FOR FISH BIODIVERSITY ASSESSMENT - T. Di Battista, F. Fortuna, F. Mauro - Journal of Environmental Informatics. Special issue of Marine and Freshwater Environmental Engineering and Management, Journal of Environmental Informatics. In press.



**Examples**

```
x=matrix(c(0.3,0.5,0.1,0.05,0.05,0.25,0.25,0.25,0.25,0,0.35,0.3,0.35,0,0),3,5)
export_plots(x,20)
```

---

radius	<i>Compute the values for the radius of curvature of the beta profile for each community in every part of the beta domain.</i>
--------	--

---

**Description**

This function provides the values of radius of the curvature for each part of the domain. The radius of curvature reflects the community composition; in particular, if we consider communities with different numbers of species, the radius of curvature is a good indicator of the lack of balance among species. This tool is alternative to the curvature because it is its inverse. Low levels of radius of curvature highlights high imbalance among different species and vice-versa.

**Usage**

```
radius(x,n)
```

**Arguments**

x	A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.
n	The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is n=20.

**Author(s)**

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**Examples**

```
x=matrix(c(0.3,0.5,0.1,0.05,0.05,0.25,0.25,0.25,0.25,0,0.35,0.3,0.35,0,0),3,5)
radius(x,20)
```

---

radius\_plot

---

*Plot the radius of curvature of the beta profiles for each community.*


---

**Description**

This function provides a plot of the radius of curvature of the diversity profiles for the considered communities. The domain "beta" represents the sensibility to changes in the presence of rare species. The graph of the radius of curvature reflects the community composition; in particular, if we consider communities with different numbers of species, the radius of curvature is a good indicator of the lack of balance among species. This graph is alternative to the curvature. Low levels of radius of curvature highlights high imbalance among different species and vice-versa.

**Usage**

```
radius_plot(x,n)
```

**Arguments**

- |   |  |
|---|--|
| x | A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.   |
| n | The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is n=20. |

**Author(s)**

Fabrizio Mauro, Francesca Fortuna, Tonio Di Battista

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issue of Marine and Freshwater Environmental Engineering and Management, Journal of Environmental Informatics. In press.

### Examples

```
x=matrix(c(0.3,0.5,0.1,0.05,0.05,0.25,0.25,0.25,0.25,0,0.35,0.3,0.35,0,0),3,5)
radius_plot(x,20)
```

---

ranking

*Compute the communities ranking according to the biodiversity computed using the functional tools.*

---

### Description

This function provides the communities ranking according to the biodiversity computed using the functional tools. Specifically, if communities present the same number of species then we can refer to the arc length. The arc length is a useful tool to establish a ranking among communities with intersecting profiles and the same number of species. It represents the length of a curve if it were rectified; it is a scalar measure extremely high in case of maximum dominance, whereas it decreases in case of high evenness. Unlike the classical indices, it considers each point of the domain corresponding to a different biodiversity value. For this reason, the arc length provides a ranking rule for communities with intersecting profiles, making possible to order them without the use of graphs. However, if communities do not present the same number of species then we must refer to the area. In an ecological framework, the area under the profiles can be used to assess biodiversity because it can rank communities, even if they have different number of species. Indeed, in a case of maximum dominance, the area is extremely low; while in a case of evenness, it increase. The main advantage of using area is that the ordering among communities can be investigated without the analysis of a graph. It provides a scalar measure of biodiversity considering the whole domain. This is not possible with the classical indices.

### Usage

```
ranking(x,n)
```

### Arguments

- |   |  |
|---|--|
| x | A data matrix with the abundance of the species (the rows are the communities and the columns indicate the species living in a community). The user can freely choose to use the absolute or relative frequencies.   |
| n | The number of points of the domain [-1,1] that the user wants to consider in computing the functional tools. It is suggested to choose a number in the interval [3,10000] because a value of less than 3 has little sense; indeed, the major indices of biodiversity are the richness index, the index of Shannon and the index of Simpson (that we get for beta equal to -1, 0, +1, respectively). On the other hand, a value greater than 10000 is not very interesting because with a value of approximately 100 we already have a good approximation. The examples provided in this package always divide the domain into 20 intervals. The default value is n=20. |

**Author(s)**

Fabrizio Mauro, Francesca Fortuna, Tonio Di Battista

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**Examples**

```
x=matrix(c(0.3,0.5,0.1,0.05,0.05,0.25,0.25,0.25,0.25,0,0.35,0.3,0.35,0,0),3,5)
ranking(x,20)
```

---

summary_species	<i>Create a species summary for each community. Based on the dataset with absolute abundance</i>
-----------------	--

---

**Description**

Create the species summary for each community (absolute abundance).

**Usage**

```
summary_species(x)
```

**Arguments**

x                    A data matrix with the absolute abundance of the species.

**Examples**

```
x=matrix(c(3,5,5,2,1,2,6,8,5,1),2,5)
x
summary_species(x)
```

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