

Package ‘Plasticity’

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Type Package

Title A package for computing plasticity indices

Version 0.2

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Description The Plasticity package allows to compute several plasticity indices as defined in Valladares et al. (2006) at Journal of Ecology

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Imports agricolae,
dplyr,
ggplot2,
psych

Encoding UTF-8

LazyData true

RoxygenNote 7.0.2

StagedInstall no

R topics documented:

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compute_rdpi	<i>compute_rdpi</i>
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Description

Function to compute a vector containing the relative distance plasticity index values (Valladares et al. 2006) of a given trait (trait) for a given categorical environmental variable (factor). It calculates rdpi for each pair of observation that does not belong to the same level of "factor", and returns a vector containing all the calculated rdpi values.

Usage

```
compute_rdpi(data, trait, factor)
```

Arguments

<code>data</code>	The dataframe that contains the data
<code>trait</code>	The bare (unquoted) name of the column that holds the trait for which to calculate RDPI. Must be numeric
<code>factor</code>	the bare (unquoted) name of the column that holds the environmental factor for which we will calculate RDPI. By definition, RDPI computes distances between pairs of observations that are at different levels of this factor.

Value

a vector containing all the calculated rdpi values for each pair of observations that do not belong to the same level of "factor"

Examples

```
data(ecophysio)
compute_rdpi(ecophysio, SB, Piso)
```

<code>rdpi</code>	<i>rdpi</i>
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Description

Function to compute the RDPI (Relative Distance Plasticity Index, Valladares et al, (2006) Quantitative estimation of phenotypic plasticity: bridging the gap between the evolutionary concept and its ecological applications, Journal of Ecology, 94(6):1103-1116.

Usage

```
rdpi(dataframe, sp, trait, factor, verbose = T)
```

Arguments

<code>dataframe</code>	The dataframe that contains the data
<code>sp</code>	The bare (unquoted) name of the column whose values will be used as independent variable. The function will compare RDPI values among values of this variable. It can be species, provenances, etc.
<code>trait</code>	The bare (unquoted) name of the column that holds the trait for which to calculate RDPI. Must be numeric
<code>factor</code>	the bare (unquoted) name of the column that holds the environmental factor for which we will calculate RDPI. By definition, RDPI computes distances between pairs of observations that are at different levels of this factor.
<code>verbose</code>	defines if we want to get a data frame with all the individual RDPI values calculated. By default is set to 'TRUE'; indicating that we will get the data frame. If set to 'FALSE', we only get a summary table and a bocplot

Value

This function computes RDPI to the environmental factor for each species of the dataset(or any other identifying variable defined in 'sp') Then it makes an ANOVA or t-test of the values of RDPI across species and plots the boxplot

Examples

```
data(ecophysio)
rdpi(ecophysio,sp,SB, Piso, verbose = F)

# if we want to store the values

foo <- rdpi(ecophysio,sp,SB, Piso, verbose = T)
```

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