

Package ‘Traitspace’

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Type Package

Title A Predictive Model for Trait Based Community Assembly of Plant Species

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Description Implements a predictive model of community assembly called 'Traitspace' (Laughlin et al. 2012, Ecology Letters). Traitspace is a hierarchical Bayesian model that translates the theory of trait-based environmental filtering into a statistical model that incorporates in-traspecific trait variation to predict the relative abundances and the distributions of species. The package includes functions to plot the predicted and the observed values. It also includes functions to compare the predicted values against the observed values using a variety of different distance measures and to implement permutation tests to test their statistical significance.

License GPL (>= 2)

Depends permute, mclust, graphics, grDevices, stats, utils

NeedsCompilation no

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R topics documented:

check	2
distTraitspace	3
plotComb	4
plotCorr	5
plotEach	6
print.traitspace	7
pval	8
spdata	9
Traitspace	10
TraitspaceMod	11
trueP	13

Index**14**

check	<i>Checks the input data</i>
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Description

Performs basic checks on the data and arranges it in a format that can be used as an input into the remaining functions of this package.

Usage

```
check(level_1, level_2, level_3, site, N)
```

Arguments

level_1	A column containing the names of the tree species
level_2	Column/s containing the trait values
level_3	Column/s containing enviromental gradient/s
site	A column containing the site names.
N	Size of the simulated trait sample.

Details

Transforms the existing data into appropriate format. This includes: 1) transform level_1 into factors; 2) transform level_2 and level_3 into dataframes; 3) generate a new factor site.name and a new dataframe site by the input site; 4) check the dimentionions of these data and 5) make sure level_2 does not has negative value.

Value

A list of transformed data that can be used as an input in the remaining functions of this package.

Examples

```
data(spdata)
species<-spdata$species #species column
trt<-cbind(spdata$t1,spdata$t2) #two traits
env<-spdata$env #one env gradient
site<-spdata$site #site information

check(species, trt, env, site)
```

distTraitspace	<i>Calculate the distances</i>
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Description

Calculates the distances between the predicted and true/observed relative abundances (by default) or species distributions if `byrow = FALSE`.

Usage

```
distTraitspace(result, obs = NULL, byrow = TRUE)
```

Arguments

<code>result</code>	The output from the <code>traitspace</code> function (class <code>traitspace</code>)
<code>obs</code>	The observed matrix - where, each row corresponds to a site and each column to a species - the order of sites and species should match with the order in which they appear in the predicted matrix. By default, <code>NULL</code> , will generate the observed matrix using the supplied trait data using the <code>trueP</code> function. See the <code>trueP</code> function for details.
<code>byrow</code>	By default, <code>TRUE</code> , will compare the relative abundances. If <code>FALSE</code> , will compare the species distribution.

Value

A list of distances calculated using the following measures: Euclidean, Manhattan, Hellinger, Kullback-Leibler and Bhattacharya. It calculates both the average distance (averages across all sites or species) as well as individual distances.

References

Basu, A., Shioya, H., & Park, C. (2011). Statistical inference: the minimum distance approach. CRC Press.

See Also

[pval](#), [Traitspace](#), [TraitspaceMod](#), [trueP](#)

Examples

```
data(spdata)
species<-spdata$species #species column
trt<-cbind(spdata$t1,spdata$t2) #two traits
env<-spdata$env #one env gradient
site<-spdata$site #site information
result1<-Traitspace(species, trt, env, site)
distTraitspace(result1)
```

plotComb *Plot traitspace results*

Description

Plots traitspace results in a single window. Plots the predicted relative abundances and the observed relative abundances (by default) or the predicted species distributions and the observed species distributions if byrow=FALSE.

Usage

```
plotComb(result, obs = NULL, byrow = TRUE, compare = TRUE)
```

Arguments

result	The output from the traitspace function (class traitspace)
obs	The observed matrix - where, each row corresponds to a site and each column to a species - the order of sites and species should match with the order in which they appear in the predicted matrix. By default, NULL, will generate the observed matrix using the supplied trait data using the <i>trueP</i> function. See the <i>trueP</i> function for details.
byrow	By default, TRUE, will plot the relative abundances. If FALSE, will plot the species distribution.
compare	By default, TRUE, will plot both the predicted as well as the observed values. If FALSE, will only plot the predicted values.

Details

Plots upto six species/sites in a single window. Will create multiple windows (multiples of six) if the number of species/sites is more.

Value

Traitspace plots.

References

Laughlin, D. C., Joshi, C., Richardson, S. J., Peltzer, D. A., Mason, N. W. H., & Wardle, D. A. (2015). Quantifying multimodal trait distributions improves trait-based predictions of species abundances and functional diversity. *Journal of Vegetation Science*, 26(1), 45-57.

Laughlin, D. C., Joshi, C., Bodegom, P. M., Bastow, Z. A., & Fule, P. Z. (2012). A predictive model of community assembly that incorporates intraspecific trait variation. *Ecology Letters*, 15(11), 1291-1299.

See Also

[plotCorr](#), [plotEach](#), [Traitspace](#), [TraitspaceMod](#), [trueP](#)

Examples

```

data(spdata)
species<-spdata$species #species column
trt<-cbind(spdata$t1,spdata$t2) #two traits
env<-spdata$env #one env gradient
site<-spdata$site #site information
result1<-Traitspace(species, trt, env, site)
plotComb(result1)

```

plotCorr

plot the predicted values against the observed values

Description

Plots the results for each species/site in a separate window and finds the correlation between the predicted and the observed values. Plots the predicted relative abundances against the observed relative abundances (by default) or the predicted species distributions against the observed species distributions if byrow=FALSE.

Usage

```
plotCorr(result, obs = NULL, byrow = TRUE)
```

Arguments

result	The output from the traitspace function (class traitspace)
obs	The observed matrix - where, each row corresponds to a site and each column to a species - the order of sites and species should match with the order in which they appear in the predicted matrix. By default, NULL, will generate the observed matrix using the supplied trait data using the <i>trueP</i> function. See the <i>trueP</i> function for details.
byrow	By default, TRUE, will plot the relative abundances. If FALSE, will plot the species distribution.

Value

Traitspace plots.

References

Laughlin, D. C., Joshi, C., Richardson, S. J., Peltzer, D. A., Mason, N. W. H., & Wardle, D. A. (2015). Quantifying multimodal trait distributions improves trait-based predictions of species abundances and functional diversity. *Journal of Vegetation Science*, 26(1), 45-57.

Laughlin, D. C., Joshi, C., Bodegom, P. M., Bastow, Z. A., & Fule, P. Z. (2012). A predictive model of community assembly that incorporates intraspecific trait variation. *Ecology Letters*, 15(11), 1291-1299.

See Also

[plotComb](#), [plotEach](#), [Traitspace](#), [TraitspaceMod](#), [trueP](#)

Examples

```
data(spdata)
species<-spdata$species #species column
trt<-cbind(spdata$t1,spdata$t2) #two traits
env<-spdata$env #one env gradient
site<-spdata$site #site information
result1<-Traitspace(species, trt, env, site)
plotCorr(result1)
```

plotEach	<i>Plot traitspace results one by one</i>
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Description

Plots the results for each species/site in a separate window. Plots the predicted relative abundances and the observed relative abundances (by default) or the predicted species distributions and the observed species distributions if `byrow=FALSE`.

Usage

```
plotEach(result, obs = NULL, byrow = TRUE, compare = TRUE)
```

Arguments

result	The output from the traitspace function (class traitspace)
obs	The observed matrix - where, each row corresponds to a site and each column to a species - the order of sites and species should match with the order in which they appear in the predicted matrix. By default, NULL, will generate the observed matrix using the supplied trait data using the <i>trueP</i> function. See the <i>trueP</i> function for details.
byrow	By default, TRUE, will plot the relative abundances. If FALSE, will plot the species distribution.
compare	By default, TRUE, will plot both the predicted as well as the observed values. If FALSE, will only plot the predicted values.

Value

Traitspace plots.

References

Laughlin, D. C., Joshi, C., Richardson, S. J., Peltzer, D. A., Mason, N. W. H., & Wardle, D. A. (2015). Quantifying multimodal trait distributions improves trait-based predictions of species abundances and functional diversity. *Journal of Vegetation Science*, 26(1), 45-57.

Laughlin, D. C., Joshi, C., Bodegom, P. M., Bastow, Z. A., & Fule, P. Z. (2012). A predictive model of community assembly that incorporates intraspecific trait variation. *Ecology Letters*, 15(11), 1291-1299.

See Also

[plotCorr](#), [plotEach](#), [Traitspace](#), [TraitspaceMod](#), [trueP](#)

Examples

```
data(spdata)
species<-spdata$species #species column
trt<-cbind(spdata$t1,spdata$t2) #two traits
env<-spdata$env #one env gradient
site<-spdata$site #site information
result1<-Traitspace(species, trt, env, site)
plotEach(result1)
```

print.traitspace	<i>prints an object of class "traitspace". This function prints out the summary of the results of the Traitspace of the TraitspaceMod functions. See details.</i>
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Description

This function prints out the summary of the results of the Traitspace of the TraitspaceMod functions. See details.

Usage

```
## S3 method for class 'traitspace'
print(x,...)
```

Arguments

x	the object with "traitspace" class
...	further arguments passed to or from other methods

Details

Print out the R-squared values, the BICs, the predicted matrix and the observed matrix. If the observed matrix is not explicitly supplied, then the Traitspace/TraitspaceMod function will generate the observed matrix using the supplied trait data using the *trueP* function and print a warning to this effect. See the *trueP* function for details.

Value

The object with "traitspace" class

References

Laughlin, D. C., Joshi, C., Richardson, S. J., Peltzer, D. A., Mason, N. W. H., & Wardle, D. A. (2015). Quantifying multimodal trait distributions improves trait-based predictions of species abundances and functional diversity. *Journal of Vegetation Science*, 26(1), 45-57.

Laughlin, D. C., Joshi, C., Bodegom, P. M., Bastow, Z. A., & Fule, P. Z. (2012). A predictive model of community assembly that incorporates intraspecific trait variation. *Ecology Letters*, 15(11), 1291-1299.

See Also

[Traitspace](#), [TraitspaceMod](#), [trueP](#)

Examples

```
data(spdata)
species<-spdata$species #species column
trt<-cbind(spdata$t1,spdata$t2) #two traits
env<-spdata$env #one env gradient
site<-spdata$site #site information
result1<-Traitspace(species, trt, env, site)
print(result1)
result1
```

pval

Permutation test on distances

Description

First calls the function *distTraitspace* to calculate the distances between the predicted and true/observed relative abundances (by default) or species distributions if `byrow = FALSE`. Then runs permutation tests to test if these distances are statistically significant and provides p-values.

Usage

```
pval(result, obs = NULL, byrow = TRUE, permutations = 999)
```

Arguments

result	the output from the traitspace function (class Traitspace)
obs	The observed matrix - where, each row corresponds to a site and each column to a species - the order of sites and species should match with the order in which they appear in the predicted matrix. By default, NULL, will generate the observed matrix using the supplied trait data using the <i>trueP</i> function. See the <i>trueP</i> function for details.

byrow	By default, TRUE, will compare the relative abundances. If FALSE, will compare the species distribution.
permutations	Number of permutations, by default 999.

Value

A list of distances calculated using the following measures: Euclidean, Manhattan, Hellinger, Kullback-Leibler and Bhattacharya. It calculates both the average distance (averages across all sites or species) as well as individual distances. Also provides p-values corresponding to each of these distances.

References

Basu, A., Shioya, H., & Park, C. (2011). Statistical inference: the minimum distance approach. CRC Press.

Phipson, B., & Smyth, G. K. (2010). Permutation p-values should never be zero: calculating exact P-values when permutations are randomly drawn. Statistical applications in genetics and molecular biology, 9(1).

See Also

[distTraitspace](#), [Traitspace](#), [TraitspaceMod](#)

Examples

```
data(spdata)
species<-spdata$species #species column
trt<-cbind(spdata$t1,spdata$t2) #two traits
env<-spdata$env #one env gradient
site<-spdata$site #site information
result1<-Traitspace(species, trt, env, site)
pval(result1)
```

spdata

Simulated species data

Description

A simulated species data to illustrate how the package works.

Usage

```
data(spdata)
```

Format

A data frame with 150 observations on the following 5 variables.

species – a factor with levels S1 S2 S3 S4 S5 S6

t1 – a numeric vector

t2 – a numeric vector

env – a numeric vector

site – a factor with levels A B C D E

Examples

```
data(spdata)
## maybe str(spdata) ; plot(spdata) ...
```

Traitspace

Traitspace Model

Description

Implements a predictive model of community assembly called the Traitspace.

Usage

```
Traitspace(level_1, level_2, level_3, site, N = 100, linear = FALSE)
```

Arguments

level_1	The data column containing species names.
level_2	The data column/s containing the trait values for one/multiple traits. One column per trait.
level_3	The data column/s containing the value of the environment gradient/s. One column per gradient.
site	The data column containing names of the sites
N	Size of the simulated trait sample per site
linear	Determines whether the trait-environment regression model is linear or quadratic. By default, FALSE, i.e. fits a quadratic model by default.

Value

A list which is an object of the 'traitspace' class.

<code>r.squared</code>	<code>TE</code>	The R-squared values for the Trait environment regression models fitted in step 1A. A separate model is fitted for each trait.
<code>BIC_TS</code>		The BIC value for the best gaussian mixture model fitted (using package <code>mclust</code>) for each species in step 1B.
<code>Predicted relative abundances</code>		A matrix containing the predicted relative abundances
<code>Predicted species distribution</code>		A matrix containing the predicted species distribution

References

Laughlin, D. C., Joshi, C., Richardson, S. J., Peltzer, D. A., Mason, N. W. H., & Wardle, D. A. (2015). Quantifying multimodal trait distributions improves trait-based predictions of species abundances and functional diversity. *Journal of Vegetation Science*, 26(1), 45-57.

Laughlin, D. C., Joshi, C., Bodegom, P. M., Bastow, Z. A., & Fule, P. Z. (2012). A predictive model of community assembly that incorporates intraspecific trait variation. *Ecology Letters*, 15(11), 1291-1299.

See Also

[Traitspace](#), [TraitspaceMod](#)

Examples

```
data(spdata)
species<-spdata$species #species column
trt<-cbind(spdata$t1,spdata$t2) #two traits
env<-spdata$env #one env gradient
site<-spdata$site #site information
result1<-Traitspace(species, trt, env, site)
result1
```

TraitspaceMod

Modified Traitspace Model

Description

Implements the modified version of the Traitspace model of community assembly.

Usage

```
TraitspaceMod(level_1, level_2, level_3, site, N = 100)
```

Arguments

level_1	The data column containing species names.
level_2	The data column/s containing the trait values for one/multiple traits. One column per trait.
level_3	The data column/s containing the value of the environment gradient/s. One column per gradient.
site	The data column containing names of the sites
N	Size of the simulated trait sample per site

Value

A list which is an object of the "traitspace" class.

BIC_TE	The BIC value for the best gaussian mixture model fitted (using package mcluse) to the trait data in step 1A. A separate model is fitted for each trait.
BIC_TS	The BIC value for the best gaussian mixture model fitted (using package mclust) for each species in step 1B.
Predicted relative abundances	A matrix containing the predicted relative abundances
Predicted species distribution	A matrix containing the predicted species distribution

References

Laughlin, D. C., Joshi, C., Richardson, S. J., Peltzer, D. A., Mason, N. W. H., & Wardle, D. A. (2015). Quantifying multimodal trait distributions improves trait-based predictions of species abundances and functional diversity. *Journal of Vegetation Science*, 26(1), 45-57.

Laughlin, D. C., Joshi, C., Bodegom, P. M., Bastow, Z. A., & Fule, P. Z. (2012). A predictive model of community assembly that incorporates intraspecific trait variation. *Ecology Letters*, 15(11), 1291-1299.

See Also

[Traitspace](#), [TraitspaceMod](#)

Examples

```
data(spdata)
species<-spdata$species #species column
trt<-cbind(spdata$t1,spdata$t2) #two traits
env<-spdata$env #one env gradient
site<-spdata$site #site information
result2<-TraitspaceMod(species, trt, env, site)
result2
```

trueP	<i>estimate observed matrix</i>
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Description

The observed relative abundances/species distributions are calculated from the input data.

Usage

```
trueP(level_1, site.name)
```

Arguments

level_1	A column containing the names of the tree species
site.name	A column containing the site names.

Details

In situations where the observed abundance data are not available, this function can be used to estimate the true abundances using the trait data. The abundances are estimated as the relative frequency of the species within a site (for relative abundance) and as the relative frequency of the species across sites (for species distribution). Relative frequency may not necessarily be a desirable measure of abundance (often relative basal area is preferred, for example) and therefore a warning is issued when this function is used. We recommend the use of actual observed abundances as far as possible. These should be manually entered using the 'obs' option.

Value

A matrix containing the estimated observed relative abundances and a matrix containing the estimated observed species distributions.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
data(spdata)
species<-spdata$species #species column
site<-spdata$site #site information

trueP(species, site)
```

Index

*Topic **datasets**

spdata, 9

check, 2

distTraitspace, 3, 9

plotComb, 4, 6

plotCorr, 4, 5, 7

plotEach, 4, 6, 6, 7

print.traitspace, 7

pval, 3, 8

spdata, 9

Traitspace, 3, 4, 6–9, 10, 11, 12

TraitspaceMod, 3, 4, 6–9, 11, 11, 12

trueP, 3, 4, 6–8, 13