

R-Package: Richness

Asymptotic estimations of species richness from spatial abundance data

Summary:

The R-Package takes spatial abundance data and return estimated species richness, including observed richness, Chao1, Chao2, ACE, Jackknife-abundance, Jackknife-incidence, Ω_o (base-version of estimator developed in citation), and Ω_T (recommended estimator developed in citation).

A wrapper function *estimateRichness.R* allows the user to provide community data as a matrix, data.frame, list, or array. Lists or arrays can be input to compare multiple communities, such as a time series.

The wrapper function calls two functions *RichnessEsts.R* and *bootstrapRichness.R* that respectively return point estimates and bootstrapped estimates for estimator precision/uncertainty quantification. These functions take in data matrix with species as columns, spatial units (e.g., transects or quadrats) as rows, and individual counts as values.

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License:	CC BY-NC-SA
URL:	https://github.com/EWTekwa/Richness
Citation:	Tekwa, Whalen, Martone, O'Connor, Theory and application of an improved species richness estimator 2023. Philosophical Transactions B. 10.1098/rstb.2022.0181.2022-0187

To download package in R, type:

```
library(devtools)
install_github("EWTekwa/RichnessEstimator", subdir = "Richness")
library(Richness)
```

To open help files in R, type:

?RichnessEsts
?estimate_richness
?bootstrapRichness

Documentation:

1. estimate_richness {Richness}

R Documentation

Estimate Richness in Community Data

Description

A wrapper function that runs RichnessEsts or bootRichnessEsts using a variety of data input types, including time series community data.

Usage

```
estimate_richness(Community, boot = FALSE, numBoot = 100,  
                  meanStates = FALSE, Apx_detectP_terms = FALSE )
```

Arguments

Community	Community data with species as columns and spatial sampling units as rows. Data can take the form of a data frame, matrix, list, or array of 3 dimensions. List and array inputs are useful when calculating richness for community time series or for different communities who richness is to be compared.
boot	logical. Should bootstrapped samples be computed?
numBoot	The number of bootstrapped samples to return.
meanStates	logical. Should mean states of correction terms bootstrapped samples be returned? Only used when boot = FALSE
Apx_detectP_terms	logical. Should approximated detection probabilities be returned? Only used when boot = FALSE

Author(s)

E.W. Tekwa and Matt Whalen

References

Tekwa, Whalen, Martone, O'Connor, Theory and application of an improved species richness estimator 2023. Philosophical Transactions B.

See Also

[RichnessEsts](#), [bootRichnessEsts](#).

Examples

```
## Use Barro Colorado Island data from the vegan package
```

```
require(vegan)
```

```
data("BCI")
```

```
## run the function for a single community data frame without bootstrapping
```

```
# point estimates only
```

```
estimate_richness(BCI)
```

```
# with mean states for correction terms and approximated detection probabilities
```

```
estimate_richness(BCI, meanStates = TRUE, Apx_detectP_terms = TRUE)
```

```
## run the function for a single community data frame with bootstrapping
```

```
estimate_richness(BCI, boot = TRUE, numBoot = 10)
```

```
## run the function on a list
```

```
# Note: this may not be the most sensible comparison
require(vegan)
data("pyrifos")
week <- gl(11, 12, labels = c(-4, -1, 0.1, 1, 2, 4, 8, 12, 15, 19, 24))
communitylist <- split(pyrifos, f = week)
estimate_richness(communitylist)
# bootstrapping on a list returns a tidy data frame
require(tidyverse)
estimate_richness(communitylist, boot = TRUE, numBoot = 10)
```

2. RichnessEsts {Richness}

R Documentation

Richness Estimates with Correction Terms and Detection Probabilities

Description

This function takes spatial abundance data and returns several richness estimates, including two defined by Tekwa et al. 2023. In addition to richness point estimates, the function returns mean states of correction terms and approximated detection probabilities used in Tekwa's estimation method.

Usage

```
RichnessEsts(Community)
```

Arguments

Community Data frame or matrix of community data with species as columns and spatial sampling units as rows.

Value

A list of 3 elements.

element1 point estimates for all richness estimators.

element2 mean states of the correction terms for $\Omega\{T\}$ and $\Omega\{0\}$.

element3 approximated detection probabilities for $\Omega\{T\}$ and $\Omega\{0\}$.

Author(s)

E.W. Tekwa and Matt Whalen

References

Tekwa, Whalen, Martone, O'Connor, Theory and application of an improved species richness estimator 2023. Philosophical Transactions B.

See Also

[estimateRichness](#), [bootstrapRichnessEsts](#).

Examples

```
## Use Barro Colorado Island data from the vegan package
```

```
require(vegan)
```

```
data("BCI")
```

```
## run the function, which returns a list
```

```
RichnessEsts(BCI)
```

```
## isolate the richness estimates
```

```
RichnessEsts(BCI)[[1]]
```

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3. bootstrapRichness {Richness}

R Documentation

Bootstrapped Richness Estimates

Description

This function takes spatial abundance data and returns several richness estimates, including two defined by Tekwa et al. 2023. The function uses a bootstrapping routine that can be used to obtain confidence intervals around richness point estimates.

Usage

```
bootstrapRichness(Community, numBoot = 100)
```

Arguments

Community Data frame or matrix of community data with species as columns and spatial sampling units as rows.

numBoot The number of bootstrapped samples to return.

Details

Point estimates are first calculated using [RichnessEsts](#) and used in the bootstrapping routine. The bootstrapping routine first resamples rows (sampling units) with replacement, with the number of sampled units the same as the number of rows in the dataset. Next, columns (e.g., species, taxa) are resampled with replacement such that the total number of columns is equal to the number of types calculated for each richness estimate, generating a data frame for each richness estimate. Then, each richness estimate is calculated on each resampled data frame, and the bootstrap routine repeats until **numBoot** is reached.

Value

A data frame of dimensions `c(numBoot, 8)`, where the columns represent the different richness estimates and rows are bootstrapped samples.

Note that the first row contains point estimates calculated using [RichnessEsts](#).

Author(s)

E.W. Tekwa and Matt Whalen

References

Tekwa, Whalen, Martone, O'Connor, Theory and application of an improved species richness estimator 2023. Philosophical Transactions B.

See Also

[estimateRichness](#), [RichnessEsts](#).

Examples

```
## Use Barro Colorado Island data from the vegan package
require(vegan)
data("BCI")
```

```
## run the function
```

```
bootstrapRichness(BCI, numBoot = 10)
```

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