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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Authors:	Matt Whalen and Eden Tekwa
Maintainers:	Matt Whalen (mawhal@gmail.com), Eden Tekwa (ewtekwa@gmail.com)
License:	CC BY-NC-SA
URL:	https://github.com/EWTekwa/RichnessEstimator/tree/main/Richness
Citation:	Tekwa, Whalen, Martone, O'Connor, Theory and application of an improved species richness estimator. bioRxiv. https://doi.org/10.1101/2022.05.02.490342

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, E.W., Whalen, M.W., Martone, P.T. and O'Connor, M.I. (2023) Theory and application of an improved species richness estimator. in revision.
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)
```

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, E.W., Whalen, M.W., Martone, P.T. and O'Connor, M.I. (2023) Theory and application of an improved species richness estimator. in revision.
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]]

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 calcuated for each richness estimate, generating a data frame for each richness estimate. Then, each richness estimate is calcualted on each resampled data frame, and the bootstap 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, E.W., Whalen, M.W., Martone, P.T. and O'Connor, M.I. (2023) Theory and application of an improved species richness estimator. in revision.
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)