Package ‘fRSE’

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Type Package

Title fRSE-predicting the total number of rare species in under-sampled sites

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Description fRSE is an R package for predicting the total number of rare species in under-sampled sites

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fRSE-package *package fRSE*

Description

fRSE: an R package for predicting the total number of rare species in under-sampled sites

Details

fRSE is an R package for estimating the total number of rare species in additional ecological samples. The methods used here include a Bayesian-weighted estimator and two unweighted estimators.

Author(s)

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References

Shen TJ, Chen Y (2019) Predicting the number of newly discovered rare species: a Bayesian weight approach. Conservation Biology, 33, 444-455.

Chen Y, Shen TJ, Nielsen SE (2019) How many rare species are present in under-sampled sites? In preparation.

Examples

```
###########################
#for abundance-based data type
data(HerpetologicalData)
## two columns represent two samples of species abundance data
X.merge = HerpetologicalData
## the first column is treated as the original sample
X.col1 = X.merge[,1]
## the second column is treated as the additional sample
X.col2 = X.merge[,2]
Xi = X.col1
## the number of individuals of the additional sample
m = sum(X.col2)
print(FullPred.abundance.rare(boot.rep = 100, f=NULL, xi=Xi, m = m, k.show = 3))

###########################
#for incidence-based data type
data(CanadaMite)
## two columns represent two samples of incidence counts
X.merge = CanadaMite
## the first column is treated as the original sample
X.col1 = X.merge[,1]
## the number of quadrats in the first sample
nT = 16
## the number of quadrats in the additional sample (i.e., the second column)
```

```
u = 16
print(FullPred.incidence.rare(boot.rep = 100, Q=NULL, xi=X.col1, nT=nT, u=u, k.show = 3))
```

---

boot.abundance.fun *Generate a bootstrap abundance-based sample*

Description

Given an abundance-based data, a bootstrap sample is generated from a reconstructed bootstrap assemblage.

Usage

```
boot.abundance.fun(S.hat, f, b)
```

Arguments

S.hat	An estimate of species richness.
f	A vector of species frequency counts, i.e., the number of singleton species (only one individual observed in the sample), the number of doubleton species (two individuals observed in the sample), and so forth.
b	A vector of estimates of two parameters for obtaining the estimated relative abundances of observed species in a given sample by Chao et al.'s (2015) method.

Value

The generated bootstrap sample is a vector of species frequency counts, i.e., the number of singleton species (only one individual observed in the bootstrap sample), the number of doubleton species (two individuals observed in the bootstrap sample), and so forth.

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Chao A, Hsieh T, Chazdon R, Colwell R, Gotelli N. 2015. Unveiling the species-rank abundance distribution by generalizing the Good-Turing sample coverage theory. Ecology 96:1189-1201.

See Also

boot.incidence.fun

Examples

```
## As an example, Herpetological assemblage data are used here.
data(HerpetologicalData)
## two columns represent two samples of species abundance data
X.merge = HerpetologicalData
## the first column is treated as the original sample
Xi = X.merge[,1]
## Convert species abundance data to species frequency counts data
```

```
f = X.to.f(Xi)
b = DetAbu(x=Xi, zero=FALSE)
## the estimated number of species
S.hat = SpEst.Chao1.abun(f)
boot.abundance.fun(S.hat=S.hat, f=f, b=b)
```

`boot.incidence.fun` *Generate a bootstrap incidence-based sample*

Description

Given an incidence-based data, a bootstrap sample is generated from a reconstructed bootstrap assemblage.

Usage

```
boot.incidence.fun(S.hat, nT, Q, b)
```

Arguments

`S.hat`	An estimate of species richness.
`nT`	The number of quadrats of the original sample
`Q`	A vector of species frequency counts, i.e., the number of species dectected once (in only one quadrat), the number of species dectected twice (in exactly two quadrats), and so forth.
`b`	A vector of estimates of two parameters for obtaining the estimated detection probabilities of observed species in a given sample by Chao et al.'s (2015) method.

Value

The generated bootstrap sample is a vector of species frequency counts, i.e., the number of species dectected once (in only one quadrat of the bootstrap sample), the number of species dectected twice (in exactly two quadrats of the bootstrap sample), and so forth.

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Chao A, Hsieh T, Chazdon R, Colwell R, Gotelli N. 2015. Unveiling the species-rank abundance distribution by generalizing the Good-Turing sample coverage theory. Ecology 96:1189-1201.

See Also

`boot.abundance.fun`

Examples

```
## As an example, Canadian-mite data are used here.
data(CanadaMite)
## two columns represent two samples of incidence counts
X.merge = CanadaMite
## the first column is treated as the sample
X.col1 = X.merge[,1]
Xi = X.col1
## Convert species incidence count data to frequency counts data
Q = X.to.f(Xi)
## the number of quadrats in the first sample
nT = 16
b = DetInc(Xi, nT)
boot.incidence.fun(S.hat=sum(Q)+b[3], nT=nT, Q=Q, b=b[1:2])
```

CanadaMite *mite incidence in moss patches of 32 locations of western Canada (Chen et al. 2015)*

Description

The mite data were collected by Youhua Chen (Chen et al. 2015) in western coasts of Canada. In Chen et al. (2015), 16 moss sampling locations were surveyed from the early days to the midst of June 2011, while another 16 moss sampling units were surveyed from the midst of June to the early days of July 2011.

Therefore, for the dataset, it has two columns, the first column contained the incidence or occurrence information of mites collected by first days of sampling (the early days to the midst of June 2011), while the second column contained the incidence of mites that were collected by the last days of the sampling

Usage

```
data(CanadaMite)
```

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Chen Y, Amundrud SL, Srivastava DS (2015) Spatial variance in soil microarthropod communities: Niche, neutrality, or stochasticity? Ecoscience 21:1-14.

Shen TJ, Chen Y (2019) Predicting the number of newly discovered rare species: a Bayesian weight approach. Conservation Biology, 33, 444-455.

Chen Y, Shen TJ, Nielsen SE (2019) How many rare species are present in under-sampled sites? In preparation.

See Also

HerpetologicalData

Examples

```
data(CanadaMite)
## two columns represent two samples of species incidence data
X.merge = CanadaMite
head(X.merge)
```

DetAbu *Abundance-based data: the estimation of parameters for obtaining the estimation of relative abundances of observed species*

Description

The estimation of parameters for obtaining the estimation of relative abundances of observed species

Usage

```
DetAbu(x, zero = FALSE)
```

Arguments

x	A vector of species abundance data, i.e., the number of individuals of species 1, the number of individuals of species 2, and so forth.
zero	A logical value for whether reserving zero frequency or not.

Value

A vector of 3 elements: the first two values are the estimates of two parameters in Chao et al. (2015) for jointly estimating relative abundances of observed species and the third one is the estimated number of unseen species in the sample by Chao 1 estimator (Chao, 1984).

Note

This function is a part of the original R code JADE by Chao et al. (2015) and is slightly modified for the output format.

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Chao A, Hsieh T, Chazdon R, Colwell R, Gotelli N. 2015. Unveiling the species-rank abundance distribution by generalizing the Good-Turing sample coverage theory. Ecology 96:1189-1201.

Chao A. 1984. Non-parametric estimation of the number of classes in a population. Scandinavian Journal of Statistics 11:265-270.

R code for JADE: http://chao.stat.nthu.edu.tw/wordpress/paper/107_Rcode.txt

See Also

DetInc

Examples

```
## As an example, Herpetological assemblage data are used here.
data(HerpetologicalData)
## two columns represent two samples of species abundance data
X.merge = HerpetologicalData
## the first column is treated as the original sample
Xi = X.merge[,1]
DetAbu(x=Xi)
```

DetInc — *DetInc(y, zero=FALSE) is a function of estimating detected species incidence probability.*

Description

DetInc(y, zero=FALSE) is a function of estimating detected species incidence probability.

Usage

```
DetInc(y, nT, zero = FALSE)
```

Arguments

`y`	a vector of species incidence frequency
`zero`	reserves zero frequency or not. Default is FALSE.

Value

a numerical vector

---

f.to.X — *Data transformation: from species frequency counts to species abundance data*

Description

This function is to convert species frequency counts data to species abundance data.

Usage

```
f.to.X(f)
```

Arguments

`f`	Species frequency counts data.

Value

Species abundance data is returned.

Author(s)

Youhua Chen & Tsung-Jen Shen

See Also

X.to.f

Examples

```
## The sample is composed of 5 singletons, two doubletons, and one tripleton species.
f = c(5, 2, 1)
f.to.X(f)
```

FullPred.abundance.rare

Abundance-based data: jointly predicting the number of rare species using all available methods

---

Description

Abundance-based prediction on the number of rare species using a Bayesian-weight and two unweighted estimators along with their bootstrap standard errors and 95% bootstrap confidence intervals.

Usage

```
FullPred.abundance.rare(boot.rep = 100, f = NULL, xi = NULL, m, k.show = 3)
```

Arguments

boot.rep	Replicate number of the bootstrapping procedure
f	A vector of species frequency counts, i.e., the number of singleton species (only one individual observed in the sample), the number of doubleton species (two individuals observed in the sample), and so forth.
xi	A vector of species abundance data, i.e., the number of individuals of species 1, the number of individuals of species 2, and so forth.
m	The number of individuals of an additional sample
k.show	Display the estimating result of the numbers of extremely rare species with abundance <= k.show in the additional sample

Value

Estimating results including point estimate, bootstrap standard error, and 95 % bootstrap confidence interval for each of three methods (a Bayesian-weight and two unweighted estimators)

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Shen TJ, Chen Y (2019) Predicting the number of newly discovered rare species: a Bayesian weight approach. Conservation Biology, 33, 444-455.

Chen Y, Shen TJ, Nielsen SE (2019) How many rare species are present in under-sampled sites? In preparation.

See Also

FullPred.incidence.rare

Examples

```
## As an example, Herpetological assemblage data are used here.
data(HerpetologicalData)
## two columns represent two samples of species abundance data
X.merge = HerpetologicalData
## the first column is treated as the original sample
X.col1 = X.merge[,1]
## the second column is treated as the additional sample
X.col2 = X.merge[,2]
Xi = X.col1
## Convert species abundance data to species frequency counts data
f = X.to.f(Xi)
## the number of individuals of the additional sample
m = sum(X.col2)
FullPred.abundance.rare(f=f, m=m)
```

FullPred.Fk.BW *Abundance-based data: Bayesian-weight estimator*

Description

Bayesian-weight estimator for predicting the number of rare species using abundance data as inputs

Usage

```
FullPred.Fk.BW(f, m, b, k.show = 3)
```

Arguments

f	A vector of species frequency counts, i.e., the number of singleton species (only one individual observed in the sample), the number of doubleton species (two individuals observed in the sample), and so forth.
m	The number of individuals of an additional sample
b	A vector of two estimated parameters for obtaining the estimated relative species abundances by Chao et al.'s (2015) method.
k.show	Display the estimating result of the numbers of extremely rare species with abundance <= k.show in the additional sample

Value

The numbers of rare species with abundance <= k.show are estimated by the abundance-based Bayesian-weight estimator and returned.

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Shen TJ, Chen Y (2019) Predicting the number of newly discovered rare species: a Bayesian weight approach. Conservation Biology, 33, 444-455.

Chen Y, Shen TJ, Nielsen SE (2019) How many rare species are present in under-sampled sites? In preparation.

See Also

FullPred.Qk.BW

Examples

```
## As an example, Herpetological assemblage data are used here.
data(HerpetologicalData)
## two columns represent two samples of species abundance data
X.merge = HerpetologicalData
## the first column is treated as the original sample
X.col1 = X.merge[,1]
## the second column is treated as the additional sample
X.col2 = X.merge[,2]
Xi = X.col1
## Convert species abundance data to species frequency counts data
f = X.to.f(Xi)
## the number of individuals of the additional sample
m = sum(X.col2)
b = DetAbu(x=Xi, zero=FALSE)
FullPred.Fk.BW(f=f, m=m, b=b)
```

FullPred.Fk.Naive *Abundance-based data: unweighted naive estimator*

Description

Abundance-based unweighted naive estimator for predicting the number of rare species

Usage

```
FullPred.Fk.Naive(f, m, k.show = 3)
```

Arguments

f	A vector of species frequency counts, i.e., the number of singleton species (only one individual observed in the sample), the number of doubleton species (two individuals observed in the sample), and so forth.
m	The number of individuals of an additional sample
k.show	Display the estimating result of the numbers of extremely rare species with abundance <= k.show in the additional sample.

Value

The numbers of rare species with abundance <= k.show are estimated by the abundance-based unweighted naive estimator and returned.

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Shen TJ, Chen Y (2019) Predicting the number of newly discovered rare species: a Bayesian weight approach. Conservation Biology, 33, 444-455.

Chen Y, Shen TJ, Nielsen SE (2019) How many rare species are present in under-sampled sites? In preparation.

See Also

FullPred.Qk.Naive

Examples

```
## As an example, Herpetological assemblage data are used here.
data(HerpetologicalData)
## two columns represent two samples of species abundance data
X.merge = HerpetologicalData
## the first column is treated as the original sample
X.col1 = X.merge[,1]
## the second column is treated as the additional sample
X.col2 = X.merge[,2]
Xi = X.col1
## Convert species abundance data to species frequency counts data
f = X.to.f(Xi)
## the number of individuals of the additional sample
m = sum(X.col2)
FullPred.Fk.Naive(f=f, m=m)
```

`FullPred.Fk.unweighted` *Abundance-based data: Unweighted estimator*

Description

Unweighted estimator based on Chao et al. (2015)'s paper using abundance-based data for predicting the number of rare species in an additional ecological sample

Usage

```
FullPred.Fk.unweighted(f, m, b, f0, k.show = 3)
```

Arguments

`f`	A vector of species frequency counts, i.e., the number of singleton species (only one individual observed in the sample), the number of doubleton species (two individuals observed in the sample), and so forth.
`m`	The number of individuals of an additional sample
`b`	A vector of two estimated parameters for obtaining the estimated relative species abundances by Chao et al.'s (2015) method.
`f0`	The estimated number of unseen species in the original sample by Chao 1 estimator (Chao 1984)
`k.show`	Display the estimating result of the numbers of extremely rare species with abundance <= k.show in the additional sample

Value

The numbers of rare species with abundance <= k.show are estimated by the abundance-based unweighted estimator and returned.

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Shen TJ, Chen Y (2019) Predicting the number of newly discovered rare species: a Bayesian weight approach. Conservation Biology, 33, 444-455.

Chen Y, Shen TJ, Nielsen SE (2019) How many rare species are present in under-sampled sites? In preparation.

Chao A, Hsieh T, Chazdon R, Colwell R, Gotelli N. 2015. Unveiling the species-rank abundance distribution by generalizing the Good-Turing sample coverage theory. Ecology 96:1189-1201.

Chao A. 1984. Non-parametric estimation of the number of classes in a population. Scandinavian Journal of Statistics 11:265-270.

See Also

`FullPred.Qk.unweighted`

Examples

```
## As an example, Herpetological assemblage data are used here.
data(HerpetologicalData)
## two columns represent two samples of species abundance data
X.merge = HerpetologicalData
## the first column is treated as the original sample
X.col1 = X.merge[,1]
## the second column is treated as the additional sample
X.col2 = X.merge[,2]
Xi = X.col1
## Convert species abundance data to species frequency counts data
f = X.to.f(Xi)
## the number of individuals of the additional sample
m = sum(X.col2)
b = DetAbu(x=Xi, zero=FALSE)
## the estimated number of unseen species in the original sample
f0 = SpEst.Chao1.abun(f)-sum(f)
FullPred.Fk.unweighted(f=f, m=m, b=b, f0=f0)
```

FullPred.incidence.rare

Incidence-based data: jointly predicting the number of rare species using all available methods

---

Description

Incidence-based prediction on the number of rare species using a Bayesian-weight and two unweighted estimators along with their bootstrap standard errors and 95% bootstrap confidence intervals.

Usage

```
FullPred.incidence.rare(boot.rep = 100, Q = NULL, xi = NULL, nT, u, k.show = 3)
```

Arguments

`boot.rep`	Replicate number of the bootstrapping procedure
`Q`	A vector of species frequency counts, i.e., the number of species dectected once (in only one quadrat), the number of species dectected twice (in exactly two quadrats), and so forth.
`xi`	A vector of species incidence counts, i.e., the number of quadrats with species 1, the number of quadrats with species 2, and so forth.
`nT`	The number of quadrats of the original sample
`u`	The number of quadrats of an additional sample
`k.show`	Display the estimating results of the numbers of rare species detected in the number of quadrats <= k.show in the additional sample

Value

Estimating results including point estimate, bootstrap standard error, and 95 % bootstrap confidence interval for each of three methods (a Bayesian-weight and two unweighted estimators)

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Shen TJ, Chen Y (2019) Predicting the number of newly discovered rare species: a Bayesian weight approach. Conservation Biology, 33, 444-455.

Chen Y, Shen TJ, Nielsen SE (2019) How many rare species are present in under-sampled sites? In preparation.

See Also

FullPred.abundance.rare

Examples

```
## As an example, Canadian-mite data are used here.
data(CanadaMite)
## two columns represent two samples of incidence counts
X.merge = CanadaMite
## the first column is treated as the original sample
X.col1 = X.merge[,1]
Xi = X.col1
## Convert species incidence count data to frequency counts data
Q = X.to.f(Xi)
## the number of quadrats in the first sample
nT = 16
## the number of quadrats in the additional sample (i.e., the second column)
u = 16
FullPred.incidence.rare(Q=Q, nT=nT, u=u)
```

FullPred.Qk.BW *Incidence-based data: Bayesian-weight estimator*

Description

Bayesian-weight estimator for predicting the number of rare species using incidence/quadrat data

Usage

```
FullPred.Qk.BW(Q, nT, u, b, k.show = 3)
```

Arguments

Q	A vector of species frequency counts, i.e., the number of species dectected once (in only one quadrat), the number of species dectected twice (in exactly two quadrats), and so forth.
nT	The number of quadrats of the original sample
u	The number of quadrats of an additional sample
b	A vector of two estimated parameters for obtaining the estimated relative species abundances by Chao et al.'s (2015) method.
k.show	Display the estimating results of the numbers of rare species detected in the number of quadrats <= k.show in the additional sample

Value

The numbers of rare species detected in the number of quadrats <= k.show are estimated by the incidence-based Bayesian-weight estimator and returned.

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Shen TJ, Chen Y (2019) Predicting the number of newly discovered rare species: a Bayesian weight approach. Conservation Biology, 33, 444-455.

Chen Y, Shen TJ, Nielsen SE (2019) How many rare species are present in under-sampled sites? In preparation.

See Also

FullPred.Fk.BW

Examples

```
## As an example, Canadian-mite data are used here.
data(CanadaMite)
## two columns represent two samples of incidence counts
X.merge = CanadaMite
## the first column is treated as the original sample
X.col1 = X.merge[,1]
Xi = X.col1
## Convert species incidence count data to frequency counts data
Q = X.to.f(Xi)
## the number of quadrats in the first sample
nT = 16
## the number of quadrats in the additional sample (i.e., the second column)
u = 16
b = DetInc(y=Xi, nT=nT)
FullPred.Qk.BW(Q=Q, nT=nT, u=u, b=b[1:2])
```

FullPred.Qk.Naive — *Incidence-based data: unweighted naive estimator*

Description

Incidence-based unweighted naive estimator for predicting the number of rare species

Usage

```
FullPred.Qk.Naive(nT, u, f, k.show = 3)
```

Arguments

nT	The number of quadrats of the original sample
u	The number of quadrats of an additional sample
f	A vector of species frequency counts, i.e., the number of species dectected once (in only one quadrat), the number of species dectected twice (in exactly two quadrats), and so forth.
k.show	Display the estimating results of the numbers of rare species detected in the number of quadrats <= k.show in the additional sample.

Value

The numbers of rare species detected in the number of quadrats <= k.show are estimated by the incidence-based unweighted naive estimator and returned.

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Shen TJ, Chen Y (2019) Predicting the number of newly discovered rare species: a Bayesian weight approach. Conservation Biology, 33, 444-455.

Chen Y, Shen TJ, Nielsen SE (2019) How many rare species are present in under-sampled sites? In preparation.

See Also

FullPred.Fk.Naive

Examples

```
## As an example, Canadian-mite data are used here.
data(CanadaMite)
## two columns represent two samples of incidence counts
X.merge = CanadaMite
## the first column is treated as the original sample
X.col1 = X.merge[,1]
Xi = X.col1
## Convert species incidence count data to frequency counts data
Q = X.to.f(Xi)
## the number of quadrats in the first sample
nT = 16
## the number of quadrats in the additional sample (i.e., the second column)
u = 16
FullPred.Qk.Naive(nT=nT,u=u,f=Q)
```

`FullPred.Qk.unweighted` *Incidence-based data: Unweighted Estimator*

Description

Unweighted Estimator derived from Chao et al. (2015)'s paper using incidence/quadrat data for predicting the number of rare species in an additional ecological sample

Usage

```
FullPred.Qk.unweighted(Q, nT, u, b, Q0, k.show = 3)
```

Arguments

`Q`	A vector of species frequency counts, i.e., the number of species dectected once (in only one quadrat), the number of species dectected twice (in exactly two quadrats), and so forth.
`nT`	The number of quadrats of the original sample
`u`	The number of quadrats of an additional sample
`b`	A vector of two estimated parameters for obtaining the estimated relative species abundances by Chao et al.'s (2015) method.
`Q0`	The estimated number of unseen species in the original sample by Chao 2 estimator (Chao 1987)
`k.show`	Display the estimating results of the numbers of rare species detected in the number of quadrats <= k.show in the additional sample

Value

The numbers of rare species detected in the number of quadrats <= k.show are estimated by the incidence-based unweighted estimator derived from Chao et al. (2015)'s paper and returned.

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Shen TJ, Chen Y (2019) Predicting the number of newly discovered rare species: a Bayesian weight approach. Conservation Biology, 33, 444-455.

Chen Y, Shen TJ, Nielsen SE (2019) How many rare species are present in under-sampled sites? In preparation.

Chao A, Hsieh T, Chazdon R, Colwell R, Gotelli N. 2015. Unveiling the species-rank abundance distribution by generalizing the Good-Turing sample coverage theory. Ecology 96:1189-1201.

Chao A. 1987. Estimating the population size for capture-recapture data with unequal catchability. Biometrics 43:783-791.

See Also

`FullPred.Fk.unweighted`

Examples

```
## As an example, Canadian-mite data are used here.
data(CanadaMite)
## two columns represent two samples of incidence counts
X.merge = CanadaMite
## the first column is treated as the original sample
X.col1 = X.merge[,1]
Xi = X.col1
## Convert species incidence count data to frequency counts data
Q = X.to.f(Xi)
## the number of quadrats in the first sample
nT = 16
## the number of quadrats in the additional sample (i.e., the second column)
u = 16
b = DetInc(Xi, nT)
FullPred.Qk.unweighted(Q=Q, nT=nT, u=u, b=b[1:2], Q0=b[3])
```

`HerpetologicalData` *Abundance of herpetofauna in the conserved and human disturbed areas of Mexico (Suazo-Ortuno et al. 2008)*

Description

Suazo-Ortuno et al. (2008) studied how the conversion of tropical forest to agricultural mosaic influenced herpetofaunal distribution and community structure in conserved and human disturbed forest areas of neotropical Mexico.

Therefore, the dataset used here, the first and second columns represented species abundance in the conserved and disturbed areas, respectively.

Usage

```
data(HerpetologicalData)
```

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Suazo-Ortuno I, Alvarado-Diaz J, Martines-Ramos M (2008) Effects of conversion of dry tropical forest to agricultural mosaic on herpetofaunal assemblages. Conservation Biology 22: 362-374.

Shen TJ, Chen Y (2019) Predicting the number of newly discovered rare species: a Bayesian weight approach. Conservation Biology, 33, 444-455.

Chen Y, Shen TJ, Nielsen SE (2019) How many rare species are present in under-sampled sites? In preparation.

See Also

CanadaMite

Examples

```
data(HerpetologicalData)
## two columns represent two samples of species abundance data
X.merge = HerpetologicalData
head(X.merge)
```

SpEst.Chao1.abun *Species richness estimation*

Description

Chao1 estimator of species richness

Usage

```
SpEst.Chao1.abun(f)
```

Arguments

f	A vector of species frequency counts, i.e., the number of singleton species (only one individual observed in the sample), the number of doubleton species (two individuals observed in the sample), and so forth.

Author(s)

Youhua Chen & Tsung-Jen Shen

References

Chao A. 1984. Non-parameteric estimation of the number of classes in a population. Scandinavian Journal of Statistics 11:265-270

Examples

```
## As an example, Herpetological assemblage data are used here.
data(HerpetologicalData)
## two columns represent two samples of species abundance data
X.merge = HerpetologicalData
## the first column is treated as the original sample
Xi = X.merge[,1]
## Convert species abundance data to species frequency counts data
f = X.to.f(Xi)
SpEst.Chao1.abun(f=f)
```

X.to.f — *Data transformation: from species abundance data to species frequency counts data*

Description

This function is to convert a vector of species abundance data to a vector of species frequency counts data.

Usage

```
X.to.f(X)
```

Arguments

X	A vector of species abundance data.

Value

Species frequency counts is returned.

Author(s)

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See Also

f.to.X

Examples

```
## As an example, Herpetological assemblage data are used here.
data(HerpetologicalData)
## two columns represent two samples of species abundance data
X.merge = HerpetologicalData
## the first column is treated as the original sample
X.col1 = X.merge[,1]
Xi = X.col1
## convert species abundance data to species frequency counts data
X.to.f(Xi)
```

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