

# Package ‘DiversitySampler’

February 19, 2015

**Type** Package

**Title** Functions for re-sampling a community matrix to compute diversity indices at different sampling levels.

**Version** 2.1

**Date** 2012-12-21

**Author** Matthew K. Lau

**Maintainer** Matthew K. Lau <mk148@nau.edu>

**Description** There are two functions in this package, which can be used together to estimate the Shannon's Diversity index at different levels of sample size. A Monte-Carlo procedure is used to re-sample a given observation at each level of sampling. The expectation being that the mean of the re-sampling will approach Shannon's diversity index at that sample level.

**License** GPL (>= 3)

**LazyLoad** yes

**Repository** CRAN

**Date/Publication** 2012-12-22 07:37:03

**NeedsCompilation** no

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count

*Counting Species Abundances*

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**Description**

Takes a vector of species names and counts the abundance of each unique species.

**Usage**

```
count(sv = "species vector", x = "species sample vector")
```

**Arguments**

sv                    A vector of species numbers or names.  
x                     A vector of species occurrences.

**Details**

This function is used within the [H.sampler](#) function.

**Value**

Returns a vector of species counts.

**Author(s)**

Matthew K. Lau

**Examples**

```
sv=1:10  
x=c(1,1,1,1,1,2,3,3,5,5,5,6,7,8,9,10)  
cbind(sv,count(sv,x))
```

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DiversitySampler-Package*Re-Sampling to Estimate Diversity Indices*

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**Description**

Contains functions for conducting analyses of expected diversity or evenness at a given sampling level. A Monte-Carlo procedure is used to re-sample a given observation at each level of sampling. The expectation being that the mean of the re-sampling will approach Shannon's diversity index at that sample level.

**Details**

Package: DiversitySampler  
Type: Package  
Version: 2.0  
Date: 2009-12-07  
License: GPL 3 or newer  
LazyLoad: yes

### Author(s)

Maintainer: Matthew K. Lau <mk148@nau.edu>, Department of Biological Sciences, Northern Arizona University, AZ, USA

Raj Whitlock, Department of Animal and Plant Sciences, University of Sheffield, Sheffield, UK

### See Also

[sample](#)

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Gd

*Genetic Evenness Index*

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### Description

This function allows calculation of a measure of compositional evenness, e.g. for a community of species or a population of genotypes (genetic individuals). Specifically, the index of evenness gives a measure of the probability that when two individuals are drawn randomly from the community (population) these individuals are of differing type (species or genotype; Nei 1987).

### Usage

```
Gd(obs, scrub=FALSE)
```

### Arguments

obs	A vector of species numbers.
scrub	Controls the treatment of species with zero abundance in the input observation. If TRUE the input vector is truncated to omit zero values.

### Details

Used within the [H.sampler](#) function.

### Value

Returns the compositional evenness calculated from the sample.

**Author(s)**

Raj Whitlock

**References**

Nei M. 1987. Molecular Evolutionary Genetics. Columbia University Press, New York, p. 180.

**See Also**

[H.sampler](#), [Hs](#)

**Examples**

```
x=rpois(25,10)
Gd(x)
```

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H.sampler

*Shannon's Diversity Re-sampler*


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**Description**

This function is a wrapper for [sample](#) and can be used to determine the expected value of a diversity index under a specified sampling intensity. A Monte-Carlo procedure is used to re-sample a given observation with replacement at each user-specified sampling intensity. The resampling can take place through one of two schemes. First, where the observed frequencies of species are assumed to represent the true underlying values, and second, where a user-specified vector of probabilities is used to control the resampling. The function calculates a diversity index over each simulated sample and summarises these for each specified level of sampling intensity via their mean.

**Usage**

```
H.sampler(x = "community matrix (spp=col,obs=row)", n = "sample size vector", nit = "number of iterations")
```

**Arguments**

x	A community matrix with observations in rows and species in columns.
n	A vector or scalar of sample size(s).
nit	Number of iterations of the Monte-Carlo procedure.
base	The base of the logarithm used to calculate Shannon's index (DEFAULT = e).
corr	Correction factor for small sample sizes.
p	A vector or matrix of weights corresponding to x, which can be used to simulate scenarios where forces other than sampling impact diversity.
method	The diversity metric: "Shannon" or "Gene diversity"

**Details**

The Monte-Carlo procedure draws random individuals based on the relative abundances of the species in a given observation. This process is repeated for the number of specified iterations at each designated sample level. For each iteration, the diversity index is calculated, and the mean is taken from all the indices produced in each iteration.

**Value**

A matrix of diversity indices for each observation (rows) at each sampling level (columns).

**Author(s)**

Matthew K. Lau and Raj Whitlock

**See Also**

[sample](#), [Gd](#), [Hs](#), [count](#)

**Examples**

```
x=array(round(runif(100,1,10)),c(10,10))
H.sampler(x,n=1:10,nit=10,base=exp(1))
```

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Hs	<i>Shannon's Diversity Index</i>
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**Description**

This function allows calculation of Shannon's diversity index (Shannon 1948).

**Usage**

```
Hs(obs,base=exp(1),corr=FALSE, scrub=TRUE)
```

**Arguments**

obs	A vector of species numbers.
base	The base of the logarithm used to calculate Shannon's index (DEFAULT = e).
corr	Correction factor for small sample sizes.
scrub	Controls the treatment of species with zero abundance in the input observation. If TRUE the input vector is truncated to omit zero values.

**Details**

This function is used within the [H.sampler](#) function.

**Value**

When `corr` is `FALSE` the value of `scrub` will not influence the value returned by this function. When `corr` is `TRUE` and `scrub` is `FALSE` observations in the input vector that have value 0 will influence the output value through the correction factor  $-(nsp-1)/(2*nsamp)$ , where `nsp` is the number of species and `nsamp` is the total number of counts. This function is used within the `H.sampler` function.

**Author(s)**

Raj Whitlock and Matthew K. Lau

**References**

Shannon C.E. (1948) A mathematical theory of communication. Bell System Technical Journal 27: 379-423 and 623-656.

**See Also**

[H.sampler](#), [Gd](#)

**Examples**

```
x=rpois(25,10)
Hs(x)
```

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