

# Package 'untb'

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**Type** Package

**Title** ecological drift under the UNTB

**Version** 1.7-2

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**Author** Robin K. S. Hankin

**SystemRequirements** PARI/GP  $\geq$  2.3.0 [strongly recommended for logkda()]

**Imports** Brobdingnag ( $\geq$  1.1-8), partitions ( $\geq$  1.9-14), polynom

**Maintainer** Robin K. S. Hankin <hankin.robin@gmail.com>

**Description** A collection of utilities for biodiversity data.  
Includes the simulation of ecological drift under Hubbell's Unified Neutral Theory of Biodiversity, and the calculation of various diagnostics such as Preston curves. Now includes functionality provided by Francois Munoz and Andrea Manica.

**License** GPL

**URL** <http://www.r-project.org>

**Depends** R ( $\geq$  2.10)

**NeedsCompilation** no

**Repository** CRAN

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**R topics documented:**

untb-package . . . . .	3
+count . . . . .	4
alonso . . . . .	5
bci . . . . .	6
butterflies . . . . .	6
caruso . . . . .	7
census . . . . .	8
copepod . . . . .	10
count . . . . .	10
display.untb . . . . .	12
etienne . . . . .	13
expected.abundance . . . . .	15
extractor . . . . .	16
fisher . . . . .	16
ghats . . . . .	17
isolate . . . . .	18
logkda . . . . .	19
logS1 . . . . .	21
no.of.ind . . . . .	22
optimal.params.gst . . . . .	24
optimal.params.sloss . . . . .	25
optimal.prob . . . . .	26
phi . . . . .	27
plot.count . . . . .	29
preston . . . . .	30
print.preston . . . . .	31
print.summary.count . . . . .	32
rand.neutral . . . . .	33
sahfos . . . . .	34
saunders . . . . .	35
simpson . . . . .	36
species.count . . . . .	38
spitale . . . . .	39
summary.count . . . . .	40
theta.prob . . . . .	41
untb . . . . .	42
vallade . . . . .	44
volkov . . . . .	46
zsm . . . . .	47

---

untb-package

*Unified neutral theory of biodiversity*

---

## Description

Numerical simulations, and visualizations, of the unified neutral theory of biodiversity

## Details

Package: untb  
Type: Package  
Version: 1.0  
Date: 2005-10-26  
License: GPL

Package untb uses two classes of object to represent an ecosystem: class count and class census. In essence, a count object is a table of species abundances and a census object is a list of individuals. See ?census and ?count for more details. Although objects of either class can be coerced to the other, class count is the preferred form: it is a more compact representation, especially for large ecosystems.

The package simulates neutral ecological drift using function untb(). Function display.untb() displays a semi-animated graphic of an ecosystem undergoing neutral drift.

## Author(s)

Robin K. S. Hankin

Maintainer: <hankin.robin@gmail.com>

## References

- S. P. Hubbell 2001. "The Unified Neutral Theory of Biodiversity". Princeton University Press.
- R. K. S. Hankin 2007. *Introducing untb, an R package for simulating ecological drift under the unified neutral theory of biodiversity*. Journal of Statistical Software, volume 22, issue 12

## Examples

```
a <- untb(start=rep(1,100),prob=0.005,gens=5000,keep=FALSE)
preston(a)
no.of.spp(a)

display.untb(start=rep(1,100),prob=0.1,gens=1000)

data(butterflies)
plot(butterflies,uncertainty=TRUE)
```

---

+.count                      *Add two count objects*

---

## Description

Adds two count objects

## Usage

```
## S3 method for class 'count'  
a + b  
## S3 method for class 'census'  
a + b
```

## Arguments

a,b                      objects of class count

## Details

Consider count objects a and b. Then a+b is a count object that records the number of each species in a and b combined. It is as though the organisms in the surveys were pooled.

Census objects are coerced to count objects, added, then the result coerced to a count object.

The operation is commutative and associative.

## Author(s)

Robin K. S. Hankin, based on an R-help tip from Gabor Grothendiek

## Examples

```
a <- count(c(dogs=4,pigs=0,slugs=5))  
b <- count(c(slugs=4,hogs=1,frogs=19))  
  
a+b
```

alonso

*Various functions from Alonso and McKane 2004***Description**

Various functions from Alonso and McKane 2004 dealing with analytical solutions of a neutral model of biodiversity

**Usage**

```
alonso.eqn6(JM, n, theta)
alonso.eqn11(J, n, theta)
alonso.eqn12(J, n, theta, give=FALSE)
```

**Arguments**

J, JM	Size of the community and metacommunity respectively
n	Abundance
theta	Biodiversity constant
give	In function <code>alonso.eqn12()</code> , Boolean with default FALSE meaning to return the value of the integral, and TRUE meaning to return the full output of <code>integrate()</code>

**Details**

Notation follows that of Alonso and McKane 2004

**Note**

Function `alonso.eqn6()` is identical to function `vallade.eqn5()`

**Author(s)**

Robin K. S. Hankin

**References**

D. Alonso and A. J. McKane 2004. "Sampling Hubbell's neutral model of biodiversity", Ecology Letters 7:901-910

**Examples**

```
J <- 100
plot(1:J , alonso.eqn11(J,n=1:J,
theta=5),log="y",type="l",xlab="n",ylab=expression(S(n)),main="Eqns
11 and 12 of Alonso and McKane")
points(1:J , alonso.eqn12(J,n=1:J, theta=5),type="l",lty=2)
legend("topright",legend=c("equation 11","equation 12"),lty=1:2)
```

bci

*Barro Colorado Island (BCI) dataset***Description**

The BCI dataset contains location and species identity for all 10cm dbh (diameter at breast height) trees on Barro Colorado Island, currently for years 1981-1983, 1985, 1990, 1995, 2000, and 2005. The subset of interest here is the abundances for each of the 252 species recorded.

The BCI dataset is not included in the **untb** package, because its licence appears to be inconsistent with the GPL.

It is discussed here because it was used as an example dataset in Hankin 2007.

**Source**

- <http://ctfs.si.edu/datasets/bci/abundance/>
- [http://www.stri.org/english/research/facilities/terrestrial/barro\\_colorado/index.php](http://www.stri.org/english/research/facilities/terrestrial/barro_colorado/index.php)

**References**

- R. Condit, S. P. Hubbell and R. B. Foster 2005. *Barro Colorado Forest Census Plot Data* <http://ctfs.si.edu/datasets/bci>
- [http://en.wikipedia.org/wiki/Barro\\_Colorado\\_Island](http://en.wikipedia.org/wiki/Barro_Colorado_Island)
- S. P. Hubbell 2001. “The Unified Neutral Theory of Biodiversity”. Princeton University Press.
- <http://ctfs.si.edu/datasets/bci/Terms%20and%20conditions.htm>
- R. K. S. Hankin 2007. “Introducing **untb**, an R package for simulating ecological drift under the unified neutral theory of biodiversity”. *Journal of Statistical Software*, volume 22, issue 12

butterflies

*abundance data for butterflies***Description**

A dataset of class “count” showing the abundance of several butterfly species

**Usage**

```
data(butterflies)
```

**Format**

A table with names of different butterfly species, and entries corresponding to the respective numbers of individuals.

**Source**

<http://texasnaturalist.net/butterflies/bflyct96.html>

**References**

Texas Birding and Naturalist Web

**Examples**

```
data(butterflies)
plot(butterflies, uncertainty=TRUE)
```

---

caruso

*Dataset due to Caruso*

---

**Description**

A dataframe in standard format due to Migliorini and Caruso presenting observations of oribatid mites.

**Usage**

```
data(caruso)
```

**Format**

Dataset caruso is a data frame with 194 observations on 5 variables. Each row corresponds to a species; the observations (rows) are the species abundances in each of 5 habitats.

Following Migliorini et al 2002, the habitats were:

- a pure beech woodland ('Beech')
- a coppice woodland ('Coppice')
- grassland ('Grassland')
- heathland ('Heathland')
- 'Biancana' badlands ('Biancana')

**Details**

Oribatid mites are rather small and very interesting free living soil microarthropods. They have a huge species diversity with populations characterised by highly aggregated distributions over multiple spatial scales ranging from a few centimetres to hundreds of meters.

Within each habitat, several soil samples were collected (five randomly located replicates per each month: see the paper Migliorini et al. 2002). So, actually, that is a network of small samples that make a single large sample.

The five study areas of this data set belong to five habitats that are very typical of that Mediterranean region. These five areas also belong to a rather homogeneous biogeographical region (southern Tuscany). On the ground of what is known on the biology and community patterns of Oribatida, several a-priori hypotheses can be made on expected changes in the diversity of their assemblages and immigration rates respectively between and within the five areas. For instance, under the Neutral Model one might expect that the Beech forest should have the highest Theta and an immigration rate of about 1, while one might expect the opposite for the Biancana (a very arid habitat, a kind of gariga/garrigue with very patchy vegetation).

### Source

Data kindly supplied by Tancredi Caruso

### References

- T. Caruso and others 2007. “The Berger-Parker index as an effective tool for monitoring the biodiversity of disturbed soils: a case study on Mediterranean oribatid (Acari: Oribatida) assemblages”. *Biodiversity Conservation*, 16:3277-3285
- M. Migliorini, A. Petrioli, and F. Bernini 2002. “Comparative analysis of two edaphic zoocoenoses (Oribatid mites and Carabid beetles) in five habitats of the ‘Pietraporciana’ and ‘Lucciolabella’ Nature Reserves (Orcia Valley, central Italy)”. *Acta Oecologica*, 23:361-374

### See Also

[extractor](#)

### Examples

```
data(caruso)

summary(count(caruso[,1]))

optimal.params.sloss(caruso)
```

---

census

*Construct, coerce, and test for a census object*

---

### Description

In package `untb`, ecosystem data is held in one of two preferred forms: census data and count data. Function `as.census()` coerces to census format.

### Usage

```
census(a)
as.census(a)
is.census(a)
```



## Arguments

`a` Ecosystem data. In function `as.census()`, if a table, interpret as species count data; otherwise, interpret as census data

## Details

A “census” object is a list of individuals in the form of an unnamed vector whose elements indicate the individuals’ species; compare “count” objects.

An object of class “census” is also an unordered factor. The levels are always in alphabetical order.

Function `census()` takes an object of class “count” and returns an object of class “census”. This function is not really intended for the end user.

Function `as.census()` coerces to class “count” then returns `census()` of the result.

## Value

Returns an object of class “census”.

## Author(s)

Robin K. S. Hankin

## See Also

[count](#)

## Examples

```
jj <- c(dogs=4,pigs=10,slugs=0,fish=1)

x <- census(jj) # slugs appear as zero abundance
extant(x) # slugs gone

x+x # count method for census objects: order of elements lost

as.census(jj) # probably NOT what you meant

a <- c(rep("oak",5) ,rep("ash",2),rep("elm",3),rep("xx",4))
# note that "a" is a plain vector here.
as.census(a)
```

---

`copepod`*Copepod data supplied by Phil Pugh*

---

**Description**

A dataset of copepod (resp: ostracod) abundances supplied by Dr Phil Pugh of the National Oceanography Centre, Southampton

**Usage**

```
data(copepod)
data(ostracod)
```

**Format**

A table with names of different copepod (resp: ostracod) species, and entries corresponding to the numbers of individuals of each species.

**Source**

<http://www.soc.soton.ac.uk/>

**Examples**

```
data(copepod)
optimize(f=theta.likelihood,interval=c(10,100), maximum=TRUE,
S=no.of.spp(copepod), J=no.of.ind(copepod), give.log=TRUE)

data(ostracod)
preston(ostracod)
```

---

`count`*Construct, coerce, and test for a count object*

---

**Description**

In package `untb`, ecosystem data is held in one of two preferred forms: census data and count data. Function `count` creates an object of class “count”, and `as.count()` coerces to this class.

**Usage**

```
as.count(a, add="")
count(a)
is.count(a)
```

**Arguments**

- a** Ecosystem data. In function `as.count()`, if a table, interpret as species count data; otherwise, interpret as census data. Special dispensation is made for single rows of a dataframe
- add** In function `as.count()`, character argument with default "" (empty string) meaning to leave the species names unchanged. A non-empty string is prepended to the species names using `paste()`. This is useful if the species names are integers because the display can become confusing

**Details**

A “count” object is a list of species together with their abundance. It also has class “table”; compare “census” objects.

An object of class “count” is a table sorted from most to least abundant species. The singletons are thus tabulated last.

Function `count()` takes a vector, the elements of which are interpreted as abundances. If any of the elements are named, the names are interpreted as species names (unnamed elements are given the null name). If the vector is unnamed, then the species names are upper case letters, with the first element being named “A”, the second “B”, and so on; this behaviour is inherited from `as.table()`. Note that this means that the species names are not necessarily in alphabetical order. From version 1.6-9, zero elements are interpreted as zero abundance species (ie extinct).

To access or change species names, use `names()` and `names<-` respectively.

Function `as.count()` coerces its argument to count form.

**Value**

Returns an object of class “count”.

**Author(s)**

Robin K. S. Hankin

**See Also**

[census](#)

**Examples**

```
a <- c(rep("oak", 5) ,rep("ash", 2), rep("elm", 3), rep("xx", 4))
as.count(a)
```

```

data(saunders)
as.count(saunders[1,-(1:150)])

jj <- sample(1:5,5,replace=TRUE)
as.count(jj)
as.count(jj,add="spp.")

```

---

display.untb

*Animation of neutral ecological drift*


---

### Description

Displays an ongoing simulation of neutral ecological drift using nice colours and a simple animation technique

### Usage

```

display.untb(start, gens=100, prob.of.mutate = 0, cex=3, individually
= TRUE, ask = FALSE, flash = FALSE, delay = 0, cols=NULL, ...)

```

### Arguments

start	Starting ecosystem; coerced to class census. Usually, pass an object of class count; see examples. To start with a monoculture of size 10, use <code>start=rep(1,10)</code> and to start with a system of maximal diversity (ie all singletons), use <code>start=1:10</code>
gens	Number of generations to simulate
prob.of.mutate	Probability of mutation. The default of zero corresponds to $\theta = 0$ and this means that any ecosystem will eventually become a monoculture (it is particularly instructive to watch this happen, especially with a starting ecosystem of maximal diversity—but be warned, this can take a long time, especially for ecosystems with a large number of individuals). Nonzero values mean that a nontrivial dominance-diversity curve will eventuate, although this too can take a long time to happen. Try a nonzero value of <code>prob.of.mutate</code> with monoculture start (use <code>individually=FALSE</code> for such experiments)
cex	The size of the dots used for plotting, defaulting to 3
individually	Boolean, with default TRUE meaning that a timestep means the death of a single individual and the simultaneous birth of a new individual; and FALSE meaning that a timestep refers to every individual in the system
ask	Boolean, with default FALSE meaning to display the generations autonomously, and TRUE meaning to wait for the user to hit the “return” before proceeding
flash	Boolean, with TRUE meaning to indicate the site of a death/birth with a flashing ring; and default FALSE meaning to omit the flashing ring. Use TRUE for pedagogic purposes, possibly with <code>ask</code> set to TRUE, or a nonzero delay. This option only kicks in if <code>individually</code> is TRUE

delay	Time delay between generations in seconds; meaningful whatever the value of flash and individually
cols	A vector of colours with default NULL meaning to choose them randomly. Useful for printing stills from a movie
...	Further arguments passed to <code>plot()</code> and <code>points()</code>

**Author(s)**

Robin K. S. Hankin

**References**

S. P. Hubbell 2001. "The Unified Neutral Theory of Biodiversity". Princeton University Press.

**Examples**

```
data(butterflies)
display.untb(start=butterflies,prob=0, gens=1e2)
```

---

etienne

*Etienne's sampling formula*

---

**Description**

Function `etienne()` returns the probability of a given dataset given  $\theta$  and  $m$  according to the Etienne's sampling formula. Function `optimal.params()` returns the maximum likelihood estimates for  $\theta$  and  $m$  using numerical optimization

**Usage**

```
etienne(theta, m, D, log.kda = NULL, give.log = TRUE, give.like = TRUE)
optimal.params(D, log.kda = NULL, start = NULL, give = FALSE, ...)
```

**Arguments**

theta	Fundamental biodiversity parameter
m	Immigration probability
D	Dataset; a count object
log.kda	The KDA as defined in equation A11 of Etienne 2005. See details section
give.log	Boolean, with default TRUE meaning to return the logarithm of the value
give.like	Boolean, with default TRUE meaning to return the likelihood and FALSE meaning to return the probability
start	In function <code>optimal.params()</code> , the start point for the optimization routine $(\theta, m)$ .
give	In function <code>optimal.params()</code> , Boolean, with TRUE meaning to return all output of the optimization routine, and default FALSE meaning to return just the point estimate
...	In function <code>optimal.params()</code> , further arguments passed to <code>optim()</code>

## Details

Function `etienne()` is just Etienne's formula 6:

$$P[D|\theta, m, J] = \frac{J!}{\prod_{i=1}^S n_i \prod_{j=1}^J \Phi_j!} \frac{\theta^S}{(\theta)_J} \times \sum_{A=S}^J \left( K(D, A) \frac{(\theta)_J}{(\theta)_A} \frac{I^A}{(I)_J} \right)$$

where  $\log K(D, A)$  is given by function `logkda()` (qv). It might be useful to know the (trivial) identity for the Pochhammer symbol [written  $(z)_n$ ] documented in `theta.prob.Rd`. For convenience, Etienne's Function `optimal.params()` uses `optim()` to return the maximum likelihood estimate for  $\theta$  and  $m$ .

Compare function `optimal.theta()`, which is restricted to no dispersal limitation, ie  $m = 1$ .

Argument `log.kda` is optional: this is the  $K(D, A)$  as defined in equation A11 of Etienne 2005; it is computationally expensive to calculate. If it is supplied, the functions documented here will not have to calculate it from scratch: this can save a considerable amount of time

## Author(s)

Robin K. S. Hankin

## References

R. S. Etienne 2005. "A new sampling formula for biodiversity". *Ecology letters* 8:253-260

## See Also

[logkda, optimal.theta](#)

## Examples

```
data(butterflies)
## Not run: optimal.params(butterflies) #takes too long without PARI/GP

#Now the one from Etienne 2005, supplementary online info:

zoo <- count(c(pigs=1, dogs=1, cats=2, frogs=3, bats=5, slugs=8))
l <- logkda.R(zoo, use.brob=TRUE) # Use logkda() if pari/gp is available
optimal.params(zoo, log.kda=1) #compare his answer of 7.047958 and 0.22635923.
```

---

expected.abundance      *Expected abundances under the neutral model*

---

**Description**

Returns a vector of expected abundances of the i-th ranked species under the neutral model

**Usage**

```
expected.abundance(J, theta)
```

**Arguments**

J	Size of the ecosystem
theta	Biodiversity parameter

**Value**

Returns an object of class count. Species names (capital letters) are assigned by function count().

**Note**

Function is very slow even for moderate J.

**Author(s)**

Robin K. S. Hankin

**References**

S. P. Hubbell 2001. "The Unified Neutral Theory of Biodiversity". Princeton University Press.

**See Also**

[rand.neutral,count](#)

**Examples**

```
expected.abundance(J=10, theta=3)

sum(expected.abundance(J=10, theta=3)) #should be 10
```

---

`extractor`*Extract rows of a database in count form*

---

**Description**

Extracts rows of a data frame and, if there is one row only, coerces to a count object, preserving the species names

**Usage**

```
extractor(x, index)
```

**Arguments**

<code>x</code>	A data frame with column headings being species names
<code>index</code>	A vector of indices to extract

**Details**

If `index` is length one, the numbers are interpreted as species counts, and the output is coerced to a count object.

**Author(s)**

Robin K. S. Hankin

**Examples**

```
data(saunders)
plot(extractor(saunders.exposed, 1))
```

---

`fisher`*Various functionality to implement Fisher's logseries*

---

**Description**

Various functions connected to Fisher's logseries including creation of synthetic datasets and estimation of Fisher's alpha

**Usage**

```
fishers.alpha(N, S, give=FALSE)
fisher.ecosystem(N, S, nmax, alpha=NULL, c=0)
```



**Arguments**

N	Size of the ecosystem. In the case of <code>fisher.ecosystem()</code> , the expected size of the ecosystem
S	Number of species in ecosystem
alpha	In function <code>fisher.ecosystem()</code> , Fisher's $\alpha$ . If not supplied, it will be calculated from N and S.
give	In function <code>fishers.alpha()</code> , Boolean variable with default FALSE meaning to return alpha, and TRUE meaning to return a list containing x and alpha.
nmax	In function <code>fisher.ecosystem()</code> , the maximum number of species abundance classes to consider
c	In function <code>fisher.ecosystem()</code> , the rare species advantage term

**Details**

Function `fishers.alpha()` solves for  $\alpha$  given  $N$  and  $S$ , as per Fisher's table 9, p55.

Given  $N$  and  $S$  (or  $\alpha$ ), function `fisher.ecosystem()` generates a Fisherian ecosystem with expected size  $N$  and expected species count  $S$ .

**Author(s)**

Robin K. S. Hankin

**References**

R. A. Fisher and A. S. Corbet and C. B. Williams 1943. "The relation between the number of species and the number of individuals in a random sample of an animal population", *Journal of Animal Ecology*, volume 12, pp 42–58

**Examples**

```
fishers.alpha(N=100000,S=100)
#compare the Table value:
100000/10^3.95991
```

---

ghats	<i>Tree counts in 1-ha plots from the Western Ghats mountains (South India)</i>
-------	---

---

**Description**

Tree species counts are given in 50 one-hectare sampling plots (species by sample matrix). This only includes trees over 10 cm dbh (diameter at breast height) and species labels (row names) are numeric.

**Usage**

```
data(ghats)
```

**Format**

Data frame displaying 304 species counts over 50 one-hectare plots.

**Source**

Ecological Archives E088-149-A1. <http://www.esapubs.org/Archive/ecol/E088/149/appendix-A.htm>

**References**

Francois Munoz, Pierre Couteron, B. R. Ramesh, and Rampal S. Etienne 2007. “Estimating parameters of neutral communities: from one single large to several small samples.” *Ecology* 88(10):2482-2488.

**Examples**

```
data(ghats)
# Rank-abundance picture of plot 1 (column 1 in ghats)
plot(extant(count(ghats[,1])))

#histogram of optimal theta across the 50 plots:
hist(apply(ghats,2,optimal.theta),col='gray')
```

---

isolate

*Randomly select a subset of an ecosystem*

---

**Description**

Return an ecosystem comprised of individuals randomly sampled from a metacommunity

**Usage**

```
isolate(a, size = no.of.ind(a), replace = TRUE)
```

**Arguments**

a	Ecosystem data
size	Number of individuals to sample
replace	Boolean, with default TRUE meaning to sample individuals from the metacommunity with replacement and FALSE meaning to sample without replacement. See details section

**Details**

Setting argument `replace` to default `TRUE` is much faster.

The canonical example is given by Leigh et al 1993, in which islands were isolated from the mainland by rising waters. The trees on the islands were held to be a randomly drawn sample from the metacommunity.

Given that the usual usage of this function is to generate a plausible ecosystem under such a scenario, one would have a hard time justifying the use of `replace=TRUE` as it allows (for example) a singleton metacommunity species to have multiple representatives in the returned ecosystem.

However, for large metacommunities and small subsamples, the distinction between `replace=TRUE` and `replace=FALSE` is small.

**Value**

Returns a count object

**Note**

If `replace=FALSE`, the returned count object includes extinct species. Use `extant(isolate(...))` to return only extant species

**Author(s)**

Robin K. S. Hankin

**References**

E. G. Leigh and others 1993. "The decline of tree diversity on newly isolated tropical islands: a test of a null hypothesis and some implications". *Evolutionary Ecology*, 7:76-102

**Examples**

```
a <- rand.neutral(1000,10)
no.of.spp(a)
no.of.spp(isolate(a))
```

---

logkda

*Etienne's  $K(D,A)$*

---

**Description**

Calculates Etienne's  $K(D, A)$  using a variety of different methods

**Usage**

```

logkda.R(a, use.brob=TRUE)
logkda.a11(a)
logkda.pari(a, numerical=TRUE, gp_binary = "gp")
logkda.polyn(a)
logkda(a, method="pari", ...)
logkda_pari_unix(a, numerical, pari_string, gp_binary)
logkda_pari_windows(a, numerical, pari_string)

```

**Arguments**

<code>a</code>	Count object
<code>use.brob</code>	In function <code>logkda.R()</code> , Boolean, with default TRUE meaning to use Brobdingnagian numbers for the calculation. This is slower but allows one to analyze larger datasets
<code>numerical</code>	Boolean, with default TRUE meaning to coerce to a numerical vector (thereby losing precision), and FALSE meaning to return the string produced by pari/gp
<code>method</code>	In function <code>logkda()</code> , a string specifying which method to use. Takes "R", "a11", or "pari"
<code>pari_string, gp_binary</code>	configuration variables (not intended to be changed by the user)
<code>...</code>	In function <code>logkda()</code> , further arguments which are passed to the other functions

**Details**

The user should use function `logkda()`, which is a wrapper for the other functions. Note that the default method, `pari`, requires the pari/gp system to be installed. This is the preferred option because it is much faster than the other methods.

Functions `logkda.R()` and `logkda.pari()` calculate  $K(D, A)$  using the method appearing in Etienne (2005), supplementary online material; they use R and pari/gp respectively. Function `logkda.a11` is a direct implementation of formula A11 in Etienne (2005). The formula is

$$K(D, A) = \sum_{\{a_1, \dots, a_S | \sum a_i = A\}} \prod_{i=1}^S \frac{\bar{s}(n_i, a_i) \bar{s}(a_i, 1)}{\bar{s}(n_i, 1)}$$

where  $\bar{s}(n_i, a_i)$  are Stirling numbers of the first kind (see `logS1`).

Function `logkda.pari()` dispatches to either `logkda_pari_unix()` or `logkda_pari_windows()` but the windows function is not guaranteed to work.

**Note**

If `method` takes its default value of "pari", and pari/gp is not installed (the test is `gp --version`), then the method is changed to R and a warning given.

Function `logkda.a11()` is included because the computational method is a direct transcription of formula A11; it is very slow.

Function `logkda.pari()` is a wrapper for `.logkda.pari.windows()` or `.logkda.pari.unix()`. It uses “`if(R.Version()$os == 'windows')`” to check for windows operating systems.

It would be nice to use `gp2c` (rather than `gp`) but I can’t make the “-g” flag work properly; and I had to hack `gp2c-run` to make it call `gp` with the `-q` flag

### Author(s)

Robin K. S. Hankin; `logkda()` is an R transliteration of `pari/gp` code appearing in Etienne 2005 (supplementary online material) due to Chave.

Function `logkda.polyn()` provided by Francois Munoz.

Function `.logkda.pari.windows()` provided by Andrea Manica and Francois Munoz.

### References

R. S. Etienne 2005. “A New Sampling Formula for Neutral Biodiversity”. *Ecology Letters*, volume 8, pp253–260. doi: 10.1111/j.1461-0248.2004.00717.x

C. Batut and K. Belabas and D. Bernardi and H. Cohen and M. Olivier 2000. “User’s guide to PARI/GP”. <http://www.parigp-home.de/>

### See Also

[etienne,logS1](#)

### Examples

```
a <- count(c(dogs=7,pigs=3,crabs=1,hogs=1,slugs=1))
## Not run: logkda(a)

logkda.R(a)
logkda.R(a, use.brob=FALSE)
logkda.a11(a)
# All four should be the same up to numerical errors
```

---

logS1

*logarithms of Stirling numbers of the first kind*

---

### Description

Natural logarithms of Stirling numbers of the first kind, used by function `logkda.a11()` (dataset `logS1`) and function `logkda.polyn()` (dataset `logS1vect`).

### Usage

logS1

**Format**

Dataset logS1 is a 100-by-100 matrix of logs of Stirling numbers of the first kind; logS1vect is a vector of length 499500

**Source**

Calculated by Maple

**See Also**

[etienne](#)

**Examples**

```
exp(logS1[1:5,1:5])
```

---

no.of.ind

*Ecosystem diagnostics*

---

**Description**

Ecosystem diagnostics such as species count, individual count, number of singletons, etc

**Usage**

```
no.of.ind(x)  
no.of.spp(x, include.extinct=FALSE)  
no.of.singletons(x)  
no.of.extinct(x)  
maximal.abundance(x)  
singletons(x)  
extinct(x)  
extant(x)
```

**Arguments**

x                    Ecosystem vector; is coerced to class count

include.extinct

In function `no.of.spp()`, Boolean argument with TRUE meaning to include extinct species (ie species with an abundance of zero), and default FALSE meaning to return the number of extant species

**Details**

- Function `no.of.spp()` returns the number of species in an ecosystem object, treating extinct species in line with argument `include.extinct`
- Function `no.of.ind()` returns the number of individuals
- Function `no.of.singletons()` returns the number of singletons
- Function `no.of.extinct()` returns the number of extinct species
- Function `maximal.abundance()` returns the abundance of the most abundant species
- Function `singletons()` returns a count object containing only the singletons: each abundance is one
- Function `extinct()` returns a count object containing only the extinct species: each abundance is zero
- Function `extant()` returns a count object containing only the extant species: each abundance is greater than zero

**Note**

It is sometimes useful to include species with an abundance of zero when, for example, taking a single row of the Saunders dataframe.

The default for `include.extinct` is `FALSE` because this is required for (eg) `optimal.theta()`

**Author(s)**

Robin K. S. Hankin

**References**

S. P. Hubbell. “The Unified Neutral Theory of Biodiversity”. Princeton University Press, 2001.

**Examples**

```
data(butterflies)
no.of.spp(butterflies)
no.of.ind(butterflies)

jj1 <- count(c(dogs=7,pigs=3,crabs=1,slugs=1))
jj2 <- count(c(squid=0,octopus=0,nautilus=0))
jj3 <- count(c(bugs=3,rats=1,crabs=0,fish=0))

extinct(jj1 + jj2)
extinct(jj3)           #cats 'n' fish
extant(jj3)           #bugs and rats

singletons(jj1)
singletons(jj2)       # empty
singletons(jj1 + jj3) # crabs, rats and slugs
```

---

optimal.params.gst      *Estimation of local immigration using GST(k) statistics*

---

### Description

Functions `optimal.params.gst()`, `GST.k()` and `I.k()` apply to count data collected over a network of community samples  $k$  (species by sample matrix). A theoretical relationship between  $GST(k)$  statistics and local immigration numbers  $I(k)$ , in the context of a spatially-implicit neutral community model (Munoz et al 2008), is used to provide  $GST(k)$  and  $I(k)$  statistics any sample  $k$ .

If requested, `optimal.params.gst()` further provides the user with confidence bounds.

### Usage

```
optimal.params.gst(D, exact = TRUE, ci = FALSE, cint = c(0.025, 0.975), nbres = 100)
GST.k(D, exact = TRUE)
I.k(D, exact = TRUE)
```

### Arguments

<code>D</code>	A data table including species counts in a network of community samples (columns)
<code>exact</code>	If TRUE, exact similarity statistics are calculated (sampling without replacement) while, if false, approximate statistics (sampling with replacement) are considered (see Munoz et al 2008 for further statistical discussion)
<code>ci</code>	Specifies whether bootstraps confidence intervals of immigration estimates are to be calculated
<code>cint</code>	Bounds of the confidence interval, if <code>ci = TRUE</code>
<code>nbres</code>	Number of rounds of the bootstrap procedure for confidence interval calculation, if <code>ci = T</code>

### Value

<code>GST</code>	A vector of 0 to 1 $GST(k)$ numbers (specific output of <code>GST.k</code> )
<code>nk</code>	Number of individuals within samples (length = number of samples)
<code>distrib</code>	Species counts of the merged dataset (output of <code>GST.k</code> and <code>I.k</code> )
<code>I</code>	Immigration estimates (output of <code>I.k</code> and <code>optimal.params.gst</code> )
<code>m</code>	Corresponding immigration rates (output of <code>I.k</code> and <code>optimal.params.gst</code> ). Specific outputs of <code>optimal.params.gst</code> when <code>ci = T</code> (bootstrap procedure)
<code>Ici</code>	Confidence interval of $I(k)$
<code>mci</code>	Confidence interval of $m(k)$
<code>Iboot</code>	Table of bootstrapped values of $I(k)$
<code>mboot</code>	Table of bootstrapped values of $im(k)$



**Author(s)**

Francois Munoz

**References**

Francois Munoz, Pierre Couteron and B.R. Ramesh (2008). “Beta-diversity in spatially implicit neutral models: a new way to assess species migration.” *The American Naturalist* 172(1): 116-127

**See Also**

[optimal.params](#), [optimal.params.sloss](#)

**Examples**

```
data(ghats)
optimal.params.gst(ghats)
```

---

`optimal.params.sloss`     *Estimation of neutral community parameters using a two-stage maximum-likelihood procedure*

---

**Description**

Function `optimal.params.sloss()` returns maximum likelihood estimates of  $\theta$  and  $m(k)$  using numerical optimization.

It differs from `untb`'s `optimal.params()` function as it applies to a network of smaller community samples  $k$  instead of to a single large community sample.

Although there is a single, common  $\theta$  for all communities, immigration estimates are provided for each local community  $k$ , sharing a same biogeographical background.

**Usage**

```
optimal.params.sloss(D, nbres = 100, ci = FALSE, cint = c(0.025, 0.975))
```

**Arguments**

<code>D</code>	Species counts over a network of community samples (species by sample table)
<code>nbres</code>	Number of resampling rounds for $\theta$ estimation
<code>ci</code>	Specifies whether bootstraps confidence intervals should be provided for estimates
<code>cint</code>	Bounds of confidence intervals, if <code>ci = T</code>

**Value**

theta	Mean theta estimate
I	The vector of estimated immigration numbers I(k)
Output of the bootstrap procedure, if ci = T:	
thetaci	Confidence interval for theta
msampleci	Confidence intervals for m(k)
thetasamp	theta estimates provided by the resampling procedure
Iboot	Bootstrapped values of I(k)
mboot	Bootstrapped values of m(k)

**Author(s)**

Francois Munoz

**References**

Francois Munoz, Pierre Couteron, B. R. Ramesh, and Rampal S. Etienne 2007. "Estimating parameters of neutral communities: from one single large to several small samples". *Ecology* 88(10):2482-2488

**See Also**

[optimal.params](#), [optimal.params.gst](#)

**Examples**

```
data(ghats)
optimal.params.sloss(ghats)
```

---

optimal.prob

*Returns an estimate of the fundamental biodiversity number*

---

**Description**

Returns a maximum likelihood estimate for the fundamental biodiversity number  $\theta$  (function `optimal.theta()`) or the probability of mutation (function `optimal.prob()`) and optionally return information about the likely error

**Usage**

```
optimal.prob(x, interval=NULL, N=NULL, like=NULL, ...)
optimal.theta(x, interval=NULL, N=NULL, like=NULL, ...)
```

**Arguments**

x	Ecosystem vector or species count table
interval	Bracketing interval for probability of mutation to be passed to the optimization routine (here <code>optimize()</code> ). Default of NULL means to use a wide interval. Note that this argument is interpreted as an interval of $\theta$ for both <code>optimal.prob()</code> and <code>optimal.theta()</code> .
N	Integer; the number of parametric resampled estimates to give. Default of NULL means to return just the maximum likelihood estimate
like	Units of likelihood to calculate credible interval. Edwards recommends using 2
...	Further arguments passed to <code>optimize()</code>

**Note**

The fundamental biodiversity parameter  $\theta$  is  $2\nu J$ , where  $\nu$  is the probability of mutation (ie, as estimated by `optimal.prob()`), and  $J$  is the size of the ecosystem.

For the general case of dispersal limitation, see functions `etienne()` and `optimal.params()`.

**Author(s)**

Robin K. S. Hankin

**See Also**

[etienne](#), [optimal.params.sloss](#), [optimal.params.gst](#)

**Examples**

```
data(butterflies)
optimal.prob(butterflies)
optimal.theta(butterflies)
```

---

 phi

*Hubbell's phi*


---

**Description**

Hubbell's phi: counts of species abundances

**Usage**

```
phi(x, addnames=TRUE)
unphi(freq, string="spp")
```

**Arguments**

x	Ecosystem vector; is coerced to class count
addnames	Boolean with default TRUE meaning to set the name of the <i>i</i> th element to the species with abundance <i>i</i> if unique. Set to FALSE to suppress this, which is useful if the species names are long
freq	Frequency data (eg as returned by phi())
string	Character; species name to prepend (using NULL can be confusing)

**Details**

Function phi() coerces its argument to a count object and by default returns a named vector whose *i*th element is the number of species with *i* individuals. The name of the *i*th element is the species with abundance *i* if unique and empty otherwise. Function phi() is used by theta.prob().

Function unphi() does the reverse: given the output of phi(), it returns a corresponding count object. Note that species names are lost.

**Note**

The code for setting the names is a dog's breakfast

**Author(s)**

Robin K. S. Hankin

**References**

S. P. Hubbell 2001. "The Unified Neutral Theory of Biodiversity". Princeton University Press.

**See Also**

[preston](#)

**Examples**

```
jj <- c(rep("oak",5) ,rep("ash",2),rep("elm",3),"pine","tea","yew")
a <- as.count(jj)

phi(a)
unphi(phi(a)) #should match 'a' except for species names (which are lost)

data(butterflies)
phi(butterflies,add=FALSE)

summary(unphi(phi(butterflies))) #should match 'summary(butterflies)'
```

---

plot.count	<i>Abundance curves</i>
------------	-------------------------

---

### Description

Plot the ranked abundance curve

### Usage

```
## S3 method for class 'count'
plot(x, uncertainty = FALSE, expectation = FALSE, theta = NULL, n = 10, ...)
## S3 method for class 'census'
plot(x, uncertainty = FALSE, expectation = FALSE, theta = NULL, n = 10, ...)
```

### Arguments

x	Ecosystem object, coerced to class count
uncertainty	Boolean, with TRUE meaning to show bootstrapped estimates for the species diversity curve, and default FALSE meaning to omit this
expectation	Boolean, with TRUE meaning to plot expected abundances, and default FALSE meaning not to plot them. <b>Warning</b> this option takes a loooong time to run, even for moderate values of $J$
theta	Fundamental biodiversity number used if argument uncertainty or expectation are TRUE. Default value of NULL means to use the maximum likelihood estimate returned by function <code>optimal.theta()</code>
n	Number of bootstrapped estimates to plot
...	Extra parameters passed to <code>untb()</code>

### Details

Plots a ranked abundance curve, optionally with parametrically resampled datasets showing the uncertainties

### Note

If using expectation, it's usually necessary to set `ylim` and possibly `xlim` manually.

### Author(s)

Robin K. S. Hankin

**Examples**

```

data(copepod)
plot(copepod)

data(butterflies)
plot(butterflies,uncertainty=TRUE)

x <- count(c(pigs=1, dogs=1, cats=2, frogs=3, bats=5, slugs=8))
plot(x,expectation=TRUE,ylim=c(0.5,10))

```

preston

*Preston diagram of an ecosystem***Description**

Gives a standard Preston diagram for an ecosystem.

**Usage**

```
preston(x,n=NULL,original=FALSE)
```

**Arguments**

x	Ecosystem vector that is coerced to class count, or a matrix whose rows are species counts
n	An integer specifying the number of species abundance classes to use, with default NULL meaning to use $1 + \log_2(J)$ . Must be greater than 1 if specified. If x is a vector, NULL is not acceptable as the program does not try to guess what is required
original	Boolean, with default FALSE meaning to use the nonoverlapping technique discussed below, and TRUE meaning to use Preston's original formulation.

**Details**

The Preston diagram is a table showing the number of species having abundances in specified abundance classes. Consider the following Preston diagram, created with `original = FALSE`:

	1	2	3-4	5-8	9-16	17-32	33-64	65-Inf
number of species	10	5	7	5	1	5	4	0

This shows that there are 10 species with abundance 1 (that is, singletons); 5 species with abundance 2; 7 species with abundance 3-4; 5 species with abundance 5-8, and so on. This method is used by Hubbell (2001), and Chisholm and Burgman (2004).

Setting argument `original` to TRUE means to follow Preston (1948) and count any species with an abundance on the boundary between two adjacent abundance classes as being split 50-50 between the classes. Thus the fourth class would be  $\phi_4/2 + \phi_5 + \phi_6 + \phi_7 + \phi_8/2$  where  $\phi_i$  is the number of species with abundance  $i$  (given by `phi(x)`).

**Value**

Function `preston()` returns an object of class “preston”.

**Author(s)**

Robin K. S. Hankin

**References**

- F. W. Preston 1948. “The Commonness, and Rarity, of Species”. *Ecology* 29(3):254-283
- R. A. Chisholm and M. A. Burgman 2004. “The unified neutral theory of biodiversity and biogeography: comment”. *Ecology* 85(11): 3172-3174
- S. P. Hubbell 2001. “The Unified Neutral Theory of Biodiversity”. Princeton University Press

**See Also**

[phi](#)

**Examples**

```
preston(untb(start=rep(1,100), prob=0.01, gens=1000, keep=FALSE))
```

```
data(butterflies)
preston(butterflies)
preston(butterflies,original=TRUE)
```

```
data(copepod)
preston(copepod)
```

---

```
print.preston          Print and plot objects of class Preston
```

---

**Description**

Print and plot objects of class `Preston`

**Usage**

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

**Arguments**

`x`                    Object of class “preston”  
`...`                further arguments passed to `print()` after class reset

**Note**

Intended to work with the output of function `preston()`.  
See the vignette for how to annotate a Preston plot.

**Author(s)**

Robin K. S. Hankin

**See Also**

[preston](#)

**Examples**

```
data(butterflies)
print(preston(butterflies))
```

---

`print.summary.count`    *Print method for summary objects*

---

**Description**

Print method for summary objects

**Usage**

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

**Arguments**

<code>x</code>	Object of class “summary.count”
<code>...</code>	extra arguments, currently ignored

**Author(s)**

Robin K. S. Hankin

**Examples**

```
data(butterflies)
summary(butterflies)
```



---

rand.neutral	<i>Random neutral ecosystem</i>
--------------	---------------------------------

---

**Description**

Given the size of the metacommunity  $J$ , and the fundamental biodiversity number  $\theta$ , generate an object of class count using a stochastic mechanism consistent with the neutral theory.

**Usage**

```
rand.neutral(J, theta=NULL, prob.of.mutate=NULL, string = NULL, pad = FALSE)
```

**Arguments**

J	Size of metacommunity
theta	Fundamental biodiversity number $\theta$ . User must supply exactly one of theta and prob.of.mutate.
prob.of.mutate	Probability of mutation $\nu$ : $\theta = 2J\nu$ .
string	String to add to species names. By default (ie string being NULL), species are named “1”, “2”,... Argument string supplies a prefix for these species names; a good one to use is “spp.”. This argument is useful because printing a count object can be confusing if the species names are all integers.
pad	Boolean, with default FALSE meaning to return a count object having only extant species, and TRUE meaning to pad the count with extinct species to J species. Use this when a vector of length J is required consistently (see examples section).

**Details**

Uses the simulation method on page 289 of Hubbell (2001).

**Note**

If pad is TRUE, and you set string to “extinct”, things will break.

**Author(s)**

Robin K. S. Hankin

**References**

S. P. Hubbell 2001. “The Unified Neutral Theory of Biodiversity”. Princeton University Press.

**See Also**

[untb](#)

**Examples**

```
rand.neutral(1000, 9)
rand.neutral(1000, 9, string="spp.")

data(butterflies)
rand.neutral(no.of.ind(butterflies), optimal.theta(butterflies), string="spp.")

# what is the distribution of abundance of the second ranked species if
# J=10, theta=0.7?
plot(table(replicate(100, rand.neutral(10, theta=0.7, pad=TRUE)[2])))
```

---

sahfos

*Biodiversity dataset provided by SAHFOS*

---

**Description**

Species counts in the North Atlantic

**Usage**

```
data(sahfos)
```

**Source**

<http://192.171.163.165/data.htm>

**References**

Warner AJ and Hays GC 1994. "Sampling by the Continuous Plankton Recorder Survey". *Progress in Oceanography*, 34: 237-256

**Examples**

```
data(sahfos)
preston(sahfos)
```

---

saunders

*Dataset due to Saunders*

---

## Description

A dataframe showing species inventories for a kelp holdfast (saunders) including a Boolean flag indicating whether the holdfast was in a sheltered or exposed location.

Also two data frames, one for the 20 exposed holdfasts (saunders.exposed) and one for the 20 sheltered holdfasts (saunders.sheltered).

Also three count objects, giving counts for all organisms (saunders.tot), all those from exposed locations (saunders.exposed.tot), and all those from sheltered locations only (saunders.sheltered.tot).

## Usage

```
data(saunders)
```

## Format

Dataset saunders is a dataframe with 40 observations on 177 variables. Each row corresponds to a holdfast. The first column is Boolean, indicating whether or not that holdfast was exposed (TRUE) or sheltered (FALSE). The other columns show species abundances for each of 176 species.

Summary datasets saunders.sheltered.tot, saunders.exposed.tot, and saunders.tot are objects of class count that are the species abundance for sheltered holdfasts, exposed holdfasts, and the entire dataset.

The user will probably be most interested in saunders.sheltered and saunders.exposed, which are the **transpose** of the appropriate rows of saunders. Thus these dataframes have 176 rows, one per species and 20 rows, one per holdfast.

## Details

Kelp are large seaweeds classified in kingdom Chromista. Kelp grows in shallow oceans in kelp forests.

The *holdfast* is a root-like structure that anchors the kelp to the ocean floor. Fauna inhabiting kelp holdfasts, being “incredibly diverse” (Anderson et al 2005), are often used as indicators of environmental change.

The data was collected in New Zealand, from eight sites along the Leigh coastline from north of Leigh Harbour down to the southern end of Kawau Island (a stretch of roughly 20 km). Four sites were wave-exposed, four were sheltered (although two of the latter were arguably quite tidally-dominated). Each site had a spatial extent of roughly one hectare. They were collected from 5 - 10 November, 2003.

The saunders dataset must be arranged as it is because if it were transposed, the first row would be the (nonsensical) observation  $c(T, T, \dots, T, F, \dots, F)$ .

**Note**

It is not entirely obvious how to derive the summary datasets from the saunders dataframe. Use function `extractor()` for this.

**Source**

Data supplied by Justine Saunders

**References**

- J. Saunders 2007. “Biodiversity of kelp holdfasts” (provisional title). PhD thesis (in preparation); School of Geography and Environmental Sciences, The University of Auckland
- M. J. Anderson and others 2005. “Consistency and variation in kelp holdfast assemblages: Spatial patterns of biodiversity for the major phyla at different taxonomic resolutions”. *Journal of Experimental Marine Biology and Ecology*. Volume 320, pages 35-56

**See Also**

[extractor](#)

**Examples**

```
data(saunders)
plot(saunders.sheltered.tot, uncertainty=TRUE, n=1)

preston(saunders.tot)

optimal.params.sloss(saunders.exposed)
```

---

simpson

*Simpson's diversity index*

---

**Description**

Simpson's diversity index

**Usage**

```
simpson(x, with.replacement=FALSE)
```

**Arguments**

`x` Ecosystem vector; coerced to class count

`with.replacement` Boolean, with default FALSE meaning to sample without replacement; see details section

**Details**

Returns the Simpson index  $D$ : the probability that two randomly sampled individuals belong to different species.

There is some confusion as to the precise definition: some authors specify that the two individuals are necessarily distinct (ie sampling without replacement), and some do not.

Simpson (1949) assumed sampling without replacement and gave

$$1 - \frac{\sum_{i=1}^S n_i (n_i - 1)}{J(J - 1)}$$

in our notation.

He and Hu (2005) assumed sampling with replacement:

$$1 - \frac{\sum_{i=1}^S n_i^2}{J^2}.$$

The difference is largely academic but is most pronounced when many species occur with low counts (ie close to 1).

**Author(s)**

Robin K. S. Hankin

**References**

- S. P. Hubbell 2001. "The Unified Neutral Theory of Biodiversity". Princeton University Press.
- F. He and X.-S. Hu 2005. "Hubbell's Fundamental Biodiversity Parameter and the Simpson Diversity Index". *Ecology Letters*, volume 8, pp386-390. doi: 10.1111/j.1461-0248.2005.00729.x
- E. H. Simpson 1949. "Measurement of diversity", *Nature*, volume 163, p688

**See Also**

[preston](#)

**Examples**

```
data(butterflies)

D <- simpson(butterflies)
theta <- optimal.prob(butterflies)*2*no.of.ind(butterflies)

# compare theta with D/(1-D) (should be roughly equal; see He & Hu 2005):
theta
D/(1-D)

# Second argument pedantic in practice.

# Mostly, the difference is small:
```

```
simpson(butterflies,FALSE) - simpson(butterflies,TRUE)

# Most extreme example:
x <- count(c(1,1))
simpson(x,TRUE)
simpson(x,FALSE)
```

---

species.count                      *Ecosystem diagnostics for output of untb()*

---

## Description

Provides ecosystem diagnostics of species count datasets (species counts and species tables), useful for the output of untb()

## Usage

```
species.count(x)
species.table(x)
```

## Arguments

`x`                      An integer matrix whose rows are integers representing the individuals' species

## Details

These functions takes a matrix argument, which is interpreted as the output of untb(...,keep=TRUE).

Function species.count() returns the total number of species present in each row (ie at each timestep).

Function species.table() returns a matrix  $M$  where  $M[i, j]$  column of the matrix is the abundance of species  $j$  at time  $i$ .

## Author(s)

Robin K. S. Hankin

## See Also

[preston](#)

**Examples**

```
a <- untb(start=rep(1,50), prob=0.01, gens=2000, keep=TRUE)

plot(species.count(a), type="b")
matplot(species.table(a), type="l", lty=1)

jj <- a[2000,]
print(jj)
as.count(jj)
```

---

spitale

*Counts of diatom species in springs of the Adamello-Brenta Nature Park*

---

**Description**

A dataset due to Spitale and Cantonati comprising abundances of different species of diatoms

**Usage**

```
data(spitale)
```

**Format**

A count object

**Source**

Data kindly provided by Daniel Spitale

**References**

D. Spitale and M. Cantonati 2011. "Understanding the natural variability of diatom assemblages in springs of the Adamello-Brenta Nature Park (south-eastern Alps) on a temporal scale". *Fundamental Applied Limnology* volume 179/2, pp137–149

**Examples**

```
data(spitale)
summary(spitale)
```

---

`summary.count`*Summary methods for count and census objects*

---

## Description

Summary methods for count and census objects

## Usage

```
## S3 method for class 'count'  
summary(object, ...)  
## S3 method for class 'census'  
summary(object, ...)
```

## Arguments

<code>object</code>	Ecosystem object coerced to class count
<code>...</code>	Further arguments, currently ignored

## Details

Prints a summary of an ecosystem object.

## Author(s)

Robin K. S. Hankin

## See Also

[phi](#)

## Examples

```
data(ostracod)  
summary(ostracod)
```



---

theta.prob	<i>Posterior probabilities for theta</i>
------------	--

---

### Description

Determines the posterior probability and likelihood for theta, given a count object

### Usage

```
theta.prob(theta, x=NULL, give.log=TRUE)
theta.likelihood(theta, x=NULL, S=NULL, J=NULL, give.log=TRUE)
```

### Arguments

theta	biodiversity parameter	
x	object of class count or census	
give.log	Boolean, with FALSE meaning to return the value, and default TRUE meaning to return the (natural) logarithm of the value	
S, J	In function theta.likelihood(), the number of individuals (J) and number of species (S) in the ecosystem, if x is not supplied. These arguments are provided so that x need not be specified if S and J are known.	

### Details

The formula was originally given by Ewens (1972) and is shown on page 122 of Hubbell (2001):

$$\frac{J! \theta^S}{1^{\phi_1} 2^{\phi_2} \dots J^{\phi_J} \phi_1! \phi_2! \dots \phi_J! \prod_{k=1}^J (\theta + k - 1)}$$

The likelihood is thus given by

$$\frac{\theta^S}{\prod_{k=1}^J (\theta + k - 1)}$$

Etienne observes that the denominator is equivalent to a Pochhammer symbol  $(\theta)_J$ , so is thus readily evaluated as  $\Gamma(\theta + J)/\Gamma(\theta)$  (Abramowitz and Stegun 1965, equation 6.1.22).

### Note

If estimating theta, use theta.likelihood() rather than theta.probability() because the former function generally executes **much** faster: the latter calculates a factor that is independent of theta.

The likelihood function  $L(\theta)$  is any function of  $\theta$  proportional, for fixed observation  $z$ , to the probability density  $f(z, \theta)$ . There is thus a slight notational inaccuracy in speaking of “the” likelihood function which is defined only up to a multiplicative constant. Note also that the “support” function is usually defined as a likelihood function with maximum value 1 (at the maximum likelihood estimator for  $\theta$ ). This is not easy to determine analytically for  $J > 5$ .

Note that  $S$  is a sufficient statistic for  $\theta$ .

Function `theta.prob()` does **not** give a PDF for  $\theta$  (so, for example, integrating over the real line does not give unity). The PDF is over partitions of  $J$ ; an example is given below.

Function `theta.prob()` requires a count object (as opposed to `theta.likelihood()`, for which  $J$  and  $S$  are sufficient) because it needs to call `phi()`.

### Author(s)

Robin K. S. Hankin

### References

- S. P. Hubbell 2001. “The Unified Neutral Theory of Biodiversity”, Princeton University Press.
- W. J. Ewens 1972. “The sampling theory of selectively neutral alleles”, *Theoretical Population Biology*, **3**:87–112
- M. Abramowitz and I. A. Stegun 1965. *Handbook of Mathematical Functions*, New York: Dover

### See Also

[phi](#), [optimal.prob](#)

### Examples

```
theta.prob(1,rand.neutral(15,theta=2))

gg <- as.count(c(rep("a",10),rep("b",3),letters[5:9]))
theta.likelihood(theta=2,gg)

optimize(f=theta.likelihood,interval=c(0,100),maximum=TRUE,x=gg)

## An example showing that theta.prob() is indeed a PMF:

a <- count(c(dogs=3,pigs=3,hogs=2,crabs=1,bugs=1,bats=1))
x <- partitions::parts(no.of.ind(a))
f <- function(x){theta.prob(theta=1.123,extant(count(x)),give.log=FALSE)}
sum(apply(x,2,f)) ## should be one exactly.
```

---

untb

*Ecological drift simulation under the Unified Neutral Theory of Biodiversity*

---

### Description

Simulates ecological drift under the UNTB. Function `untb()` carries out the simulation; function `select()` carries out a single generational step.

**Usage**

```
untb(start, prob=0, D=1, gens=150, keep=FALSE, meta=NULL)
select(a, D=length(a), prob=0, meta=NULL)
select.mutate(a, D=length(a), prob.of.mutate=0)
select.immigrate(a, D=length(a), prob.of.immigrate=0, meta)
```

**Arguments**

<code>a, start</code>	Starting ecosystem; coerced to class census. Usually, pass an object of class count; see examples. To start with a monoculture of size 10, use <code>start=rep(1,10)</code> and to use <code>start=1:10</code> .
<code>prob, prob.of.immigrate, prob.of.mutate</code>	Probability of “new” organism not being a descendent of an existing individual
<code>D</code>	Number of organisms that die in each timestep
<code>gens</code>	Number of generations to simulate
<code>keep</code>	In function <code>untb()</code> Boolean with default FALSE meaning to return the system at the end of the simulation and TRUE meaning to return a matrix whose rows are the ecosystem at successive times
<code>meta</code>	In function <code>untb()</code> , the metacommunity; coerced to a count object. Default of NULL means to use a “greedy” system in which every mutation gives rise to a new, previously unencountered species. This would correspond to an infinitely large, infinitely diverse, Hubbellian ecosystem (which is not too ridiculous an assumption for a small island near a large diverse mainland). In function <code>select.immigrate()</code> , a simplified representation of a metacommunity.

**Details**

Functions `select.immigrate()` and `select.mutate()` are not really intended for the end user; they use computationally efficient (and opaque) integer arithmetic.

**Author(s)**

Robin K. S. Hankin

**References**

S. P. Hubbell 2001. “The Unified Neutral Theory of Biodiversity”. Princeton University Press.

**Examples**

```
data(butterflies)
untb(start=butterflies, prob=0, gens=100)

a <- untb(start=1:10,prob=0.005, gens=1000,keep=TRUE)
plot(species.count(a),type="b")
matplot(species.table(a),type="l",lty=1)
```

---

 vallade

*Various functions from Vallade and Houchmandzadeh*


---

### Description

Various functions from Vallade and Houchmandzadeh (2003), dealing with analytical solutions of a neutral model of biodiversity

### Usage

```
vallade.eqn5(JM, theta, k)
vallade.eqn7(JM, theta)
vallade.eqn12(J, omega, m, n)
vallade.eqn14(J, theta, m, n)
vallade.eqn16(J, theta, mu)
vallade.eqn17(mu, theta, omega, give=FALSE)
```

### Arguments

J, JM	Size of the community and metacommunity respectively
theta	Biodiversity number $\theta = (J_M - 1)\nu/(1 - \nu)$ as discussed in equation 6
k, n	Abundance
omega	Relative abundance $\omega = k/J_M$
m	Immigration probability
mu	Scaled immigration probability $\mu = (J - 1)m/(1 - m)$
give	In function <code>vallade.eqn17()</code> , Boolean with default FALSE meaning to return the numerical value of the integral and TRUE meaning to return the entire output of <code>integrate()</code> including the error estimates

### Details

Notation follows Vallade and Houchmandzadeh (2003) exactly.

### Note

Function `vallade.eqn16()` requires the `polynom` library, which is not loaded by default. It will not run for  $J > 50$  due to some stack overflow error.

Function `vallade.eqn5()` is identical to function `alonso.eqn6()`

### Author(s)

Robin K. S. Hankin

## References

M. Vallade and B. Houchmandzadeh 2003. "Analytical Solution of a Neutral Model of Biodiversity", *Physical Review E*, volume 68. doi: 10.1103/PhysRevE.68.061902

## Examples

```
# A nice check:
JM <- 100
k <- 1:JM
sum(k*vallade.eqn5(JM,theta=5,k)) # should be JM=100 exactly.

# Now, a replication of Figure 3:
omega <- seq(from=0.01, to=0.99,len=100)
f <- function(omega,mu){
  vallade.eqn17(mu,theta=5, omega=omega)
}
plot(omega,
     omega*5,type="n",xlim=c(0,1),ylim=c(0,5),
     xlab=expression(omega),
     ylab=expression(omega*g[C](omega)),
     main="Figure 3 of Vallade and Houchmandzadeh")
points(omega,omega*sapply(omega,f,mu=0.5),type="l")
points(omega,omega*sapply(omega,f,mu=1),type="l")
points(omega,omega*sapply(omega,f,mu=2),type="l")
points(omega,omega*sapply(omega,f,mu=4),type="l")
points(omega,omega*sapply(omega,f,mu=8),type="l")
points(omega,omega*sapply(omega,f,mu=16),type="l")
points(omega,omega*sapply(omega,f,mu=Inf),type="l")

# Now a discrete version of Figure 3 using equation 14:
J <- 100
omega <- (1:J)/J

f <- function(n,mu){
  m <- mu/(J-1+mu)
  vallade.eqn14(J=J, theta=5, m=m, n=n)
}
plot(omega,omega*0.03,type="n",main="Discrete version of Figure 3 using
     eqn 14")
points(omega,omega*sapply(1:J,f,mu=16))
points(omega,omega*sapply(1:J,f,mu=8))
points(omega,omega*sapply(1:J,f,mu=4))
points(omega,omega*sapply(1:J,f,mu=2))
points(omega,omega*sapply(1:J,f,mu=1))
points(omega,omega*sapply(1:J,f,mu=0.5))
```

volkov

*Expected frequency of species***Description**

Given a community size, biodiversity parameter  $\theta$ , and an immigration rate  $m$ , returns the expected frequency of species with  $n$  individuals, for  $0 < n \leq J$ .

**Usage**

```
volkov(J, params, bins = FALSE, give = FALSE)
```

**Arguments**

J	Size of community
params	A two-element vector with first element interpreted as theta, the Fundamental biodiversity parameter and the second, m, interpreted as the probability of immigration. This argument will accept the output of <code>optimal.params()</code>
bins	Boolean, with default FALSE meaning to return the expected number of species with $1, 2, \dots, J$ individuals, and TRUE meaning to return the binned total, using a Preston-like binning system as used in <code>preston()</code>
give	Boolean, with TRUE meaning to return <i>all</i> the output of <code>integrate()</code> , and default FALSE meaning to return just the value of the integral

**Value**

Returns an object of class “phi”.

**Note**

The method used is slightly inefficient: the terms to the left of the integral sign [in Volkov’s equation 7] are integrated and this is, strictly, unnecessary as it is not a function of  $y$ . However, taking advantage of this fact results in messy code.

**Author(s)**

Robin K. S. Hankin

**References**

I. Volkov and others 2003. “Neutral theory and relative species abundance in ecology”. *Nature*, volume 424, number 28.

**See Also**

[phi](#), [preston](#)

**Examples**

```
## Not run:
  volkov(J=21457,c(theta=47.226, m=0.1)) # Example in figure 1

## End(Not run)

volkov(J=20,params=c(theta=1,m=0.4))

data(butterflies)
r <- plot( Preston(butterflies,n=9,orig=TRUE))

## Not run:  jj <- optimal.params(butterflies)    # needs PARI/GP

jj <- c(9.99980936124759, 0.991791987473506)

points(r,volkov(no.of.ind(butterflies), jj, bins=TRUE),type="b")
```

zsm

*Zero sum multinomial distribution as derived by McKane***Description**

The Zero sum multinomial distribution of species abundances as derived by McKane 2004.

**Usage**

```
zsm(J, P, m)
```

**Arguments**

J	Size of local community
P	Abundance in metacommunity
m	Probability of immigration

**Value**

Returns a vector of size J showing the probability of the stationary abundance being  $1, \dots, J$ .

**Note**

The function uses `lgamma()` to avoid numerical overflow

**Author(s)**

Robin K. S. Hankin

## References

A. J. McKane and others 2004. "Analytic solution of Hubbell's model of local community dynamics". *Theoretical Population Biology* 65:67-73

## Examples

```
sum(zsm(164,0.1,0.5)) # should be 1

# McKane et al 2004: figure 1.
layout(matrix(1:4,2,2))
par(mai=0.2+rep(0,4))
plot(1,type="n",log="y",ylim=c(1e-9,1),xlim=c(0,64),xlab="",ylab="Ps(N)",
      axes=FALSE,main=expression(J==64))
axis(1,pos=1e-9)
axis(2,pos=0,at=10^(-(0:9)))
segments(64,1e-9,64,1)
segments(60,1e-9,64,1e-9)
f <- function(P){points(0:64,zsm(64,P=P,m=0.05),type="l")}
for(i in 1:9){f(i/10)}
f(0.99)
f(0.999)
f(0.01)
f(0.001)
text(07,3.2e-7,adj=0,expression(P==0.999))
text(49,3.2e-7,adj=0,expression(P==0.001))
text(45,0.1,expression(m==0.05))

plot(1,type="n",log="y",ylim=c(1e-5,1),xlim=c(0,64),xlab="",ylab="Ps(N)",
      axes=FALSE,main="")
axis(1,pos=1e-5)
axis(2,pos=0,at=10^(-(0:5)))
segments(60,1e-5,64,1e-5)
segments(64,1e-5,64,1)
par(xpd=FALSE)
g <- function(m){points(0:64,pmax(zsm(64,P=0.1,m=m),1e-5),type="l")}
g(0.0001)
g(0.0005)
g(0.002)
g(0.01)
g(0.02)
g(0.05)
g(0.5)
g(0.999)
text(50,0.4,expression(P==0.1))

plot(1,type="n",log="y",ylim=c(1e-9,1),xlim=c(0,1e5),xlab="",ylab="Ps(N)",
      axes=FALSE,main=expression(J==10000))
axis(1,pos=1e-9)
axis(2,pos=0)
```



```
segments(1e5,1e-9,1e5,0.1)

h <- function(P){points(0:1e5,pmax(zsm(1e5,P=P,m=0.05),1e-9),type="l")}
for(i in 1:9){h(i/10)}
h(0.01)
h(0.99)
text(75000,0.1,expression(m==0.5))

plot(1,type="n",log="y",ylim=c(1e-40,1),xlim=c(0,1e5),xlab="",ylab="Ps(N)",
      axes=FALSE,main="")
axis(1,pos=1e-40)
axis(2,pos=0,at=1/10^c(40,32,24,16,8,0))
segments(1e5,1e-40,1e5,1)

i <- function(m){points(0:1e5,pmax(zsm(1e5,P=0.1,m=m),1e-40),type="l")}
i(0.0001)
i(0.0002)
i(0.0005)
i(0.001)
i(0.002)
i(0.005)
i(0.01)
i(0.02)
i(0.5)
text(60000,1e-4,expression(P==0.1))
```

# Index

## \*Topic **datasets**

- bci, 6
- butterflies, 6
- caruso, 7
- copepod, 10
- ghats, 17
- logS1, 21
- sahfos, 34
- saunders, 35
- spitale, 39

## \*Topic **math**

- +.count, 4
- alonso, 5
- census, 8
- count, 10
- display.untb, 12
- etienne, 13
- expected.abundance, 15
- extractor, 16
- fisher, 16
- isolate, 18
- logkda, 19
- no.of.ind, 22
- optimal.prob, 26
- phi, 27
- plot.count, 29
- preston, 30
- print.preston, 31
- print.summary.count, 32
- rand.neutral, 33
- simpson, 36
- species.count, 38
- summary.count, 40
- theta.prob, 41
- untb, 42
- untb-package, 3
- vallade, 44
- volkov, 46
- zsm, 47

## \*Topic **optimize**

- optimal.params.gst, 24
- optimal.params.sloss, 25
- +.census (+.count), 4
- +.count, 4
- alonso, 5
- as.census (census), 8
- as.count (count), 10
- BCI (bci), 6
- bci, 6
- butterflies, 6
- butterfly (butterflies), 6
- Caruso (caruso), 7
- caruso, 7
- census, 8, 11
- copepod, 10
- count, 9, 10, 15
- display.untb, 12
- Etienne (etienne), 13
- etienne, 13, 21, 22, 27
- expected.abundance, 15
- extant (no.of.ind), 22
- extinct (no.of.ind), 22
- extractor, 8, 16, 36
- fisher, 16
- fishers.alpha (fisher), 16
- ghats, 17
- GST.k (optimal.params.gst), 24
- I.k (optimal.params.gst), 24
- is.census (census), 8
- is.count (count), 10
- isolate, 18
- logkda, 14, 19

- logkda\_pari\_unix (logkda), 19
- logkda\_pari\_windows (logkda), 19
- logS1, 21, 21
- logS1vect (logS1), 21
  
- maximal.abundance (no.of.ind), 22
  
- no.of.extinct (no.of.ind), 22
- no.of.ind, 22
- no.of.singletons (no.of.ind), 22
- no.of.spp (no.of.ind), 22
  
- optimal.params, 25, 26
- optimal.params (etienne), 13
- optimal.params.gst, 24, 26, 27
- optimal.params.sloss, 25, 25, 27
- optimal.prob, 26, 42
- optimal.theta, 14
- optimal.theta (optimal.prob), 26
- Oribatid (caruso), 7
- oribatid (caruso), 7
- ostracod (copepod), 10
  
- phi, 27, 31, 40, 42, 46
- plot.census (plot.count), 29
- plot.count, 29
- plot.preston (print.preston), 31
- Preston (preston), 30
- preston, 28, 30, 32, 37, 38, 46
- print.preston, 31
- print.summary.census  
    (print.summary.count), 32
- print.summary.count, 32
  
- rand.neutral, 15, 33
  
- sahfos, 34
- saunders, 35
- select (untb), 42
- simpson, 36
- singletons (no.of.ind), 22
- species.count, 38
- species.table (species.count), 38
- spitale, 39
- summary.census (summary.count), 40
- summary.count, 40
  
- theta.likelihood (theta.prob), 41
- theta.prob, 41
  
- unphi (phi), 27
- untb, 33, 42
- untb-package, 3
  
- Vallade (vallade), 44
- vallade, 44
- volkov, 46
  
- zsm, 47