

# Package ‘emdbook’

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**Description** Auxiliary functions and data sets for “Ecological Models and Data”, a book presenting maximum likelihood estimation and related topics for ecologists (ISBN 978-0-691-12522-0).

**Suggests** R2WinBUGS, ellipse, SuppDists, numDeriv, testthat, rgl

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emdbook-package	<i>Support Functions and Data for "Ecological Models and Data"</i>
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### Description

Auxiliary functions and data sets for "Ecological Models and Data", a book presenting maximum likelihood estimation and related topics for ecologists (ISBN 978-0-691-12522-0).

### References

*Bolker, Benjamin M. Ecological Models and Data in R. Princeton University Press, 2008*

---

apply2d	<i>Apply a function to a combination of vectors</i>
---------	---

---

### Description

applies a (non-vectorized) function to a combination of vectors; substitute for outer

### Usage

```
apply2d(fun, x, y, ..., use_plyr = TRUE, .progress="none")
```

**Arguments**

fun	a function of two arguments (or a character string such as "*")
x	first vector
y	second vector
...	additional arguments to fun
use_plyr	use methods from the plyr package?
.progress	progress bar type ("none", "text", "tk", "win": see <a href="#">create_progress_bar</a> )

**Value**

a matrix of the function applied to the combinations of the vector values

**Author(s)**

Ben Bolker

**See Also**

outer

**Examples**

```
outer(1:3,1:3)
## this example would work with outer() too
apply2d("*",1:3,1:3)
```

---

as.mcmc.bugs

*Convert WinBUGS output to CODA format*

---

**Description**

Converts results of a bugs run (class "bugs") to a form that can be used by CODA (class "mcmc")

**Usage**

```
as.mcmc.bugs(x)
```

**Arguments**

x an object of class bugs (output from bugs())

**Value**

an object of class mcmc

**Author(s)**

Ben Bolker

---

calcslice	<i>Negative log-likelihood slice</i>
-----------	--------------------------------------

---

**Description**

Calculate the negative log-likelihood along a line connecting two mle fits

**Usage**

```
calcslice(fit1, fit2, fn = fit1@minuslogl, range = c(-0.1, 1.1), n = 400)
```

**Arguments**

fit1	An mle object
fit2	Another mle object
fn	Negative log-likelihood function
range	Numeric vector: range of parameters to try, where 0 corresponds to <code>coef(fit1)</code> and 1 corresponds to <code>coef(fit2)</code>
n	Number of points to evaluate

**Details**

Calculates the negative log-likelihood (not a profile, just a "slice") along the line connecting the two sets of coefficients. Intended for diagnosing and visualizing multiple minima in a likelihood surface, especially in higher-dimensional models.

**Value**

x	Parameter values, along the 0-1 scale described above
y	Negative log-likelihood values

**Author(s)**

Ben Bolker

---

contour3d	<i>Superimpose contour lines on a 3D plot</i>
-----------	---

---

**Description**

Plot contour lines computed from data in 3D, or add them to an existing 3D (RGL) surface

**Usage**

```
contour3d(x, y, z, contourArgs=NULL, ...)
```

**Arguments**

x	numeric vector of x values (as in <a href="#">contour</a> ), or a list with components x, y and z
y	numeric vector of y values (as in <a href="#">contour</a> )
z	numeric z matrix (as in <a href="#">contour</a> )
contourArgs	list of arguments to <a href="#">contourLines</a>
...	other arguments to <a href="#">lines3d</a>

**Value**

Returns a list of contour lines (as in [contourLines](#)), invisibly.

**Note**

You have to install the rgl package before you can use this function.

**Note**

If you are superimposing the contour lines on a surface, it helps to draw the surface with some level of transparency (alpha parameter: see [material3d](#)) so the contour lines are not obscured by the surface.

**Author(s)**

Ben Bolker

---

credint *Calculate Bayesian credible intervals*

---

### Description

Calculate Bayesian credible intervals based on various types of information about the posterior distribution

### Usage

```
tcredint(dist, parlist, ranges, level = 0.95, eps = 1e-05, verbose=FALSE)
ncredint(pvec, npost, level=0.95, tol=0.01, verbose=FALSE)
```

### Arguments

dist	character string giving the name of a distribution for which "d", "q", and "p" function exist, e.g. "beta"
parlist	list of parameters to pass to distribution functions
ranges	lower, middle, and upper values to bracket lower and upper boundaries of the credible interval
level	confidence level
eps	if ranges is missing, set lower and upper brackets to the eps and 1-eps quantiles of the distribution
tol	tolerance on credible interval
verbose	if TRUE, return detailed information on the probability cutoff and realized area of the credible interval; if FALSE, just lower and upper bounds of the credible region
...	additional arguments to <a href="#">density</a>
pvec	numeric vector of parameter values
npost	numeric vector of posterior density values corresponding to pvec

### Details

tcredint gives credible intervals for a theoretical posterior density with defined density, cumulative density, and quantile functions; ncredint gives credible intervals for a numerical posterior density.

### Value

A numeric vector giving the credible interval. If verbose=FALSE, gives just lower and upper bounds; if verbose=TRUE, also gives information on the probability cutoff and realized area of the credible interval

### Note

For credible intervals from a sample (e.g. from an MCMC run), see HPDinterval in the coda package.

**Author(s)**

Ben Bolker

**Examples**

```
tcredint("beta",list(shape1=5,shape2=10),verbose=TRUE)
pvec = seq(0,1,length=100)
postvec = dbeta(pvec,shape1=5,shape2=10)
ncredint(pvec,postvec,verbose=TRUE)
set.seed(1001)
```

curve3d

*Plot a 3D surface representing a 2D curve***Description**

Two-dimensional analogue of curve: generates a surface and plots it

**Usage**

```
curve3d(expr, from = c(0, 0), to = c(1, 1), n = c(41, 41),
xlim, ylim, add = FALSE,
xlab=varnames[1],
ylab=varnames[2],
zlab = NULL, log = NULL, sys3d = c("persp", "wireframe", "rgl",
"contour", "image", "none"),
varnames=c("x", "y"),use_plyr=TRUE, .progress="none",...)
```

**Arguments**

expr	a mathematical expression using x and y as the independent variables
from	minimum values for x and y
to	maximum values for x and y
xlim	range of values for x
ylim	range of values for y
n	number of grid points in each direction
add	(logical) add to an existing plot? (only possible for contour plots or rgl)
xlab	x label
ylab	y label
zlab	z label
log	(character): "x", "y", or "xy" for logarithmic axes
sys3d	3D plotting system to use: one of "persp", "wireframe", "rgl", "contour", "image", or "none"
varnames	names of variables to substitute

use_plyr	use methods from the plyr package?
.progress	progress bar type ("none", "text", "tk", "win": see <a href="#">create_progress_bar</a> )
...	additional arguments to the plotting functions

**Value**

invisibly, a list of

x	x values
y	y values
z	z matrix

**Note**

- You must explicitly install the rgl package (via `install.packages("rgl")`) before using `sys3d="persp"`.
- if you encounter the error ‘Results must have one or more dimensions’, try `use_plyr=FALSE` or use `c()` to remove attributes from the result of your expression

**See Also**

[outer](#), [curve](#)

**Examples**

```
curve3d(cos(2*pi*x)+sin(2*pi*y/3),
  from=c(0,0),to=c(1,1))
x <- 1
y <- 3
curve3d(cos(2*pi*x)+sin(2*pi*y/3),
  from=c(0,0),to=c(1,1),sys3d="wireframe")
curve3d(x*cos(2*pi*a/x)+sin(2*pi*b/y),
  from=c(0,0),to=c(1,1),sys3d="wireframe",
  varnames=c("a","b")) ## identical
op <- par(mfrow=c(2,2))
curve3d(cos(2*pi*x)+sin(2*pi*y/3),
  from=c(0,0),to=c(1,1),sys3d="image")
curve3d(x*cos(2*pi*a/x)+sin(2*pi*b/y),
  from=c(0,0),to=c(1,1),sys3d="image",
  varnames=c("a","b")) ## identical
x <- 4
curve3d(cos(2*pi*a/x)+y*sin(2*pi*b/y),
  from=c(0,0),to=c(1,1),sys3d="image",
  varnames=c("a","b"))
curve3d(cos(2*pi*x)+sin(2*pi*y/3),
  from=c(0,0),to=c(1,1),sys3d="image")
curve3d(cos(2*pi*x)+sin(2*pi*y/3),
  sys3d="contour",add=TRUE)
par(op)
```

---

Damselfish

*Reef fish (damselfish) data*

---

## Description

Two data sets on *Dascyllus trimaculatus* (three-spot damselfish), one on the distribution of settlement densities to empty anemones across time and space, the other on survival (recruitment) of arriving settlers as a function of experimentally manipulated densities from Schmitt et al. (1999).

## Usage

```
data(DamselSettlement)
data(DamselRecruitment)
data(DamselRecruitment_sum)
```

## Format

Three data frames:

site settlement site (location)

pulse monthly settlement pulse

obs observation within pulse

density density of settlers per 0.1 m<sup>2</sup> anemone

area anemone area in cm<sup>2</sup>

init initial settler density

surv surviving density after 6 months

settler.den target experimental density of settlers on experimental anemones

surv.den mean surviving density after 6 months, by target density

SE standard error of survivor density, by target density

## Source

Schmitt et al. (1999), "Quantifying the effects of multiple processes on local abundance", Ecology Letters 2:294-303. DOI: 10.1046/j.1461-0248.1999.00086.x (Original data kindly provided by Schmitt and Holbrook.) The original version of this data set is available from the [Moorea Coral Reef LTER data repository](#).

---

 dbetabinom

*Beta-binomial distribution*


---

### Description

Density function and random variate generator for the beta-binomial function, parameterized in terms of probability and overdispersion

### Usage

```
dbetabinom(x, prob, size, theta, shape1, shape2, log = FALSE)
rbetabinom(n, prob, size, theta, shape1, shape2)
```

### Arguments

x	a numeric vector of integer values
prob	numeric vector: mean probability of underlying beta distribution
size	integer: number of samples
theta	overdispersion parameter
shape1	shape parameter of per-trial probability distribution
shape2	shape parameter of per-trial probability distribution
log	(logical) return log probability density?
n	integer number of random variates to return

### Details

The beta-binomial distribution is the result of compounding a beta distribution of probabilities with a binomial sampling process. The density function is

$$p(x) = \frac{C(N, x) \text{Beta}(N - x + \theta(1 - p), x + \theta p)}{\text{Beta}(\theta(1 - p), \theta p)}$$

The parameters shape1 and shape2 are the more traditional parameterization in terms of the parameters of the per-trial probability distribution.

### Value

A vector of probability densities or random deviates. If x is non-integer, the result is zero (and a warning is given).

### Note

Although the quantile (qbetabinom) and cumulative distribution (pbetabinom) functions are not available, in a pinch they could be computed from the pghyper and qghyper functions in the SuppDists package – provided that shape2 > 1. As described in ?pghyper, pghyper(q, a = -shape1, N = -shape1 - shape2, should give the cumulative distribution for the beta-binomial distribution with parameters (shape1, shape2, size), and similarly for qghyper. (Translation to the (theta, size, prob) parameterization is left as an exercise.)

**Author(s)**

Ben Bolker

**References**

Morris (1997), American Naturalist 150:299-327

**See Also**[dbeta](#), [dbinom](#)**Examples**

```

set.seed(100)
n <- 9
z <- rbetabinom(1000, 0.5, size=n, theta=4)
par(las=1,bty="l")
plot(table(z)/length(z),ylim=c(0,0.34),col="gray",lwd=4,
      ylab="probability")
points(0:n,dbinom(0:n,size=n,prob=0.5),col=2,pch=16,type="b")
points(0:n,dbetabinom(0:n,size=n,theta=4,
                     prob=0.5),col=4,pch=17,type="b")
## correspondence with SuppDists
if (require(SuppDists)) {
  d1a <- dghyper(0:5,a=-5,N=-10,k=5)
  d1b <- dbetabinom(0:5,shape1=5,shape2=5,size=5)
  max(abs(d1a-d1b))
  p1a <- pghyper(0:5,a=-5,N=-10,k=5,lower.tail=TRUE)
  p1b <- cumsum(d1b)
  max(abs(p1a-p1b))
}

```

---

**dchibarsq***Mixed chi-squared distributions*

---

**Description**

Calculates "mixed" chi-squared distributions (mixtures of chi-square(n) and chi-square(n-1)); useful for Likelihood Ratio Tests when parameters are on the boundary

**Usage**

```

dchibarsq(x, df = 1, mix = 0.5, log = FALSE)
pchibarsq(p, df = 1, mix = 0.5, lower.tail=TRUE, log.p = FALSE)
qchibarsq(q, df = 1, mix = 0.5)
rchibarsq(n, df = 1, mix = 0.5)

```

**Arguments**

x	numeric vector of positive values
p	numeric vector of positive values
q	numeric vector of quantiles (0-1)
n	integer: number of random deviates to pick
df	degrees of freedom (positive integer)
mix	mixture parameter: fraction of distribution that is chi-square(n-1) distributed
log	return log densities?
log.p	return log probabilities?
lower.tail	return lower tail values?

**Value**

Vectors of probability densities (`dchibarsq`), cumulative probabilities (`pchibarsq`), quantiles (`qchibarsq`), or random deviates (`rchibarsq`) from Goldman and Whelan's "chi-bar-squared" distribution. `qchibarsq` uses simple algebra for `df=1` and `uniroot` for `df>1`.

**Author(s)**

Ben Bolker

**References**

N. Goldman and S. Whelan (2000) "Statistical Tests of Gamma-Distributed Rate Heterogeneity in Models of Sequence Evolution in Phylogenetics", *Mol. Biol. Evol.* 17:975-978. D. O. Stram and J. W. Lee (1994) "Variance Components Testing in the Longitudinal Fixed Effects Model", *Biometrics* 50:1171-1177.

**Examples**

```
x <- rchibarsq(100)
plot(density(x, from=0))
curve(dchibarsq(x), add=TRUE, col=2, from=0)
## Not run:
library(lattice)
print(qqmath(~ simdist,
  distribution=qchibarsq,
  panel = function(x, ...) {
    panel.qqmathline(x, ...)
    panel.qqmath(x, ...)
  })))

## End(Not run)
## create first line of table in Goldman and Whelan 2000
round(qchibarsq(c(0.01,0.05,0.9,0.95,0.975,0.99,0.995),df=1),2)
## check second line of table
round(pchibarsq(c(3.81,5.14,6.48,8.27,9.63),df=2),3)
```

```
## create middle column
round(qchibarsq(0.95,df=1:10))
```

---

deltamethod                      *Delta method functions*

---

### Description

Delta-method implementations for Jensen's inequality and prediction uncertainty

### Usage

```
deltamethod(fun, z, var = "x", params = NULL, max.order = 2)
deltavar(fun, meanval=NULL, vars, Sigma, verbose=FALSE)
```

### Arguments

fun	Function of one (deltamethod) or more arguments, expressed in raw form (e.g. $a*x/(b+x)$ )
z	numeric vector of values
var	variable name
vars	list of variable names: needed if params does not have names, or if some of the values specified in params should be treated as constant
params	list or numeric vector of parameter values to substitute
meanval	possibly named vector of mean values of parameters
Sigma	numeric vector of variances or variance-covariance matrix
max.order	maximum order of delta method to compute
verbose	print details?

### Details

deltamethod() is for computing delta-method approximations of the mean of a function of data; deltavar() is for estimating variances of a function based on the mean values and variance-covariance matrix of the parameters. If Sigma is a vector rather than a matrix, the parameters are assumed to be independently estimated.

### Value

For deltavar(), a vector of predicted variances; for deltamethod() a vector containing the observed value of the function average, the function applied to the average, and a series of delta-method approximations

### Author(s)

Ben Bolker

**References**

Lyons (1991), "A practical guide to data analysis for physical science students", Cambridge University Press

**Examples**

```
deltamethod(a*x/(b+x),runif(50),params=list(a=1,b=1),max.order=9)
deltavar(scale*gamma(1+1/shape),meanval=c(scale=0.8,shape=12),
  Sigma=matrix(c(0.015,0.125,0.125,8.97),nrow=2))
## more complex deltavar example
xvec = seq(-4,4,length=101)
x1 = xvec
x2 = xvec
v = matrix(0.2,nrow=3,ncol=3)
diag(v) = 1
m = c(b0=1,b1=1.5,b2=1)
v3 = deltavar(1/(1+exp(-(b0+b1*x1+b2*x2))),meanval=m,Sigma=v)
plot(xvec,v3)
```

---

 deprecated

*Deprecated (obsolete) functions*


---

**Description**

Functions that are obsolete for one reason or another

**Author(s)**

Ben Bolker

---

 dmvnorm

*Multivariate normal distribution density function*


---

**Description**

Calculates the probability density function of the multivariate normal distribution

**Usage**

```
dmvnorm(x, mu, Sigma, log = FALSE, tol = 1e-06)
```

**Arguments**

x	a vector or matrix of multivariate observations
mu	a vector or matrix of mean values
Sigma	a square variance-covariance matrix
log	(logical) return log-likelihood?
tol	tolerance for positive definiteness

**Details**

uses naive linear algebra – could probably use QR decomposition and/or crossprod.

**Value**

vector of log-likelihoods

**Author(s)**

Ben Bolker

**See Also**

[mvrnorm](#) (in MASS package), [dmvnorm](#) (in mvtnorm package)

**Examples**

```
M = matrix(c(1,0.5,0.5,0.5,1,0.5,0.5,0.5,1),nrow=3)
dmvnorm(1:3,mu=1:3,Sigma=M,log=TRUE)
dmvnorm(matrix(1:6,nrow=2),mu=1:3,Sigma=M,log=TRUE)
dmvnorm(matrix(1:6,nrow=2),mu=matrix(1:6,nrow=2),Sigma=M,log=TRUE)
```

---

 dzinbinom

*Zero-inflated negative binomial distribution*


---

**Description**

Probability distribution function and random variate generation for the zero-inflated negative binomial distribution

**Usage**

```
dzinbinom(x, mu, size, zprob, log=FALSE)
rzinbinom(n, mu, size, zprob)
```

**Arguments**

x	vector of integer values
n	number of values to draw
mu	mean parameter (or vector of parameters) of negative binomial
size	number of trials/overdispersion parameter (or vector of parameters) of negative binomial
zprob	probability of structural zeros
log	return log probability?

**Details**

The zero-inflated negative binomial distribution is widely used to model extra zero counts in count data that otherwise follows a negative binomial distribution. The probability distribution is

$$p(0) = p_z + (1 - p_z)NB(0, \mu, k)$$

and

$$p(x) = (1 - p_z)NB(x, \mu, k)$$

for  $x > 0$ .

**Value**

Probabilities of x or random deviates.

**Note**

Only the "ecological" parameterization is included here (must specify mu, not prob)

**Author(s)**

Ben Bolker

**References**

Tyre et al., "Improving precision and reducing bias in biological surveys: estimating false-negative error rates", *Ecological Applications* 13:1790-1801 (2003)

**See Also**

[dnbinom](#), Simon Jackman's pscl package

**Examples**

```
dzinbinom(0:9, mu=2, zprob=0.3, size=0.9)
dnbinom(0:9, mu=2, size=0.9)
rzinbinom(10, mu=2, zprob=0.3, size=0.9)
```

---

Fir

*Data on fir (Abies) life history*

---

**Description**

Data on various aspects of life history (diameter at breast height, onset of reproduction, crowding, fecundity) from subalpine *Abies balsamea*, from Dodd and Silvertown

**Usage**

```
data(FirDBHFec)
data(FirDBHFec_sum)
```

**Format**

DBH diameter in m at breast height (1.4 m)  
fecundity number of cone rachises [per year?]  
pop which population (wave, nonwave) an individual was sampled from  
VAR1 location  
WAVE\_NON non-wave (n) or wave (w)  
TREE\_NO tree number  
C1991 1991 cones  
C1992 1992 cones  
C1993 1993 cones  
C1994 1994 cones  
C1995 1995 cones  
C1996 1996 cones  
C1997 1997 cones  
C1998 1998 cones  
C1999 1999 cones  
NOTES\_IN notes  
G1990 1990 growth  
G1991 1991 growth  
G1992 1992 growth  
G1993 1993 growth  
G1994 1994 growth  
G1995 1995 growth  
G1996 1996 growth  
G1997 1997 growth  
G1998 1998 growth  
DBH diameter at breast height  
DBH\_MM dbh in mm  
DBH\_2 ?  
DBH\_2MM ?  
AGE ?  
GOOD\_OR ?  
PC1998 ?  
AC1998 ?  
PC1994 ?  
AC1994 ?  
R3PC1998 ?

RPC1994 ?  
 RAC1994 ?  
 RLOOKOUT ?  
 RSHREWYS ?  
 RWILLS a factor with levels 0 1 Fajita  
 C8TOT ?  
 G8TOT ?  
 RAC1994I ?  
 RPC1994I ?  
 R3PC1998.1 ?  
 AC1998I ?  
 TOTCONES total cones

### Source

J. Silvertown and M. Dodd, Evolution of life history in balsam fir (*Abies balsamea*) in subalpine forests, Proc. Roy. Soc. Lond. B (1999) 266, 729-733.

### References

M. Dodd and J. Silvertown, Size-specific fecundity and the influence of lifetime size variation upon effective population size in *Abies balsamea*

### Examples

```

data(FirDBHFec_sum)
attach(FirDBHFec_sum)
plot(DBH, fecundity, col=as.numeric(pop), pch=as.numeric(pop))
lms = lapply(split(FirDBHFec_sum, pop), lm, formula=fecundity~DBH)
for (i in 1:2) abline(lms[[i]], col=i)
detach(FirDBHFec_sum)

```

---

get.emdbook.packages *install and update auxiliary packages*

---

### Description

convenience function for downloading and installing all the packages needed for the book (just a list and a wrapper around [install.packages](#))

### Usage

```
get.emdbook.packages()
```

**Value**

none: installs packages as a side effect

**Author(s)**

Ben Bolker

**See Also**

[install.packages](#)

---

GobySurvival

*Goby (reef fish) survivorship data*

---

**Description**

Survivorship data from experimental manipulations on gobies *Elacatinus evelynae* and *E. prochilos* in the US Virgin Islands, 2000-2002

**Format**

exper experiment  
year year  
site site (factor: backreef, patchreef)  
head coral head (factor)  
density treatment "density" (number of "target" fish)  
qual treatment "quality"; background settlement rate  
d1 last day observed (starting at 1)  
d2 first day not observed

**Details**

These data have been made available by the author for pedagogical use; out of courtesy, please don't redistribute (outside of the context of this package) or use in an academic publication without requesting permission (via the package maintainer).

**Source**

J. Wilson, pers. comm.; "Habitat quality, competition and recruitment processes in two marine gobies", Ph.D. thesis, University of Florida (2004); <http://uf.catalog.fcla.edu/permalink.jsp?20UF022544524>

**Examples**

```
## midpoint of survival times
gg <- transform(GobySurvival, mid=(d1+d2)/2)
plot(table(gg$mid))
```

---

`gridsearch2d`*Graphical grid search in 2D*

---

**Description**

Given an objective function and starting ranges, computes the values over the ranges and displays them in the graphics window. User can then interactively zoom in to view interesting parts of the surface.

**Usage**

```
gridsearch2d(fun, v1min, v2min, v1max, v2max,  
n1 = 20, n2 = 20, logz = FALSE,  
sys3d = c("both", "contour", "image"), ...)
```

**Arguments**

<code>fun</code>	Objective function to be minimized: function of two arguments
<code>v1min</code>	Minimum starting value of variable 1
<code>v2min</code>	Minimum starting value of variable 2
<code>v1max</code>	Maximum starting value of variable 1
<code>v2max</code>	Maximum starting value of variable 2
<code>n1</code>	Number of grid points for variable 1
<code>n2</code>	Number of grid points for variable 2
<code>logz</code>	Display image or contour on log scale?
<code>sys3d</code>	Display surface as an image, contour, or both?
<code>...</code>	Other arguments to fun

**Details**

If `log=TRUE`, the value of the surface is rescaled to  $\log_{10}(m - \min(m) + \text{mindm})$ , where `mindm` is the difference between the minimum and the next-largest value (or  $1e-10$  if this difference is zero).

At each iteration, the user is prompted to select two corners of the new range with the mouse; if this choice is confirmed then the view zooms in. When the user chooses to quit, they are asked whether they want to choose a final point (e.g. an estimate of the minimum) with the mouse.

**Value**

If a final point is chosen, a list with elements `x` and `y`, otherwise `NULL`.

**Author(s)**

Ben Bolker

**See Also**

[curve3d](#)

---

`HPDregionplot`*Plot highest posterior density region*

---

**Description**

Given a sample from a posterior distribution (an `mcmc` object from the `coda` package), plot the bivariate region of highest marginal posterior density for two variables, using `kde2d` from `MASS` to calculate a bivariate density.

**Usage**

```
HPDregionplot(x, vars = 1:2, h, n = 50, lump = TRUE, prob = 0.95, xlab =  
NULL, ylab = NULL, lims=NULL, ...)
```

**Arguments**

<code>x</code>	an <code>mcmc</code> or <code>mcmc.list</code> object
<code>vars</code>	which variables to plot: numeric or character vector
<code>h</code>	bandwidth of 2D kernel smoother (previous default value was <code>c(1,1)</code> , which worked poorly with some plots with very small scales; if not specified, defaults to values in <a href="#">kde2d</a> )
<code>n</code>	number of points at which to evaluate the density grid
<code>lump</code>	if <code>x</code> is an <code>mcmc.list</code> object, lump the chains together for plotting?
<code>prob</code>	probability level
<code>xlab</code>	x axis label
<code>ylab</code>	y axis label
<code>lims</code>	limits, specified as <code>(x.lower,x.upper,y.lower,y.upper)</code> (passed to <code>kde2d</code> )
<code>...</code>	other arguments to <a href="#">contour</a>

**Details**

Uses `kde2d` to calculate a bivariate density, then normalizes the plot and calculates the contour corresponding to a contained volume of `prob` of the total volume under the surface (a two-dimensional Bayesian credible region).

**Value**

Draws a plot on the current device, and invisibly returns a list of contour lines ([contourLines](#)).

**Note**

Accuracy may be limited by density estimation; you may need to tinker with `h` and `n` (see `kde2d` in the `MASS` package).

**Author(s)**

Ben Bolker

**See Also**

HPDinterval in the coda package, ellipse package

**Examples**

```
library(MASS)
library(coda)
z <- mvrnorm(1000,mu=c(0,0),Sigma=matrix(c(2,1,1,2),nrow=2))
z2 <- mvrnorm(1000,mu=c(0,0),Sigma=matrix(c(2,1,1,2),nrow=2))
HPDregionplot(mcmc(z))
HPDregionplot(mcmc.list(mcmc(z),mcmc(z2)))
```

lambertW

*Lambert W function***Description**

Computes the Lambert W function, giving efficient solutions to the equation  $x \cdot \exp(x) = z$

**Usage**

```
lambertW_base(z, b = 0, maxiter = 10, eps = .Machine$double.eps, min.imag =
1e-09)
lWasymp(z, logz)
lambertW(z, ...)
```

**Arguments**

<code>z</code>	(complex) vector of values for which to compute the function
<code>logz</code>	(complex (?)) vector of $\log(z)$ values (to be specified by name instead of <code>z</code> )
<code>b</code>	(integer) <code>b=0</code> specifies the principal branch, 0 and -1 are the ones that can take non-complex values
<code>maxiter</code>	maximum numbers of iterations for convergence
<code>eps</code>	convergence tolerance
<code>min.imag</code>	maximum magnitude of imaginary part to chop when returning solutions
<code>...</code>	arguments to pass to <code>lambertW_base</code>

**Details**

Compute the Lambert W function of  $z$ . This function satisfies  $W(z) \exp(W(z)) = z$ , and can thus be used to express solutions of transcendental equations involving exponentials or logarithms. For  $z > 10^307$ , an asymptotic formula (from Corless et al by way of <http://mathworld.wolfram.com/LambertW-Function.html>) is used: `lambertW` is a wrapper that automatically selects the asymptotic formula where appropriate.

- In ecology, the Lambert W can be used to solve the so-called "Rogers equation" for predator functional response with depletion.
- In epidemiology, the Lambert W function solves the final-size equation of a simple SIR epidemic model.

**Value**

Complex or real vector of solutions.

**Note**

This implementation should return values within  $2.5 \cdot \text{eps}$  of its counterpart in Maple V, release 3 or later. Please report any discrepancies to the author or translator.

The derivative of the `lambertW` function is `plogis(-lambertW)`.

**Author(s)**

Nici Schraudolph <[schraudo@inf.ethz.ch](mailto:schraudo@inf.ethz.ch)> (original version (c) 1998), Ben Bolker (R translation)

**References**

Corless, Gonnet, Hare, Jeffrey, and Knuth (1996), "On the Lambert W Function", *Advances in Computational Mathematics* 5(4):329-359

**See Also**

?`Lambert` in the `gsl` package by Robin Hankin, which uses Gnu Scientific Library code; also ?`lambertW` in the `VGAM` and `pracma` packages, and the `lambertW` package

**Examples**

```
curve(lambertW(x), from=0, to=10)
pvec <- seq(-1,1,length=40)
m <- outer(pvec,pvec,function(x,y)Re(lambertW(x+y*1i)))
persp(pvec,pvec,m,
      theta=290,shade=0.5,zlab="lambertW")
num1 <- uniroot(function(x) {x*exp(x)-1},lower=0,upper=1,tol=1e-9)
abs(lambertW(1)-num1$root)<1e-9
###
## Rogers random predator equation:
rogers.pred <- function(N0,a,h,T) {
  N0 - lambertW(a*h*N0*exp(-a*(T-h*N0)))/(a*h)
}
```

```

holling2.pred <- function(N0,a,h) {
  a*N0/(1+a*h*N0)
}
curve(rogers.pred(x,a=1,h=0.2,T=1),from=0,to=60,
  ylab="Number eaten/unit time",xlab="Initial number",ylim=c(0,5),
  main="Predation: a=1, h=0.2")
curve(rogers.pred(x,a=1,h=0.2,T=5)/5,add=TRUE,lty=2,from=0)
curve(rogers.pred(x,a=1,h=0.2,T=0.2)*5,add=TRUE,lty=3,from=0)
curve(rogers.pred(x,a=1,h=0.2,T=10)/10,add=TRUE,lty=4,from=0)
curve(holling2.pred(x,a=1,h=0.2),add=TRUE,lty=1,lwd=2,from=0)
abline(h=5)
legend(30,2,
  c(paste("Rogers, T=",c(0.2,1,5,10),sep=""),
    "Holling type II"),lwd=c(rep(1,4),2),lty=c(3,1,2,4,1))
## final size of an epidemic
finalsize <- function(R0) {
  1+1/R0*lambertW(-R0*exp(-R0))
}
curve(finalsize,from=1,to=10,xlab=expression(R[0]),ylab="Final size")
## comparison of asymptotic results
tmpf <- function(x) {
  L0 <- lambertW_base(10^x)
  L1 <- lWasymp(logz=x*log(10))
  (L1-L0)/L0
}
curve(tmpf,from=1,to=307,log="y")

## derivative
## don't run (avoid numDeriv dependency)
## require(numDeriv)
## grad(lambertW(1))
## plogis(-lambertW(1))

```

---

Lily

*Glacier lily occurrence and fecundity data*


---

## Description

Data on sample quadrats of the glacier lily, *Erythronium grandiflorum*, from Thomson et al 1996

## Usage

```
data(Lily_sum)
```

## Format

```

x location of quadrat
y location of quadrat
flowers number of flowers

```

seedlings number of seedlings  
 vegetative number of vegetative plants  
 gopher index of gopher activity  
 rockiness rockiness index  
 moisture moisture index  
 flowcol inverse quintile of flowering plants  
 seedcol inverse quintile of seedlings  
 vegcol inverse quintile of number of vegetative plants for image plots  
 gophcol inverse quintile of gopher activity  
 rockcol inverse quintile of rockiness  
 moiscol inverse quintile of moisture

### Details

16x16 grid of 2x2m quadrats in Washington Gulch, sampled 1992

### Source

Thomson et al 1996, "Untangling multiple factors in spatial distributions", Ecology 77:1698-1715.  
 Data from James D. Thomson, with file format conversion help from Jennifer Schmidt

### Examples

```
data(Lily_sum)
par(mfrow=c(3,2))
for (i in 9:14) {
  image(matrix(Lily_sum[,i],nrow=16),main=names(Lily_sum)[i])
}
```

---

lseq

*Log-spaced sequence*

---

### Description

Generates a logarithmically spaced sequence

### Usage

```
lseq(from, to, length.out)
```

### Arguments

from	starting value
to	ending value
length.out	number of intervening values

**Details**

lseq() is just a wrapper for `exp(seq(log(from), log(to), length.out = length.out))`

**Value**

logarithmically spaced sequence

**Author(s)**

Ben Bolker

**See Also**

[seq](#)

**Examples**

```
lseq(10, 1000, 9)
```

---

lump.mcmc.list

*Utility functions for mcmc objects*

---

**Description**

Creates traceplots or combine mcmc list into mcmc objects

**Usage**

```
lump.mcmc.list(x)
```

**Arguments**

x                    an mcmc.list object

**Value**

a single mcmc object with the chains lumped together

**Author(s)**

Ben Bolker

**See Also**

coda package

metropSB

*Metropolis-Szymura-Barton algorithm***Description**

Stochastic global optimization using the Metropolis-Szymura-Barton algorithm. New parameters are chosen from a uniform candidate distribution with an adaptively tuned scale, and accepted or rejected according to a Metropolis rule.

**Usage**

```
metropSB(fn, start, deltap = NULL, scale = 1, rptfreq = -1, acceptscale
= 1.01, rejectscale = 0.99, nmax = 10000,
retvals = FALSE, retfreq = 100, verbose = FALSE, ...)
```

**Arguments**

fn	Objective function, taking a vector of parameters as its first argument. The function is minimized, so it should be a negative log-likelihood or a negative log-posterior density.
start	Vector of starting values
deltap	Starting jump size; half-width of uniform distribution
scale	Scaling factor for acceptance
rptfreq	Frequency for reporting interim results (<0 means no reporting)
acceptscale	Amount to inflate candidate distribution if last jump was accepted
rejectscale	Amount to shrink candidate distribution if last jump was rejected
nmax	Number of iterations
retvals	Return detailed statistics?
retfreq	Sampling frequency for detailed statistics
verbose	Print status?
...	Other arguments to fn

**Details**

Metropolis-Szymura-Barton algorithm: given function and starting value, try to find parameters that minimize the function Algorithm: at a given step, 1. pick a new set of parameters, each of which is uniformly distributed in  $(p[i]-deltap[i], p[i]+deltap[i])$  2. calculate function value at new parameter values 3. if  $f(\text{new}) < f(\text{old})$ , accept 4. if  $f(\text{new}) > f(\text{old})$ , accept with probability  $(\exp(-scale * (f(\text{new}) - f(\text{old}))))$  5. if accept, increase all deltap values by acceptscale; if reject, decrease by rejectscale 6. if better than min so far, save function and parameter values 7. if reject, restore old values

**Value**

minimum	minimum value achieved
estimate	parameters corresponding to minimum
funcalls	number of function evaluations
If retvals=TRUE:	
retvals	matrix of periodic samples including parameters, jump scale, current value, and minimum achieved value

**Note**

If scale=1 the algorithm satisfies MCMC rules, provided that the other properties of the MC (irreducibility and aperiodicity) are satisfied.

**Author(s)**

Ben Bolker

**References**

Szymura and Barton (1986) Genetic analysis of a hybrid zone between the fire-bellied toads, *Bombina bombina* and *B. variegata*, near Cracow in southern Poland. *Evolution* 40(6):1141-1159.

**See Also**

[optim](#), [MCMCmetrop1R](#) (MCMCpack package)

---

Myxo

*Myxomatosis titer data*

---

**Description**

Myxomatosis viral titer in blood samples from European rabbits, as a function of day-of-infection and virus grade, from Dwyer et al. 1990, ultimately from Fenner et al. 1956

**Usage**

```
data(MyxoTiter_sum)
```

**Format**

```
grade virus grade (1, least virulent; 5, most virulent)
day day of infection
titer blood virus titer (in log10 rabbit infectious doses)
```

**Note**

Pulled graphically from figure in Dwyer et al.; to be replaced (eventually) with original tabular data in Fenner et al.

**Source**

Dwyer, Levin and Buttel, "A Simulation Model of the Population Dynamics and Evolution of Myxomatosis", Ecological Monographs 60(4):423-447 (1990). Original source: Fenner et al. 1956

**Examples**

```
data(MyxoTiter_sum)
library(lattice)
xyplot(titer~day|factor(grade),data=MyxoTiter_sum,xlim=c(0,30))
```

---

perturb.params                      *Create a list of perturbed parameters*

---

**Description**

Takes a baseline set of parameters and perturbs it to create a variety of starting points for maximum likelihood estimation or MCMC

**Usage**

```
perturb.params(base, alt, which, mult = FALSE, use.base = TRUE)
```

**Arguments**

base	a named list (or vector) of parameters
alt	a list of lists (or vectors) of alternative parameter values or multipliers
which	which parameters to perturb (currently unused)
mult	(logical) multiply baseline values rather than replacing them?
use.base	(logical) include baseline parameters in the list?

**Details**

Takes the baseline parameter list and substitutes alternative values.

**Value**

A list of named lists of parameters.

**Note**

To be extended.

**Author(s)**

Ben Bolker

**Examples**

```
perturb.params(list(x=1,y=2,z=3),alt=list(x=c(2,4),z=5))
```

Reedfrog

*Data on reed frog predation experiments***Description**

Data on lab experiments on the density- and size-dependent predation rate of an African reed frog, *Hyperolius spinigularis*, from Vonesh and Bolker 2005

**Usage**

```
data(ReedfrogPred)
data(ReedfrogSizepred)
data(ReedfrogFuncresp)
```

**Format**

Various data with variables:

density initial tadpole density (number of tadpoles in a 1.2 x 0.8 x 0.4 m tank) [experiment 1]

pred factor: predators present or absent [experiment 1]

size factor: big or small tadpoles [experiment 1]

surv number surviving

propsurv proportion surviving (=surv/density) [experiment 1]

TBL tadpole body length in mm [size-predation experiment]

Kill number killed out of 10, in 3 days [size-predation]

Initial initial number/density (300 L tank) [functional response]

Killed number killed by 3 dragonfly larvae in 14 days [functional response]

**Source**

Vonesh and Bolker (2005) Compensatory larval responses shift trade-offs associated with predator-induced hatching plasticity. *Ecology* 86:1580-1591

**Examples**

```
data(ReedfrogPred)
boxplot(propsurv~size*density*pred,data=ReedfrogPred)
data(ReedfrogSizepred)
data(ReedfrogFuncresp)
```

---

scinot	<i>Scientific notation as LaTeX/expression()</i>
--------	--

---

### Description

Takes a number and returns a version formatted in LaTeX (suitable for use with `Sexpr()` in an Sweave document) or in `expression()` (suitable for plotting), or plots an axis with labels in scientific notation

### Usage

```
scinot(x, format = c("latex", "expression"), delim="$",
pref="", ...)
axis.scinot(side,at)
```

### Arguments

<code>x</code>	a numeric vector (of length 1)
<code>format</code>	produce LaTeX or <code>expression()</code> format?
<code>delim</code>	delimiter to add at beginning and end (latex only)
<code>pref</code>	text to put before expression (expression only)
<code>side</code>	side on which to plot axis
<code>at</code>	list of locations/labels
<code>...</code>	additional arguments to <code>formatC</code>

### Value

a character vector (if latex) or `expression` (if `expression`); `axis.scinot` draws an axis on the current plot

### Author(s)

Ben Bolker

### See Also

`formatC`, `expression`, `plotmath`, `axis`, `axTicks`, `latexSN` in the `Hmisc` package, `eaxis` in the `sfsmisc` package

### Examples

```
scinot(1e-5)
scinot(1e-5,digits=0)
scinot(1e-5,"expression")
scinot(1e-5,"expression",pref="p=")
set.seed(1001)
```

```
plot(1:100,rlnorm(100,0,2),log="y",axes=FALSE)
axis(side=1)
axis.scinot(side=2) ## fix bug!
```

---

SeedPred

*Seed predation data set from Duncan and Duncan 2000*

---

### Description

Data on seed predation over time from Duncan and Duncan (2000)

### Usage

```
data(SeedPred)
data(SeedPred_wide)
data(SeedPred_mass)
```

### Format

station a factor specifying the station number  
species a factor with levels abz cd cor dio mmu pol psd uva  
date sample date  
seeds number of seeds present  
tcum cumulative time elapsed  
tint time since last sample  
taken seeds removed since last sample  
dist distance from forest edge (m)

### Details

SeedPred is in long format, SeedPred\_wide is in wide format; SeedPred\_wide has lots of NA values because stations at 10 and 25 m from the forest were sampled on different days. SeedPred\_mass is a numeric vector containing the approximate seed masses for each species.

### Source

R. Scot Duncan and Virginia E. Duncan (2000) Forest Succession and Distance from Forest Edge in an Afro-Tropical Grassland, *Biotropica* 32(1):33-41. (Data from Scot Duncan.)

### Examples

```
data(SeedPred)
```

---

trcoef	<i>Transform coefficients</i>
--------	-------------------------------

---

**Description**

Perform standard transformations of coefficients based on information encoded in the names or the `transf` attribute of the vector or list

**Usage**

```
trcoef(x, inverse = FALSE)
```

**Arguments**

<code>x</code>	A numeric vector of coefficients with names and/or a <code>transf</code> attribute
<code>inverse</code>	(logical) Perform inverse transform?

**Details**

If `inverse=FALSE` and coefficient names begin with "logit", "log", or "sqrt" the function will back-transform them (using `plogis`, `exp`, or squaring), strip the descriptor from the names, and set the `transf` attribute. Naturally, `inverse=TRUE` will do the opposite. If the `transf` attribute is all empty strings after an inverse transformation, it will be deleted.

**Value**

A vector of transformed variables with modified names and `transf` attributes.

**Author(s)**

Ben Bolker

**Examples**

```
x = c(loga=1, logitb=2, sqrtc=2)
trx = trcoef(x); trx
trcoef(trx, inverse=TRUE)
```

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