

# Package: emdbook (via r-universe)

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**Type** Package

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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 " $\times$ ")                  |
| 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(" $\times$ ",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

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

|                |                                                       |
|----------------|-------------------------------------------------------|
| <code>x</code> | Parameter values, along the 0-1 scale described above |
| <code>y</code> | 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 |
| 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",
data = NULL, ...)
```

**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> ) |
| data      | additional data (as a list) to use in evaluating expr                                     |
| ...       | 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)
```

---

Damsel fish

Reef fish (damsel fish) 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 m2 anemone  
area anemone area in cm2  
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.)

---

|            |                                   |
|------------|-----------------------------------|
| dbetabinom | <i>Beta-binomial distribution</i> |
|------------|-----------------------------------|

---

## 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

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

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, k=size) 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; [https://en.wikipedia.org/wiki/Beta-binomial\\_distribution](https://en.wikipedia.org/wiki/Beta-binomial_distribution)

**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**

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

---

## 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 | <i>Deprecated (obsolete) functions</i> |
|------------|----------------------------------------|

---

Description

Functions that are obsolete for one reason or another

Author(s)

Ben Bolker

---

|         |                                                          |
|---------|----------------------------------------------------------|
| dmvnorm | <i>Multivariate normal distribution density function</i> |
|---------|----------------------------------------------------------|

---

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**

[mvnorm](#) (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); <https://ufdc.ufl.edu/UFE0004180/00001/pdf>

**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**

|       |                                                               |
|-------|---------------------------------------------------------------|
| fun   | Objective function to be minimized: function of two arguments |
| v1min | Minimum starting value of variable 1                          |
| v2min | Minimum starting value of variable 2                          |
| v1max | Maximum starting value of variable 1                          |
| v2max | Maximum starting value of variable 2                          |
| n1    | Number of grid points for variable 1                          |
| n2    | Number of grid points for variable 2                          |
| logz  | Display image or contour on log scale?                        |
| sys3d | Display surface as an image, contour, or both?                |
| ...   | 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  $z > 10^3 07$ , 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  $2.5 \times \text{eps}$  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 | <i>Log-spaced sequence</i> |
|------|----------------------------|

---

### 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 | <i>Myxomatosis titer data</i> |
|------|-------------------------------|

---

**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 | <i>Create a list of perturbed parameters</i> |
|----------------|----------------------------------------------|

---

**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 <a href="#">formatC</a>    |

## 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**

|         |                                                                       |
|---------|-----------------------------------------------------------------------|
| x       | A numeric vector of coefficients with names and/or a transf attribute |
| inverse | (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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