Package ‘bbmle’

December 19, 2019

Title Tools for General Maximum Likelihood Estimation

Description Methods and functions for fitting maximum likelihood models in R.

Version 1.0.22

Depends R (>= 3.0.0), stats4

Imports stats, numDeriv, lattice, MASS, methods, bdsmatrix, Matrix, mvtnorm

Suggests emdbook, rms, ggplot2, RUnit, MuMIn, AICcmodavg, Hmisc, optimx (>= 2013.8.6), knitr, testthat

VignetteBuilder knitr
BuildVignettes yes

Description: Methods and functions for fitting maximum likelihood models in R. This package modifies and extends the 'mle' classes in the 'stats4' package.

License GPL

URL https://github.com/bbolker/bbmle

Collate 'mle2-class.R' 'mle2-methods.R' 'mle.R' 'confint.R' 'predict.R' 'profile.R' 'update.R' 'dists.R' 'IC.R' 'slice.R' 'impsamp.R' 'TMB.R'

RoxygenNote 6.1.1

Encoding UTF-8

NeedsCompilation no

Author Ben Bolker [aut, cre], R Development Core Team [aut], Iago Giné-Vázquez [ctb]

Maintainer Ben Bolker <bolker@mcmaster.ca>

Repository CRAN

Date/Publication 2019-12-19 17:30:02 UTC
as.data.frame.profile.mle2

convert profile to data frame

Description

converts a profile of a fitted mle2 object to a data frame

Usage

```r
## S3 method for class 'profile.mle2'
as.data.frame(x, row.names=NULL, 
optional=FALSE, ...)
```

Arguments

- `x` a profile object
- `row.names` row names (unused)
- `optional` unused
- `...` unused
Value

a data frame with columns

- **param**  name of parameter being profiled
- **z**  signed square root of the deviance difference from the minimum parameter values
  named par.vals.parname
- **focal**  value of focal parameter: redundant, but included for plotting convenience

Author(s)

Ben Bolker

Examples

```r
## use as.data.frame and lattice to plot profiles
x <- 0:10
y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)
library(bbmle)
LL <- function(ymax=15, xhalf=6) {
    -sum(stats::dpois(y, lambda=ymax/(1+x/xhalf), log=TRUE))
}
## uses default parameters of LL
fit1 <- mle2(LL)
p1 <- profile(fit1)
d1 <- as.data.frame(p1)
library(lattice)
xyplot(abs(z)~focal|param,data=d1,
    subset=abs(z)<3,
    type="b",
    xlab="",
    ylab=expression(paste(abs(z),
                         " (square root of \(\Delta\) deviance)")),
    scale=list(x=list(relation="free")))
```

---

**BIC-methods**

Log likelihoods and model selection for mle2 objects

---

**Description**

Various functions for likelihood-based and information-theoretic model selection of likelihood models
Usage

## S4 method for signature 'ANY,mle2,logLik'
AICc(object,...,nobs,k=2)
## S4 method for signature 'ANY,mle2,logLik'
qAIC(object,...,k=2)
## S4 method for signature 'ANY,mle2,logLik'
qAICc(object,...,nobs,k=2)

Arguments

object
A logLik or mle2 object

...  
An optional list of additional logLik or mle2 objects (fitted to the same data set).

nobs  
Number of observations (sometimes obtainable as an attribute of the fit or of the log-likelihood)

k
penalty parameter (nearly always left at its default value of 2)

Details

Further arguments to BIC can be specified in the ... list: delta (logical) specifies whether to include a column for delta-BIC in the output.

Value

A table of the BIC values, degrees of freedom, and possibly delta-BIC values relative to the minimum-BIC model

Methods

logLik signature(object = "mle2")  
: Extract maximized log-likelihood.

AIC signature(object = "mle2")  
: Calculate Akaike Information Criterion

AICc signature(object = "mle2")  
: Calculate small-sample corrected Akaike Information Criterion

anova signature(object="mle2")  
: Likelihood Ratio Test comparision of different models

Note

This is implemented in an ugly way and could probably be improved!

Examples

d <- data.frame(x=0:10,y=c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8))
(fit <- mle2(y~dpois(lambda=ymax/(1+x/xhalf)),
    start=list(ymax=25,xhalf=3),data=d))
(fit2 <- mle2(y~dpois(lambda=(x+1)*slope),
    start=list(slope=1),data=d))
BIC(fit)
call.to.char

BIC(fit, fit2)

call.to.char  Convert calls to character

Description

Utility function (hack) to convert calls such as y~x to their character equivalent

Usage

call.to.char(x)

Arguments

x  a formula (call)

Details

It would be nice if as.character(y~x) gave "y~x", but it doesn’t, so this hack achieves the same goal

Value

a character vector of length 1

Author(s)

Ben Bolker

Examples

as.character(y~x)
call.to.char(y~x)
dnorm_n

Normal distribution with profiled-out standard deviation

**Description**

Returns the Normal probability densities for a distribution with the given mean values and the standard deviation equal to the root mean-squared deviation between x and mu

**Usage**

dnorm_n(x, mean, log = FALSE)

**Arguments**

- **x**: numeric vector of data
- **mean**: numeric vector or mean values
- **log**: logical: return the log-density?

**Details**

This is a convenience function, designed for the case where you're trying to compute a MLE for the mean but don't want to bother estimating the MLE for the standard deviation at the same time

**Value**

Numeric vector of probability densities

**Examples**

```r
set.seed(101)
x <- rnorm(5, mean=3, sd=2)
dnorm_n(x, mean=3, log=TRUE)
```

---

get.mnames

**extract model names**

**Description**

given a list of models, extract the names (or "model n")

**Usage**

get.mnames(Call)
Arguments

Call a function call (usually a list of models)

Value

a vector of model names

Author(s)

Ben Bolker

---

ICtab

*Compute table of information criteria and auxiliary info*

Description

Computes information criteria for a series of models, optionally giving information about weights, differences between ICs, etc.

Usage

```
ICtab(..., type=c("AIC","BIC","AICc","qAIC","qAICc"),
       weights = FALSE, delta = TRUE, base = FALSE,
       logLik=FALSE, sort = TRUE,
       nobs=NULL, dispersion = 1, mnames, k = 2)
AICtab(...,mnames)
BICtab(...,mnames)
AICctab(...,mnames)
```

## S3 method for class `ICtab`

```
print(x,...,min.weight)
```

Arguments

... a list of (logLik or?) mle objects; in the case of AICtab etc., could also include other arguments to ICtab

type specify information criterion to use

base (logical) include base IC (and log-likelihood) values?

weights (logical) compute IC weights?

logLik (logical) include log-likelihoods in the table?

delta (logical) compute differences among ICs (and log-likelihoods)?

sort (logical) sort ICs in increasing order?

nobs (integer) number of observations: required for type="BIC" or type="AICc"

unless objects have a `nobs` method

dispersion overdispersion estimate, for computing qAIC: required for type="qAIC" or type="qAICc"

unless objects have a "dispersion" attribute
mnames names for table rows: defaults to names of objects passed
k penalty term (largely unused: left at default of 2)
x an ICl tab object
min.weight minimum weight for exact reporting (smaller values will be reported as "<[min.weight]")

Value

A data frame containing:

IC information criterion
df degrees of freedom/number of parameters
dIC difference in IC from minimum-IC model
weights exp(-dIC/2)/sum(exp(-dIC/2))

Note

(1) The print method uses sensible defaults; all ICs are rounded to the nearest 0.1, and IC weights are printed using format.pval to print an inequality for values <0.001. (2) The computation of degrees of freedom/number of parameters (e.g., whether variance parameters are included in the total) varies enormously between packages. As long as the df computations for a given set of models is consistent, differences don’t matter, but one needs to be careful with log likelihoods and models taken from different packages. If necessary one can change the degrees of freedom manually by saying attr(obj,"df") <-df.new where df.new is the desired number of parameters. (3) Defaults have changed to sort=TRUE, base=FALSE, delta=TRUE, to match my conviction that it rarely makes sense to report the overall values of information criteria

Author(s)

Ben Bolker

References

Burnham and Anderson 2002

Examples

set.seed(101)
d <- data.frame(x=1:20,y=rpois(20,lambda=2))
m0 <- glm(y~1,data=d)
m1 <- update(m0,.~x)
m2 <- update(m0,.~poly(x,2))
AICtab(m0,m1,m2,mnames=LETTERS[1:3])
AICtab(m0,m1,m2,base=TRUE,logLik=TRUE)
AICtab(m0,m1,m2,logLik=TRUE)
AICctab(m0,m1,m2,weights=TRUE)
print(AICctab(m0,m1,m2,weights=TRUE),min.weight=0.1)
**mle2**

**Maximum Likelihood Estimation**

**Description**

Estimate parameters by the method of maximum likelihood.

**Usage**

```r
mle2(minuslogl, start, method, optimizer, 
     fixed = NULL, data=NULL, 
     subset=NULL, 
     default.start=TRUE, eval.only = FALSE, vecpar=FALSE, 
     parameters=NULL, 
     parnames=NULL, 
     skip.hessian=FALSE, 
     hessian.opts=NULL, 
     use.ginv=TRUE, 
     trace=FALSE, 
     browse_obj=FALSE, 
     gr=NULL, 
     optimfun,...)
calc_mle2_function(formula,parameters, links, start, 
     parnames, use.deriv=FALSE, data=NULL,trace=FALSE)
```

**Arguments**

- `minuslogl`: Function to calculate negative log-likelihood, or a formula
- `start`: Named list. Initial values for optimizer
- `method`: Optimization method to use. See `optim`.
- `optimizer`: Optimization function to use. Currently available choices are "optim" (the default), "nlm", "nlminb", "constrOptim", "optimx", and "optimize". If "optimx" is used, (1) the `optimx` package must be explicitly loaded with `load` or `require` (Warning: Options other than the default may be poorly tested, use with caution.)
- `fixed`: Named list. Parameter values to keep fixed during optimization.
- `data`: list of data to pass to negative log-likelihood function: must be specified if `minuslogl` is specified as a formula
- `subset`: logical vector for subsetting data (STUB)
- `default.start`: Logical: allow default values of `minuslogl` as starting values?
- `eval.only`: Logical: return value of `minuslogl(start)` rather than optimizing
- `vecpar`: Logical: is first argument a vector of all parameters? (For compatibility with `optim`.) If `vecpar` is TRUE, then you should use `parnames` to define the parameter names for the negative log-likelihood function.
parameters  List of linear models for parameters. MUST BE SPECIFIED IN THE SAME ORDER as the start vector (this is a bug/restriction that I hope to fix soon, but in the meantime beware)

links  (unimplemented) specify transformations of parameters

parnames  List (or vector?) of parameter names

gr  gradient function

...  Further arguments to pass to optimizer

formula  a formula for the likelihood (see Details)

trace  Logical: print parameter values tested?

browse_obj  Logical: drop into browser() within the objective function?

skip.hessian  Bypass Hessian calculation?

hessian.opts  Options for Hessian calculation, passed through to the hessian function

use.ginv  Use generalized inverse (ginv) to compute approximate variance-covariance

optimfun  user-supplied optimization function. Must take exactly the same arguments and return exactly the same structure as optim.

use.deriv  (experimental, not yet implemented): construct symbolic derivatives based on formula?

Details

The optim optimizer is used to find the minimum of the negative log-likelihood. An approximate covariance matrix for the parameters is obtained by inverting the Hessian matrix at the optimum.

The minuslogl argument can also specify a formula, rather than an objective function, of the form \( x \sim ddistn(param1, \ldots, paramn) \). In this case, \( ddistn \) is taken to be a probability or density function, which must have (literally) \( x \) as its first argument (although this argument may be interpreted as a matrix of multivariate responses) and which must have a \( \log \) argument that can be used to specify the log-probability or log-probability-density is required. If a formula is specified, then parameters can contain a list of linear models for the parameters.

If a formula is given and non-trivial linear models are given in parameters for some of the variables, then model matrices will be generated using model.matrix. start can be given:

- as a list containing lists, with each list corresponding to the starting values for a particular parameter;
- just for the higher-level parameters, in which case all of the additional parameters generated by model.matrix will be given starting values of zero (unless a no-intercept formula with \(-1\) is specified, in which case all the starting values for that parameter will be set equal)
- (to be implemented!) as an exhaustive (flat) list of starting values (in the order given by model.matrix)

The trace argument applies only when a formula is specified. If you specify a function, you can build in your own print() or cat() statement to trace its progress. (You can also specify a value for trace as part of a control list for optim(): see optim.)

The skip.hessian argument is useful if the function is crashing with a "non-finite finite difference value" error when trying to evaluate the Hessian, but will preclude many subsequent confidence
interval calculations. (You will know the Hessian is failing if you use method="Nelder-Mead" and still get a finite-difference error.)

If convergence fails, see the manual page of the relevant optimizer (optim) by default, but possibly nlm, nlminb, optimx, or constrOptim if you have set the value of optimizer) for the meanings of the error codes/messages.

Value

An object of class "mle2".

Warning

Do not use a higher-level variable named .i in parameters – this is reserved for internal use.

Note

Note that the minuslogl function should return the negative log-likelihood, -log L (not the log-likelihood, log L, nor the deviance, -2 log L). It is the user’s responsibility to ensure that the likelihood is correct, and that asymptotic likelihood inference is valid (e.g. that there are “enough” data and that the estimated parameter values do not lie on the boundary of the feasible parameter space). If lower, upper, control$parscale, or control$ndeps are specified for optim fits, they must be named vectors.

The requirement that data be specified when using the formula interface is relatively new: it saves many headaches on the programming side when evaluating the likelihood function later on (e.g. for profiling or constructing predictions). Since data.frame uses the names of its arguments as column names by default, it is probably the easiest way to package objects that are lying around in the global workspace for use in mle2 (provided they are all of the same length).

When optimizer is set to "optimx" and multiple optimization methods are used (i.e. the methods argument has more than one element, or all.methods=TRUE is set in the control options), the best (minimum negative log-likelihood) solution will be saved, regardless of reported convergence status (and future operations such as profiling on the fit will only use the method that found the best result).

See Also

mle2-class

Examples

```r
x <- 0:10
y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)
d <- data.frame(x,y)

## in general it is best practice to use the 'data' argument,
## but variables can also be drawn from the global environment
LL <- function(ymax=15, xhalf=6)
  -sum(stats::dpois(y, lambda=ymax/(1+x/xhalf), log=TRUE))
## uses default parameters of LL
(fit <- mle2(LL))
fit1F <- mle2(LL, fixed=list(xhalf=6))
```
coef(fit1F)
coef(fit1F, exclude.fixed=TRUE)

(fit0 <- mle2(y~dpois(lambda=ymean), start=list(ymean=mean(y)), data=d))
anova(fit0, fit)
summary(fit)
logLik(fit)
vcov(fit)
p1 <- profile(fit)
plot(p1, absVal=FALSE)
confint(fit)

## use bounded optimization
## the lower bounds are really > 0, but we use >=0 to stress-test
## profiling; note lower must be named
(fit1 <- mle2(LL, method="L-BFGS-B", lower=c(ymax=0, xhalf=0)))
p1 <- profile(fit1)
plot(p1, absVal=FALSE)

## a better parameterization:
LL2 <- function(lymax=log(15), lxhalf=log(6))
  -sum(stats::dpois(y, lambda=exp(lymax)/(1+x/exp(lxhalf)), log=TRUE))
(fit2 <- mle2(LL2))
plot(profile(fit2), absVal=FALSE)
exp(confint(fit2))
vcov(fit2)
cov2cor(vcov(fit2))

mle2(y~dpois(lambda=exp(lymax)/(1+x/exp(lhalf))),
     start=list(lymax=0,lhalf=0),
     data=d,
     parameters=list(lymax~1,lhalf~1))

## Not run:
## try bounded optimization with nlminb and constrOptim
(fit1B <- mle2(LL, optimizer="nlminb", lower=c(lymax=1e-7, lhalf=1e-7)))
p1B <- profile(fit1B)
confint(p1B)
(fit1C <- mle2(LL, optimizer="constrOptim", ui = c(lymax=1,lhalf=1), ci=2, method="Nelder-Mead")

set.seed(1001)
lymax <- c(0,2)
lhalf <- 0
x <- sort(runif(200))
g <- factor(sample(c("a","b"), 200, replace=TRUE))
y <- rnbinom(200,mu=exp(lymax[g])/(1+x/exp(lhalf)),size=2)
d2 <- data.frame(x,g,y)

fit3 <- mle2(y~dnbinom(mu=exp(lymax)/(1+x/exp(lhalf)),size=exp(logk)),
            parameters=list(lymax~g), data=d2,
            start=list(lymax=0,lhalf=0,logk=0))
Class "mle2". Result of Maximum Likelihood Estimation.

Description
This class encapsulates results of a generic maximum likelihood procedure.

Objects from the Class
Objects can be created by calls of the form `new("mle2",...), but most often as the result of a call to `mle2``.

Slots
call: (language) The call to `mle2``.
call.orig: (language) The call to `mle2`` saved in its original form (i.e. without data arguments evaluated).
coef: (numeric) Vector of estimated parameters.
data: (data frame or list) Data with which to evaluate the negative log-likelihood function
fullcoef: (numeric) Fixed and estimated parameters.
vcov: (numeric matrix) Approximate variance-covariance matrix, based on the second derivative matrix at the MLE.
min: (numeric) Minimum value of objective function = minimum negative log-likelihood.
details: (list) Return value from `optim``.
minuslogl: (function) The negative log-likelihood function.
optimizer: (character) The optimizing function used.
method: (character) The optimization method used.
formula: (character) If a formula was specified, a character vector giving the formula and parameter specifications.

Methods
coef signature(object = "mle2") : Extract coefficients. If `exclude.fixed=TRUE` (it is `FALSE` by default), only the non-fixed parameter values are returned.
confint signature(object = "mle2") : Confidence intervals from likelihood profiles, or quadratic approximations, or root-finding.
show signature(object = "mle2") : Display object briefly.
show signature(object = "summary.mle2") : Display object briefly.
summary signature(object = "mle2") : Generate object summary.
update signature(object = "mle2") : Update fit.
vcov signature(object = "mle2") : Extract variance-covariance matrix.
formula signature(object="mle2") : Extract formula
plot signature(object="profile.mle2,missing") : Plot profile.
Details on the confint method

When the parameters in the original fit are constrained using lower or upper, or when prof.lower or prof.upper are set, and the confidence intervals lie outside the constraint region, confint will return NA. This may be too conservative – in some cases, the appropriate answer would be to set the confidence limit to the lower/upper bound as appropriate – but it is the most general answer.

(If you have a strong opinion about the need for a new option to confint that sets the bounds to the limits automatically, please contact the package maintainer.)

Examples

```r
x <- 0:10
y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)
lowerbound <- c(a=2,b=-0.2)
d <- data.frame(x,y)
fit1 <- mle2(y~dpois(lambda=exp(a+b*x)),start=list(a=0,b=2),data=d,
method="L-BFGS-B",lower=c(a=2,b=-0.2))
(cc <- confint(fit1,quietly=TRUE))
## to set the lower bounds to the limit
na_lower <- is.na(cc[,1])
cc[na_lower,1] <- lowerbound[na_lower]
cc
```

mle2.options

Options for maximum likelihood estimation

Description

Query or set MLE parameters

Usage

`mle2.options(...)`

Arguments

... names of arguments to query, or a list of values to set

Details

- `optim.method` name of optimization method (see `optim` for choices)
- `confint` name of confidence interval method: choices are "spline", "uniroot", "hessian" corresponding to spline inversion, attempt to find best answer via uniroot, information-matrix approximation
- `optimizer` optimization function to use by default (choices: "optim", "nlm", "nlminb", "constrOptim")
Value

Values of queried parameters, or (invisibly) the full list of parameters

See Also

`mle2-class`

Description

goes through a list (containing a combination of single- and multiple-element vectors) and removes redundant names that will make trouble for `mle`.

Usage

`namedrop(x)`

Arguments

x 
a list of named or unnamed, typically numeric, vectors

Details

examines each element of `x`. If the element has length one and is a named vector, the name is removed; if `length(x)` is greater than 1, but all the names are the same, the vector is renamed.

Value

the original list, with names removed/added

Author(s)

Ben Bolker

Examples

```r
x = list(a=c(a=1), b=c(d=1, d=2), c=c(a=1, b=2, c=3))
names(unlist(namedrop(x)))
```

```r
names(unlist(namedrop(x)))
```
parnames  

get and set parameter names

Description

Gets and sets the "parnames" attribute on a negative log-likelihood function

Usage

parnames(obj)
parnames(obj) <- value

Arguments

obj  
a negative log-likelihood function

value  
a character vector of parameter names

Details

The parnames attribute is used by mle2() when the negative log-likelihood function takes a parameter vector, rather than a list of parameters; this allows users to use the same objective function for optim() and mle2()

Value

Returns the parnames attribute (a character vector of parameter names) or sets it.

Author(s)

Ben Bolker

Examples

```r
x <- 1:5
set.seed(1001)
y <- rbinom(5, prob=x/(1+x), size=10)
mfun <- function(p) {
a <- p[1]
b <- p[2]
-sum(dbinom(y, prob=a*x/(b+x), size=10, log=TRUE))
}
optim(fn=mfun, par=c(1,1))
parnames(mfun) <- c("a","b")
mle2(minuslogl=mfun, start=c(a=1,b=1), method="Nelder-Mead")
```
pop_pred_samp

generate population prediction sample from parameters

Description

This [EXPERIMENTAL] function combines several sampling tricks to compute a version of an importance sample (based on flat priors) for the parameters.

Usage

pop_pred_samp(object, n = 1000, n_imp = n * 10, return_wts = FALSE, impsamp = FALSE, PDify = FALSE, PDmethod = NULL, tol = 1e-06, return_all = FALSE, rmvnorm_method = c("mvtnorm", "MASS"), fix_params = NULL)

Arguments

object a fitted mle2 object
n number of samples to return
n_imp number of total samples from which to draw, if doing importance sampling
return_wts return a column giving the weights of the samples, for use in weighted summaries?
impsamp subsample values (with replacement) based on their weights?
PDify use Gill and King generalized-inverse procedure to correct non-positive-definite variance-covariance matrix if necessary?
PDmethod method for fixing non-positive-definite covariance matrices
tol tolerance for detecting small eigenvalues
return_all return a matrix including all values, and weights (rather than taking a sample)
rmvnorm_method package to use for generating MVN samples
fix_params parameters to fix (in addition to parameters that were fixed during estimation)

References

**predict-methods**

*Predicted values from an mle2 fit*

**Description**

Given an mle2 fit and an optional list of new data, return predictions (more generally, summary statistics of the predicted distribution)

**Usage**

```r
## S4 method for signature 'mle2'
predict(object, newdata=NULL, location="mean", newparams=NULL, ...)
## S4 method for signature 'mle2'
simulate(object, nsim, seed, newdata=NULL, newparams=NULL, ...)
## S4 method for signature 'mle2'
residuals(object, type=c("pearson","response"), location="mean", ...)
```

**Arguments**

- `object` an mle2 object
- `newdata` optional list of new data
- `newparams` optional vector of new parameters
- `location` name of the summary statistic to return
- `nsim` number of simulations
- `seed` random number seed
- `type` residuals type
- `...` additional arguments (for generic compatibility)

**Methods**

- `x = "mle2"` an mle2 fit

**Note**

For some models (e.g. constant models), predict may return a single value rather than a vector of the appropriate length.
Examples

```r
set.seed(1002)
lymax <- c(0, 2)
lhalf <- 0
x <- runif(200)
g <- factor(rep(c("a", "b"), each=100))
y <- rnbinom(200, mu=exp(lymax[g])/(1+x/exp(lhalf)), size=2)
dat <- data.frame(y, g, x)

fit3 <- mle2(y~dnbinom(mu=exp(lymax)/(1+x/exp(lhalf)), size=exp(logk)),
parameters=list(lymax~g),
start=list(lymax=0, lhalf=0, logk=0),
data=dat)

plot(y~x,col=g)
## true curves
curve(exp(0)/(1+x/exp(0)), add=TRUE)
curve(exp(2)/(1+x/exp(0)), col=2, add=TRUE)
## model predictions
xvec = seq(0, 1, length=100)
lines(xvec, predict(fit3, newdata=list(g=factor(rep("a", 100), levels=c("a", "b")),
          x = xvec)), col=1, lty=2)
lines(xvec, predict(fit3, newdata=list(g=factor(rep("b", 100), levels=c("a", "b")),
          x = xvec)), col=2, lty=2)

## comparing automatic and manual predictions
p1 = predict(fit3)
p2A = with(as.list(coef(fit3)), exp(lymax.(Intercept))/(1+x[1:100]/exp(lhalf)))
p2B = with(as.list(coef(fit3)), exp(lymax.(Intercept)+lymax.gb)/(1+x[101:200]/exp(lhalf)))
all(p1==c(p2A, p2B))
## simulate(fit3)
```

profile-methods

Likelihood profiles

Description

Compute likelihood profiles for a fitted model

Usage

```r
profplot(fitted, which = 1:p, maxsteps = 100,
alpha = 0.01, zmax = sqrt(qchisq(1 - alpha/2, p)),
del = zmax/5, trace = FALSE, skiperrs=TRUE, std.err,
```
tol.newmin = 0.001, debug=FALSE, 
prof.lower, prof.upper, 
skip.hessian = TRUE, 
continuation = c("none", "naive", "linear"), 
try_harder=FALSE, ...) 

## S4 method for signature 'mle2'
profile(fitted, ...)

Arguments

fitted A fitted maximum likelihood model of class “mle2”
which a numeric or character vector describing which parameters to profile (default is to profile all parameters)
maxsteps maximum number of steps to take looking for an upper value of the negative log-likelihood
alpha maximum (two-sided) likelihood ratio test confidence level to find
zmax maximum value of signed square root of deviance difference to find (default value corresponds to a 2-tailed chi-squared test at level alpha)
del step size for profiling
trace (logical) produce tracing output?
skiperrs (logical) ignore errors produced during profiling?
std.err Optional numeric vector of standard errors, for cases when the Hessian is badly behaved. Will be replicated if necessary, and NA values will be replaced by the corresponding values from the fit summary
tol.newmin tolerance for diagnosing a new minimum below the minimum deviance estimated in initial fit is found
debug (logical) debugging output?
prof.lower optional vector of lower bounds for profiles
prof.upper optional vector of upper bounds for profiles
continuation use continuation method to set starting values? ”none” sets starting values to best fit; ”naive” sets starting values to those of previous profiling fit; ”linear” (not yet implemented) would use linear extrapolation from the previous two profiling fits
skip.hessian skip hessian (defunct?)
try_harder (logical) ignore NA and flat spots in the profile, try to continue anyway?
... additional arguments (not used)

Details

proffun is the guts of the profile method, exposed so that other packages can use it directly.
See the vignette (vignette("mle2", package="bbmle")) for more technical details of how profiling is done.

See Also

profile.mle-class
Description

Definition of the mle2 likelihood profile class, and applicable methods

Usage

## S4 method for signature 'profile.mle2'
plot(x,
 levels, which=1:p, conf = c(99, 95, 90, 80, 50)/100, 
plot.confstr = TRUE, 
confstr = NULL, absVal = TRUE, add = FALSE, 
col.minval="green", lty.minval=2, 
col.conf="magenta", lty.conf=2, 
col.prof="blue", lty.prof=1, 
xlabs=nm, ylab="z", 
onepage=TRUE, 
ask=(!prod(par("mfcol")) < length(which)) && dev.interactive() && !onepage),
show.points=FALSE,
main, xlim, ylim, ...)

## S4 method for signature 'mle2'
confint(object, parm, level = 0.95, method, 
trace=FALSE,quietly=!interactive(), 
tol.newmin=0.001,...)

## S4 method for signature 'profile.mle2'
confint(object, parm, level = 0.95, trace=FALSE, ...)

Arguments

x An object of class profile.mle2

object An object of class mle2 or profile.mle2 (as appropriate)

levels levels at which to plot likelihood cutoffs (set by conf by default)

level level at which to compute confidence interval

which (numeric or character) which parameter profiles to plot

parm (numeric or character) which parameter(s) to find confidence intervals for

method (character) "spline", "uniroot", or "quad", for spline-extrapolation-based (default), root-finding, or quadratic confidence intervals. By default it uses the value of mle2.options("confint") – the factory setting is "spline".

trace trace progress of confidence interval calculation when using 'uniroot' method?

conf (1-alpha) levels at which to plot likelihood cutoffs/confidence intervals

quietly (logical) suppress “Profiling ...” message when computing profile to get confidence interval?
tol.newmin see profile-methods
plot.confstr (logical) plot labels showing confidence levels?
confstr (character) labels for confidence levels (by default, constructed from conf levels)
absVal (logical) plot absolute values of signed square root deviance difference ("V" plot rather than straight-line plot)?
add (logical) add profile to existing graph?
col.minval color for minimum line
lty.minval line type for minimum line
col.conf color for confidence intervals
lty.conf line type for confidence intervals
col.prof color for profile
lty.prof line type for profile
xlabs x labels
ylab y label
onepage (logical) plot all profiles on one page, adjusting par(mfcol) as necessary?
ask (logical) pause for user input between plots?
show.points (logical) show computed profile points as well as interpolated spline?
main (logical) main title
xlim x limits
ylim y limits
... other arguments

Details

The default confidence interval calculation computes a likelihood profile and uses the points therein, or uses the computed points in an existing profile.mle2 object, to construct an interpolation spline (which by default has three times as many points as were in the original set of profile points). It then uses linear interpolation between these interpolated points (!)

Objects from the Class

Objects can be created by calls of the form new("profile.mle2",...), but most often by invoking profile on an "mle2" object.

Slots

profile: Object of class "list". List of profiles, one for each requested parameter. Each profile is a data frame with the first column called z being the signed square root of the deviance, and the others being the parameters with names prefixed by par.vals.
summary: Object of class "summary.mle2". Summary of object being profiled.
profile.mle2-class

Methods

confint signature(object = "profile.mle2"): Use profile to generate approximate confidence intervals for parameters.

plot signature(x = "profile.mle2", y = "missing"): Plot profiles for each parameter.

summary signature(x = "profile.mle2"): Plot profiles for each parameter.

show signature(object = "profile.mle2"): Show object.

See Also

mle2, mle2-class, summary.mle2-class

Examples

```r
x <- 0:10
y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)
d <- data.frame(x, y)
## we have a choice here: (1) don't impose boundaries on the parameters,
## put up with warning messages about NaN values:
fit1 <- mle2(y ~ dpois(lambda = ymax/(1 + x/xhalf)),
start = list(ymax = 1, xhalf = 1),
data = d)
p1 <- suppressWarnings(profile(fit1))
plot(p1, main = c("first", "second"),
xlab = c(~y[max], ~x[1/2]), ylab = "Signed square root deviance",
show.points = TRUE)
suppressWarnings(confint(fit1)) ## recomputes profile
confint(p1) ## operates on existing profile
suppressWarnings(confint(fit1, method = "uniroot"))
## alternatively, we can use box constraints to keep ourselves
## to positive parameter values ...
fit2 <- update(fit1, method = "L-BFGS-B", lower = c(ymax = 0.001, xhalf = 0.001))
## Not run:
p2 <- profile(fit2)
plot(p2, show.points = TRUE)
## but the fit for ymax is just bad enough that the spline gets wonky
confint(p2) ## now we get a warning
confint(fit2, method = "uniroot")
## bobyqa is a better-behaved bounded optimizer ...
## BUT recent (development, 2012.5.24) versions of
## optimx no longer allow single-parameter fits!
if (require(optimx)) {
  fit3 <- update(fit1,
    optimizer = "optimx",
    method = "bobyqa", lower = c(ymax = 0.001, xhalf = 0.001))
p3 <- profile(fit3)
plot(p3, show.points = TRUE)
confint(p3)
}
## End(Not run)
```
\textbf{relist2} \quad \textit{reconstruct the structure of a list}

\textbf{Description}

reshapes a vector according to a list template

\textbf{Usage}

\texttt{relist2(v, l)}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{v} \quad vector, probably numeric, of values to reshape
  \item \texttt{l} \quad template list giving structure
\end{itemize}

\textbf{Details}

attempts to coerce \texttt{v} into a list with the same structure and names as \texttt{l}

\textbf{Value}

a list with values corresponding to \texttt{v} and structure corresponding to \texttt{l}

\textbf{Author(s)}

Ben Bolker

\textbf{Examples}

\begin{verbatim}
l = list(b=1,c=2:5,d=matrix(1:4,nrow=2))
relist2(1:9,l)
\end{verbatim}

\textbf{sbinom} \quad \textit{Abstract definitions of distributions}

\textbf{Description}

Functions returning values for summary statistics (mean, median, etc.) of distributions
Usage

sbetabinom(size, prob, theta)
sbinom(size, prob)
snbinom(size, prob, mu)

Arguments

prob probability as defined for dbinom, dnbinom, or beta-binomial distribution (dbetabinom in the emdbook package)
size size parameter as defined for dbinom or dbetabinom in the emdbook package, or size/overdispersion parameter as in dnbinom
mean mean parameter as defined for dnorm
mu mean parameter as defined for dnbinom
sd standard deviation parameter as defined for dnorm
shape1 shape parameter for dbeta
shape2 shape parameter for dbeta
lambda rate parameter as defined for dpois
theta overdispersion parameter for beta-binomial (see dbetabinom in the emdbook package)
meanlog as defined for dlnorm
sdlog as defined for dlnorm

Value

title name of the distribution
[parameters] input parameters for the distribution
mean theoretical mean of the distribution
median theoretical median of the distribution
mode theoretical mode of the distribution
variance theoretical variance of the distribution
sd theoretical standard deviation of the distribution

Note

these definitions are tentative, subject to change as I figure this out better. Perhaps construct functions that return functions? Strip down results? Do more automatically?

Author(s)

Ben Bolker
See Also
dbinom, dpois, dnorm, dnbinom

Examples
sbinom(prob=0.2, size=10)

snbinom(mu=2, size=1.2)

slice Calculate likelihood "slices"

Description
Computes cross-section(s) of a multi-dimensional likelihood surface

Usage
slice(x, dim=1, ...)  
sliceOld(fitted, which = 1:p, maxsteps = 100,  
alpha = 0.01, zmax = sqrt(qchisq(1 - alpha/2, p)),  
del = zmax/5, trace = FALSE,  
tol.newmin=0.001, ...)

slice1D(params, fun, nt=101, lower=-Inf,  
upper=Inf, verbose=TRUE, tranges=NULL, ...)

slice2D(params, fun, nt=31, lower=-Inf,  
upper=Inf,  
cutoff=10, verbose=TRUE,  
tranges=NULL, ...)

slicetrans(params, params2, fun, extend=0.1, nt=401,  
lower=-Inf, upper=Inf)

Arguments
x a fitted model object of some sort
dim dimensionality of slices (1 or 2)
params a named vector of baseline parameter values
params2 a vector of parameter values
fun an objective function
nt (integer) number of slice-steps to take
lower lower bound(s) (stub?)
upper upper bound(s) (stub?)
cutoff maximum increase in objective function to allow when computing ranges
extend (numeric) fraction by which to extend range beyond specified points
verbose print verbose output?
A fitted maximum likelihood model of class “mle2”

which

a numeric or character vector describing which parameters to profile (default is to profile all parameters)

maxsteps

maximum number of steps to take looking for an upper value of the negative log-likelihood

alpha

maximum (two-sided) likelihood ratio test confidence level to find

zmax

maximum value of signed square root of deviance difference to find (default value corresponds to a 2-tailed chi-squared test at level alpha)

del

step size for profiling

trace

(logical) produce tracing output?

tol.newmin

tolerance for diagnosing a new minimum below the minimum deviance estimated in initial fit is found

tranges

a two-column matrix giving lower and upper bounds for each parameter

... additional arguments (not used)

Details

Slices provide a lighter-weight way to explore likelihood surfaces than profiles, since they vary a single parameter rather than optimizing over all but one or two parameters.

slice is a generic method

slice1D creates one-dimensional slices, by default of all parameters of a model

slice2D creates two-dimensional slices, by default of all pairs of parameters in a model. In each panel the closed point represents the parameters given (typically the MLEs), while the open point represents the observed minimum value within the 2D slice. If everything has gone according to plan, these points should coincide (at least up to grid precision).

slicetrans creates a slice along a transect between two specified points in parameter space (see calcslice in the emdbook package)

Value

An object of class slice with

slices a list of individual parameter (or parameter-pair) slices, each of which is a data frame with elements

var1 name of the first variable

var2 (for 2D slices) name of the second variable

x parameter values

y (for 2D slices) parameter values

z slice values

ranges a list (?) of the ranges for each parameter

params vector of baseline parameter values

dim 1 or 2

sliceOld returns instead a list with elements profile and summary (see profile.mle2)
Author(s)

Ben Bolker

See Also

profile

Examples

```r
x <- 0:10
y <- c(26, 17, 13, 12, 20, 5, 8, 5, 4, 8)
d <- data.frame(x,y)
fit1 <- mle2(y~dpois(lambda=exp(lymax)/(1+x/exp(lhalf))),
start=list(lymax=0,lhalf=0),
data=d)
s1 <- bbmle::slice(fit1,verbose=FALSE)
s2 <- bbmle::slice(fit1,dim=2,verbose=FALSE)
require(lattice)
plot(s1)
plot(s2)
## 'transect' slice, from best-fit values to another point
st <- bbmle::slice(fit1,params2=c(5,0.5))
plot(st)
```

Description

evaluations of log-likelihood along transects in parameter space

Objects from the Class

Objects can be created by calls of the form `new("slice.mle2",...)`. The objects are similar to likelihood profiles, but don’t involve any optimization with respect to the other parameters.

Slots

- `profile`: Object of class "list". List of slices, one for each requested parameter. Each slice is a data frame with the first column called `z` being the signed square root of the -2 log likelihood ratio, and the others being the parameters with names prefixed by `par.vals`.

- `summary`: Object of class "summary.mle2". Summary of object being profiled.

Methods

- `plot` signature(x = "profile.mle2", y = "missing"): Plot profiles for each parameter.

See Also

`profile.mle2-class`
strwrapx

Wrap strings at white space and + symbols

Description

Extended (hacked) version of strwrap: wraps a string at whitespace and plus symbols

Usage

strwrapx(x, width = 0.9 * getOption("width"), indent = 0, 
exdent = 0, prefix = "", simplify = TRUE, 
parsplit = "\n[ \t\n]*\n", wordsplit = "[ \t\n"])

Arguments

x a character vector, or an object which can be converted to a character vector by as.character.
width a positive integer giving the target column for wrapping lines in the output.
indent a non-negative integer giving the indentation of the first line in a paragraph.
exdent a non-negative integer specifying the indentation of subsequent lines in para-
graphs.
prefix a character string to be used as prefix for each line.
simplify a logical. If TRUE, the result is a single character vector of line text; otherwise, it is a list of the same length as x the elements of which are character vectors of line text obtained from the corresponding element of x. (Hence, the result in the former case is obtained by unlisting that of the latter.)
parsplit Regular expression describing how to split paragraphs
wordsplit Regular expression describing how to split words

Details

Whitespace in the input is destroyed. Double spaces after periods (thought as representing sentence
ends) are preserved. Currently, possible sentence ends at line breaks are not considered specially.

Indentation is relative to the number of characters in the prefix string.

Examples

## Read in file 'THANKS'.
x <- paste(readLines(file.path(R.home("doc"), "THANKS")), collapse = "\n")
## Split into paragraphs and remove the first three ones
x <- unlist(strsplit(x, "\n[ \t\n]*\n")[-(1:3)])
## Join the rest
x <- paste(x, collapse = "\n\n")
## Now for some fun:
writeLines(strwrap(x, width = 60))
writeLines(strwrap(x, width = 60, indent = 5))
writeLines(strwrap(x, width = 60, exdent = 5))
writeLines(strwrap(x, prefix = "THANKS"))

## Note that messages are wrapped AT the target column indicated by
## 'width' (and not beyond it).
## From an R-devel posting by J. Hosking <jh910@juno.com>.
x <- paste(sapply(sample(10, 100, rep=TRUE),
               function(x) substring("aaaaaaaaaa", 1, x)), collapse = " ")
sapply(1:10, function(m)
               c(target = m, actual = max(nchar(strwrap(x, m))))

summary.mle2-class  Class "summary.mle2", summary of "mle2" objects

Description

Extract of "mle2" object

Objects from the Class

Objects can be created by calls of the form new("summary.mle2",...), but most often by invoking summary on an "mle2" object. They contain values meant for printing by show.

Slots

call: Object of class "language" The call that generated the "mle2" object.
coef: Object of class "matrix". Estimated coefficients and standard errors
m2logL: Object of class "numeric". Minus twice the log likelihood.

Methods

show signature(object = "summary.mle2"): Pretty-prints object
coeff signature(object = "summary.mle2"): Extracts the contents of the coef slot

See Also

summary, mle2, mle2-class
Index

*Topic character
   strwrapx, 29

*Topic classes
   mle2-class, 13
   profile.mle2-class, 21
   slice.mle2-class, 28
   summary.mle2-class, 30

*Topic distribution
   dnorm_n, 6

*Topic methods
   BIC-methods, 3
   predict-methods, 18
   profile-methods, 19

*Topic misc
   as.data.frame.profile.mle2, 2
   call.to.char, 5
   get.mnames, 6
   ICtab, 7
   namedrop, 15
   parnames, 16
   relist2, 24
   sbinom, 24
   slice, 26

*Topic models
   mle2, 9
   mle2.options, 14
   AIC,mle2-method (BIC-methods), 3
   AIC-methods (BIC-methods), 3
   AICc (BIC-methods), 3
   AICc,ANY,mle2,logLik-method (BIC-methods), 3
   AICc,ANY-method (BIC-methods), 3
   AICc,logLik-method (BIC-methods), 3
   AICc,mle2-method (BIC-methods), 3
   AICc-methods (BIC-methods), 3
   AICctab (ICtab), 7
   AICtab (ICtab), 7
   anova,mle2-method (BIC-methods), 3
   as.character, 29
   as.data.frame.profile.mle2, 2
   BIC-methods, 3
   BICtab (ICtab), 7
   calc_mle2_function (mle2), 9
   call.to.char, 5
   coef,mle2-method (mle2-class), 13
   coef,summary.mle2-method (summary.mle2-class), 30
   coerce,mle2-method (mle2-class), 13
   coerce,profile.mle2, data.frame-method (as.data.frame.profile.mle2), 2
   coerce,profile.mle2-method (as.data.frame.profile.mle2), 2
   confint,mle2-method (profile.mle2-class), 21
   confint,profile.mle2-method (profile.mle2-class), 21
   confint.mle2 (profile.mle2-class), 21
   constrOptim, 11
   dbeta, 25
   dbinom, 25, 26
   deviance,mle2-method (mle2-class), 13
   dlnorm, 25
   dnbinom, 25, 26
   dnorm, 25, 26
   dnorm_n, 6
   dpois, 25, 26
   format.pval, 8
   formula,mle2-method (mle2-class), 13
   get.mnames, 6
   gfun (predict-methods), 18
   ginv, 10
   hessian, 10
   ICtab, 7
<table>
<thead>
<tr>
<th>Function</th>
<th>Line(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>load</td>
<td>9</td>
</tr>
<tr>
<td>logLik, mle2-method (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>logLik-methods (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>mle (mle2)</td>
<td>9</td>
</tr>
<tr>
<td>mle2, 9, 13, 23, 30</td>
<td></td>
</tr>
<tr>
<td>mle2-class</td>
<td>13</td>
</tr>
<tr>
<td>mle2.options</td>
<td>14</td>
</tr>
<tr>
<td>namedrop</td>
<td>15</td>
</tr>
<tr>
<td>nlm</td>
<td>11</td>
</tr>
<tr>
<td>nlminb</td>
<td>11</td>
</tr>
<tr>
<td>nobs</td>
<td>7</td>
</tr>
<tr>
<td>optim</td>
<td>9–11, 13, 14</td>
</tr>
<tr>
<td>optimx</td>
<td>11</td>
</tr>
<tr>
<td>parnames</td>
<td>9, 16</td>
</tr>
<tr>
<td>parnames&lt;- (parnames)</td>
<td>16</td>
</tr>
<tr>
<td>plot, profile.mle2, missing-method (profile.mle2-class)</td>
<td>21</td>
</tr>
<tr>
<td>plot, profile.mle2-method</td>
<td></td>
</tr>
<tr>
<td>plot.profile.mle2</td>
<td></td>
</tr>
<tr>
<td>plot,profile.mle2-method</td>
<td></td>
</tr>
<tr>
<td>plot.profile.mle2 (profile.mle2-class)</td>
<td>21</td>
</tr>
<tr>
<td>pop_pred_samp</td>
<td>17</td>
</tr>
<tr>
<td>predict, mle2-method (predict-methods)</td>
<td>18</td>
</tr>
<tr>
<td>predict-methods</td>
<td>18</td>
</tr>
<tr>
<td>print.ICtab</td>
<td>7</td>
</tr>
<tr>
<td>proffun (profile-methods)</td>
<td>19</td>
</tr>
<tr>
<td>profile</td>
<td>28</td>
</tr>
<tr>
<td>profile, mle2-method (profile-methods)</td>
<td>19</td>
</tr>
<tr>
<td>profile-methods</td>
<td>19</td>
</tr>
<tr>
<td>profile.mle2</td>
<td>27</td>
</tr>
<tr>
<td>profile.mle2 (profile-methods)</td>
<td>19</td>
</tr>
<tr>
<td>profile.mle2 (profile-methods)</td>
<td>21</td>
</tr>
<tr>
<td>qAIC (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>qAIC, ANY, mle2, logLik-method (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>qAIC, ANY-method (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>qAIC, logLik-method (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>qAIC, mle2-method (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>qAIC-methods (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>qAICc, mle2-method (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>qAICc-methods (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>qAICc, ANY-method (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>qAICc, logLik-method (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>qAICc, mle2-method (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>qAICc-methods (BIC-methods)</td>
<td>3</td>
</tr>
<tr>
<td>relist2</td>
<td>24</td>
</tr>
<tr>
<td>require</td>
<td>9</td>
</tr>
<tr>
<td>residuals, mle2-method</td>
<td></td>
</tr>
<tr>
<td>(predict-methods)</td>
<td>18</td>
</tr>
<tr>
<td>sbeta (sbinom)</td>
<td>24</td>
</tr>
<tr>
<td>sbetabinom (sbinom)</td>
<td>24</td>
</tr>
<tr>
<td>sbinom</td>
<td>24</td>
</tr>
<tr>
<td>show, mle2-method (mle2-class)</td>
<td>13</td>
</tr>
<tr>
<td>show, profile.mle2-method</td>
<td></td>
</tr>
<tr>
<td>show, profile.mle2</td>
<td></td>
</tr>
<tr>
<td>show, summary.mle2-method</td>
<td></td>
</tr>
<tr>
<td>show, summary.mle2-class</td>
<td>21</td>
</tr>
<tr>
<td>simulate, mle2-method (predict-methods)</td>
<td>18</td>
</tr>
<tr>
<td>simulate, mle2-class</td>
<td>13</td>
</tr>
<tr>
<td>slice</td>
<td>26</td>
</tr>
<tr>
<td>slice, mle2-method (mle2-class)</td>
<td>13</td>
</tr>
<tr>
<td>slice.mle2-class</td>
<td>13</td>
</tr>
<tr>
<td>slice1D (slice)</td>
<td>26</td>
</tr>
<tr>
<td>slice2D (slice)</td>
<td>26</td>
</tr>
<tr>
<td>sliceOld (slice)</td>
<td>26</td>
</tr>
<tr>
<td>slicetrans (slice)</td>
<td>26</td>
</tr>
<tr>
<td>slnorm (sbinom)</td>
<td>24</td>
</tr>
<tr>
<td>sbinom (sbinom)</td>
<td>24</td>
</tr>
<tr>
<td>snorm (sbinom)</td>
<td>24</td>
</tr>
<tr>
<td>spois (sbinom)</td>
<td>24</td>
</tr>
<tr>
<td>spois</td>
<td>24</td>
</tr>
<tr>
<td>stdEr (mle2-class)</td>
<td>13</td>
</tr>
<tr>
<td>stdEr, mle2-method (mle2-class)</td>
<td>13</td>
</tr>
<tr>
<td>strwrapx</td>
<td>29</td>
</tr>
<tr>
<td>summary</td>
<td>30</td>
</tr>
<tr>
<td>summary, mle2-method (mle2-class)</td>
<td>30</td>
</tr>
<tr>
<td>summary, mle2-class</td>
<td>30</td>
</tr>
<tr>
<td>update, mle2-method (mle2-class)</td>
<td>13</td>
</tr>
<tr>
<td>vcov, mle2-method (mle2-class)</td>
<td>13</td>
</tr>
</tbody>
</table>