Package ‘ashr’

February 22, 2022

Encoding UTF-8
Type Package
Maintainer Peter Carbonetto <pcarbo@uchicago.edu>
Version 2.2-54
Date 2022-02-22
Title Methods for Adaptive Shrinkage, using Empirical Bayes
Description The R package ‘ashr’ implements an Empirical Bayes
approach for large-scale hypothesis testing and false discovery
rate (FDR) estimation based on the methods proposed in
<DOI:10.1093/biostatistics/kxw041>. These methods can be applied
whenever two sets of summary statistics---estimated effects and
standard errors---are available, just as ‘qvalue’ can be applied
to previously computed p-values. Two main interfaces are
provided: ash(), which is more user-friendly; and ash.workhorse(),
which has more options and is geared toward advanced users. The
ash() and ash.workhorse() also provides a flexible modeling
interface that can accommodate a variety of likelihoods (e.g.,
normal, Poisson) and mixture priors (e.g., uniform, normal).

Depends R (>= 3.1.0)
Imports Matrix, stats, graphics, Rcpp (>= 0.10.5), truncnorm, mixsqp,
       SQUAREM, etrunct, invgamma
Suggests testthat, knitr, rmarkdown, ggplot2, REBayes
LinkingTo Rcpp
License GPL (>= 3)
NeedsCompilation yes
URL https://github.com/stephens999/ashr
BugReports https://github.com/stephens999/ashr/issues
VignetteBuilder knitr
RoxygenNote 7.1.2
Author  Matthew Stephens [aut],  
        Peter Carbonetto [aut, cre],  
        Chaoxing Dai [ctb],  
        David Gerard [aut],  
        Mengyin Lu [aut],  
        Lei Sun [aut],  
        Jason Willwerscheid [aut],  
        Nan Xiao [aut],  
        Mazon Zeng [ctb]  

Repository  CRAN  

Date/Publication  2022-02-22 16:10:07 UTC  

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### Description

Implements Empirical Bayes shrinkage and false discovery rate methods based on unimodal prior distributions.

### Usage

```r
ash(
  betaHat,
  seBetaHat,
  mixcompDist = c("uniform", "halfuniform", "normal", "+uniform", "-uniform", "halfnormal"),
  df = NULL,
  ...
)

ash.workhorse(
  betaHat,
  seBetaHat,
  method = c("fdr", "shrink"),
  mixcompDist = c("uniform", "halfuniform", "normal", "+uniform", "-uniform", "halfnormal"),
  optmethod = c("mixSQP", "mixIP", "cxxMixSquarem", "mixEM", "mixVBEM", "w_mixEM"),
  df = NULL,
)```

---

**ash**  
*Adaptive Shrinkage*

---
nullweight = 10,
pointmass = TRUE,
prior = c("nullbiased", "uniform", "unit"),
mixsd = NULL,
gridmult = sqrt(2),
outputlevel = 2,
g = NULL,
fixg = FALSE,
mode = 0,
alpha = 0,
grange = c(-Inf, Inf),
control = list(),
lik = NULL,
weights = NULL,
pi_thresh = 1e-10
)

Arguments

betahat a p vector of estimates
sebetahat a p vector of corresponding standard errors
mixcompdist distribution of components in mixture used to represent the family G. Depending on the choice of mixture component, the family G becomes more or less flexible. Options are:

uniform G is (approximately) any symmetric unimodal distribution
normal G is (approximately) any scale mixture of normals
halfuniform G is (approximately) any unimodal distribution
+uniform G is (approximately) any unimodal distribution with support constrained to be greater than the mode.
-uniform G is (approximately) any unimodal distribution with support constrained to be less than the mode.
halfnormal G is (approximately) any scale mixture of truncated normals where the normals are truncated at the mode

If you are happy to assume a symmetric distribution for effects, you can use "uniform" or "normal". If you believe your effects may be asymmetric, use "halfuniform" or "halfnormal". If you want to allow only positive/negative effects use "+uniform"/"-uniform". The use of "normal" and "halfnormal" is permitted only if df=NULL.

df appropriate degrees of freedom for (t) distribution of (betahat-beta)/sebetahat; default is NULL which is actually treated as infinity (Gaussian)

... Further arguments of function ash to be passed to ash.workhorse.

method specifies how ash is to be run. Can be "shrinkage" (if main aim is shrinkage) or "fdr" (if main aim is to assess false discovery rate or false sign rate (fsr)). This is simply a convenient way to specify certain combinations of parameters: "shrinkage" sets pointmass=FALSE and prior="uniform"; "fdr" sets pointmass=TRUE and prior="nullbiased".
optmethod specifies the function implementing an optimization method.
nullweight scalar, the weight put on the prior under "nullbiased" specification, see prior
pointmass Logical, indicating whether to use a point mass at zero as one of components for a mixture distribution.
prior string, or numeric vector indicating Dirichlet prior on mixture proportions (defaults to "uniform", or (1,1,...,1); also can be "nullbiased" (nullweight,1,...,1) to put more weight on first component), or "unit" (1/K,...,1/K) [for optmethod=mixVBEM version only].
mixsd Vector of standard deviations for underlying mixture components.
gridmult the multiplier by which the default grid values for mixsd differ by one another. (Smaller values produce finer grids.)
outputlevel Determines amount of output. There are several numeric options: 0 = just fitted g; 1 = also PosteriorMean and PosteriorSD; 2 = everything usually needed; 3 = also include results of mixture fitting procedure (including matrix of log-likelihoods used to fit mixture). 4 and 5 are reserved for outputting additional data required by the (in-development) flashr package. The user can also specify the output they require in detail (see Examples).
g The prior distribution for beta. Usually this is unspecified (NULL) and estimated from the data. However, it can be used in conjunction with fixg=TRUE to specify the g to use (e.g. useful in simulations to do computations with the "true" g). Or, if g is specified but fixg=FALSE, the g specifies the initial value of g used before optimization, (which also implicitly specifies mixcompdist).
fixg If TRUE, don’t estimate g but use the specified g - useful for computations under the "true" g in simulations.
mode either numeric (indicating mode of g) or string "estimate", to indicate mode should be estimated, or a two dimension numeric vector to indicate the interval to be searched for the mode.
alpha Numeric value of alpha parameter in the model.
grange Two dimension numeric vector indicating the left and right limit of g. Default is c(-Inf, Inf).
control A list of control parameters passed to optmethod.
lik Contains details of the likelihood used; for general ash. Currently, the following choices are allowed: normal (see function lik_normal()); binomial likelihood (see function lik_binom); likelihood based on logF error distribution (see function lik_logF); mixture of normals likelihood (see function lik_normalmix); and Poisson likelihood (see function lik_pois).
weights a vector of weights for observations; use with optmethod = "w_mixEM"; this is currently beta-functionality.
pi_thresh a threshold below which to prune out mixture components before computing summaries (speeds up computation since empirically many components are usually assigned negligible weight). The current implementation still returns the full fitted distribution; this only affects the posterior summaries.
Details

The ash function provides a number of ways to perform Empirical Bayes shrinkage estimation and false discovery rate estimation. The main assumption is that the underlying distribution of effects is unimodal. Novice users are recommended to start with the examples provided below.

In the simplest case the inputs to ash are a vector of estimates (betahat) and their corresponding standard errors (sebetahat), and degrees of freedom (df). The method assumes that for some (unknown) "true" vector of effects beta, the statistic (betahat[j]-beta[j])/sebetahat[j] has a $t$ distribution on $df$ degrees of freedom. (The default of df=NULL assumes a normal distribution instead of a t.)

By default the method estimates the vector beta under the assumption that beta ~ g for a distribution g in G, where G is some unimodal family of distributions to be specified (see parameter mixcompdist). By default is to assume the mode is 0, and this is suitable for settings where you are interested in testing which beta[j] are non-zero. To estimate the mode see parameter mode.

As is standard in empirical Bayes methods, the fitting proceeds in two stages: i) estimate g by maximizing a (possibly penalized) likelihood; ii) compute the posterior distribution for each beta[j] | betahat[j],sebetahat[j] using the estimated g as the prior distribution.

A more general case allows that beta[j]/sebetahat[j]^alpha | sebetahat[j] ~ g.

Value

ash returns an object of class "ash", a list with some or all of the following elements (determined by outputlevel)

- fitted_g: fitted mixture
- loglik: log P(D|fitted_g)
- logLR: log[P(D|fitted_g)/P(D|beta==0)]
- result: A dataframe whose columns are:
  - NegativeProb: A vector of posterior probability that beta is negative.
  - PositiveProb: A vector of posterior probability that beta is positive.
  - lfsr: A vector of estimated local false sign rate.
  - lfdr: A vector of estimated local false discovery rate.
  - qvalue: A vector of q values.
  - svalue: A vector of s values.
  - PosteriorMean: A vector consisting the posterior mean of beta from the mixture.
  - PosteriorSD: A vector consisting the corresponding posterior standard deviation.
- call: a call in which all of the specified arguments are specified by their full names
- data: a list containing details of the data and models used (mostly for internal use)
- fit_details: a list containing results of mixture optimization, and matrix of component log-likelihoods used in this optimization

Functions

- ash.workhorse: Adaptive Shrinkage with full set of options.
See Also

ashci for computation of credible intervals after getting the ash object return by ash()

Examples

```r
beta = c(rep(0,100),rnorm(100))
sebetahat = abs(rnorm(200,0,1))
betahat = rnorm(200,beta,sebetahat)
beta.ash = ash(betahat, sebetahat)
names(beta.ash)
head(beta.ash$result) # the main dataframe of results
head(get_pm(beta.ash)) # get_pm returns posterior mean
head(get_lfsr(beta.ash)) # get_lfsr returns the local false sign rate
graphics::plot(betahat,get_pm(beta.ash),xlim=c(-4,4),ylim=c(-4,4))

## Not run:
# Why is this example included here? -Peter
CIMatrix=ashci(beta.ash,level=0.95)
print(CIMatrix)

## End(Not run)

# Illustrating the non-zero mode feature.
betahat=betahat+5
beta.ash = ash(betahat, sebetahat)
graphics::plot(betahat,get_pm(beta.ash))
betan.ash=ash(betahat, sebetahat,mode=5)
graphics::plot(betahat,get_pm(betan.ash))
summary(betan.ash)

# Running ash with different error models
beta.ash1 = ash(betahat, sebetahat, lik = lik_normal())
beta.ash2 = ash(betahat, sebetahat, lik = lik_t(df=4))
e = rnorm(100)+log(rf(100,df1=10,df2=10)) # simulated data with log(F) error
e.ash = ash(e,1,lik=lik_logF(df1=10,df2=10))

# Specifying the output
beta.ash = ash(betahat, sebetahat, output = c("fitted_g","logLR","lfsr"))

#Running ash with a pre-specified g, rather than estimating it
beta = c(rep(0,100),rnorm(100))
sebetahat = abs(rnorm(200,0,1))
betahat = rnorm(200,beta,sebetahat)
true_g = normalmix(c(0.5,0.5),c(0,0),c(0,1)) # define true g
## Passing this g into ash causes it to i) take the sd and the means
## for each component from this g, and ii) initialize pi to the value
## from this g.
beta.ash = ash(betahat, sebetahat,g=true_g,fixg=TRUE)

# running with weights
```
```
beta.ash = ash(betahat, sebetahat, optmethod="w_mixEM",
               weights = c(rep(0.5,100),rep(1,100)))

# Different algorithms can be used to compute maximum-likelihood
# estimates of the mixture weights. Here, we illustrate use of the
# EM algorithm and the (default) SQP algorithm.
set.seed(1)
betahat <- c(8.115,9.027,9.289,10.097,9.463)
sebeta <- c(0.6157,0.4129,0.3197,0.3920,0.5496)
fit.em <- ash(betahat,sebeta,mixcompdist = "normal",optmethod = "mixEM")
fit.sqp <- ash(betahat,sebeta,mixcompdist = "normal",optmethod = "mixSQP")
range(fit.em$fitted$pi - fit.sqp$fitted$pi)

ashci

---

## Credible Interval Computation for the ash object

### Description

Given the ash object returned by the main function ash, this function computes a posterior credible interval (CI) for each observation. The ash object must include a data component to use this function (which it does by default).

### Usage

```r
ashci(
  a,
  level = 0.95,
  betaindex,
  lfsr_threshold = 1,
  tol = 0.001,
  trace = FALSE
)
```

### Arguments

- `a`:
  - the fitted ash object
- `level`:
  - the level for the credible interval, (default=0.95)
- `betaindex`:
  - a vector consisting of locations of betahat where you would like to compute the credible interval
- `lfsr_threshold`:
  - a scalar, if specified then computes CIs only for observations more significant than that threshold.
- `tol`:
  - passed to uniroot; indicates desired accuracy.
- `trace`:
  - a logical variable denoting whether some of the intermediate results of iterations should be displayed to the user. Default is FALSE.
```
Details

Uses uniroot to find credible interval, one at a time for each observation. The computation cost is linear in number of observations.

Value

A matrix, with 2 columns, ith row giving CI for ith observation

Examples

```r
beta = c(rep(0,20),rnorm(20))
sebetahat = abs(rnorm(40,0,1))
betahat = rnorm(40,beta,sebetahat)
beta.ash = ash(betahat, sebetahat)

CImatrix=ashci(beta.ash,level=0.95)

CImatrix1=ashci(beta.ash,level=0.95,betaindex=c(1,2,5))
CImatrix2=ashci(beta.ash,level=0.95,lfsr_threshold=0.1)
```

Description

The main function in the ashr package is `ash`, which should be examined for more details. For simplicity only the most commonly-used options are documented under `ash`. For expert or interested users the documentation for function `ash.workhorse` provides documentation on all implemented options.

ash_pois

Performs adaptive shrinkage on Poisson data

Description

Uses Empirical Bayes to fit the model

\[ y_j | \lambda_j \sim Pois(c_j \lambda_j) \]

with

\[ h(\lambda_j) \sim g() \]

where \( h \) is a specified link function (either "identity" or "log" are permitted).

Usage

```r
ash_pois(y, scale = 1, link = c("identity", "log"), ...)
```
calc_loglik

Arguments

- **y**: vector of Poisson observations.
- **scale**: vector of scale factors for Poisson observations: the model is $y[j] \sim \text{Pois}(\text{scale}[j] \ast \lambda[j])$.
- **link**: string, either "identity" or "log", indicating the link function.
- **...**: other parameters to be passed to ash

Details

The model is fit in two stages: i) estimate $g$ by maximum likelihood (over the set of symmetric unimodal distributions) to give estimate $\hat{g}$; ii) Compute posterior distributions for $\lambda_j$ given $y_j, \hat{g}$. Note that the link function $h$ affects the prior assumptions (because, e.g., assuming a unimodal prior on $\lambda$ is different from assuming unimodal on $\log \lambda$), but posterior quantities are always computed for the for $\lambda$ and *not* $h(\lambda)$.

Examples

```r
beta = c(rep(0,50),rexp(50))
y = rpois(100,beta) # simulate Poisson observations
y.ash = ash_pois(y,scale=1)
```

Description

Return the log-likelihood of the data for a given g() prior

Usage

`calc_loglik(g, data)`

Arguments

- **g**: the fitted g, or an ash object containing g
- **data**: a data object, see `set_data`
calc_logLR

Compute loglikelihood ratio for data from ash fit

Description

Return the log-likelihood ratio of the data for a given g() prior

Usage

calc_logLR(g, data)

Arguments

g  the fitted g, or an ash object containing g
data  a data object, see set_data

calc_mixmean

Generic function of calculating the overall mean of the mixture

Description

Generic function of calculating the overall mean of the mixture

Usage

calc_mixmean(m)

Arguments

m  a mixture of k components generated by normalmix() or unimix() or igmix()

Value

it returns scalar, the mean of the mixture distribution.
calc_mixsd

Generic function of calculating the overall standard deviation of the mixture

Description

Generic function of calculating the overall standard deviation of the mixture

Usage

calc_mixsd(m)

Arguments

m a mixture of k components generated by normalmix() or unimix() or igmix()

Value

it returns scalar

calc_null_loglik

Compute loglikelihood for data under null that all beta are 0

Description

Return the log-likelihood of the data betahat, with standard errors betahatsd, under the null that beta==0

Usage

calc_null_loglik(data)

Arguments

data a data object; see set_data
calc_null_vloglik  
*Compute vector of loglikelihood for data under null that all beta are 0*

**Description**

Return the vector of log-likelihoods of the data points under the null

**Usage**

```
calc_null_vloglik(data)
```

**Arguments**

- `data`  
a data object; see `set_data`

---

calc_vloglik  
*Compute vector of loglikelihood for data from ash fit*

**Description**

Return the vector of log-likelihoods of the data betahat, with standard errors betahatsd, for a given g() prior on beta, or an ash object containing that

**Usage**

```
calc_vloglik(g, data)
```

**Arguments**

- `g`  
the fitted g, or an ash object containing g
- `data`  
a data object, see `set_data`
**calc_vlogLR**

**Description**

Return the vector of log-likelihood ratios of the data betahat, with standard errors betahatsd, for a given g() prior on beta, or an ash object containing that, vs the null that g() is point mass on 0.

**Usage**

`calc_vlogLR(g, data)`

**Arguments**

- `g` - the fitted g, or an ash object containing g
- `data` - a data object, see set_data

---

**cdf.ash**

**Description**

Computed the cdf of the underlying fitted distribution.

**Usage**

`cdf.ash(a, x, lower.tail = TRUE)`

**Arguments**

- `a` - the fitted ash object
- `x` - the vector of locations at which cdf is to be computed
- `lower.tail` - (default=TRUE) whether to compute the lower or upper tail

**Details**

None
Description

compute cdf of mixture m convoluted with error distribution either normal of sd (s) or student t with df v at locations x

Usage

cdf_conv(m, data)

Arguments

m mixture distribution with k components
data details depend on the model

Description

evaluate cdf of posterior distribution of beta at c. m is the prior on beta, a mixture; c is location of evaluation assumption is betahat | beta ~ t_v(beta,sebetahat)

Usage

cdf_post(m, c, data)

Arguments

m mixture distribution with k components
c a scalar
data details depend on model

Value

an n vector containing the cdf for beta_i at c

Examples

beta = rnorm(100,0,1)
betahat= beta+rnorm(100,0,1)
sebetahat=rep(1,100)
ash.beta = ash(betahat,1,mixcompdist="normal")
cdf0 = cdf_post(ash.beta$fitted_g,0,set_data(betahat,sebetahat))
graphics::plot(cdf0,1-get_pp(ash.beta))
**compute_lfsr**

*Function to compute the local false sign rate*

**Description**

Function to compute the local false sign rate

**Usage**

```r
compute_lfsr(NegativeProb, ZeroProb)
```

**Arguments**

- **NegativeProb**
  A vector of posterior probability that beta is negative.
- **ZeroProb**
  A vector of posterior probability that beta is zero.

**Value**

The local false sign rate.

**comp_cdf**

*Generic function of computing the cdf for each component*

**Description**

Generic function of computing the cdf for each component

**Usage**

```r
comp_cdf(m, y, lower.tail = TRUE)
```

**Arguments**

- **m**
  a mixture (eg of type normalmix or unimix)
- **y**
  locations at which cdf to be computed
- **lower.tail**
  boolean indicating whether to report lower tail

**Value**

it returns a vector of probabilities, with length equals to number of components in m
Description

compute the cdf of data for each component of mixture when convolved with error distribution

Usage

comp_cdf_conv(m, data)

Arguments

m mixture distribution with k components
data details depend on the model

Value

a k by n matrix of cdfs

Description

returns cdf of convolution of each component of a normal mixture with N(0,s^2) at x. Note that convolution of two normals is normal, so it works that way

Usage

## S3 method for class 'normalmix'
comp_cdf_conv(m, data)

Arguments

m mixture distribution with k components
data a list with components x and s to be interpreted as a normally-distributed observation and its standard error

Value

a k by n matrix
**Description**

cdf of convolution of each component of a unif mixture

**Usage**

```r
## S3 method for class 'unimix'
comp_cdf_conv(m, data)
```

**Arguments**

- `m` a mixture of class `unimix`
- `data`, see `set_data()`

**Value**

a k by n matrix

---

**Description**

evaluate cdf of posterior distribution of beta at c. m is the prior on beta, a mixture; c is location of evaluation assumption is betahat | beta ~ t_v(beta,sebetahat)

**Usage**

`comp_cdf_post(m, c, data)`

**Arguments**

- `m` mixture distribution with k components
- `c` a scalar
- `data` details depend on model

**Value**

a k by n matrix
Examples

```r
beta = rnorm(100, 0, 1)
betahat = beta + rnorm(100, 0, 1)
sebetahat = rep(1, 100)
ash.beta = ash(betahat, 1, mixcompdist="normal")
comp_cdf_post(get_fitted_g(ash.beta), 0, data = set_data(beta, sebetahat))
```

---

### comp_dens

**Generic function of calculating the component densities of the mixture**

#### Description

Generic function of calculating the component densities of the mixture

#### Usage

```r
comp_dens(m, y, log = FALSE)
```

#### Arguments

- `m`: mixture of k components generated by `normalmix()` or `unimix()` or `igmix()`
- `y`: is an n-vector of location
- `log`: whether to use log-scale on densities

#### Value

A k by n matrix of densities

---

### comp_dens_conv

**comp_dens_conv**

#### Description

Compute the density of data for each component of mixture when convolved with error distribution

#### Usage

```r
comp_dens_conv(m, data)
```

#### Arguments

- `m`: mixture distribution with k components
- `data`: details depend on the model

#### Value

A k by n matrix of densities
comp_dens_conv.normalmix

Description
returns density of convolution of each component of a normal mixture with N(0,s^2) at x. Note that convolution of two normals is normal, so it works that way

Usage
## S3 method for class 'normalmix'
comp_dens_conv(m, data)

Arguments
m mixture distribution with k components
data a list with components x and s to be interpreted as a normally-distributed observation and its standard error

Value
a k by n matrix

comp_dens_conv.unimix density of convolution of each component of a unif mixture

Description
density of convolution of each component of a unif mixture

Usage
## S3 method for class 'unimix'
comp_dens_conv(m, data)

Arguments
m a mixture of class unimix
data, see set_data()

Value
a k by n matrix
**comp_mean**

*Generic function of calculating the first moment of components of the mixture*

**Description**

Generic function of calculating the first moment of components of the mixture

**Usage**

```r
comp_mean(m)
```

**Arguments**

- `m` : a mixture of k components generated by normalmix() or unimix() or igmix()

**Value**

it returns a vector of means.

---

**comp_mean.normalmix**

**Description**

returns mean of the normal mixture

**Usage**

```r
## S3 method for class 'normalmix'
comp_mean(m)
```

**Arguments**

- `m` : a normal mixture distribution with k components

**Value**

a vector of length k
Description

Returns mean of the truncated-normal mixture.

Usage

```r
## S3 method for class 'tnormalmix'
comp_mean(m)
```

Arguments

- `m` A truncated normal mixture distribution with k components.

Value

A vector of length k.

Description

Generic function of calculating the second moment of components of the mixture

Usage

```r
comp_mean2(m)
```

Arguments

- `m` a mixture of k components generated by normalmix() or unimix() or igmix()

Value

it returns a vector of second moments.
**comp_postmean**

**Description**

output posterior mean for beta for each component of prior mixture m, given data

**Usage**

`comp_postmean(m, data)`

**Arguments**

- `m`  
mixture distribution with k components
- `data`  
details depend on the model

---

**comp_postmean2**

**Description**

output posterior mean-squared value given prior mixture m and data

**Usage**

`comp_postmean2(m, data)`

**Arguments**

- `m`  
mixture distribution with k components
- `data`  
details depend on the model
### Description

**comp_postprob**

compute the posterior prob that each observation came from each component of the mixture m. Output a k by n vector of probabilities computed by weighting the component densities by pi and then normalizing.

**Usage**

```r
comp_postprob(m, data)
```

**Arguments**

- `m`: mixture distribution with k components
- `data`: details depend on the model

### Description

**comp_postsd**

output posterior sd for beta for each component of prior mixture m, given data.

**Usage**

```r
comp_postsd(m, data)
```

**Arguments**

- `m`: mixture distribution with k components
- `data`: details depend on the model

**Examples**

```r
beta = rnorm(100,0,1)
betahat = beta + rnorm(100,0,1)
ash.beta = ash(betahat,1,mixcompdist="normal")
data = set_data(betahat,rep(1,100))
comp_postmean(get_fitted_g(ash.beta),data)
comp_postsd(get_fitted_g(ash.beta),data)
comp_postprob(get_fitted_g(ash.beta),data)
```
comp_sd

Generic function to extract the standard deviations of components of the mixture

Description

Generic function to extract the standard deviations of components of the mixture

Usage

comp_sd(m)

Arguments

m a mixture of k components generated by normalmix() or unimix() or igmix()

Value

it returns a vector of standard deviations

comp_sd.normalmix

Description

returns sds of the normal mixture

Usage

## S3 method for class 'normalmix'
comp_sd(m)

Arguments

m a normal mixture distribution with k components

Value

a vector of length k
**Description**

Returns standard deviations of the truncated normal mixture.

**Usage**

```
## S3 method for class 'tnormalmix'
comp_sd(m)
```

**Arguments**

- `m`: A truncated normal mixture distribution with k components.

**Value**

A vector of length k.

---

**cxxMixSquarem**

_Brief description of function._

---

**Description**

Explain here what this function does.

**Usage**

```
cxxMixSquarem(matrix_lik, prior, pi_init, control)
```

**Arguments**

- `matrix_lik`: Description of argument goes here.
- `prior`: Description of argument goes here.
- `pi_init`: Description of argument goes here.
- `control`: Description of argument goes here.
dens

*Find density at y, a generic function*

**Description**

Find density at y, a generic function

**Usage**

dens(x, y)

**Arguments**

- **x**  
  A mixture of k components generated by `normalmix` or `unimix`.
- **y**  
  An n-vector of the location.

---

dens_conv

*compute density of mixture m convoluted with normal of sd (s) or student t with df v at locations x*

**Description**

compute density of mixture m convoluted with normal of sd (s) or student t with df v at locations x

**Usage**

dens_conv(m, data)

**Arguments**

- **m**  
  mixture distribution with k components
- **data**  
  details depend on the model
**dlogf**  
*The log-F distribution*

**Description**
Density function for the log-F distribution with \(df1\) and \(df2\) degrees of freedom (and optional non-centrality parameter \(ncp\)).

**Usage**
```
dlogf(x, df1, df2, ncp, log = FALSE)
```

**Arguments**
- \(x\) vector of quantiles
- \(df1\) degrees of freedom
- \(df2\) degrees of freedom
- \(ncp\) non-centrality parameter. If omitted the central F is assumed.
- \(log\) logical; if TRUE, probabilities \(p\) are given as \(\log(p)\).

**Value**
The density function.

---

**estimate_mixprop**  
*Estimate mixture proportions of a mixture \(g\) given noisy (error-prone) data from that mixture.*

**Description**
Estimate mixture proportions of a mixture \(g\) given noisy (error-prone) data from that mixture.

**Usage**
```
estimate_mixprop(  
data,  
g,  
prior,  
optmethod = c("mixSQP", "mixEM", "mixVBEM", "cxxMixSquarem", "mixIP", "w_mixEM"),  
control,  
weights = NULL)
)```
Arguments

data
- list to be passed to log_comp_dens_conv; details depend on model

g
- an object representing a mixture distribution (e.g., normalmix for mixture of normals; unimix for mixture of uniforms). The component parameters of g (e.g., the means and variances) specify the components whose mixture proportions are to be estimated. The mixture proportions of g are the parameters to be estimated; the values passed in may be used to initialize the optimization (depending on the optmethod used)

prior
- numeric vector indicating parameters of “Dirichlet prior” on mixture proportions

optmethod
- name of function to use to do optimization

control
- list of control parameters to be passed to optmethod, typically affecting things like convergence tolerance

weights
- vector of weights (for use with w_mixEM; in beta)

Details

This is used by the ash function. Most users won’t need to call this directly, but is exported for use by some other related packages.

Value

list, including the final loglikelihood, the null loglikelihood, an n by k likelihood matrix with (j,k)th element equal to $f_k(x_j)$, the fit and results of optmethod

Description

Produce function to compute expectation of truncated error distribution from log cdf and log pdf (using numerical integration)

Usage

gen_etruncFUN(lcdfFUN, lpdfFUN)

Arguments

lcdfFUN
- the log cdfFUN of the error distribution

lpdfFUN
- the log pdfFUN of the error distribution
get_density  

*Density method for ash object*

**Description**

Return the density of the underlying fitted distribution

**Usage**

```r
get_density(a, x)
```

**Arguments**

- `a`: the fitted ash object
- `x`: the vector of locations at which density is to be computed

**Details**

None

---

get_lfsr  

*Return lfsr from an ash object*

**Description**

These functions simply return elements of an ash object, generally without doing any calculations. (So if the value was not computed during the original call to ash, eg because of how outputlevel was set in the call, then NULL will be returned.) Accessing elements in this way rather than directly from the ash object will help ensure compatibility moving forward (e.g. if the internal structure of the ash object changes during software development.)

**Usage**

```r
get_lfsr(x)
get_lfdr(a)
get_svalue(a)
get_qvalue(a)
get_pm(a)
get_psd(a)
```
get_lfsr

get_pp(a)
get_np(a)
get_loglik(a)
get_logLR(a)
get_fitted_g(a)
get_pi0(a)

Arguments

x an ash fit (e.g. from running ash)
a an ash fit (e.g. from running ash)

Value

a vector (ash) of local false sign rates

Functions

• get_lfsr: local false sign rate
• get_lfdr: local false discovery rate
• get_svalue: svalue
• get_qvalue: qvalue
• get_pm: posterior mean
• get_psd: posterior standard deviation
• get_pp: positive probability
• get_np: negative probability
• get_loglik: log-likelihood
• get_logLR: log-likelihood ratio
• get_fitted_g: fitted g mixture
• get_pi0: pi0, the proportion of nulls
**get_post_sample**

**Sample from posterior**

**Description**

Returns random samples from the posterior distribution for each observation in an ash object. A matrix is returned, with columns corresponding to observations and rows corresponding to samples.

**Usage**

```r
get_post_sample(a, nsamp)
```

**Arguments**

- `a`: the fitted ash object
- `nsamp`: number of samples to return (for each observation)

**Examples**

```r
beta = rnorm(100,0,1)
betahat = beta+rnorm(100,0,1)
ash.beta = ash(betahat,1,mixcompdist="normal")
post.beta = get_post_sample(ash.beta,1000)
```

---

**igmix**

**Constructor for igmix class**

**Description**

Creates an object of class igmix (finite mixture of univariate inverse-gammas)

**Usage**

```r
igmix(pi, alpha, beta)
```

**Arguments**

- `pi`: vector of mixture proportions
- `alpha`: vector of shape parameters
- `beta`: vector of rate parameters

**Details**

None
lik_binom

Value

an object of class igmix

Examples

igmix(c(0.5,0.5),c(1,1),c(1,2))
lik_logF

Description

Creates a likelihood object for ash for use with logF error distribution

Usage

lik_logF(df1, df2)

Arguments

df1  first degree of freedom parameter of F distribution

df2  second degree of freedom parameter of F distribution

Examples

e = rnorm(100) + log(rf(100,df1=10,df2=10)) # simulate some data with log(F) error
ash(e,1,lik=lik_logF(df1=10,df2=10))

lik_normal

Description

Creates a likelihood object for ash for use with normal error distribution

Usage

lik_normal()

Examples

z = rnorm(100) + rnorm(100) # simulate some data with normal error
ash(z,1,lik=lik_normal())
lik_normalmix  
*Likelihood object for normal mixture error distribution*

**Description**

Creates a likelihood object for ash for use with normal mixture error distribution

**Usage**

```
lik_normalmix(pilik, sdlik)
```

**Arguments**

- **pilik**: a `k` vector of mixture proportions (`k` is the number of mixture components), or an `n*k` matrix that the `j`th row the is mixture proportions for `betahat_j`
- **sdlik**: a `k` vector of component-wise standard deviations, or an `n*k` matrix that the `j`th row the is component-wise standard deviations for `betahat_j`

**Examples**

```
e = rnorm(100,0,0.8)
e[seq(1,100,by=2)] = rnorm(50,0,1.5)  # generate e~0.5*N(0,0.8^2)+0.5*N(0,1.5^2)
betahat = rnorm(100)+e
ash(betahat, 1, lik=lik_normalmix(c(0.5,0.5),c(0.8,1.5)))
```

lik_pois  
*Likelihood object for Poisson error distribution*

**Description**

Creates a likelihood object for ash for use with Poisson error distribution

**Usage**

```
lik_pois(y, scale = 1, link = c("identity", "log"))
```

**Arguments**

- **y**: Poisson observations.
- **scale**: Scale factor for Poisson observations: `y~Pois(scale*lambda)`.
- **link**: Link function. The "identity" link directly puts unimodal prior on Poisson intensities `lambda`, and "log" link puts unimodal prior on `log(lambda)`. 
Details
Suppose we have Poisson observations $y_i \sim \text{Poisson}(c_i \lambda_i)$. We either put an unimodal prior $g$ on the (scaled) intensities $\lambda_i \sim g$ (by specifying link="identity") or on the log intensities $\logit(\lambda_i) \sim g$ (by specifying link="log"). Either way, ASH with this Poisson likelihood function will compute the posterior mean of the intensities $\lambda_i$.

Examples

```r
beta = c(rnorm(100,50,5)) # prior mode: 50
y = rpois(100,beta) # simulate Poisson observations
ash(rep(0,length(y)),1,lik=lik_pois(y))
```

---

**lik_t**

Likelihood object for $t$ error distribution

**Description**

Creates a likelihood object for ash for use with $t$ error distribution

**Usage**

```r
lik_t(df)
```

**Arguments**

- **df**: degree of freedom parameter of $t$ distribution

**Examples**

```r
z = rnorm(100) + rt(100,df=4) # simulate some data with $t$ error
ash(z,1,lik=lik_t(df=4))
```

---

**loglik_conv**

loglik_conv

**Description**

find log likelihood of data using convolution of mixture with error distribution

**Usage**

```r
loglik_conv(m, data)
```

**Arguments**

- **m**: mixture distribution with k components
- **data**: details depend on the model
### Description

The default version of `loglik_conv`.

### Usage

```r
## Default S3 method:
loglik_conv(m, data)
```

### Arguments

- `m` : mixture distribution with k components
- `data` : data whose details depend on model

### Value

A `k` by `n` matrix of log densities
Description
returns log-density of convolution of each component of a normal mixture with \( N(0, s^2) \) or \( s^t(v) \) at \( x \). Note that convolution of two normals is normal, so it works that way

Usage
```r
## S3 method for class 'normalmix'
log_comp_dens_conv(m, data)
```

Arguments
- `m`: mixture distribution with \( k \) components
- `data`: a list with components \( x \) and \( s \) to be interpreted as a normally-distributed observation and its standard error

Value
a \( k \) by \( n \) matrix

Description
log density of convolution of each component of a unif mixture

Usage
```r
## S3 method for class 'unimix'
log_comp_dens_conv(m, data)
```

Arguments
- `m`: a mixture of class unimix
- `data`: see `set_data`

Value
a \( k \) by \( n \) matrix of densities
mixcdf.default

Description

Returns cdf for a mixture (generic function)

Usage

mixcdf(x, y, lower.tail = TRUE)

Arguments

x
a mixture (eg of type normalmix or unimix)
y
locations at which cdf to be computed
lower.tail
boolean indicating whether to report lower tail

Details

None

Value

an object of class normalmix

Examples

mixcdf(normalmix(c(0.5,0.5),c(0,0),c(1,2)),seq(-4,4,length=100))

mixcdf.default

Description

The default version of mixcdf.

Usage

## Default S3 method:
mixcdf(x, y, lower.tail = TRUE)

Arguments

x
a mixture (eg of type normalmix or unimix)
y
locations at which cdf to be computed
lower.tail
boolean indicating whether to report lower tail
mixEM

Description

Given the individual component likelihoods for a mixture model, estimates the mixture proportions by an EM algorithm.

Usage

mixEM(matrix_lik, prior, pi_init = NULL, control = list())

Arguments

matrix_lik, a n by k matrix with (j,k)th element equal to \( f_k(x_j) \).
prior, a k vector of the parameters of the Dirichlet prior on \( \pi \). Recommended to be rep(1,k).
pi_init, the initial value of \( \pi \) to use. If not specified defaults to \((1/k,\ldots,1/k)\).
control A list of control parameters for the SQUAREM algorithm, default value is set to control.default=list(K = 1, method=3, square=TRUE, step.min0=1, step.max0=1, mstep=4, kr=1, objfn.inc=1, tol=1.e-07, maxiter=5000, trace=FALSE).

Details

Fits a k component mixture model

\[
f(x|\pi) = \sum_k \pi_k f_k(x)
\]

to independent and identically distributed data \( x_1,\ldots,x_n \). Estimates mixture proportions \( \pi \) by maximum likelihood, or by maximum a posteriori (MAP) estimation for a Dirichlet prior on \( \pi \) (if a prior is specified). Uses the SQUAREM package to accelerate convergence of EM. Used by the ash main function; there is no need for a user to call this function separately, but it is exported for convenience.

Value

A list, including the estimates (pihat), the log likelihood for each iteration (B) and a flag to indicate convergence.
mixIP

Estimate mixture proportions of a mixture model by Interior Point method

Description

Given the individual component likelihoods for a mixture model, estimates the mixture proportions.

Usage

mixIP(matrix_lik, prior, pi_init = NULL, control = list(), weights = NULL)

Arguments

matrix_lik, a n by k matrix with (j,k)th element equal to \( f_k(x_j) \).
prior, a k vector of the parameters of the Dirichlet prior on \( \pi \). Recommended to be \( \text{rep}(1,k) \).
pi_init, the initial value of \( \pi \) to use. If not specified defaults to \( (1/k, \ldots, 1/k) \).
control A list of control parameters to be passed to REBayes::KWDual
weights weights to be assigned to the observations (an n vector)

Details

Optimizes

\[ L(\pi) = \sum_j w_j \log(\sum_k \pi_k f_{jk}) + h(\pi) \]

subject to \( \pi_k \) non-negative and \( \sum_k \pi_k = 1 \). Here

\[ h(\pi) \]

is a penalty function \( h(\pi) = \sum_k (\text{prior}_k-1) \log \pi_k \). Calls REBayes::KWDual in the REBayes package, which is in turn a wrapper to the mosek convex optimization software. So REBayes must be installed to use this. Used by the ash main function; there is no need for a user to call this function separately, but it is exported for convenience.

Value

A list, including the estimates (pihat), the log likelihood for each iteration (B) and a flag to indicate convergence
### mixmean2

**Generic function of calculating the overall second moment of the mixture**

**Description**

Generic function of calculating the overall second moment of the mixture

**Usage**

```r
mixmean2(m)
```

**Arguments**

- **m**
  - a mixture of k components generated by normalmix() or unimix() or igmix()

**Value**

- it returns scalar

---

### mixprop

**Generic function of extracting the mixture proportions**

**Description**

Generic function of extracting the mixture proportions

**Usage**

```r
mixprop(m)
```

**Arguments**

- **m**
  - a mixture of k components generated by normalmix() or unimix() or igmix()

**Value**

- it returns a vector of component probabilities, summing up to 1.
mixSQP

Estimate mixture proportions of a mixture model using mix-SQP algorithm.

Description

Estimate mixture proportions of a mixture model using mix-SQP algorithm.

Usage

mixSQP(matrix_lik, prior, pi_init = NULL, control = list(), weights = NULL)

Arguments

- **matrix_lik**: A matrix containing the conditional likelihood values, possibly normalized.
- **prior**: A vector of the parameters of the Dirichlet prior on the mixture weights.
- **pi_init**: The initial estimate of the mixture weights.
- **control**: A list of settings for the mix-SQP optimization algorithm; see `mixsqp` for details.
- **weights**: The weights to be assigned to the observations. Must be a vector of length equal the number of rows of `matrix_lik`. If `weights = NULL`, all observations are assigned the same weight.

Value

A list object including the estimates (pihat) and a flag (control) indicating convergence success or failure.

mixVBEM

Estimate posterior distribution on mixture proportions of a mixture model by a Variational Bayes EM algorithm

Description

Given the individual component likelihoods for a mixture model, estimates the posterior on the mixture proportions by a VBEM algorithm. Used by the ash main function; there is no need for a user to call this function separately, but it is exported for convenience.

Usage

mixVBEM(matrix_lik, prior, pi_init = NULL, control = list())
Arguments

- matrix_lik: an n by k matrix with \((j,k)\)th element equal to \(f_k(x_j)\).
- prior: a k vector of the parameters of the Dirichlet prior on \(\pi\). Recommended to be \(\text{rep}(1,k)\).
- pi_init: the initial value of the posterior parameters. If not specified defaults to the prior parameters.
- control: A list of control parameters for the SQUAREM algorithm, default value is set to be \(\text{control.default}=\text{list}(K = 1, \text{method}=3, \text{square}=\text{TRUE}, \text{step.min0}=1, \text{step.max0}=1, \text{mstep}=4, \text{kr}=1, \text{objfn.inc}=1, \text{tol}=1.\text{e-07}, \text{maxiter}=5000, \text{trace}=\text{FALSE})\).

Details

Fits a k component mixture model

\[
  f(x|\pi) = \sum_k \pi_k f_k(x)
\]

to independent and identically distributed data \(x_1, \ldots, x_n\). Estimates posterior on mixture proportions \(\pi\) by Variational Bayes, with a Dirichlet prior on \(\pi\). Algorithm adapted from Bishop (2009), Pattern Recognition and Machine Learning, Chapter 10.

Value

A list, whose components include point estimates (pihat), the parameters of the fitted posterior on \(\pi\) (pipost), the bound on the log likelihood for each iteration (b) and a flag to indicate convergence (converged).

Description

Compute second moment of the truncated Beta.

Usage

\[
  \text{my_e2truncbeta}(a, b, \alpha, \beta)
\]

Arguments

- a: left limit of distribution
- b: right limit of distribution
- alpha, beta: shape parameters of Beta distribution
my_e2truncgamma  
**second moment of truncated gamma distribution**

**Description**
Compute second moment of the truncated gamma.

**Usage**
\[
\text{my_e2truncgamma}(a, b, \text{shape}, \text{rate})
\]

**Arguments**
- \(a\): left limit of distribution
- \(b\): right limit of distribution
- \(\text{shape}\): shape of gamma distribution
- \(\text{rate}\): rate of gamma distribution

my_e2truncnorm  
**Expected Squared Value of Truncated Normal**

**Description**
Computes the expected squared values of truncated normal distributions with parameters \(a, b, \text{mean}, \text{and sd}\). Arguments can be scalars, vectors, or matrices. Arguments of shorter length will be recycled according to the usual recycling rules, but \(a\) and \(b\) must have the same length. Missing values are accepted for all arguments.

**Usage**
\[
\text{my_e2truncnorm}(a, b, \text{mean} = 0, \text{sd} = 1)
\]

**Arguments**
- \(a\): The lower limit for the support of the truncated normal. Can be -\(\text{Inf}\).
- \(b\): The upper limit for the support. Can be \(\text{Inf}\). \(a\) and \(b\) must have the same length, and each element of \(a\) should be less than or equal to the corresponding element of \(b\).
- \(\text{mean}\): The mean of the untruncated normal.
- \(\text{sd}\): The standard deviation of the untruncated normal. Standard deviations of zero are interpreted as numerically (rather than exactly) zero, so that the square of the untruncated mean is returned if it lies within \([a, b]\) and the square of the nearer of \(a\) and \(b\) is returned otherwise.
Value

The expected squared values of truncated normal distributions with parameters $a$, $b$, mean, and sd. If any of the arguments is a matrix, then a matrix will be returned.

See Also

my_etruncnorm, my_vtruncnorm

---

my_e2trunct

**Description**

Compute second moment of the truncated t. Uses results from O'Hagan, Biometrika, 1973

**Usage**

my_e2trunct(a, b, df)

**Arguments**

- **a**: left limit of distribution
- **b**: right limit of distribution
- **df**: degree of freedom of error distribution

---

my_etruncbeta

**Description**

Compute mean of the truncated Beta.

**Usage**

my_etruncbeta(a, b, alpha, beta)

**Arguments**

- **a**: left limit of distribution
- **b**: right limit of distribution
- **alpha, beta**: shape parameters of Beta distribution
my_etruncgamma  mean of truncated gamma distribution

Description
Compute mean of the truncated gamma.

Usage
my_etruncgamma(a, b, shape, rate)

Arguments
a  left limit of distribution
b  right limit of distribution
shape  shape of gamma distribution
rate  rate of gamma distribution

my_etrunclogf  my_etrunclogf

Description
Compute expectation of truncated log-F distribution.

Usage
my_etrunclogf(a, b, df1, df2)

Arguments
a  Left limit of distribution.
b  Right limit of distribution.
df1, df2  degrees of freedom
my_etrunctnorm

Expected Value of Truncated Normal

Description
Computes the means of truncated normal distributions with parameters a, b, mean, and sd. Arguments can be scalars, vectors, or matrices. Arguments of shorter length will be recycled according to the usual recycling rules, but a and b must have the same length. Missing values are accepted for all arguments.

Usage
my_etrunctnorm(a, b, mean = 0, sd = 1)

Arguments
- a: The lower limit for the support of the truncated normal. Can be -Inf.
- b: The upper limit for the support. Can be Inf. a and b must have the same length, and each element of a should be less than or equal to the corresponding element of b.
- mean: The mean of the untruncated normal.
- sd: The standard deviation of the untruncated normal. Standard deviations of zero are interpreted as numerically (rather than exactly) zero, so that the untruncated mean is returned if it lies within [a, b] and the nearer of a and b is returned otherwise.

Value
The expected values of truncated normal distributions with parameters a, b, mean, and sd. If any of the arguments is a matrix, then a matrix will be returned.

See Also
my_e2truncnorm, my_vtruncnorm

my_etrunct

Description
Compute second moment of the truncated t. Uses results from O'Hagan, Biometrika, 1973

Usage
my_etrunct(a, b, df)
Arguments

- **a**: left limit of distribution
- **b**: right limit of distribution
- **df**: degree of freedom of error distribution

Description

Computes the variance of truncated normal distributions with parameters `a`, `b`, `mean`, and `sd`. Arguments can be scalars, vectors, or matrices. Arguments of shorter length will be recycled according to the usual recycling rules, but `a` and `b` must have the same length. Missing values are accepted for all arguments.

Usage

```r
my_vtruncnorm(a, b, mean = 0, sd = 1)
```

Arguments

- **a**: The lower limit for the support of the truncated normal. Can be `-Inf`.
- **b**: The upper limit for the support. Can be `Inf`. `a` and `b` must have the same length, and each element of `a` should be less than or equal to the corresponding element of `b`.
- **mean**: The mean of the untruncated normal.
- **sd**: The standard deviation of the untruncated normal.

Value

The variance of truncated normal distributions with parameters `a`, `b`, `mean`, and `sd`. If any of the arguments is a matrix, then a matrix will be returned.

See Also

`my_etruncnorm, my_e2truncnorm`
Description

ncomp

Usage

ncomp(m)

Arguments

m a mixture of k components generated by normalmix() or unimix() or igmix()

Description

The default version of ncomp.

Usage

## Default S3 method:
ncomp(m)

Arguments

m a mixture of k components generated by normalmix() or unimix() or igmix()

Constructor for normalmix class

Description

Creates an object of class normalmix (finite mixture of univariate normals)

Usage

normalmix(pi, mean, sd)
Arguments

\( \pi \)  
vector of mixture proportions

\( \text{mean} \)  
vector of means

\( \text{sd} \)  
vector of standard deviations

Details

None

Value

an object of class normalmix

Examples

\[
\text{normalmix}(c(0.5,0.5),c(0,0),c(1,2))
\]
**plogf**

*The log-F distribution*

**Description**

Distribution function for the log-F distribution with df1 and df2 degrees of freedom (and optional non-centrality parameter ncp).

**Usage**

\[ plogf(q, \text{df1}, \text{df2}, \text{ncp}, \text{lower.tail} = \text{TRUE}, \text{log.p} = \text{FALSE}) \]

**Arguments**

- `q`: vector of quantiles
- `df1`, `df2`: degrees of freedom
- `ncp`: non-centrality parameter. If omitted the central F is assumed.
- `lower.tail`: logical; if TRUE (default), probabilities are \( P[X \leq x] \), otherwise, \( P[X > x] \).
- `log.p`: logical; if TRUE, probabilities \( p \) are given as \( \log(p) \).

**Value**

The distribution function.

---

**plot.ash**

*Plot method for ash object*

**Description**

Plot the cdf of the underlying fitted distribution

**Usage**

```
## S3 method for class 'ash'
plot(x, ..., xmin, xmax)
```

**Arguments**

- `x`: the fitted ash object
- `...`: Arguments to be passed to methods, such as graphical parameters (see `plot`)
- `xmin`: xlim lower range, default is the lowest value of betahat
- `xmax`: xlim upper range, default is the highest value of betahat

**Details**

None
plot_diagnostic  Diagnostic plots for ash object

Description

Generate several plots to diagnose the fitness of ASH on the data

Usage

plot_diagnostic(
  x,
  plot.it = TRUE,
  sebetahat.tol = 0.001,
  plot.hist,
  xmin,
  xmax,
  breaks = "Sturges",
  alpha = 0.01,
  pch = 19,
  cex = 0.25
)

Arguments

- **x**: the fitted ash object
- **plot.it**: logical. whether to plot the diagnostic result
- **sebetahat.tol**: tolerance to test the equality of betahat
- **plot.hist**: logical. whether to plot the histogram of betahat when sebetahat is not constant
- **xmin, xmax**: range of the histogram of betahat to be plotted
- **breaks**: histograms parameter (see `hist`)
- **alpha**: error level for the de-trended diagnostic plot
- **pch, cex**: plot parameters for dots

Details

None.
pm_on_zero

Generic function to extract which components of mixture are point mass on 0

Description

Generic function to extract which components of mixture are point mass on 0

Usage

pm_on_zero(m)

Arguments

m  
a mixture of k components generated by normalmix() or unimix() or igmix()

Value

a boolean vector indicating which components are point mass on 0

posterior_dist

Compute Posterior

Description

Return the posterior on beta given a prior (g) that is a mixture of normals (class normalmix) and observation betahat $N(\beta, \text{sebetahat})$

Usage

posterior_dist(g, betahat, sebetahat)

Arguments

g  
a normalmix with components indicating the prior; works only if g has means 0
betahat  
(n vector of observations)
sebetahat  
(n vector of standard errors/deviations of observations)

Details

This can be used to obt

Value

A list, (pi1,mu1,sigma1) whose components are each k by n matrices where k is number of mixture components in g, n is number of observations in betahat
postmean

Description
postmean

Usage
postmean(m, data)

Arguments
m mixture distribution with k components
data details depend on the model

postmean2

Description
output posterior mean-squared value given prior mixture m and data

Usage
postmean2(m, data)

Arguments
m mixture distribution with k components
data details depend on the model

postsd

Description
output posterior sd given prior mixture m and data

Usage
postsd(m, data)

Arguments
m mixture distribution with k components
data details depend on the model
Description
returns random samples from the posterior, given a prior distribution m and n observed datapoints.

Usage
post_sample(m, data, nsamp)

Arguments
m prior distribution (eg of type normalmix)
data a list with components x and s, each vectors of length n, to be interpreted as a normally-distributed observations and corresponding standard errors
nsamp number of random samples to return for each observation

Details
exported, but mostly users will want to use ‘get_post_sample’

Value
an nsamp by n matrix

Description
returns random samples from the posterior, given a prior distribution m and n observed datapoints.

Usage
## S3 method for class 'normalmix'
post_sample(m, data, nsamp)

Arguments
m mixture distribution with k components
data a list with components x and s to be interpreted as a normally-distributed observation and its standard error
nsamp number of samples to return for each observation
Description
returns random samples from the posterior, given a prior distribution \( m \) and \( n \) observed datapoints.

Usage

```r
## S3 method for class 'unimix'
post_sample(m, data, nsamp)
```

Arguments

- **m**: mixture distribution with \( k \) components
- **data**: a list with components \( x \) and \( s \) to be interpreted as a normally-distributed observation and its standard error
- **nsamp**: number of samples to return for each observation

Value

a \( nsamp \) by \( n \) matrix

---

print.ash

*Print method for ash object*

Description
Print the fitted distribution of beta values in the EB hierarchical model

Usage

```r
## S3 method for class 'ash'
print(x, ...)
```

Arguments

- **x**: the fitted ash object
- **...**: not used, included for consistency as an S3 generic/method.

Details

None
prune

Description

prunes out mixture components with low weight

Usage

prune(m, thresh = 1e-10)

Arguments

m
  What is this argument?
thresh
  the threshold below which components are removed

qval.from.lfdr

Function to compute q values from local false discovery rates

Description

Computes q values from a vector of local fdr estimates

Usage

qval.from.lfdr(lfdr)

Arguments

lfdr,
  a vector of local fdr estimates

Details

The q value for a given lfdr is an estimate of the (tail) False Discovery Rate for all findings with a smaller lfdr, and is found by the average of the lfdr for all more significant findings. See Storey (2003), Annals of Statistics, for definition of q value.

Value

vector of q values
set_data

Takes raw data and sets up data object for use by ash

Description
Takes raw data and sets up data object for use by ash

Usage
set_data(betahat, sebetahat, lik = NULL, alpha = 0)

Arguments
- betahat: vector of betahats
- sebetahat: vector of standard errors
- lik: a likelihood (see e.g., lik_normal())
- alpha: specifies value of alpha to use (model is for betahat/sebetahat^alpha | sebetahat)

Details
The data object stores both the data, and details of the model to be used for the data. For example, in the generalized version of ash the cdf and pdf of the likelihood are stored here.

Value
data object (list)

summary.ash

Summary method for ash object

Description
Print summary of fitted ash object

Usage
## S3 method for class 'ash'
summary(object, ...)

Arguments
- object: the fitted ash object
- ...: not used, included for consistency as an S3 generic/method.
**tnormalmix**

**Details**
summary prints the fitted mixture, the fitted log likelihood with 10 digits and a flag to indicate convergence

**Description**
Creates an object of class tnormalmix (finite mixture of truncated univariate normals).

**Usage**
```r
tnormalmix(pi, mean, sd, a, b)
```

**Arguments**
- `pi` Cector of mixture proportions (length k say).
- `mean` Vector of means (length k).
- `sd` Vector of standard deviations (length k).
- `a` Vector of left truncation points of each component (length k).
- `b` Vector of right truncation points of each component (length k).

**Value**
An object of class “tnormalmix”.

**Examples**
```r
tnormalmix(c(0.5,0.5),c(0,0),c(1,2),c(-10,0),c(0,10))
```

---

**unimix**

**Constructor for unimix class**

**Description**
Creates an object of class unimix (finite mixture of univariate uniforms)

**Usage**
```r
unimix(pi, a, b)
```
vcdf_post

Arguments

- pi: vector of mixture proportions
- a: vector of left hand ends of uniforms
- b: vector of right hand ends of uniforms

Details

None

Value

an object of class unimix

Examples

```r
unimix(c(0.5,0.5),c(0,0),c(1,2))
```

---

vcdf_post

Description

vectorized version of `cdf_post`

Usage

```r
vcdf_post(m, c, data)
```

Arguments

- m: mixture distribution with k components
- c: a numeric vector
- data: depends on context

Value

an n vector containing the cdf for beta_i at c

Examples

```r
beta = rnorm(100,0,1)
betahat= beta+rnorm(100,0,1)
sebetahat=rep(1,100)
ash.beta = ash(betahat,1,mixcompdist="normal")
c = vcdf_post(get_fitted_g(ash.beta),seq(-5,5,length=1000),data = set_data(betahat,sebetahat))
```
Estimate mixture proportions of a mixture model by EM algorithm (weighted version)

Description

Given the individual component likelihoods for a mixture model, and a set of weights, estimates the mixture proportions by an EM algorithm.

Usage

`w_mixEM(matrix_lik, prior, pi_init = NULL, weights = NULL, control = list())`

Arguments

- `matrix_lik`, a n by k matrix with (j,k)th element equal to $f_k(x_j)$.
- `prior`, a k vector of the parameters of the Dirichlet prior on $\pi$. Recommended to be `rep(1,k)`.
- `pi_init`, the initial value of $\pi$ to use. If not specified defaults to $(1/k,\ldots,1/k)$.
- `weights`, an n vector of weights
- `control` A list of control parameters for the SQUAREM algorithm, default value is set to be `control.default=list(K = 1, method=3, square=TRUE, step.min0=1, step.max0=1, mstep=4, kr=1, objfn.inc=1, to1=1.e-07, maxiter=5000, trace=FALSE)`.

Details

Fits a k component mixture model

$$ f(x|\pi) = \sum_k \pi_k f_k(x) $$

to independent and identically distributed data $x_1,\ldots,x_n$ with weights $w_1,\ldots,w_n$. Estimates mixture proportions $\pi$ by maximum likelihood, or by maximum a posteriori (MAP) estimation for a Dirichlet prior on $\pi$ (if a prior is specified). Here the log-likelihood for the weighted data is defined as $l(\pi) = \sum_j w_j \log f(x_j|\pi)$. Uses the SQUAREM package to accelerate convergence of EM. Used by the ash main function; there is no need for a user to call this function separately, but it is exported for convenience.

Value

A list, including the estimates (pihat), the log likelihood for each iteration (B) and a flag to indicate convergence.
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