Package 'DEmixR'

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Type Package

Title Fit Two-Component Normal and Lognormal Mixture Models

Version 0.2.0

Description Fits, bootstraps, and evaluates two-component normal and lognormal mixture models. Parameters are estimated by combining differential-evolution global optimization, as implemented in the 'DEoptim' package (Mullen, Ardia, Gil, Windover and Cline, 2011) <doi:10.18637/jss.v040.i06>, with a local 'L-BFGS-B' refinement step via optim(). Also provides preliminary diagnostic plots, automatic normal-versus-lognormal model selection by information criteria, and parametric or nonparametric bootstrap confidence intervals for the fitted parameters.

Imports DEoptim (>= 2.0.0), pbapply (>= 1.0.0)

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Author Farrokh Habibzadeh [aut, cre] (ORCID: <https://orcid.org/0000-0001-5360-2900>)

Maintainer Farrokh Habibzadeh <farrokh.habibzadeh@gmail.com>

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Contents

bootstrap_mix2 2
evaluate_init 3

fit_lognorm2 4
fit_norm2 5
plot.demixr_fit 5
prelim_plots 6
print.demixr_boot 7
print.demixr_fit 8
print.demixr_select 9
print.summary.demixr_fit 9
select_best_mixture 10
summary.demixr_fit 11

Index **12**

`bootstrap_mix2` *Bootstrap mixture parameters*

Description

Bootstrap mixture parameters

Usage

```
bootstrap_mix2(
  fit = NULL,
  x = NULL,
  par = NULL,
  family = NULL,
  B = 1000,
  parametric = TRUE,
  boot_size = NULL,
  parallelType = 0,
  quiet = 2,
  ci_level = 0.95
)
```

Arguments

`fit`	fitted object from fit_lognorm2 or fit_norm2
`x`	numeric vector (if fit not provided)
`par`	numeric vector of parameters (if fit not provided)
`family`	"lognormal" or "normal" (if fit not provided)
`B`	number of bootstrap replicates
`parametric`	logical, parametric bootstrap if TRUE
`boot_size`	size or fraction (if between 0 and 1) of bootstrap sample
`parallelType`	integer for DEoptim/pbapply parallelism
`quiet`	0/1/2 for verbosity
`ci_level`	confidence level

Value

an object of class `demixr_boot`: a list with cleaned bootstrap estimates (`ests_clean`), central tendency (`central`), and confidence intervals (`ci`). Has a `print` method.

Examples

```
set.seed(1)
x <- c(rnorm(150, 0, 1), rnorm(50, 4, 1))
fit <- fit_norm2(x, n_runs = 1, NP = 20, itermax = 200, quiet = 0)
boot <- bootstrap_mix2(fit, B = 20, quiet = 0)
boot
```

---

evaluate_init *Evaluate initial parameter values for mixture fitting*

Description

Evaluate initial parameter values for mixture fitting

Usage

```
evaluate_init(
  par_init,
  x,
  family = c("lognormal", "normal"),
  lower = NULL,
  upper = NULL,
  pgtol = 1e-08
)
```

Arguments

`par_init`	numeric vector of initial parameters
`x`	numeric vector of data
`family`	"lognormal" or "normal"
`lower`	numeric vector of lower bounds
`upper`	numeric vector of upper bounds
`pgtol`	numeric, gradient tolerance for optim

Value

list with success flag, optimized parameters, log-likelihood, and convergence

Examples

```
set.seed(1)
x <- c(rnorm(150, 0, 1), rnorm(50, 4, 1))
ev <- evaluate_init(par_init = c(0.7, 0, 1, 4, 1), x = x, family = "normal")
ev$success
```

`fit_lognorm2` *Fit 2-component lognormal mixture*

Description

Fit 2-component lognormal mixture

Usage

```
fit_lognorm2(x, ...)
```

Arguments

`x`	numeric vector of data to fit
`...`	additional arguments passed to `.fit_mix2_core`

Value

an object of class `demixr_fit`: a list with the fitted parameters (`par`), `logLik`, `AIC`, `BIC`, and convergence information. Has `print`, `summary`, and `plot` methods.

Examples

```
set.seed(1)
x <- c(rlnorm(150, 0, 0.5), rlnorm(50, 2, 0.3))
fit <- fit_lognorm2(x, n_runs = 1, NP = 20, itermax = 200, quiet = 0)
fit

plot(fit)
```

fit_norm2 *Fit 2-component normal mixture*

Description

Fit 2-component normal mixture

Usage

```
fit_norm2(x, ...)
```

Arguments

x	numeric vector of data to fit
...	additional arguments passed to .fit_mix2_core

Value

an object of class demixr_fit: a list with the fitted parameters (par), logLik, AIC, BIC, and convergence information. Has print, summary, and plot methods.

Examples

```
set.seed(1)
x <- c(rnorm(150, 0, 1), rnorm(50, 4, 1))
fit <- fit_norm2(x, n_runs = 1, NP = 20, itermax = 200, quiet = 0)
fit

plot(fit)
```

plot.demixr_fit *Plot a fitted DEmixR mixture model over a histogram of the data*

Description

Plot a fitted DEmixR mixture model over a histogram of the data

Usage

```
## S3 method for class 'demixr_fit'
plot(
  x,
  hist_bins = 60,
  col_hist = "gray85",
  col_total = "black",
```

```
  col_comp1 = "steelblue",
  col_comp2 = "firebrick",
  ...
)
```

Arguments

x	an object of class demixr_fit
hist_bins	number of histogram bins
col_hist	histogram fill color
col_total	color of the fitted overall mixture density
col_comp1	color of the first fitted component density
col_comp2	color of the second fitted component density
...	further arguments passed to hist

Value

no return value, called for side effects (generating a plot)

Examples

```
set.seed(1)
x <- c(rnorm(150, 0, 1), rnorm(50, 4, 1))
fit <- fit_norm2(x, n_runs = 1, NP = 20, itermax = 200, quiet = 0)
plot(fit)
```

---

prelim_plots *Preliminary diagnostic plots*

Description

Preliminary diagnostic plots

Usage

```
prelim_plots(
  x,
  which = c("hist"),
  hist_bins = 60,
  col_hist = "gray85",
  col_density = "darkorange",
  col_qq = "gray60",
  col_line = "darkorange"
)
```

Arguments

x	numeric vector
which	character vector: "hist", "qq", "pp", "logqq"
hist_bins	number of bins for histogram
col_hist	color for histogram
col_density	color for the kernel-density curve drawn over the histogram. Set to NA to omit the density curve entirely; in that case the histogram title is "Histogram" instead of "Histogram with density".
col_qq	color for qq points
col_line	color for lines in "qq", "pp", "logqq" plots

Value

no return value, called for side effects (generating plots)

Examples

```
set.seed(1)
x <- c(rnorm(150, 0, 1), rnorm(50, 4, 1))
prelim_plots(x, c("hist", "qq"), hist_bins = 15)

# Histogram without the kernel-density overlay (title becomes "Histogram")
prelim_plots(x, "hist", col_density = NA)
```

---

print.demixr_boot *Print bootstrap results from a DEmixR mixture fit*

Description

Print bootstrap results from a DEmixR mixture fit

Usage

```
## S3 method for class 'demixr_boot'
print(x, digits = 4, ...)
```

Arguments

x	an object of class demixr_boot, as returned by bootstrap_mix2
digits	number of significant digits to print
...	further arguments passed to or from other methods (currently unused)

Value

x, invisibly

Examples

```
set.seed(1)
x <- c(rnorm(150, 0, 1), rnorm(50, 4, 1))
fit <- fit_norm2(x, n_runs = 1, NP = 20, itermax = 200, quiet = 0)
boot <- bootstrap_mix2(fit, B = 20, quiet = 0)
print(boot)
```

`print.demixr_fit` *Print a fitted DEmixR mixture model*

Description

Print a fitted DEmixR mixture model

Usage

```
## S3 method for class 'demixr_fit'
print(x, digits = 4, ...)
```

Arguments

`x`	an object of class `demixr_fit`, as returned by `fit_norm2` or `fit_lognorm2`
`digits`	number of significant digits to print
`...`	further arguments passed to or from other methods (currently unused)

Value

`x`, invisibly

Examples

```
set.seed(1)
x <- c(rnorm(150, 0, 1), rnorm(50, 4, 1))
fit <- fit_norm2(x, n_runs = 1, NP = 20, itermax = 200, quiet = 0)
print(fit)
```

print.demixr_select *Print model-selection results from DEmixR*

Description

Print model-selection results from DEmixR

Usage

```
## S3 method for class 'demixr_select'
print(x, digits = 4, ...)
```

Arguments

x	an object of class demixr_select, as returned by select_best_mixture
digits	number of significant digits to print
...	further arguments passed to or from other methods (currently unused)

Value

x, invisibly

Examples

```
set.seed(1)
x <- c(rnorm(150, 0, 1), rnorm(50, 4, 1))
mix <- select_best_mixture(x, n_runs = 1, NP = 20, itermax = 200, quiet = 0)
print(mix)
```

print.summary.demixr_fit *Print a summary of a fitted DEmixR mixture model*

Description

Print a summary of a fitted DEmixR mixture model

Usage

```
## S3 method for class 'summary.demixr_fit'
print(x, digits = 4, ...)
```

Arguments

x	an object of class summary.demixr_fit, as returned by summary.demixr_fit
digits	number of significant digits to print
...	further arguments passed to or from other methods (currently unused)

Value

x, invisibly

Examples

```
set.seed(1)
x <- c(rnorm(150, 0, 1), rnorm(50, 4, 1))
fit <- fit_norm2(x, n_runs = 1, NP = 20, itermax = 200, quiet = 0)
print(summary(fit))
```

---

select_best_mixture *Select best mixture model (lognormal or normal) based on BIC*

Description

Select best mixture model (lognormal or normal) based on BIC

Usage

```
select_best_mixture(x, n_runs = 1, NP = 50, itermax = 10000, quiet = 2)
```

Arguments

x	numeric vector
n_runs	number of DEoptim runs
NP	population size for DEoptim
itermax	maximum iterations
quiet	verbosity

Value

an object of class demixr_select: a list with the best-fitting model (best), all fitted models (all), and the BIC of each (BICs). Has a print method.

Examples

```
set.seed(1)
x <- c(rnorm(150, 0, 1), rnorm(50, 4, 1))
mix <- select_best_mixture(x, n_runs = 1, NP = 20, itermax = 200, quiet = 0)
mix
mix$best$family
```

`summary.demixr_fit` *Summarize a fitted DEmixR mixture model*

Description

Summarize a fitted DEmixR mixture model

Usage

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

Arguments

`object`	an object of class `demixr_fit`
`...`	further arguments passed to or from other methods (currently unused)

Value

an object of class `summary.demixr_fit`: a list holding the per-component weight/location/scale table together with the family, sample size, log-likelihood, AIC, BIC, and convergence code. Has a `print` method.

Examples

```
set.seed(1)
x <- c(rnorm(150, 0, 1), rnorm(50, 4, 1))
fit <- fit_norm2(x, n_runs = 1, NP = 20, itermax = 200, quiet = 0)
summary(fit)
```

Index

.fit_mix2_core, *4*, *5*

bootstrap_mix2, 2, *7*

evaluate_init, 3

fit_lognorm2, 4, *8*
fit_norm2, 5, *8*

hist, *6*

plot.demixr_fit, 5
prelim_plots, 6
print.demixr_boot, 7
print.demixr_fit, 8
print.demixr_select, 9
print.summary.demixr_fit, 9

select_best_mixture, *9*, 10
summary.demixr_fit, *10*, 11