Package ‘DEmixR’

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Type Package

Title Fit Two-Component Normal and Lognormal Mixture Models

Version 0.1.1

Description Fits, bootstraps, and evaluates two-component normal and lognormal mixture models. Includes diagnostic plots and statistical evaluation of mixture model fits using differential evolution optimization.

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

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Encoding UTF-8

RoxygenNote 7.3.3

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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Contents

`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

list with cleaned bootstrap estimates, central tendency, and CI

`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

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`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

list with fitted parameters and metrics

`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

list with fitted parameters and metrics

`prelim_plots` *Preliminary diagnostic plots*

Description

Preliminary diagnostic plots

Usage

```
prelim_plots(
  x,
  which = c("hist"),
  hist_bins = 60,
  col_hist = "grey85",
  col_density = "darkorange",
  col_qq = "grey60",
  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 density line in histogram
`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)

`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

list with best fit, all fits, and BICs

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