

# Package: DEmixR (via r-universe)

May 26, 2026

**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 ( $\geq 2.0.0$ ), pbapply ( $\geq 1.0.0$ ), parallelly ( $\geq 1.0.0$ )

**License** MIT + file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.3.3

**Suggests** knitr, rmarkdown, testthat ( $\geq 3.0.0$ )

**VignetteBuilder** knitr

**NeedsCompilation** no

**Author** Farrokh Habibzadeh [aut, cre]

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

**Repository** <https://fhabibzadeh.r-universe.dev>

**Date/Publication** 2025-09-27 08:40:08 UTC

**RemoteUrl** <https://github.com/cran/DEmixR>

**RemoteRef** HEAD

**RemoteSha** 339bd9301b167dde0171cc6041599993b85c4fc3

## Contents

bootstrap_mix2 . . . . .	2
evaluate_init . . . . .	3
fit_lognorm2 . . . . .	3
fit_norm2 . . . . .	4
prelim_plots . . . . .	4
select_best_mixture . . . . .	5

<b>Index</b>	<b>6</b>
--------------	----------

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	<i>Evaluate initial parameter values for mixture fitting</i>
---------------	--------------------------------------------------------------

---

**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

---

fit_lognorm2	<i>Fit 2-component lognormal mixture</i>
--------------	------------------------------------------

---

**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	<i>Fit 2-component normal mixture</i>
-----------	---------------------------------------

---

**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	<i>Preliminary diagnostic plots</i>
--------------	-------------------------------------

---

**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

# Index

`.fit_mix2_core`, 4  
`bootstrap_mix2`, 2  
`evaluate_init`, 3  
`fit_lognorm2`, 3  
`fit_norm2`, 4  
`prelim_plots`, 4  
`select_best_mixture`, 5