

Package ‘semisup’

April 10, 2023

Version 1.22.0

Title Semi-Supervised Mixture Model

Description Implements a parametric semi-supervised mixture model. The permutation test detects markers with main or interactive effects, without distinguishing them. Possible applications include genome-wide association analysis and differential expression analysis.

biocViews SNP, GenomicVariation, SomaticMutation, Genetics, Classification, Clustering, DNaseq, Microarray, MultipleComparison

Depends R (>= 3.0.0)

Imports VGAM

Suggests knitr, testthat, SummarizedExperiment

VignetteBuilder knitr

License GPL-3

LazyData true

RoxygenNote 7.0.0

URL <https://github.com/rauschenberger/semisup>

BugReports <https://github.com/rauschenberger/semisup/issues>

git_url <https://git.bioconductor.org/packages/semisup>

git_branch RELEASE_3_16

git_last_commit 5a87e13

git_last_commit_date 2022-11-01

Date/Publication 2023-04-10

Author Armin Rauschenberger [aut, cre]

Maintainer Armin Rauschenberger <armin.rauschenberger@uni.lu>

R topics documented:

semisup-package	2
mixtura	2
scrutor	4

semisup-package	<i>Semi-supervised mixture model</i>
-----------------	--------------------------------------

Description

This R package implements the semi-supervised mixture model. Use [mixtura](#) for model fitting, and [scrutor](#) for hypothesis testing.

Getting started

Please type the following commands:

```
utils::vignette("semisup")
```

```
?semisup::mixtura
```

```
?semisup::scrutor
```

More information

A Rauschenberger, RX Menezes, MA van de Wiel, NM van Schoor, and MA Jonker (2020). "Semi-supervised mixture test for detecting markers associated with a quantitative trait", *Manuscript in preparation*.

<a.rauschenberger@vumc.nl>

mixtura	<i>Model fitting</i>
---------	----------------------

Description

This function fits a semi-supervised mixture model. It simultaneously estimates two mixture components, and assigns the unlabelled observations to these.

Usage

```
mixtura(y, z, dist = "norm",  
        phi = NULL, pi = NULL, gamma = NULL,  
        test = NULL, iter = 100, kind = 0.05,  
        debug = TRUE, ...)
```

Arguments

y	observations: numeric vector of length n
z	class labels: integer vector of length n, with entries 0, 1 and NA
dist	distributional assumption: character "norm" (Gaussian), "nbinom" (negative binomial), or "zinb" (zero-inflated negative binomial)
phi	dispersion parameters: numeric vector of length q, or NULL
pi	zero-inflation parameter(s): numeric vector of length q, or NULL
gamma	offset: numeric vector of length n, or NULL
test	resampling procedure: character "perm" (permutation) or "boot" (parametric bootstrap), or NULL
iter	(maximum) number of resampling iterations : positive integer, or NULL
kind	resampling accuracy: numeric between 0 and 1, or NULL; all p-values above kind are approximate
debug	verification of arguments: TRUE or FALSE
...	settings EM algorithm: starts, it.em and epsilon (see arguments)

Details

By default, phi and pi are estimated by the maximum likelihood method, and gamma is replaced by a vector of ones.

Value

This function fits and compares a one-component (H_0) and a two-component (H_1) mixture model.

posterior	probability of belonging to class 1: numeric vector of length n
converge	path of the log-likelihood: numeric vector with maximum length it.em
estim0	parameter estimates under H_0: data frame
estim1	parameter estimates under H_1: data frame
loglik0	log-likelihood under H_0: numeric
loglik1	log-likelihood under H_1: numeric
lrts	likelihood-ratio test statistic: positive numeric
p.value	H_0 versus H_1: numeric between 0 and 1, or NULL

Reference

A Rauschenberger, RX Menezes, MA van de Wiel, NM van Schoor, and MA Jonker (2020). "Semi-supervised mixture test for detecting markers associated with a quantitative trait", *Manuscript in preparation*.

See Also

Use [scrutor](#) for hypothesis testing. All other functions are [internal](#).

Examples

```
# data simulation
n <- 100
z <- rep(0:1,each=n/2)
y <- rnorm(n=n,mean=2,sd=1)
z[(n/4):n] <- NA

# model fitting
mixtura(y,z,dist="norm",test="perm")
```

scrutor

*Hypothesis testing***Description**

This function tests whether the unlabelled observations come from a mixture of two distributions.

Usage

```
scrutor(Y, Z, dist = "norm",
        phi = NULL, pi = NULL, gamma = NULL,
        test = "perm", iter = NULL, kind = NULL,
        debug = TRUE, ...)
```

Arguments

Y	observations: numeric vector of length n, or numeric matrix with n rows (samples) and q columns (variables)
Z	class labels: numeric vector of length n, or numeric matrix with n rows (samples) and p columns (variables), with entries 0 and NA
dist	distributional assumption: character "norm" (Gaussian), "nbinom" (negative binomial), or "zinb" (zero-inflated negative binomial)
phi	dispersion parameter(s): numeric vector of length q, or NULL (norm: none, nbinom: MLE)
pi	zero-inflation parameter(s): numeric vector of length q, or NULL (norm: none, nbinom: MLE)
gamma	offset: numeric vector of length n, or NULL
test	resampling procedure: character "perm" (permutation) or "boot" (parametric bootstrap), or NULL
iter	(maximum) number of resampling iterations : positive integer, or NULL
kind	resampling accuracy: numeric between 0 and 1, or NULL; all p-values above kind are approximate
debug	verification of arguments: TRUE or FALSE
...	settings EM algorithm: starts, it.em and epsilon (see arguments)

Details

By default, ϕ and π are estimated by the maximum likelihood method, and γ is replaced by a vector of ones.

Value

This function tests a one-component (H_0) against a two-component mixture model (H_1).

y	index observations
z	index class labels
lrts	test statistic
p.value	p-value

Reference

A Rauschenberger, RX Menezes, MA van de Wiel, NM van Schoor, and MA Jonker (2020). "Semi-supervised mixture test for detecting markers associated with a quantitative trait", *Manuscript in preparation*.

See Also

Use [mixtura](#) for model fitting. All other functions are [internal](#).

Examples

```
# data simulation
n <- 100
z <- rep(0:1, each=n/2)
y <- rnorm(n=n, mean=2*z, sd=1)
z[(n/4):n] <- NA

# hypothesis testing
scrutor(y,z,dist="norm")
```

Index

* **documentation**

semisup-package, [2](#)

* **methods**

mixtura, [2](#)

scrutor, [4](#)

arguments, [3](#), [4](#)

internal, [3](#), [5](#)

mixtura, [2](#), [2](#), [5](#)

scrutor, [2](#), [3](#), [4](#)

semisup (semisup-package), [2](#)

semisup-package, [2](#)