Package: semisup (via r-universe)

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Version 1.37.0

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

Repository https://bioc.r-universe.dev

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`semisup-package` *Semi-supervised mixture model*

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` *Model fitting*

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 bionomial), 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 (H0) and a two-component (H1) 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 H0**:** data frame
estim1	parameter estimates under H1**:** data frame
loglik0	log-likelihood under H0**:** numeric
loglik1	log-likelihood under H1**:** numeric
lrts	likelihood-ratio test statistic**:** positive numeric
p.value	H0 versus H1**:** 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")
```

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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 bionomial), 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, `phi` and `pi` are estimated by the maximum likelihood method, and `gamma` is replaced by a vector of ones.

Value

This function tests a one-component (`H0`) against a two-component mixture model (`H1`).

`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")
```

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