

Package ‘semisup’

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Version 1.6.0

Title Semi-Supervised Mixture Model

Description Useful for detecting SNPs with interactive effects on a quantitative trait. This R package moves away from testing interaction terms, and moves towards testing whether an individual SNP is involved in any interaction. This reduces the multiple testing burden to one test per SNP, and allows for interactions with unobserved factors. Analysing one SNP at a time, it splits the individuals into two groups, based on the number of minor alleles. If the quantitative trait differs in mean between the two groups, the SNP has a main effect. If the quantitative trait differs in distribution between some individuals in one group and all other individuals, it possibly has an interactive effect. Implicitly, the membership probabilities may suggest potential interacting variables.

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

Depends R (>= 3.0.0)

Imports SummarizedExperiment, VGAM

Suggests knitr, testthat

VignetteBuilder knitr

License GPL-3

LazyData true

RoxygenNote 6.0.1

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

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

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semisup-package	<i>Semi-supervised mixture model</i>
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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 (2017). "Detecting SNPs with interactive effects on a quantitative trait", *Manuscript in preparation*.

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mixtura	<i>Model fitting</i>
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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 parameter: positive numeric, or NULL
pi	zero-inflation parameter: numeric between 0 and 1, 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 <code>it.em</code>
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 (2017). "Detecting SNPs with interactive effects on 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
mixture(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, 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 (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 (2017). "Detecting SNPs with interactive effects on 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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