Package ‘pipeGS’

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get.phat.linear

Get the pvalue for the linear statistic

Description

Get the pvalue for the linear statistic

Usage

get.phat.linear(x, y, method = c("phat2", "saddlepoint", "phat1", "phat3", "nested", "mc", "exact"), N.mc = 10^3, mc.cores = 1, N.level = 1000, q = 0.2, B = 5 * length(x), do.sd = FALSE)

Arguments

x binary vector of treatment assignment
y gene expression measurement matrix
method method to estimate pvalue for the linear statistic
N.mc number of mc samples is method == "mc"
mc.cores number of cores to use in mcapply
N.level number of samples in each level if method == "nested"
q progression quantile if method == "nested"
B number of burn-ins to use if method == "nested"
do.sd logical to indicate whether calculating sd or not

Value

a list containing phat from different methods

Examples

x <- c(rep(0, 4), rep(1, 4))
y <- c(rnorm(4, 0, 1), rnorm(4, 2, 1))
get.phat.linear(x, y, method = "saddlepoint")
get.phat.linear(x, y, method = "phat1")
get.phat.linear(x, y, method = "phat2")
get.phat.linear(x, y, method = "phat3")
get.phat.linear(x, y, method = "nested")
get.phat.linear(x, y, method = "mc")
get.phat.linear(x, y, method = "exact")
get.phat.linear(x, y, method = "saddlepoint", do.sd = TRUE)
get.phat.linear(x, y, method = "phat1", do.sd = TRUE)
get.phat.linear(x, y, method = "phat2", do.sd = TRUE)
get.phat.linear(x, y, method = "phat3", do.sd = TRUE)
get.phat.linear(x, y, method = "nested", do.sd = TRUE)
get.phat.linear(x, y, method = "mc", do.sd = TRUE)
get.phat.linear(x, y, method = "exact", do.sd = TRUE)
get.phat.quadratic

Get the pvalue for the quadratic statistic

Description
Get the pvalue for the quadratic statistic

Usage
get.phat.quadratic(x, y, method = c("is", "nested", "mc", "exact"),
N.mc = 10^3, N.is = 10^3, N.level = 1000, q = 0.2, B = 5 *
length(x), mc.cores = 1, do.sd = FALSE)

Arguments
x binary vector of treatment assignment
y gene expression measurement matrix
method method to estimate pvalue for the linear statistic
N.mc number of mc samples is method == "mc"
N.is number of mc samples is method == "is"
N.level number of samples in each level if method == "nested"
q progression quantile if method == "nested"
B number of burn-ins to use if method == "nested"
mc.cores number of cores to use in mcapply
do.sd logical to indicate whether calculating sd or not

Value
a list containing phat from different methods

Examples
x <- c(rep(0, 4), rep(1, 4))
y <- matrix(c(rnorm(4*5, 0, 1), rnorm(4*5, 2,1)), nrow = 8)
get.phat.quadratic(x, y, method = "is")
get.phat.quadratic(x, y, method = "nested")
get.phat.quadratic(x, y, method = "mc")
get.phat.quadratic(x, y, method = "exact")
get.phat.quadratic(x, y, method = "is", do.sd = TRUE)
get.phat.quadratic(x, y, method = "nested", do.sd = TRUE)
get.phat.quadratic(x, y, method = "mc", do.sd = TRUE)
get.phat.quadratic(x, y, method = "exact", do.sd = TRUE)
Description

The package calculates the approximation for permutation p-values of linear statistic.
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