Package ‘logitT’

January 30, 2017

Version 1.32.0
Date 2008-09-14
Title logit-t Package
Author Tobias Guennel <tguennel@vcu.edu>
Maintainer Tobias Guennel <tguennel@vcu.edu>
Depends affy
Suggests SpikeInSubset
Description The logitT library implements the Logit-t algorithm introduced in
--A high performance test of differential gene expression for oligonucleotide arrays--
by William J Lemon, Sandya Liyanarachchi and Ming You for use with Affymetrix data
stored in an AffyBatch object in R.
License GPL (>= 2)
URL http://www.bioconductor.org
biocViews Microarray, DifferentialExpression
NeedsCompilation yes

R topics documented:

logitTAffy ............................................................... 1

Index

logitTAffy Testing for differential gene expression using the Logit-t algorithm

Description
This function takes an instance of AffyBatch and calculates t-statistics for tests of differential gene
expression for oligonucleotide arrays using the Logit-t algorithm.

Usage
logitTAffy(object, group)
logitTAffy

Arguments

object an instance of AffyBatch

group a vector specifying the group label for each array

Details

For more details see the package vignette.

Value

A named vector containing the t-statistics for each probe set for each array.

Author(s)

Tobias Guennel <tguennel@vcu.edu>

References


See Also

AffyBatch

Examples

if(require(SpikeInSubset)){
library(SpikeInSubset)
data(spikein95)
logitTex<-logitTAffy(spikein95, group=c("A","A","A","B","B","B"))
logitTex[1:10] # extract t-statistics for first ten probe sets
logitTex[grep("AFFX-BioB-5_at", names(logitTex))] # extract t-statistics for specific probe set
pvals<-(1-pt(abs(logitTex),df=4))*2 # calculate two-sided p-values
signifgenes<-names(logitTex)[pvals<0.01] # find significant probe sets at 0.01 significance level
}
else{
stop("Please install the SpikeInSubset package to run the example.")
}
Index

AffyBatch, 2
logitTAffy, 1