Package ‘logitT’

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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:

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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)
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.")
}
}
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