Package ‘logitT’

December 21, 2016

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 (&gt;= 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)
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

```r
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 se
  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