Package 'logitT'

October 18, 2022

Version 1.54.0

Date 2008-09-14

Title logit-t Package

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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.

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URL http://www.bioconductor.org

biocViews Microarray, DifferentialExpression

git_url https://git.bioconductor.org/packages/logitT

git_branch RELEASE_3_15

git_last_commit 9428862

git_last_commit_date 2022-04-26

Date/Publication 2022-10-18

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)

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References

William J Lemon, Sandya Liyanarachchi and Ming You (2003). A high performance test of differ-
ential gene expression for oligonucleotide arrays. Genome Biology 2003, 4:R67. http://genomebiology.com/2003/4/10/R67.

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 significanc
}else{
```

```
  stop("Please install the SpikeInSubset package to run the example.")
  }
```

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