Package ‘logitT’

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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.
License GPL (>= 2)
URL http://www.bioconductor.org
biocViews Microarray, DifferentialExpression
NeedsCompilation yes

R topics documented:

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.

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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 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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