logitT

November 11, 2009

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.

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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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