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)
```

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 differential gene expression for oligonucleotide arrays. Genome Biology 2003, 4:R67. http://genomebiology.com/2003/4/10/R

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 s
logitTex[grep("AFFX-BioB-5_at",names(logitTex))]                    # extract t-statistics for specific prob
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 s
}else{
stop("Please install the SpikeInSubset package to run the example.")
}
```

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