

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.

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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

| | |
|---------------------|--|
| <code>object</code> | an instance of <code>AffyBatch</code> |
| <code>group</code> | 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/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 sets
  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
}else{
  stop("Please install the SpikeInSubset package to run the example.")
}
```

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