

# Package ‘logitT’

October 18, 2017

**Version** 1.34.0

**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.

**License** GPL (>= 2)

**URL** <http://www.bioconductor.org>

**biocViews** Microarray, DifferentialExpression

**NeedsCompilation** yes

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logitTAffy                      *Testing for differential gene expression using the Logit-t algorithm*

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### 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)**

Tobias Guennel <tguennel@vcu.edu>

**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 level
}else{
  stop("Please install the SpikeInSubset package to run the example.")
}
```

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