

# 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

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## R topics documented:

logitTAffy . . . . . 2

**Index** 4

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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

<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)

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 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
}else{
```

```
stop("Please install the SpikeInSubset package to run the example.")  
}
```

# Index

AffyBatch, [2](#)

logitTAffy, [2](#)