

# logitT

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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)

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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-s
  logitTex[grep("AFFX-BioB-5_at",names(logitTex))] # extract t-stat
  pvals<-(1-pt(abs(logitTex),df=4))*2 # calculate t
  signifgenes<-names(logitTex)[pvals<0.01] # find signif
}else{
  stop("Please install the SpikeInSubset package to run the example.")
}
```

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