logiT
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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
logiTAffy(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

See Also
AffyBatch
Examples

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