

# dFDRscore

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dFDRscore	<i>Function to transform <math>fdr</math> into scores according to log-likelihood ratio between the true positives and the false positives and/or after controlling false discovery rate</i>
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## Description

dFDRscore is supposed to take as input a vector of  $fdr$ , which are transformed into scores according to according to log-likelihood ratio between the true positives and the false positives. Also if the FDR threshold is given, it is used to make sure that  $fdr$  below threshold are considered significant and thus scored positively. Instead, those  $fdr$  above the given threshold are considered insignificant and thus scored negatively.

## Usage

```
dFDRscore(fdr, fdr.threshold = NULL, scatter = F)
```

## Arguments

fdr	a vector containing a list of input $fdr$
fdr.threshold	the given FDR threshold. By default, it is set to NULL, meaning there is no constraint. If given, those $fdr$ with the FDR below threshold are considered significant and thus scored positively. Instead, those $fdr$ with the FDR above given threshold are considered insignificant and thus scored negatively
scatter	logical to indicate whether the scatter graph of scores against p-values should be drawn. Also indicated is the score corresponding to the given FDR threshold (if any)

## Value

- scores: a vector of scores

## Note

none

## See Also

[dSVDsignif](#), [dNetPipeline](#)

**Examples**

```
# 1) generate data with an iid matrix of 1000 x 9
data <- cbind(matrix(rnorm(1000*3,mean=0,sd=1), nrow=1000, ncol=3),
matrix(rnorm(1000*3,mean=0.5,sd=1), nrow=1000, ncol=3),
matrix(rnorm(1000*3,mean=-0.5,sd=1), nrow=1000, ncol=3))

# 2) calculate the significance according to SVD
# using "fdr" significance
fdr <- dSVDsignif(data, signif="fdr", num.permutation=10)

# 3) calculate the scores according to the fitted BUM and fdr=0.01
# no fdr threshold
scores <- dFDRscore(fdr)
# using fdr threshold of 0.01
scores <- dFDRscore(fdr, fdr.threshold=0.1, scatter=TRUE)
```