

dFDRscore

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dFDRscore	<i>Function to transform fdr into scores according to log-likelihood ratio between the true positives and the false positivies 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 positivies. 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)
```