dSVDsignif

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`dSVDsignif` *Function to obtain SVD-based gene significance from the input gene-sample matrix*

Description

`dSVDsignif` is supposed to obtain gene signficance from the given gene-sample matrix according to singular value decomposition (SVD)-based method. The method includes: 1) singular value decomposition of the input matrix; 2) determination of the eigens in consideration (if not given); 3) construction of the gene-specific project vector based on the considered eigens; 4) calculation of the distance statistic from the projection vector to zero point vector; and 5) based on distance statistic to obtain the gene significance.

Usage

```
dSVDsignif(data, num.eigen = NULL, pval.eigen = 0.01, signif = c("fdr",
"pval"), orient.permutation = c("row", "column", "both"),
num.permutation = 100, fdr.procedure = c("stepup", "stepdown"),
verbose = T)
```

Arguments

`data`	an input gene-sample data matrix used for singular value decomposition
`num.eigen`	an integer specifying the number of eigens in consideration. If NULL, this number will be automatically decided on based on the observed relative eigenexpression against randomised relative eigenexpression calculated from a list (here 100) of permutated input matrix
`pval.eigen`	p-value used to call those eigens as dominant. This parameter is used only when parameter 'num.eigen' is NULL. Here, p-value is calcualted to assess how likely the observed relative eigenexpression are more than the maximum relative eigenexpression calculated from permutated matrix
`signif`	the singificance to return. It can be either "pval" for using the p-value as the gene significance, or "fdr" for using the fdr as the gene significance
`orient.permutation`	the orientation of matrix being permutated. It can be either "row" to permutate values within each row, or "column" to permutate values within each column, or "both" to permutate values both within rows and columns. Notably, when using the p-value as the gene significance, it is always to permutate values within each row.

`num.permutation`
: an integer specifying how many permutations are used

`fdr.procedure`
: the procedure to adjust the fdr. To ensure that the high distance statistic the more significance, the fdr should be adjusted either using "stepup" for step-up procedure (from the most significant to the least significant) or using "stepdown" for step-down procedure (from the least significant to the most significant)

`verbose`
: logical to indicate whether the messages will be displayed in the screen. By default, it sets to true for display

Value

a vector storing gene significance

Note

none

See Also

`dFDRscore`

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)
# using "pval" significance
pval <- dSVDsignif(data, signif="pval", num.permutation=10)
```