Package: TDbasedUFEadv (via r-universe)

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Type Package

Title Advanced package of tensor decomposition based unsupervised feature extraction

Version 1.5.0

Language en-US

Description This is an advanced version of TDbasedUFE, which is a comprehensive package to perform Tensor decomposition based unsupervised feature extraction. In contrast to TDbasedUFE which can perform simple the feature selection and the multiomics analyses, this package can perform more complicated and advanced features, but they are not so popularly required. Only users who require more specific features can make use of its functionality.

biocViews GeneExpression, FeatureExtraction, MethylationArray, SingleCell, Software

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Imports TDbasedUFE, Biobase, GenomicRanges, utils, rTensor, methods, graphics, RTCGA, stats, enrichplot, DOSE, STRINGdb, enrichR, hash, shiny

RoxygenNote 7.2.3

BugReports https://github.com/tagtag/TDbasedUFEadv/issues

URL https://github.com/tagtag/TDbasedUFEadv

Suggests knitr, rmarkdown, testthat (>= 3.0.0), RTCGA.rnaseq, RTCGA.clinical, BiocStyle, MOFAdata

VignetteBuilder knitr

Config/testthat/edition 3

Repository https://bioc.r-universe.dev

RemoteUrl https://github.com/bioc/TDbasedUFEadv

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Contents

`computeSVD` *Title Perform SVD toward reduced matrix generated from a tensor with partial summation*

Description

Title Perform SVD toward reduced matrix generated from a tensor with partial summation

Usage

```
computeSVD(matrix1, matrix2, dim = 10L, scale = TRUE)
```

Arguments

`matrix1`	The first original matrix that generates a tensor
`matrix2`	The second original matrix that generates a tensor
`dim`	The number of singular value vectors to be computed
`scale`	If matrix should be scaled or not

Value

Singular value vectors attributed to two sets of objects associated with singular value vectors attributed to features, by multiplying

Examples

```
matrix1 <- matrix(runif(200),20)
matrix2 <- matrix(runif(400),20)
SVD <- computeSVD(matrix1,matrix2)
```

prepareCondDrugandDisease *Prepare condition matrix for expDrug*

Description

Prepare condition matrix for expDrug

Usage

```
prepareCondDrugandDisease(expDrug)
```

Arguments

expDrug	input gene expression profile

Value

Condition matrix for expDrug

Examples

```
library(RTCGA.rnaseq)
Cancer_cell_lines <- list(ACC.rnaseq,BLCA.rnaseq,BRCA.rnaseq)
Drug_and_Disease <- prepareexpDrugandDisease(Cancer_cell_lines)
Cond <- prepareCondDrugandDisease(Drug_and_Disease$expDrug)
```

prepareCondTCGA *Prepare Sample label for TCGA data*

Description

Prepare Sample label for TCGA data

Usage

```
prepareCondTCGA(
  Multi_sample,
  Clinical,
  ID_column_of_Multi_sample,
  ID_column_of_Clinical
)
```

Arguments

`Multi_sample`	list of sample ids
`Clinical`	List of clinical data matrix from RTCGA.clinical
`ID_column_of_Multi_sample`	Column numbers used for conditions
`ID_column_of_Clinical`	Column numbers that include corresponding sample ids in clinical data

Value

list of sample labels

Examples

```
library(RTCGA.clinical)
library(RTCGA.rnaseq)
Clinical <- list(BLCA.clinical, BRCA.clinical, CESC.clinical, COAD.clinical)
Multi_sample <- list(
  BLCA.rnaseq[seq_len(100), 1, drop = FALSE],
  BRCA.rnaseq[seq_len(100), 1, drop = FALSE],
  CESC.rnaseq[seq_len(100), 1, drop = FALSE],
  COAD.rnaseq[seq_len(100), 1, drop = FALSE]
)
ID_column_of_Multi_sample <- c(770, 1482, 773, 791)
ID_column_of_Clinical <- c(20, 20, 12, 14)
cond <- prepareCondTCGA(
  Multi_sample, Clinical,
  ID_column_of_Multi_sample, ID_column_of_Clinical
)
```

`prepareexpDrugandDisease` *Generating gene expression of drug treated cell lines and a disease cell line*

Description

Generating gene expression of drug treated cell lines and a disease cell line

Usage

```
prepareexpDrugandDisease(Cancer_cell_lines)
```

Arguments

`Cancer_cell_lines`	<- list(ACC.rnaseq,BLCA.rnaseq,BRCA.rnaseq) list that includes individual data set from RTCGA.rnaseq

Value

list of expDrug and expDisease

Examples

```
library(RTCGA.rnaseq)
Cancer_cell_lines <- list(ACC.rnaseq,BLCA.rnaseq,BRCA.rnaseq)
Drug_and_Disease <- prepareexpDrugandDisease(Cancer_cell_lines)
```

---

prepareTensorfromList *Prepare tensor from a list that includes multiple profiles*

Description

Prepare tensor from a list that includes multiple profiles

Usage

```
prepareTensorfromList(Multi, proj_dim)
```

Arguments

Multi	a list that includes multiple profiles
proj_dim	the number of projection dimensions

Value

a tensor as a bundle of singular value vectors obtained by applying SVD to individual omics

Examples

```
library(MOFAdata)
data("CLL_data")
data("CLL_covariates")
Z <- prepareTensorfromList(CLL_data,10L)
```

prepareTensorfromMatrix *Generate tensor from two matrices*

Description

Generate tensor from two matrices

Usage

```
prepareTensorfromMatrix(matrix1, matrix2)
```

Arguments

matrix1	the first input matrix
matrix2	the second input matrix

Value

A tensor generated from the first and second matrices

Examples

```
Z <- prepareTensorfromMatrix(matrix(runif(100),10),matrix(runif(100),10))
```

prepareTensorRect *Prepare tensor generated from two matrices that share samples*

Description

Prepare tensor generated from two matrices that share samples

Usage

```
prepareTensorRect(
  sample,
  feature,
  value,
  featureRange = GRanges(NULL),
  sampleData = list(NULL)
)
```

Arguments

sample	Character vector of sample names
feature	list of features from two matrices
value	array, contents of
featureRange	Genomic Ranges to be associated with features
sampleData	List of conditional labeling associated with samples

Value

Tensor generated from two matrices that share samples

Examples

```
matrix1 <- matrix(runif(1000),200) #row features, column samples
matrix2 <- matrix(runif(2000),400) #row features, column samples
Z <- prepareTensorfromMatrix(t(matrix1),t(matrix2))
Z <- prepareTensorRect(sample=as.character(seq_len(50)),
feature=list(as.character(seq_len(200)),as.character(seq_len(400))),
sampleData=list(rep(seq_len(2),each=25)),value=Z)
```

---

selectFeatureProj *Select feature when projection strategy is employed for the case where features are shared with multiple omics profiles*

Description

Select feature when projection strategy is employed for the case where features are shared with multiple omics profiles

Usage

```
selectFeatureProj(
  HOSVD,
  Multi,
  cond,
  de = 1e-04,
  p0 = 0.01,
  breaks = 100L,
  input_all = NULL
)
```

Arguments

HOSVD	HOSVD
Multi	list of omics profiles, row: sample, column: feature
cond	list of conditions for individual omics profiles
de	initial value for optimization of standard deviation
p0	Threshold P-value
breaks	The number of bins of histogram of P-values
input_all	The number of selected feature. if null, interactive mode is activated

Value

list composed of logical vector that represent which features are selected and p-values

Examples

```
library(TDbasedUFE)
Multi <- list(matrix(runif(1000),10),matrix(runif(1000),10),
matrix(runif(1000),10),matrix(runif(1000),10))
Z <- prepareTensorfromList(Multi,10L)
Z <- aperm(Z,c(2,1,3))
Z <- PrepareSummarizedExperimentTensor(feature =as.character(1:10),
                                       sample=array("",1),value=Z)
HOSVD <- computeHosvd(Z)
cond <- rep(list(rep(1:2,each=5)),4)
index <- selectFeatureProj(HOSVD,Multi,cond,de=0.1,input_all=2)
```

---

selectFeatureRect *Select features through the selection of singular value vectors*

Description

Select features through the selection of singular value vectors

Usage

```
selectFeatureRect(
  SVD,
  cond,
  de = rep(1e-04, 2),
  p0 = 0.01,
  breaks = 100L,
  input_all = NULL
)
```

Arguments

SVD	SVD computed from matrix generated by partial summation of a tensor
cond	Condition to select singular value vectors
de	Initial values to be used for optimization of standard deviation
p0	Threshold value for the significance
breaks	Number of bins of histogram of P-values
input_all	The ID of selected singular value vectors. If it is null, interactive mode is activated.

Value

List of lists that includes P-vales as well as if individual features selected.

Examples

```
set.seed(0)
matrix1 <- matrix(runif(2000),200)
matrix2 <- matrix(runif(4000),200)
SVD <- computeSVD(matrix1,matrix2)
index_all <- selectFeatureRect(SVD,
list(NULL,rep(seq_len(2),each=5),rep(seq_len(2),each=10)),de=rep(0.5,2),
input_all=1)
```

---

selectFeatureTransRect

Select features for a tensor generated from two matrices that share samples.

Description

Select features for a tensor generated from two matrices that share samples.

Usage

```
selectFeatureTransRect(
  HOSVD,
  cond,
  de = rep(1e-04, 2),
  p0 = 0.01,
  breaks = 100L,
  input_all = NULL
)
```

Arguments

HOSVD	HOSVD
cond	list of conditions
de	initial values for optimization of standard deviation
p0	threshold value for the significance
breaks	number of bins of the histogram of P-values
input_all	The selected singular value vectors attributed to samples. if NULL, interactive mode

Value

list of logical vector that represent if the individual features are selected and P-values.

Examples

```
library(TDbasedUFE)
set.seed(0)
matrix1 <- matrix(runif(1000),20) #row features, column samples
matrix2 <- matrix(runif(2000),40) #row features, column samples
Z <- prepareTensorfromMatrix(t(matrix1),t(matrix2))
Z <- prepareTensorRect(sample=as.character(seq_len(50)),
feature=list(as.character(seq_len(20)),as.character(seq_len(40))),
sampleData=list(rep(seq_len(2),each=25)),value=Z)
HOSVD <- computeHosvd(Z)
cond <- list(attr(Z,"sampleData")[[1]],NULL,NULL)
index_all <- selectFeatureTransRect(HOSVD,cond,de=c(0.1,0.1),
input_all=2,p0=1e-10)
```

TensorRect-class *Class definitions*

Description

Class definitions

Slots

`sample` character.

`feature` list.

`value` array.

`featureRange` GRanges.

`sampleData` list.

`transSVD` *Convert SVD to that for the case where samples are shared between two matrices*

Description

Convert SVD to that for the case where samples are shared between two matrices

Usage

```
transSVD(SVD)
```

Arguments

`SVD`	input SVD object generated from computeSVD function

Value

converted SVD objects

Examples

```
matrix1 <- matrix(runif(200),20)
matrix2 <- matrix(runif(400),20)
SVD <- computeSVD(matrix1,matrix2)
SVD <- transSVD(SVD)
```

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