

# Package ‘TDbasedUFEadv’

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**Type** Package

**Title** Advanced package of tensor decomposition based unsupervised feature extraction

**Version** 1.0.0

**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

**License** GPL-3

**Encoding** UTF-8

**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, MOFAdat

**VignetteBuilder** knitr

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TDbasedUFEadv-package *TDbasedUFEadv: Advanced package of tensor decomposition based unsupervised feature extraction*

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## 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.

## Author(s)

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## See Also

Useful links:

- <https://github.com/tagtag/TDbasedUFEadv>
- Report bugs at <https://github.com/tagtag/TDbasedUFEadv/issues>

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computeSVD	<i>Title Perform SVD toward reduced matrix generated from a tensor with partial summation</i>
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**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)
```

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prepareCondDrugandDisease	<i>Prepare condition matrix for expDrug</i>
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**Description**

Prepare condition matrix for expDrug

**Usage**

```
prepareCondDrugandDisease(expDrug)
```

**Arguments**

expDrug	input gene expression profile
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**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)
```

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prepareCondTCGA	<i>Prepare Sample label for TCGA data</i>
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---

**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	<i>Prepare tensor generated from two matrices that share samples</i>
-------------------	--

---

**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	<i>Select feature when projection strategy is employed for the case where features are shared with multiple omics profiles</i>
-------------------	--

---

### 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)
```



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selectFeatureRect	<i>Select features through the selection of singular value vectors</i>
-------------------	--

---

## 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-values 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)
```

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TensorRect-class	<i>Class definitions</i>
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**Description**

Class definitions

**Slots**

sample character.  
feature list.  
value array.  
featureRange GRanges.  
sampleData list.

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transSVD	<i>Convert SVD to that for the case where samples are shared between two matrices</i>
----------	---

---

**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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