

# Package ‘TDbasedUFEadv’

June 20, 2025

**Type** Package

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

**Version** 1.9.1

**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, MOFAdata

**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> |
|------------|-----------------------------------------------------------------------------------------------|

---

**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 | <i>Prepare condition matrix for expDrug</i> |
|---------------------------|---------------------------------------------|

---

**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 | <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)
```

---

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-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)

```

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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