

Package ‘TDbasedUFE’

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Type Package

Title Tensor Decomposition Based Unsupervised Feature Extraction

Version 1.5.0

Description This is a comprehensive package to perform
Tensor decomposition based unsupervised feature extraction.
It can perform unsupervised feature extraction.
It uses tensor decomposition.
It is applicable to gene expression, DNA methylation, and
histone modification etc.
It can perform multiomics analysis.
It is also potentially applicable to single cell omics data sets.

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SingleCell

License GPL-3

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LazyData false

URL <https://github.com/tagtag/TDbasedUFE>

BugReports <https://github.com/tagtag/TDbasedUFE/issues>

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| | |
|--------------------|---|
| TDbasedUFE-package | <i>TDbasedUFE: Tensor Decomposition Based Unsupervised Feature Extraction</i> |
|--------------------|---|

Description

This is a comprehensive package to perform Tensor decomposition based unsupervised feature extraction. It can perform unsupervised feature extraction. It uses tensor decomposition. It is applicable to gene expression, DNA methylation, and histone modification etc. It can perform multiomics analysis. It is also potentially applicable to single cell omics data sets.

Author(s)

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See Also

- Useful links:
- <https://github.com/tagtag/TDbasedUFE>
 - Report bugs at <https://github.com/tagtag/TDbasedUFE/issues>

computeHosvd

*Title Compute higher order singular value decomposition***Description**

Title Compute higher order singular value decomposition

Usage

```
computeHosvd(Z, dims = c(10, dim(attr(Z, "value"))[-1]), scale = TRUE)
```

Arguments

| | |
|-------|------------------------------------|
| Z | array that includes omics data |
| dims | dimensions to be computed by HOSVD |
| scale | If value is scaled |

Value

List that includes output from HOSVD

Examples

```
Z <- PrepareSummarizedExperimentTensor(
  sample=matrix(as.character(seq_len(6)),c(3,2)),
  feature=as.character(seq_len(10)),
  value=array(runif(10*3*2),c(10,3,2)))
HOSVD <- computeHosvd(Z)
```

computeHosvdSquire

*Title Compute higher order singular value decomposition from the tensor generated from squared matrix***Description**

Title Compute higher order singular value decomposition from the tensor generated from squared matrix

Usage

```
computeHosvdSquire(
  Z,
  dims = unlist(lapply(dim(attr(Z, "value")), function(x) {
    min(10, x)
  })),
  scale = TRUE
)
```

Arguments

| | |
|--------------------|--|
| <code>Z</code> | A tensor including sample names, feature values, associated with <code>featureRange</code> and sample properties |
| <code>dims</code> | dimensions to be computed by HOSVD |
| <code>scale</code> | If value is scaled |

Value

List that includes output from HOSVD

Examples

```
omics1 <- matrix(runif(100),10)
dimnames(omics1) <- list(seq_len(10),seq_len(10))
omics2 <- matrix(runif(100),10)
dimnames(omics2) <- dimnames(omics1)
Multi <- list(omics1,omics2)
Z <- PrepareSummarizedExperimentTensorSquare(
  sample=matrix(colnames(omics1),1),
  feature=list(omics1=rownames(omics1),
    omics2=rownames(omics2)),
  value=convertSquare(Multi),
  sampleData=list(NA))
HOSVD <- computeHosvdSqure(Z)
```

convertSquare

Generate squared tensor from multiomics data

Description

Generate squared tensor from multiomics data

Usage

```
convertSquare(Multi)
```

Arguments

| | |
|--------------------|-------------------------------------|
| <code>Multi</code> | A list that include multiomics data |
|--------------------|-------------------------------------|

Value

A tensor computed from multiomics data

Examples

```
omics1 <- matrix(runif(100),10)
dimnames(omics1) <- list(seq_len(10),seq_len(10))
omics2 <- matrix(runif(100),10)
dimnames(omics2) <- dimnames(omics1)
Multi <- list(omics1,omics2)
Z <- convertSquare(Multi)
```

```
PrepareSummarizedExperimentTensor
```

Title Generate feature values formatted as a tensor format

Description

Title Generate feature values formatted as a tensor format

Usage

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

Arguments

| | |
|--------------|--|
| sample | Sample names |
| feature | Feature id names |
| value | Feature values |
| featureRange | Genomic coordinate attributed to feature id (if any) |
| sampleData | Sample property (labels etc) |

Value

A tensor including sample names, feature id, feature values, associated with featureRange and sample properties

Examples

```
require(GenomicRanges)
Z <- PrepareSummarizedExperimentTensor(
  sample=matrix(as.character(seq_len(6)),c(3,2)),
  feature=as.character(seq_len(10)),
  value=array(runif(10*3*2),c(10,3,2)))
```

```
PrepareSummarizedExperimentTensorSquare
```

Title Generate feature values formatted as a tensor format from Squared matrix

Description

Title Generate feature values formatted as a tensor format from Squared matrix

Usage

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

Arguments

| | |
|--------------|--|
| sample | Sample names |
| feature | Feature id names |
| value | Squared Feature values |
| featureRange | Genomic coordinate attributed to feature id (if any) |
| sampleData | Sample property (labels etc) |

Value

A tensor including sample names, feature values, associated with featureRange and sample properties

Examples

```
omics1 <- matrix(runif(100),10)
dimnames(omics1) <- list(seq_len(10),seq_len(10))
omics2 <- matrix(runif(100),10)
dimnames(omics2) <- dimnames(omics1)
Multi <- list(omics1,omics2)
Z <- PrepareSummarizedExperimentTensorSquare(
  sample=matrix(colnames(omics1),1),
  feature=list(omics1=rownames(omics1),
    omics2=rownames(omics2)),
  value=convertSquare(Multi),
  sampleData=list(NA))
```

| | |
|---------------|------------------------------|
| selectFeature | <i>Title Select features</i> |
|---------------|------------------------------|

Description

Title Select features

Usage

```
selectFeature(HOSVD, input_all, de = 1e-04, p0 = 0.01, breaks = 100)
```

Arguments

- | | |
|-----------|--|
| HOSVD | output from HOSVD |
| input_all | Selected singular value IDs |
| de | Initial value for optimization of standard deviation |
| p0 | Threshold P-value |
| breaks | The number of bins |

Value

List that includes selected features and computed P-value

Examples

```
set.seed(2)
require(rTensor)
HOSVD <- hosvd(as.tensor(array(runif(10000*3*3),c(10000,3,3))),c(10,3,3))
input_all <- c(2,2)
index <- selectFeature(HOSVD,input_all,de=0.01,p0=0.01)
```

| | |
|---------------------|---|
| selectFeatureSquare | <i>Title Select features (for tensor generated from squared matrix)</i> |
|---------------------|---|

Description

Title Select features (for tensor generated from squared matrix)

Usage

```
selectFeatureSquare(
  HOSVD,
  input_all,
  Multi,
  de = rep(1e-04, dim(HOSVD$U[[3]])[2]),
  p0 = 0.01,
  breaks = 100,
  interact = TRUE
)
```

Arguments

| | |
|-----------|---|
| HOSVD | output from HOSVD applied to tensor generated from squared matrix |
| input_all | Selected singular value vector IDs |
| Multi | Multionomics data |
| de | Initial value for optimization of standard deviation |
| p0 | Threshold P-value |
| breaks | The number of bins |
| interact | if interact mode or not |

Value

List that includes selected features and computed P-value

Examples

```
omics1 <- matrix(runif(100000),ncol=10)
dimnames(omics1) <- list(seq_len(10000),seq_len(10))
omics2 <- matrix(runif(100000),ncol=10)
dimnames(omics2) <- dimnames(omics1)
Multi <- list(omics1,omics2)
Z <- PrepareSummarizedExperimentTensorSquare(
  sample=matrix(colnames(omics1),1),
  feature=list(omics1=rownames(omics1),
    omics2=rownames(omics2)),
  value=convertSquare(Multi),
  sampleData=list(NA))
HOSVD <- computeHosvdSquare(Z)
cond <- list(0,rep(seq_len(2),each=5),c("A","B"))
input_all <- selectSingularValueVectorLarge(HOSVD,cond,input_all=c(1,1))
index <- selectFeatureSquare(HOSVD,input_all,Multi,de=c(0.1,0.1),
  interact=FALSE)
```

selectSingularValueVectorLarge

Title Select singular value vectors from HOSVD (boxplot version)

Description

Title Select singular value vectors from HOSVD (boxplot version)

Usage

```
selectSingularValueVectorLarge(HOSVD, cond, input_all = NULL)
```

Arguments

| | |
|-----------|---|
| HOSVD | output from HOSVD |
| cond | Labels to select singular value vector number |
| input_all | if list is not null, no interactive mode is activated but provided values are used. |

Value

Selected singular value vector IDs

Examples

```
Z <- PrepareSummarizedExperimentTensor(
  sample=matrix(as.character(seq_len(6)),c(3,2)),
  feature=as.character(seq_len(10)),
  value=array(runif(10*3*2),c(10,3,2)))
HOSVD <- computeHosvd(Z)
cond <- list(0,c("A","B","C"),c("A","B"))
input_all <- selectSingularValueVectorLarge(HOSVD,cond,input_all=c(1,1))
```

selectSingularValueVectorSmall

Title Select singular value vectors from HOSVD

Description

Title Select singular value vectors from HOSVD

Usage

```
selectSingularValueVectorSmall(HOSVD, input_all = NULL)
```

Arguments

HOSVD output from HOSVD
input_all if ist is no null, no interactive mode is activated but provided values are used.

Value

Selected singular value vector IDs

Examples

```
Z <- PrepareSummarizedExperimentTensor(
  sample=matrix(as.character(seq_len(6)),c(3,2)),
  feature=as.character(seq_len(10)),
  value=array(runif(10*3*2),c(10,3,2)))
HOSVD <- computeHosvd(Z)
input_all <- selectSingularValueVectorSmall(HOSVD,input_all=c(1,1))
```

| | |
|---------------|--|
| tableFeatures | <i>Title Show selected features as Table</i> |
|---------------|--|

Description

Title Show selected features as Table

Usage

```
tableFeatures(Z, index)
```

Arguments

Z Tensor of features
index List that includes selected features and P-values

Value

Table list of selected features

Examples

```
set.seed(2)
require(rTensor)
HOSVD <- hosvd(as.tensor(array(runif(10000*3*3),c(10000,3,3))),c(10,3,3))
input_all <- c(2,2)
index <- selectFeature(HOSVD,input_all,de=0.01,p0=0.01)
index$index[seq_len(100)] <- TRUE
Z <- PrepareSummarizedExperimentTensor(
  sample=matrix(as.character(seq_len(9)),c(3,3)),
  feature=as.character(seq_len(10000)),
  value=array(runif(10000*3*3),c(10,3,3)))
head(tableFeatures(Z,index))
```

| | |
|---------------------|--|
| tableFeaturesSquare | <i>Title Show selected features as Table (for Squared one)</i> |
|---------------------|--|

Description

Title Show selected features as Table (for Squared one)

Usage

```
tableFeaturesSquare(Z, index, id)
```

Arguments

| | |
|-------|---|
| Z | Tensor of features |
| index | List that includes selected features and P-values |
| id | feature to be shown |

Value

Table list of selected features

Examples

```
omics1 <- matrix(runif(100000),ncol=10)
dimnames(omics1) <- list(seq_len(10000),seq_len(10))
omics2 <- matrix(runif(100000),ncol=10)
dimnames(omics2) <- dimnames(omics1)
Multi <- list(omics1,omics2)
Z <- PrepareSummarizedExperimentTensorSquare(
  sample=matrix(colnames(omics1),1),
  feature=list(omics1=rownames(omics1),
    omics2=rownames(omics2)),
  value=convertSquare(Multi),
  sampleData=list(NA))
HOSVD <- computeHosvdSquare(Z)
cond <- list(0,rep(seq_len(2),each=5),c("A","B"))
input_all <- selectSingularValueVectorLarge(HOSVD,cond,input_all=c(1,1))
index <- selectFeatureSquare(HOSVD,input_all,Multi,de=c(0.1,0.1),
  interact=FALSE)
index[[1]]$index[1:100]<-TRUE
index[[1]]$p.value[1:100] <- 1e-3
tableFeaturesSquare(Z,index,1)
```

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