

# Package ‘Rtpca’

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**Title** Thermal proximity co-aggregation with R

**Version** 1.0.0

**Description** R package for performing thermal proximity co-aggregation analysis with thermal proteome profiling datasets to analyse protein complex assembly and (differential) protein-protein interactions across conditions.

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**BugReports** <https://support.bioconductor.org/>

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---

CommonFeatures, tpcaResult-method

*Extract CommonFeatures*

---

## Description

Extract CommonFeatures

**Usage**

```
## S4 method for signature 'tpcaResult'  
CommonFeatures(object)
```

**Arguments**

object                    and object of class tpcaResult

**Value**

a vector of common features across replicates

**Examples**

```
m1 <- matrix(1:12, ncol = 4)  
m2 <- matrix(2:13, ncol = 4)  
m3 <- matrix(c(2:10, 1:7), ncol = 4)  
  
rownames(m1) <- 1:3  
rownames(m2) <- 2:4  
rownames(m3) <- 2:5  
  
mat_list <- list(  
  m1, m2, m3  
)  
  
ppi_anno <- tibble(  
  x = "2",  
  y = "3",  
  combined_score = 700,  
  pair = "2:3")  
  
tpcaObj <- runTPCA(  
  objList = mat_list,  
  complexAnno = NULL,  
  ppiAnno = ppi_anno  
)  
  
CommonFeatures(tpcaObj)
```

---

ComplexAnnotation,tpcaResult-method

*Extract ComplexAnnotation*

---

**Description**

Extract ComplexAnnotation

**Usage**

```
## S4 method for signature 'tpcaResult'  
ComplexAnnotation(object)
```

**Arguments**

object                    and object of class tpcaResult

**Value**

a data frame containing the complex annotation

**Examples**

```
m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
ComplexAnnotation(tpcaObj)
```

---

ComplexBackgroundDistributionList,tpcaResult-method  
*Extract ComplexBackgroundDistributionList*

---

**Description**

Extract ComplexBackgroundDistributionList

**Usage**

```
## S4 method for signature 'tpcaResult'
ComplexBackgroundDistributionList(object)
```

**Arguments**

object                    and object of class tpcaResult

**Value**

a list of data frames containing distances of random complexes with different number of members

**Examples**

```
m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5
```

```
mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
ComplexBackgroundDistributionList(tpcaObj)
```

---

ComplexRocTable, tpcaResult-method

*Extract ComplexRocTable*

---

## Description

Extract ComplexRocTable

## Usage

```
## S4 method for signature 'tpcaResult'
ComplexRocTable(object)
```

## Arguments

object                    and object of class tpcaResult

## Value

a data frame containing a complex analysis roc table

## Examples

```
m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
ComplexRocTable(tpcaObj)
```

---

ContrastCondName, tpcaResult-method

*Extract ContrastCondName*

---

**Description**

Extract ContrastCondName

**Usage**

```
## S4 method for signature 'tpcaResult'  
ContrastCondName(object)
```

**Arguments**

object                    and object of class tpcaResult

**Value**

a character string describing the contrast condition

**Examples**

```
tpcaObj <- new("tpcaResult")  
ContrastCondName(tpcaObj)
```

---

ContrastDistMat, tpcaResult-method

*Extract ContrastDistMat*

---

**Description**

Extract ContrastDistMat

**Usage**

```
## S4 method for signature 'tpcaResult'  
ContrastDistMat(object)
```

**Arguments**

object                    an object of class tpcaResult

**Value**

a matrix containing the contrast distance matrix of all pairwise protein-protein melting curve distances computed from a TPP experiment

**Examples**

```
m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
ContrastDistMat(tpcaObj)
```

---

ContrastList,tpcaResult-method

*Extract ContrastList*

---

**Description**

Extract ContrastList

**Usage**

```
## S4 method for signature 'tpcaResult'
ContrastList(object)
```

**Arguments**

object            an object of class tpcaResult

**Value**

an object list containing TPP data

**Examples**

```
m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
ContrastList(tpcaObj)
```

---

createDistMat	<i>Create distance matrix of all vs all protein melting profiles</i>
---------------	--

---

## Description

Create distance matrix of all vs all protein melting profiles

## Usage

```
createDistMat(  
  objList,  
  rownameCol = NULL,  
  summaryMethodStr = "median",  
  distMethodStr = "euclidean"  
)
```

## Arguments

objList	list of objects suitable for the analysis, currently allowed classes of objects are: matrices, data.frames, tibbles and ExpressionSets
rownameCol	in case the input objects are tibbles this parameter takes in the name (character) of the column specifying protein names or ids
summaryMethodStr	character string indicating a method to use to summarize measurements across replicates, default is "median", other options are c("mean", "rbind")
distMethodStr	method to use within dist function, default is 'euclidean'

## Value

a distance matrix of all pairwise protein melting profiles

## Examples

```
library(Biobase)  
  
m1 <- matrix(1:12, ncol = 4)  
m2 <- matrix(2:13, ncol = 4)  
m3 <- matrix(c(2:10, 1:7), ncol = 4)  
  
rownames(m1) <- 1:3  
rownames(m2) <- 2:4  
rownames(m3) <- 2:5  
  
colnames(m1) <- paste0("X", 1:4)  
colnames(m2) <- paste0("X", 1:4)  
colnames(m3) <- paste0("X", 1:4)  
  
mat_list <- list(  
  m1, m2, m3  
)  
  
createDistMat(mat_list)
```



```
expr1 <- ExpressionSet(m1)
expr2 <- ExpressionSet(m2)
expr3 <- ExpressionSet(m3)

exprSet_list <- list(
  expr1, expr2, expr3
)

createDistMat(exprSet_list)
```

---

*CtrlCondName,tpcaResult-method*  
*Extract CtrlCondName*

---

**Description**

Extract CtrlCondName

**Usage**

```
## S4 method for signature 'tpcaResult'
CtrlCondName(object)
```

**Arguments**

object                    and object of class tpcaResult

**Value**

a character string describing the control condition

**Examples**

```
tpcaObj <- new("tpcaResult")
CtrlCondName(tpcaObj)
```

---

*diffTpcaResultTable,tpcaResult-method*  
*Extract diffTpcaResultTable*

---

**Description**

Extract diffTpcaResultTable

**Usage**

```
## S4 method for signature 'tpcaResult'
diffTpcaResultTable(object)
```

**Arguments**

object            an object of class tpcaResult

**Value**

a data frame containing the results from a diffTpca analysis

**Examples**

```
m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
diffTpcaResultTable(tpcaObj)
```

---

DistMat,tpcaResult-method

*Extract DistMat*

---

**Description**

Extract DistMat

**Usage**

```
## S4 method for signature 'tpcaResult'
DistMat(object)
```

**Arguments**

object            an object of class tpcaResult

**Value**

a matrix containing the distance matrix of all pairwise protein-protein melting curve distances computed from a TPP experiment

**Examples**

```
m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
```

```
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
DistMat(tpcaObj)
```

---

DistMethod,tpcaResult-method

*Extract DistMethod*

---

### Description

Extract DistMethod

### Usage

```
## S4 method for signature 'tpcaResult'
DistMethod(object)
```

### Arguments

object                    and object of class tpcaResult

### Value

a character string of the dist method

### Examples

```
tpcaObj <- new("tpcaResult")
DistMethod(tpcaObj)
```

---

ObjList,tpcaResult-method

*Extract ObjList*

---

### Description

Extract ObjList

### Usage

```
## S4 method for signature 'tpcaResult'
ObjList(object)
```

### Arguments

object                    an object of class tpcaResult

**Value**

an object list containing TPP data

**Examples**

```
m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
ObjList(tpcaObj)
```

---

ori\_et\_al\_complexes\_df

*Data frame of annotated protein complexes by Ori et al.*

---

**Description**

data frame assigning proteins to annotated protein complexes

**Usage**

```
data("ori_et_al_complexes_df")
```

**Format**

data frame with columns `ensembl_id`, `protein` and `id` (complex identifier)

**References**

Ori et al. (2016), *Genome Biology*, 17, 47

**Examples**

```
data("ori_et_al_complexes_df")
```

---

`ori_et_al_complex_ppis`

*Data frame of eukaryotic protein-protein interactions inferred from annotated protein complexes by Ori et al. and StringDB interactions with a combined score of at least 900*

---

**Description**

data frame assigning proteins to (in)directly interacting proteins within protein complexes

**Usage**

```
data("ori_et_al_complex_ppis")
```

**Format**

data frame with columns `complex_name`, `x`, `y`, `pair` (unique pair id)

**References**

Ori et al. (2016), *Genome Biology*, 17, 47; Jensen et al. (2009), *Nucleic Acids Research*, 37, D412–D416

**Examples**

```
data("ori_et_al_complex_ppis")
```

---

`plotComplexRoc`

*Plot Complex ROC curve*

---

**Description**

Plots a ROC curve representing how well a given TPP dataset recovers annotated proteins complexes. The ROC curve is generated based on the supplied protein complex annotation specificity is assessed by comparing the given complex annotation to random permutations of that table, i.e. proteins randomly grouped together.

**Usage**

```
plotComplexRoc(tpcaObj, computeAUC = FALSE)
```

**Arguments**

<code>tpcaObj</code>	tpcaResult object
<code>computeAUC</code>	logical parameter indicating whether area under the ROC should be computed and indicated in the lower right corner of the plot

**Value**

ggplot object of a receiver operating curve (ROC)

**Examples**

```

rocTab = data.frame(
  TPR = c(0, 0.1, 0.2, 0.4, 0.5, 0.7, 0.9, 1),
  FPR = c(0, 0.05, 0.1, 0.2, 0.5, 0.7, 0.9, 1)
)

tpcaTest <- new(
  "tpcaResult",
  ComplexRocTable = rocTab)

plotComplexRoc(tpcaTest)

```

---

plotDiffTpcaVolcano *Plot differential TPCA analysis results*

---

**Description**

Plot differential TPCA analysis results

**Usage**

```

plotDiffTpcaVolcano(
  tpcaObj,
  alpha = 0.1,
  setXLim = FALSE,
  xlimit = c(-0.75, 0.75)
)

```

**Arguments**

tpcaObj	a tpcaObj after having performed a differential analysis, see runDiffTPCA
alpha	significance level / FDR at which null hypothesis should be rejected
setXLim	logical determining whether x-axis limits should be set according to xlimit
xlimit	numeric vector with two elements determining the x-axis limits, only is implemented if setXLim is set to TRUE

**Value**

ggplot displaying a volcano plot

**Examples**

```

library(dplyr)
library(Biobase)

m1 <- matrix(1:28, ncol = 4)
m2 <- matrix(2:25, ncol = 4)
m3 <- matrix(c(2:10, 1:19), ncol = 4)

rownames(m1) <- 1:7
rownames(m2) <- 3:8

```

```
rownames(m3) <- 2:8

mat_list <- list(
  m1, m2, m3
)

c1 <- matrix(29:2, ncol = 4)
c2 <- matrix(26:3, ncol = 4)
c3 <- matrix(c(11:3, 20:2), ncol = 4)

rownames(c1) <- 1:7
rownames(c2) <- 3:8
rownames(c3) <- 2:8

contrast_list <- list(
  c1, c2, c3
)

ppi_anno <- tibble(
  x = c("3", "3"),
  y = c("5", "7"),
  pair = c("3:5", "3:7"))

ref_df <- tibble(
  pair = c("3:5", "3:7"),
  valueC2 = c(4, 8)
)

diff_tpca <- runDiffTPCA(
  mat_list, contrast_list, ppiAnno = ppi_anno)

plotDiffTpcaVolcano(diff_tpca)
```

---

plotPPiProfiles

*Plot thermal profile of protein pairs*

---

### Description

Plot thermal profile of protein pairs

### Usage

```
plotPPiProfiles(tpcaObj, pair, splinesDf = 4)
```

### Arguments

tpcaObj	a tpcaObj after having performed a differential analysis, see runDiffTPCA
pair	character vector of one or more protein names
splinesDf	numeric, degree of freedom of the spline fit to the melting curves

### Value

ggplot displaying the thermal profile of a protein pair across conditions

**Examples**

```

library(Biobase)

set.seed(12)
m1 <- matrix(rnorm(50), ncol = 10)
m2 <- matrix(rnorm(50), ncol = 10)

rownames(m1) <- letters[1:5]
rownames(m2) <- letters[1:5]

colnames(m1) <- paste("fc", 1:10, sep = "_")
colnames(m2) <- paste("fc", 1:10, sep = "_")

pheno <- data.frame(
  temperature = seq(37, 67, length.out = 10))
rownames(pheno) <- paste("fc", 1:10, sep = "_")

eset1 <- ExpressionSet(
  assayData = m1,
  phenoData = AnnotatedDataFrame(pheno)
)

eset2 <- ExpressionSet(
  assayData = m2,
  phenoData = AnnotatedDataFrame(pheno)
)

tpcaObj <- new("tpcaResult",
  ObjList = list(eset1),

ContrastList = list(eset2),
  CtrlCondName = "control",
  ContrastCondName = "treatment")

plotPPiProfiles(tpcaObj, pair = c("b", "d"))

```

---

plotPPiRoc

*Plot PPI ROC curve*


---

**Description**

Plot PPI ROC curve

**Usage**

```
plotPPiRoc(tpcaObj, computeAUC = FALSE)
```

**Arguments**

tpcaObj	tpcaResult object
computeAUC	logical parameter indicating whether area under the ROC should be computed and indicated in the lower right corner of the plot



**Value**

ggplot object of a receiver operating curve (ROC)

**Examples**

```
rocTab = data.frame(
  TPR = c(0, 0.1, 0.2, 0.4, 0.5, 0.7, 0.9, 1),
  FPR = c(0, 0.05, 0.1, 0.2, 0.5, 0.7, 0.9, 1)
)

tpcaTest <- new(
  "tpcaResult",
  PPIRocTable = rocTab)

plotPPIRoc(tpcaTest)
```

---

plotTpcaVolcano      *Plot TPCA analysis results*

---

**Description**

Plot TPCA analysis results

**Usage**

```
plotTpcaVolcano(tpcaObj, alpha = 0.1)
```

**Arguments**

tpcaObj      a tpcaObj after having performed a differential analysis, see runDiffTPCA  
alpha      significance level / FDR at which null hypothesis should be rejected

**Value**

ggplot displaying a volcano plot

**Examples**

```
library(dplyr)
library(Biobase)

m1 <- matrix(1:28, ncol = 4)
m2 <- matrix(2:25, ncol = 4)
m3 <- matrix(c(2:10, 1:19), ncol = 4)

rownames(m1) <- 1:7
rownames(m2) <- 3:8
rownames(m3) <- 2:8

mat_list <- list(
  m1, m2, m3
)
```

```
complex_anno <- tibble(
  protein = c("3", "4", "5",
             "4", "5", "6", "7"),
  id = c(rep("1", 3), rep("2", 4)),
  count = c(rep(3, 3), rep(4, 4)))

tpca_result <- runTPCA(
  mat_list, complexAnno = complex_anno)

plotTpcaVolcano(tpca_result)
```

---

PPiAnnotation,tpcaResult-method  
*Extract PPiAnnotation*

---

## Description

Extract PPiAnnotation

## Usage

```
## S4 method for signature 'tpcaResult'
PPiAnnotation(object)
```

## Arguments

object                    and object of class tpcaResult

## Value

a data frame containing the results from a tpca analysis

## Examples

```
m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
PPiAnnotation(tpcaObj)
```

---

PPiRocTable, tpcaResult-method  
*Extract PPIRocTable*

---

**Description**

Extract PPIRocTable

**Usage**

```
## S4 method for signature 'tpcaResult'  
PPiRocTable(object)
```

**Arguments**

object            an object of class tpcaResult

**Value**

a data frame containing the results from a tpca analysis

**Examples**

```
m1 <- matrix(1:12, ncol = 4)  
m2 <- matrix(2:13, ncol = 4)  
m3 <- matrix(c(2:10, 1:7), ncol = 4)  
  
rownames(m1) <- 1:3  
rownames(m2) <- 2:4  
rownames(m3) <- 2:5  
  
mat_list <- list(  
  m1, m2, m3  
)  
tpcaObj <- new("tpcaResult", ObjList = mat_list)  
PPiRocTable(tpcaObj)
```

---

PPiRocTableAnno, tpcaResult-method  
*Extract PPIRocTableAnno*

---

**Description**

Extract PPIRocTableAnno

**Usage**

```
## S4 method for signature 'tpcaResult'  
PPiRocTableAnno(object)
```

**Arguments**

object            an object of class `tpcaResult`

**Value**

a data frame containing annotation information for `PPiRocTable`

**Examples**

```
m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
PPiRocTableAnno(tpcaObj)
```

---

runDiffTPCA

*Run differential TPCA analysis*

---

**Description**

Run differential TPCA analysis

**Usage**

```
runDiffTPCA(
  objList,
  contrastList,
  ctrlCondName = "control",
  contrastCondName = "treatment",
  ppiAnno = NULL,
  complexAnno = NULL,
  rownameCol = NULL,
  summaryMethodStr = "median",
  distMethodStr = "euclidean",
  n = 10000,
  p_adj_method = "BH"
)
```

**Arguments**

`objList`            input list of objects, e.g. `ExpressionSets` retrieved after TPP data import or matrices or data frames

`contrastList`       input list of objects for comparison at e.g. different treatment condition, same file formats work as for `objList`

ctrlCondName	character string indicating the name of the control condition, default is "control"
contrastCondName	character string indicating the name of the contrast condition, default is "treatment"
ppiAnno	data frame annotation known protein-protein interactions (PPI) to test
complexAnno	data frame annotating known protein complexes of interest to test
rownameCol	in case the input objects are tibbles this parameter takes in the name (character) of the column specifying protein names or ids
summaryMethodStr	character string indicating a method to use to summarize measurements across replicates, default is "median", other options are c("mean", "rbind")
distMethodStr	method to use within dist function, default is 'euclidean'
n	number of random protein pair draws to obtain empirical p-value, default is 10000
p_adj_method	method to be used for multiple testing adjustment, default is "BH"

**Value**

an object of class `tpcaResult` with the following slots: 1) `ObjList`: containing the supplied list of objects

**Examples**

```
library(dplyr)
library(Biobase)

m1 <- matrix(1:28, ncol = 4)
m2 <- matrix(2:25, ncol = 4)
m3 <- matrix(c(2:10, 1:19), ncol = 4)

rownames(m1) <- 1:7
rownames(m2) <- 3:8
rownames(m3) <- 2:8

mat_list <- list(
  m1, m2, m3
)

c1 <- matrix(29:2, ncol = 4)
c2 <- matrix(26:3, ncol = 4)
c3 <- matrix(c(11:3, 20:2), ncol = 4)

rownames(c1) <- 1:7
rownames(c2) <- 3:8
rownames(c3) <- 2:8

contrast_list <- list(
  c1, c2, c3
)

ppi_anno <- tibble(
  x = c("3", "3"),
  y = c("5", "7"),
```

```

pair = c("3:5", "3:7"))

ref_df <- tibble(
  pair = c("3:5", "3:7"),
  valueC2 = c(4, 8)
)

diff_tpca <- Rtpca:::runDiffTPCA(
  mat_list, contrast_list, ppiAnno = ppi_anno)

```

---

runTPCA

*Run the TPCA analysis*


---

## Description

Run the TPCA analysis

## Usage

```

runTPCA(
  objList,
  complexAnno = NULL,
  ppiAnno = NULL,
  rownameCol = NULL,
  summaryMethodStr = "median",
  distMethodStr = "euclidean",
  doRocAnalysis = TRUE,
  minCount = 3,
  nSamp = 10000,
  p_adj_method = "BH"
)

```

## Arguments

objList	inout list of objects, e.g. ExpressionSets retrieved after TPP data import or matrices or data frames
complexAnno	data frame annotating known protein complexes of interest to test
ppiAnno	data frame annotation known protein-protein interactions (PPI) to test
rownameCol	in case the input objects are tibbles this parameter takes in the name (character) of the column specifying protein names or ids
summaryMethodStr	character string indicating a method to use to summarize measurements across replicates, default is "median", other options are c("mean", "rbind")
distMethodStr	method to use within dist function, default is 'euclidean'
doRocAnalysis	logical indicating whether a ROC analysis should be performed which can be used to assess the predictive power of the dataset for protein-protein interactions / protein complexes based on distanc between melting curves of protein interactions partners

minCount	integer indicating how many subunits of a complex should be quantified to include it into the analysis, default is 3
nSamp	integer indicating the number of random samples which should be performed to estimate empirical null distributions, default is 10000
p_adj_method	character string indicating a valid method to be used for multiple testing adjustment, default is "BH" which makes p.adjust use benjamini-hochberg, for additional options check ?p.adjust

**Value**

an object of class `tpcaResult` with the following slots: 1) `ObjList`: containing the supplied list of objects

**Examples**

```

m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

colnames(m1) <- paste0("X", 1:4)
colnames(m2) <- paste0("X", 1:4)
colnames(m3) <- paste0("X", 1:4)

mat_list <- list(
  m1, m2, m3
)

ppi_anno <- tibble(
  x = "2",
  y = "3",
  combined_score = 700,
  pair = "2:3")

runTPCA(
  objList = mat_list,
  complexAnno = NULL,
  ppiAnno = ppi_anno
)

```

---

SetCommonFeatures, tpcaResult-method

*Set CommonFeatures*

---

**Description**

Set CommonFeatures

**Usage**

```
## S4 method for signature 'tpcaResult'  
SetCommonFeatures(object, commonFeatures)
```

**Arguments**

`object` and object of class `tpcaResult`  
`commonFeatures` a vector of characters indicating the common features across replicates

**Value**

a vector of common features across replicates

**Examples**

```
m1 <- matrix(1:12, ncol = 4)  
m2 <- matrix(2:13, ncol = 4)  
m3 <- matrix(c(2:10, 1:7), ncol = 4)  
  
rownames(m1) <- 1:3  
rownames(m2) <- 2:4  
rownames(m3) <- 2:5  
  
mat_list <- list(  
  m1, m2, m3  
)  
  
tpcaObj <- new("tpcaResult", ObjList = mat_list)  
SetCommonFeatures(tpcaObj, c("2", "3"))
```

---

SetComplexAnnotation,tpcaResult-method

*Set ComplexAnnotation*

---

**Description**

Set ComplexAnnotation

**Usage**

```
## S4 method for signature 'tpcaResult'  
SetComplexAnnotation(object, df)
```

**Arguments**

`object` an object of class `tpcaResult`  
`df` data frame containing complex annotation

**Value**

an object of class `tpcaResult`



**Examples**

```

m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
SetComplexAnnotation(tpcaObj, data.frame(id = "complex1"))

```

---

SetComplexBackgroundDistributionList,tpcaResult-method  
*Set ComplexBackgroundDistributionList*

---

**Description**

Set ComplexBackgroundDistributionList

**Usage**

```

## S4 method for signature 'tpcaResult'
SetComplexBackgroundDistributionList(object, lt)

```

**Arguments**

object	an object of class tpcaResult
lt	a list of data frames containing distances of random complexes with different number of members

**Value**

an object of class tpcaResult

**Examples**

```

m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
SetComplexBackgroundDistributionList(tpcaObj,
  list('3' = data.frame(pair = "A:B")))

```

---

SetComplexRocTable, tpcaResult-method  
*Set ComplexRocTable*

---

**Description**

Set ComplexRocTable

**Usage**

```
## S4 method for signature 'tpcaResult'
SetComplexRocTable(object, df)
```

**Arguments**

object            and object of class tpcaResult  
df                data.frame containg ComplexRocTable to set

**Value**

a data frame containing the results from a tpca analysis

**Examples**

```
m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
SetComplexRocTable(tpcaObj, data.frame(FPR = 1, TPR = 1))
```

---

SetContrastCondName, tpcaResult-method  
*Set ContrastCondName*

---

**Description**

Set ContrastCondName

**Usage**

```
## S4 method for signature 'tpcaResult'
SetContrastCondName(object, name)
```

**Arguments**

object            an object of class tpcaResult  
name             a character string describing the contrast condition

**Value**

an object of class tpcaResult

**Examples**

```
tpcaObj <- new("tpcaResult")  
SetContrastCondName(tpcaObj, "DMSO")
```

---

SetContrastDistMat,tpcaResult-method  
*Set ContrastDistMat*

---

**Description**

Set ContrastDistMat

**Usage**

```
## S4 method for signature 'tpcaResult'  
SetContrastDistMat(object, mat)
```

**Arguments**

object            and object of class tpcaResult  
mat               matrix containg contrast distance matrix to set

**Value**

a data frame containing the results from a tpca analysis

**Examples**

```
m1 <- matrix(1:12, ncol = 4)  
m2 <- matrix(2:13, ncol = 4)  
m3 <- matrix(c(2:10, 1:7), ncol = 4)  
  
rownames(m1) <- 1:3  
rownames(m2) <- 2:4  
rownames(m3) <- 2:5  
  
mat_list <- list(  
  m1, m2, m3  
)  
tpcaObj <- new("tpcaResult", ObjList = mat_list)  
SetContrastDistMat(tpcaObj, matrix(c(0, 1, 0, 1), ncol = 2))
```

SetCtrlCondName, tpcaResult-method  
*Set CtrlCondName*

---

**Description**

Set CtrlCondName

**Usage**

```
## S4 method for signature 'tpcaResult'  
SetCtrlCondName(object, name)
```

**Arguments**

object            an object of class tpcaResult  
name             a character string describing the control condition

**Value**

an object of class tpcaResult

**Examples**

```
tpcaObj <- new("tpcaResult")  
SetCtrlCondName(tpcaObj, "DMSO")
```

---

SetDiffTpcaResultTable, tpcaResult-method  
*Set diffTpcaResultTable*

---

**Description**

Set diffTpcaResultTable

**Usage**

```
## S4 method for signature 'tpcaResult'  
SetDiffTpcaResultTable(object, df)
```

**Arguments**

object            an object of class tpcaResult  
df                a data frame containing the results from a differential tpca analysis

**Value**

an object of class tpcaResult

**Examples**

```

m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
SetDiffTpcarResultTable(tpcaObj, data.frame(pair = "A:B"))

```

---

SetDistMat, tpcaResult-method

*Set DistMat*


---

**Description**

Set DistMat

**Usage**

```

## S4 method for signature 'tpcaResult'
SetDistMat(object, mat)

```

**Arguments**

object	an object of class tpcaResult
mat	matrix containing distance matrix to set

**Value**

a data frame containing the results from a tpca analysis

**Examples**

```

m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
SetDistMat(tpcaObj, matrix(c(0, 1, 0, 1), ncol = 2))

```

---

SetDistMethod,tpcaResult-method  
*Set distMethod*

---

**Description**

Set distMethod

**Usage**

```
## S4 method for signature 'tpcaResult'
SetDistMethod(object, method)
```

**Arguments**

object	an object of class tpcaResult
method	character string of dist method

**Value**

an object of class tpcaResult

**Examples**

```
tpcaObj <- new("tpcaResult")
SetDistMethod(tpcaObj, "euclidean")
```

---

SetPPiRocTable,tpcaResult-method  
*Set PPIRocTable*

---

**Description**

Set PPIRocTable

**Usage**

```
## S4 method for signature 'tpcaResult'
SetPPiRocTable(object, df)
```

**Arguments**

object	an object of class tpcaResult
df	data.frame containg PPIRocTable to set

**Value**

an object of class tpcaResult

**Examples**

```

m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
SetPPiRocTable(tpcaObj, data.frame(FPR = 1, TPR = 1))

```

---

SetPPiRocTableAnno,tpcaResult-method

*Set PPiRocTableAnno*


---

**Description**

Set PPiRocTableAnno

**Usage**

```

## S4 method for signature 'tpcaResult'
SetPPiRocTableAnno(object, df)

```

**Arguments**

object	an object of class tpcaResult
df	data.frame containg PPiRocTable annotation to set

**Value**

an object of class tpcaResult

**Examples**

```

m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
SetPPiRocTableAnno(tpcaObj, data.frame(pair = "A:B"))

```

---

SetSummaryMethod, tpcaResult-method  
*Set summaryMethod*

---

**Description**

Set summaryMethod

**Usage**

```
## S4 method for signature 'tpcaResult'
SetSummaryMethod(object, method)
```

**Arguments**

object	an object of class tpcaResult
method	character string of summary method

**Value**

an object of class tpcaResult

**Examples**

```
tpcaObj <- new("tpcaResult")
SetSummaryMethod(tpcaObj, "median")
```

---

SetTpcaResultTable, tpcaResult-method  
*Set TpcaResultTable*

---

**Description**

Set TpcaResultTable

**Usage**

```
## S4 method for signature 'tpcaResult'
SetTpcaResultTable(object, df)
```

**Arguments**

object	an object of class tpcaResult
df	a data frame containing the results from a tpca analysis

**Value**

an object of class tpcaResult



**Examples**

```

m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
SetTpcaResultTable(tpcaObj, data.frame(pair = "A:B"))

```

---

string_ppi_df	<i>Data frame of annotated human protein-protein interactions retrieved from stringDB with a combined interaction score equal or higher than 700</i>
---------------	--

---

**Description**

data frame assigning proteins to interacting proteins

**Usage**

```
data("string_ppi_df")
```

**Format**

data frame with columns x, y (gene symbol of interactors), combined\_score, pair (unique pair id)

**References**

Jensen et al. (2009), Nucleic Acids Research, 37, D412–D416

**Examples**

```
data("string_ppi_df")
```

---

SummaryMethod, tpcaResult-method	<i>Extract SummaryMethod</i>
----------------------------------	------------------------------

---

**Description**

Extract SummaryMethod

**Usage**

```
## S4 method for signature 'tpcaResult'
SummaryMethod(object)
```

**Arguments**

object                    and object of class tpcaResult

**Value**

a character string of the summary method

**Examples**

```
tpcaObj <- new("tpcaResult")
SummaryMethod(tpcaObj)
```

---

tpcaResult-class	<i>S4 TPCA Result Class</i>
------------------	-----------------------------

---

**Description**

S4 TPCA Result Class

**Value**

an object of class tpcaResult with the following slots: 1) ObjList: containing the supplied list of objects (e.g. a list of Expression Sets summarizing a TPP experiment) 2) ContrastList: containing the supplied list of contrast objects (if supplied for performance of a differential Rtpca analysis) 3) CtrlCondName: character string indicating the control condition, e.g. "control" 4) ContrastCondName: character string indicating the contrast condition, e.g. "drug treatment" 5) DistMat: a matrix containing all pairwise protein-protein distances obtained from comparing their melting curves in the control condition 6) ContrastDistMat: a matrix containing all pairwise protein-protein distances obtained from comparing their melting curves in the contrast condition 7) CommonFeatures: a vector containing the features (proteins) found in common between control and contrast condition 8) ComplexAnnotation: a data frame supplied by the user annotating protein to protein complexes 9) ComplexBackgroundDistributionList: a list of distances drawn for random groups of proteins with different number of members 10) PPIAnnotation: a data frame supplied by the user annotating protein-protein interactions 11) PPIRocTable: data frame containing false positive rate and true positive rate based on ranking the TPCA analysis results by euclidean distance of melting curves of protein pairs, annotated PPIs are considered true positives 12) PPIRocTableAnno: annotation to PPIRocTable 13) ComplexRocTable: data frame containing false positive rate and true positive rate based on ranking the TPCA analysis results by euclidean distance of melting curves of proteins within annotated complexes, annotated complexes are considered true positives, proteins in randomly permuted complex annotations are considered false positives 14) summaryMethod: character string of summarization method used to summarize data across replicates 15) distMethod: character string of distance method used to compare melting curves of proteins 16) tpcaResultTable: data frame containing the results from a tpca analysis 17) diffTpcaResultTable: data frame containing the results from a differential tpca analysis

**Slots**

ObjList list.

ContrastList list.

CtrlCondName character.

ContrastCondName character.  
 DistMat matrix.  
 ContrastDistMat matrix  
 CommonFeatures vector.  
 ComplexAnnotation data.frame.  
 ComplexBackgroundDistributionList list.  
 PPIAnnotation data.frame.  
 PPIRocTable data.frame  
 PPIRocTableAnno data.frame  
 ComplexRocTable data.frame  
 summaryMethod character.  
 distMethod character.  
 tpcaResultTable data.frame.  
 diffTpcaResultTable data.frame.

### Examples

```

m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
  
```

---

tpcaResultTable, tpcaResult-method  
*Extract tpcaResultTable*

---

### Description

Extract tpcaResultTable

### Usage

```

## S4 method for signature 'tpcaResult'
tpcaResultTable(object)
  
```

### Arguments

object            an object of class tpcaResult

**Value**

a data frame containing the results from a tpca analysis

**Examples**

```
m1 <- matrix(1:12, ncol = 4)
m2 <- matrix(2:13, ncol = 4)
m3 <- matrix(c(2:10, 1:7), ncol = 4)

rownames(m1) <- 1:3
rownames(m2) <- 2:4
rownames(m3) <- 2:5

mat_list <- list(
  m1, m2, m3
)
tpcaObj <- new("tpcaResult", ObjList = mat_list)
tpcaResultTable(tpcaObj)
```

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