

# Package: fCI (via r-universe)

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**Type** Package

**Title** f-divergence Cutoff Index for Differential Expression Analysis  
in Transcriptomics and Proteomics

**Version** 1.43.0

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**Description** (f-divergence Cutoff Index), is to find DEGs in the transcriptomic & proteomic data, and identify DEGs by computing the difference between the distribution of fold-changes for the control-control and remaining (non-differential) case-control gene expression ratio data. fCI provides several advantages compared to existing methods.

**License** GPL (>= 2)

**Depends** R (>= 3.1),FNN, psych, gtools, zoo, rgl, grid, VennDiagram

**Suggests** knitr, rmarkdown, BiocStyle

**VignetteBuilder** knitr

**NeedsCompilation** no

**biocViews** Proteomics

**Config/pak/sysreqs** cmake libfreetype6-dev libglu1-mesa-dev make texlive libpng-dev libuv1-dev libgl1-mesa-dev zlib1g-dev

**Repository** <https://bioc.r-universe.dev>

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---

|                        |                              |
|------------------------|------------------------------|
| <code>call.npci</code> | <i>the s4 class function</i> |
|------------------------|------------------------------|

---

**Description**

the s4 class function

**Usage**

`call.npci(.Object)`

**Arguments**

`.Object`            the fCI object

**Details**

The S4 method will compute DEGs and save the results to the original s4 object `.Object`

**Value**

NA                    No values will be returned

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

`print("See README")`

---

|                   |                                             |
|-------------------|---------------------------------------------|
| call.npci-methods | ~~ <i>Methods for Function</i> call.npci ~~ |
|-------------------|---------------------------------------------|

---

### Description

~~ Methods for function call.npci ~~

### Methods:

signature(.Object = "NPCI")

---

|         |                                                    |
|---------|----------------------------------------------------|
| compute | <i>the generic function 'compute' for s4 class</i> |
|---------|----------------------------------------------------|

---

### Description

the generic function 'compute' for s4 class

### Usage

```
compute(.Object)
```

### Arguments

.Object

### Details

TBD

### Value

NA                      No values will be returned

### Note

TBD

### Author(s)

Shaojun Tang

### References

<http://software.steenlab.org/fCI/>

See Also

TBD

Examples

```
print("See README")
```

---

|                 |                                    |
|-----------------|------------------------------------|
| compute-methods | ~~ Methods for Function compute ~~ |
|-----------------|------------------------------------|

---

Description

~~ Methods for function compute ~~

Methods:

```
signature(.Object = "NPCI")
```

---

|                          |                                                                                                              |
|--------------------------|--------------------------------------------------------------------------------------------------------------|
| deg.pairwise.fold.change | <i>find targets that have a consistent fold change in the same direction (either up- or down-regulation)</i> |
|--------------------------|--------------------------------------------------------------------------------------------------------------|

---

Description

find targets that have a consistent fold change in the same direction

Usage

```
deg.pairwise.fold.change(pairwise.wt.up.down.fold, pairwise.df.up.down.fold,  
  d = 1, min.fold = 1.2)
```

Arguments

- pairwise.wt.up.down.fold  
a list of numeric values representing the fold changes between control replicates for every gene
- pairwise.df.up.down.fold  
a list of numeric values representing the fold changes between case and control replicates for every gene
- d  
the dimensionality of the database, if the dataset is from proteogenomics, then d=2
- min.fold  
minimum fold change to declare a gene to be dysregulated, by default, min.fold=2

**Details**

TBD

**Value**

expression ratio

a dataframe of fCI gene expression ratios (folds) with none zero values defined by given control-control index (i.e. 1 & 2) and control-case index (i.e. 3&4)

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
wt.fold.changes=list(c(1.2,1.3,1.5,1.6))
df.fold.changes=list(c(1.1,1.3,1.4,1.6))
deg.pairwise.fold.change(wt.fold.changes,df.fold.changes)
```

---

deg.up.down.info

*find targets and their detailed expression changes*

---

**Description**

given expression matrix, find targets and their detailed expression changes

**Usage**

```
deg.up.down.info(wt.index.in.list, df.index.in.list, npc1,  
use.normalization = FALSE, target.ratio = 0.5)
```

**Arguments**

|                                |                                                                                   |
|--------------------------------|-----------------------------------------------------------------------------------|
| <code>wt.index.in.list</code>  | a list of numeric values representing the column indexes for control samples      |
| <code>df.index.in.list</code>  | a list of numeric values representing the column indexes for experimental samples |
| <code>npci</code>              | the object <code>npci</code>                                                      |
| <code>use.normalization</code> | a boolean value indicating if the normalization will be applied or not            |
| <code>target.ratio</code>      | a numeric value indicating the expected fold changes, i.e, 1.5                    |

**Details**

TBD

**Value**

|                  |                                                                                                           |
|------------------|-----------------------------------------------------------------------------------------------------------|
| expression ratio | a dataframe of fCI gene expression ratios (folds) defined by control-control index and control-case index |
|------------------|-----------------------------------------------------------------------------------------------------------|

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
print("TBC")
```

---

`deseq.median.ratio.normalization`*data matrix normalization method*

---

**Description**

normalize expression matrix by first replicate's median gene expression values

**Usage**

```
deseq.median.ratio.normalization(npqi.data)
```

**Arguments**

|                        |                                                                                                                |
|------------------------|----------------------------------------------------------------------------------------------------------------|
| <code>npqi.data</code> | a data frame containing non-zero numeric values (the data frame must contain more than one row and one column) |
|------------------------|----------------------------------------------------------------------------------------------------------------|

**Details**

TBD

**Value**

|                         |                                                               |
|-------------------------|---------------------------------------------------------------|
| <code>data.frame</code> | a new dataframe with each column having the same median value |
|-------------------------|---------------------------------------------------------------|

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
udata=data.frame(matrix(sample(3:100, 6*4), 6,4))
normalized.udata=deseq.median.ratio.normalization(udata)
```

---

`divergence.multivariate.distributions`*estimate fCI divergence for given samples of arbitrary dimensions*

---

**Description**

estimate fCI divergence for given samples of arbitrary dimensions

**Usage**

```
divergence.multivariate.distributions(null.data, diff.data, choice = 2)
```

**Arguments**

|                        |                                                                                 |
|------------------------|---------------------------------------------------------------------------------|
| <code>null.data</code> | the empirical null dataset (a dataframe of none-zero ratio values)              |
| <code>diff.data</code> | the case-control dataset (a dataframe of none-zero ratio values)                |
| <code>choice</code>    | choice=1 => cross entropy choice=2 => Helligan distance choice=3 => KL distance |

**Details**

TBD

**Value**

|                          |                                                                                   |
|--------------------------|-----------------------------------------------------------------------------------|
| <code>divergences</code> | The estimated divergence given control-control and case-control expression ratios |
|--------------------------|-----------------------------------------------------------------------------------|

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

## Examples

```
null.data=data.frame(matrix(sample(seq(from=0.1,to=10, by=0.01), 100), 100,1))
diff.data=data.frame(matrix(sample(seq(from=0.1,to=10, by=0.01), 100), 100,1))
divergence.multivariate.distributions(null.data, diff.data, choice = 2)
```

---

|           |                    |
|-----------|--------------------|
| fCI-class | <i>Class "fCI"</i> |
|-----------|--------------------|

---

## Description

The main Class that defines the slots values

## Objects from the Class

Objects can be created by calls of the form `new("fCI", ...)`.

## Slots

```
sample.data.file: Object of class "character" ~~
distance.matrix: Object of class "matrix" ~~
sample.data.normalized: Object of class "data.frame" ~~
attr.info: Object of class "data.frame" ~~
null.data.start: Object of class "matrix" ~~
diff.data.start: Object of class "matrix" ~~
expr.by.fold: Object of class "matrix" ~~
fold.cutoff.list: Object of class "list" ~~
rank.index.to.be.removed: Object of class "list" ~~
diff.gene.ids: Object of class "list" ~~
wt.index: Object of class "numeric" ~~
df.index: Object of class "numeric" ~~
ctr.indexes: Object of class "numeric" ~~
trt.indexes: Object of class "numeric" ~~
method.option: Object of class "numeric" ~~
use.ratio: Object of class "logical" ~~
percent.genes.to.scan: Object of class "numeric" ~~
num.genes.to.skip.each: Object of class "numeric" ~~
use.fold.change: Object of class "logical" ~~
wt.comb: Object of class "list" ~~
df.comb: Object of class "list" ~~
diff.ids: Object of class "list" ~~
```

```
result: Object of class "numeric" ~~  
indexes.reconsidered: Object of class "numeric" ~~  
center.by.gaussian.kernel: Object of class "logical" ~~  
symmetric.fold: Object of class "logical" ~~  
pairwise.diff.gene.ids: Object of class "list" ~~
```

**Methods**

No methods defined with class "fCI" in the signature.

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
showClass("fCI")
```

---

|                   |                                                                                                        |
|-------------------|--------------------------------------------------------------------------------------------------------|
| fCI.call.by.index | <i>top level function call to find targets based on expression data and control &amp; case indexes</i> |
|-------------------|--------------------------------------------------------------------------------------------------------|

---

**Description**

top level function call to find targets based on expression data and control & case indexes

**Usage**

```
fCI.call.by.index(wt.indexes, df.indexes, data.file, use.normalization = FALSE,  
  npc=NULL, short.report=TRUE)
```

**Arguments**

|                                |                                                                 |
|--------------------------------|-----------------------------------------------------------------|
| <code>wt.indexes</code>        | The wild type sample column indexes in the matrix, i.e. 1,2     |
| <code>df.indexes</code>        | The diseases type sample column indexes in the matrix, i.e. 3,4 |
| <code>data.file</code>         | The expression matrix                                           |
| <code>use.normalization</code> | boolean value whether you want the data to be normalized or not |
| <code>npci</code>              | the fCI object                                                  |
| <code>short.report</code>      | whether you want to have a report summary                       |

**Details**

TBD

**Value**

`rtable` A data frame of the detected targets

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
wt.indexes=1:2
df.indexes=3:4
data.file=data.frame(matrix(sample(3:100, 100*4, replace=TRUE), 100,4))
use.normalization=FALSE
npci=NULL
short.report=TRUE
fCI.call.by.index(wt.indexes, df.indexes, data.file, use.normalization,
  npc, short.report)
```

---

|          |                                      |
|----------|--------------------------------------|
| fci.data | <i>data frame of gene expression</i> |
|----------|--------------------------------------|

---

**Description**

This data set gives the gene expression values for multiple control and case samples.

**Usage**

```
fci.data
```

**Format**

a matrix containing 1043 genes and 4 samples.

**Value**

dataframe      A data frame of expression values

**Source**

[software.steenlab.org](http://software.steenlab.org)

**References**

<http://software.steenlab.org/fCI/>

---

|         |                                                                 |
|---------|-----------------------------------------------------------------|
| figures | <i>generic function to draw figures of the current analysis</i> |
|---------|-----------------------------------------------------------------|

---

**Description**

generic function to draw figures of the current analysis

**Usage**

```
figures(.Object)
```

**Arguments**

.Object

**Details**

TBD

**Value**

NA                      No values will be returned

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
print("See README")
```

---

figures-methods

*generate figures for empirical null and case-control distributions*

---

**Description**

~~ Methods for function figures ~~

**Methods:**

```
signature(.Object = "NPCI")
```

---

|                  |                                                |
|------------------|------------------------------------------------|
| find.fci.targets | <i>identify differentially expressed genes</i> |
|------------------|------------------------------------------------|

---

**Description**

identify differentially expressed genes

**Usage**

```
find.fci.targets(.Object, wt.indexes, df.indexes, data.file, use.normalization)
```

**Arguments**

|                   |                                                                 |
|-------------------|-----------------------------------------------------------------|
| .Object           | the fCI object                                                  |
| wt.indexes        | The wild type sample column indexes in the matrix, i.e. 1,2     |
| df.indexes        | The diseases type sample column indexes in the matrix, i.e. 3,4 |
| data.file         | The expression matrix                                           |
| use.normalization | boolean value whether you want the data to be normalized or not |

**Details**

TBD

**Value**

|    |                            |
|----|----------------------------|
| NA | No values will be returned |
|----|----------------------------|

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

Examples

```
fci=new("NPCI")
fci.data=data.frame(matrix(sample(3:100, 1043*6, replace=TRUE), 1043,6))
targets=find.fci.targets(fci, c(1,2,3), c(4,5,6), fci.data)
head(show.targets(targets))
```

---

|                                                    |
|----------------------------------------------------|
| find.fci.targets-methods                           |
| ~~ <i>Methods for Function find.fci.targets</i> ~~ |

---

Description

~~ Methods for function find.fci ~~

Methods:

signature(.Object = "NPCI") the built-in method to compute fCI DEGs.

---

|                |                                                          |
|----------------|----------------------------------------------------------|
| find.mid.point | <i>find the middle value of the density distribution</i> |
|----------------|----------------------------------------------------------|

---

Description

find the middle value of the density distribution

Usage

```
find.mid.point(Y)
```

Arguments

Y

Details

TBD

Value

position            The value the separates density into two halves

Note

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
Y=density(sample(1:100, 50), bw=0.5)
find.mid.point(Y)
```

---

|                                  |                                                                          |
|----------------------------------|--------------------------------------------------------------------------|
| <code>get.fold.large.step</code> | <i>generate fold change cutoff values for fCI divergence computation</i> |
|----------------------------------|--------------------------------------------------------------------------|

---

**Description**

generate fold change cutoff with a large step of 0.5 fold

**Usage**

```
get.fold.large.step()
```

**Details**

TBD

**Value**

`fold_values`      A vector of predefined fold changes for fCI computation

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
get.fold.large.step()
```

---

|               |                                                           |
|---------------|-----------------------------------------------------------|
| get.npci.data | <i>return a fCI object given the gene expression data</i> |
|---------------|-----------------------------------------------------------|

---

**Description**

return a fCI object given the gene expression data

**Usage**

```
get.npci.data(sample.data.normalized, wt.index, df.index)
```

**Arguments**

sample.data.normalized

wt.index

df.index

**Details**

TBD

**Value**

expression ratio

a dataframe of fCI gene expression ratios (folds) defined by control-control index and control-case index

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
sample.data.normalized=data.frame(matrix(sample(3:100, 100*4, replace=TRUE),
100,4))
wt.index=c(1,2)
df.index=c(1,3)
get.npci.data(sample.data.normalized, wt.index, df.index)
```

---

`get.npci.distance.matrix`*generate the divergence estimation based of fold change cutoff values*

---

**Description**

generate the divergence estimation based of fold change cutoff values

**Usage**`get.npci.distance.matrix(npci.data, null.data.start, diff.data.start, choice = 2, rank.index.to.be.removed)`**Arguments**

`npci.data`  
`null.data.start`  
  
`diff.data.start`  
  
`choice`  
`rank.index.to.be.removed`  
  
`expr.by.fold`  
`ctr.indexes`  
`trt.indexes`  
`use.intersect`  
`symmetric.fold`  
`fold.cutoff.list`

**Details**

TBD

**Value**

divergence      A matrix of computed divergences

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
data.file=data.frame(matrix(sample(3:100, 100*4, replace=TRUE), 100,4))
wt.index=c(1,2)
df.index=c(1,3)
npci=new("NPCI")
npci@wt.index=wt.index
npci@df.index=df.index
npci@sample.data.normalized=data.file
npci=initialize(npci)
npci=normalization(npci)
npci=populate(npci)

null.data.start=npci@null.data.start
diff.data.start=npci@diff.data.start
choice=2
rank.index.to.be.removed=npci@rank.index.to.be.removed
expr.by.fold=npci@expr.by.fold
ctr.indexes=npci@wt.index
trt.indexes=npci@df.index
use.intersect=FALSE
symmetric.fold=TRUE
fold.cutoff.list=npci@fold.cutoff.list

get.npci.distance.matrix(npci.data, null.data.start, diff.data.start,
  choice = 2, rank.index.to.be.removed, expr.by.fold, ctr.indexes, trt.indexes,
  use.intersect, symmetric.fold, fold.cutoff.list)
```

---

get.outline.index      *find the outline genes of a given distribution*

---

### Description

find the outline genes of a given distribution

### Usage

```
get.outline.index(values)
```

### Arguments

values

### Details

TBD

### Value

indexes      remove the index of values that are outliers based on the t-test with  $\alpha=0.05$

### Note

TBD

### Author(s)

Shaojun Tang

### References

<http://software.steenlab.org/fCI/>

### See Also

TBD

### Examples

```
values=rnorm(100)
get.outline.index(values)
```

---

get.protein.fold.step    *generate fold-change cutoff on proteomics data (with large steps of 0.2-0.5 fold)*

---

**Description**

generate fold-change cutoff on proteomics data (with large steps of 0.2-0.5 fold)

**Usage**

```
get.protein.fold.step()
```

**Details**

TBD

**Value**

     folds                    returning a vector of recommended fold ratios for proteomic study

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
get.protein.fold.step()
```

---

get.rank.combinations *fold change values*

---

**Description**

identify the fold change value indexes beyond the fCI estimation

**Usage**

```
get.rank.combinations(rank.index.to.be.removed, symmetric.fold)
```

**Arguments**

`rank.index.to.be.removed`  
a list of integers representing the genes to be removed because it exceeds the predefined fold change, i.e 1.2 fold

`symmetric.fold` a boolean value indicating the upregulation and downregulation are treatedly equally

**Details**

TBD

**Value**

`combinations` a data frame of gene indexes

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
rank.index.to.be.removed=list(sample(1:100, 20))
symmetric.fold=TRUE
get.rank.combinations(rank.index.to.be.removed, symmetric.fold)
```

---

|                                |                                                                        |
|--------------------------------|------------------------------------------------------------------------|
| <code>get.rna.fold.step</code> | <i>generate fCI fold-change cutoff values for typical RNA-Seq data</i> |
|--------------------------------|------------------------------------------------------------------------|

---

**Description**

generate fCI fold-change cutoff values for typical RNA-Seq data

**Usage**

```
get.rna.fold.step()
```

**Details**

TBD

**Value**

`folds`                      a vector of fold changes fCI used for divergence computation

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
get.rna.fold.step()
```

---

|                                 |                                              |
|---------------------------------|----------------------------------------------|
| <code>initialize-methods</code> | <i>~~ Methods for Function initialize ~~</i> |
|---------------------------------|----------------------------------------------|

---

**Description**

~~ Methods for function initialize ~~

**Methods:**

`signature(.Object = "NPCI")` this s4 class generic method initialize the fCI object once it is made

---

|                    |                                                        |
|--------------------|--------------------------------------------------------|
| intersect.of.lists | <i>find the common values of all vectors of a list</i> |
|--------------------|--------------------------------------------------------|

---

**Description**

find the common values of all vectors of a list

**Usage**

```
intersect.of.lists(vectorlist)
```

**Arguments**

|            |                                                                  |
|------------|------------------------------------------------------------------|
| vectorlist | a list of list values which we want to use to find common values |
|------------|------------------------------------------------------------------|

**Details**

TBD

**Value**

|            |                            |
|------------|----------------------------|
| intersects | the common values of lists |
|------------|----------------------------|

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
print("this function will be disabled!")
```

---

|                           |                |
|---------------------------|----------------|
| <code>is.installed</code> | <i>package</i> |
|---------------------------|----------------|

---

**Description**

test if a package is installed in the R library

**Usage**

```
is.installed(mypkg)
```

**Arguments**

|                    |                               |
|--------------------|-------------------------------|
| <code>mypkg</code> | a R library name, such as FNN |
|--------------------|-------------------------------|

**Details**

TBD

**Value**

|                           |                                           |
|---------------------------|-------------------------------------------|
| <code>installation</code> | boolean value indicating the installation |
|---------------------------|-------------------------------------------|

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
is.installed('fCI')
```

---

|                            |                                      |
|----------------------------|--------------------------------------|
| multi dimensional.fci.data |                                      |
|                            | <i>data frame of gene expression</i> |

---

**Description**

This data set gives the gene expression values for 14204 genes and the control and case samples were generated at two time points (bivariate data).

**Usage**

```
fci.data
```

**Format**

a matrix containing 14204 genes and 8 samples.

**Value**

|           |                                   |
|-----------|-----------------------------------|
| dataframe | A data frame of expression values |
|-----------|-----------------------------------|

**Source**

[software.steenlab.org](http://software.steenlab.org)

**References**

<http://software.steenlab.org/fCI/>

---

|               |                                                             |
|---------------|-------------------------------------------------------------|
| normalization | <i>generic function to normalize gene expression matrix</i> |
|---------------|-------------------------------------------------------------|

---

**Description**

generic function to normalize gene expression matrix

**Usage**

```
normalization(.Object)
```

**Arguments**

|         |                                                   |
|---------|---------------------------------------------------|
| .Object | the predefined class object (i.e fCI=new("NPCI")) |
|---------|---------------------------------------------------|

**Details**

TBD

**Value**

NA                      No values will be returned

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
print("See README")
```

---

normalization-methods    *~~ Methods for Function normalization ~~*

---

**Description**

*~~ Methods for function normalization ~~*

**Methods:**

`signature(.Object = "NPCI")` the built-in method for fCI data normalization, by default, the data is normalized according to mean excluding the top 5 and bottom 5 percent.

---

 NPCI-class

 Class "NPCI"
 

---

## Description

The main Class that defines the slots values

## Objects from the Class

Objects can be created by calls of the form `new("NPCI", ...)`.

## Slots

```

sample.data.file: Object of class "character" ~~
distance.matrix: Object of class "matrix" ~~
sample.data.normalized: Object of class "data.frame" ~~
attr.info: Object of class "data.frame" ~~
null.data.start: Object of class "matrix" ~~
diff.data.start: Object of class "matrix" ~~
expr.by.fold: Object of class "matrix" ~~
fold.cutoff.list: Object of class "list" ~~
rank.index.to.be.removed: Object of class "list" ~~
diff.gene.ids: Object of class "list" ~~
wt.index: Object of class "numeric" ~~
df.index: Object of class "numeric" ~~
ctr.indexes: Object of class "numeric" ~~
trt.indexes: Object of class "numeric" ~~
method.option: Object of class "numeric" ~~
use.ratio: Object of class "logical" ~~
percent.genes.to.scan: Object of class "numeric" ~~
num.genes.to.skip.each: Object of class "numeric" ~~
use.fold.change: Object of class "logical" ~~
wt.comb: Object of class "list" ~~
df.comb: Object of class "list" ~~
diff.ids: Object of class "list" ~~
result: Object of class "numeric" ~~
indexes.reconsidered: Object of class "numeric" ~~
center.by.gaussian.kernel: Object of class "logical" ~~
symmetric.fold: Object of class "logical" ~~
pairwise.diff.gene.ids: Object of class "list" ~~

```

**Methods**

No methods defined with class "NPCI" in the signature.

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/NPCI/>

**See Also**

TBD

**Examples**

```
showClass("NPCI")
```

---

`npci.gene.by.pvalues` *find most significantly change fCI targets*

---

**Description**

identify the genes that change most significantly using inverse of log ratio the smaller the results, the more significant the changes.

**Usage**

```
npci.gene.by.pvalues(npci.data, gene.indexes, ctr.indexes, trt.indexes)
```

**Arguments**

|                           |                                                                                                                |
|---------------------------|----------------------------------------------------------------------------------------------------------------|
| <code>npci.data</code>    | a data frame containing non-zero numeric values (the data frame must contain more than one row and one column) |
| <code>gene.indexes</code> | the row ids of genes used for p-value calculation                                                              |
| <code>ctr.indexes</code>  | The wild type sample column indexes in the matrix, i.e. 1,2                                                    |
| <code>trt.indexes</code>  | The experimental sample column indexes in the matrix, i.e. 1,2                                                 |

**Details**

TBD

**Value**

pvalues            a vector of pvalues

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
npci.data=data.frame(matrix(sample(3:100, 100*4, replace=TRUE), 100,4))
gene.indexes=sample(1:97, 25)
ctr.indexes=c(1,2)
trt.indexes=c(3,4)
npci.gene.by.pvalues(npci.data, gene.indexes, ctr.indexes, trt.indexes)
```

---

`npci.index.reconsidered`

*find targets that have little evidence to be differentially expressed*

---

**Description**

the function will be depreciated

**Usage**

```
npci.index.reconsidered(npci.data, expr.by.fold, null.data.start, diff.data.start, gene.indexes, ctr.
```

**Arguments**

|                              |                                                                                                                |
|------------------------------|----------------------------------------------------------------------------------------------------------------|
| <code>npci.data</code>       | a data frame containing non-zero numeric values (the data frame must contain more than one row and one column) |
| <code>expr.by.fold</code>    | a 1xN matrix of case-control fold changes for every gene of the total N genes                                  |
| <code>null.data.start</code> | a Nx1 matrix of control-control fold changes                                                                   |
| <code>diff.data.start</code> | a Nx1 matrix of case-control fold changes                                                                      |
| <code>gene.indexes</code>    | the genes used for differential expression analysis.                                                           |
| <code>ctr.indexes</code>     | the control sample column indexes                                                                              |
| <code>trt.indexes</code>     | the case sample column indexes                                                                                 |
| <code>left.fold</code>       | the minimum fold changes for downregulation                                                                    |
| <code>right.fold</code>      | the minimum fold changes for upregulation                                                                      |

**Details**

TBD

**Value**

values                      genes wrongly considered as differentially expressed

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
data.file=data.frame(matrix(sample(3:100, 100*4, replace=TRUE), 100,4))
wt.index=c(1,2)
df.index=c(1,3)
npci=new("NPCI")
npci@wt.index=wt.index
npci@df.index=df.index
npci@sample.data.normalized=data.file
npci=initialize(npci)
```

```

npci=normalization(npci)
npci=populate(npci)
npci=compute(npci)
npci=summarize(npci)

npci.data=npci@sample.data.normalized
null.data.start=npci@null.data.start
diff.data.start=npci@diff.data.start
choice=2
rank.index.to.be.removed=npci@rank.index.to.be.removed
expr.by.fold=npci@expr.by.fold

ctr.indexes=1:2
trt.indexes=3:4
use.intersect=FALSE
symmetric.fold=TRUE
fold.cutoff.list=npci@fold.cutoff.list
gene.indexes=npci@diff.gene.ids
left.fold=2
right.fold=2

```

---

```
npci.index.to.be.removed
```

*gene indexes that will be considered as targets*

---

## Description

This function will be depreciated.

## Usage

```
npci.index.to.be.removed(expr.by.fold, d, symmetric.fold, max.rank,
  l.max.rank, r.max.rank)
```

## Arguments

|                             |                                                                                                              |
|-----------------------------|--------------------------------------------------------------------------------------------------------------|
| <code>expr.by.fold</code>   | a 1xN matrix of fold change between case and control for every genes in N genes                              |
| <code>d</code>              | the dimension of the data, if RNA-Seq or LC-MS/MS data, d=1                                                  |
| <code>symmetric.fold</code> | a boolean valuable indicating whether to use the same fold change cutoff for upregulation and downregulation |
| <code>max.rank</code>       | the maximum fold change, i.e 3 fold                                                                          |
| <code>l.max.rank</code>     | the maximum fold change for downregulation, i.e 1.5 fold                                                     |
| <code>r.max.rank</code>     | the maximum fold change for upregulation, i.e 1.5 fold                                                       |

**Details**

TBD

**Value**

indexes                      gene (indexes) considered as differentially expressed

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
print("Function to be discarded!")
```

---

|                                |                                                        |
|--------------------------------|--------------------------------------------------------|
| <code>npci.venn.diagram</code> | <i>generate venn diagram for multiple fCI analysis</i> |
|--------------------------------|--------------------------------------------------------|

---

**Description**

plot the overlap differentially expressed genes by pairwise fCI analysis

**Usage**

```
npci.venn.diagram(diff.gene.ids, i = 1, k = 1)
```

**Arguments**

`diff.gene.ids`    gene ids for genes that are differentially expressed  
`i`                      number of comparisons for fCI analysis, i.e 1 or 2  
`k`                      number of genes for fCI analysis

**Details**

TBD

**Value**

figure                      the venn diagram plot

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
targets.run1=c(2:10)
targets.run2=c(1:8)
targets.run3=c(6:12)
diff.gene.ids=list(targets.run1, targets.run2, targets.run3)
npci.venn.diagram(diff.gene.ids)
```

---

`pairwise.change.occupancy`

*find the targets whose fold changes occur consistently (upregulated or downregulated) in all fCI analysis*

---

**Description**

find the targets whose fold changes occur consistently (upregulated or downregulated) in all fCI analysis

**Usage**

```
pairwise.change.occupancy(common.ids, pairwise.index,
  pairwise.up.down, target.ratio)
```



---

|          |                                                                           |
|----------|---------------------------------------------------------------------------|
| populate | <i>generic function to populate the fCI object based on provided data</i> |
|----------|---------------------------------------------------------------------------|

---

**Description**

generic function to populate the fCI object based on provided data

**Usage**

```
populate(.Object)
```

**Arguments**

.Object

**Details**

TBD

**Value**

NA                      No values will be returned

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
print("See README")
```

---

populate-methods      *~~ Methods for Function populate ~~*

---

### Description

~~ Methods for function populate ~~

### Methods:

signature(.Object = "NPCI") after fCI object is initialized, popular the slot values for the object

---

report.target.summary    *generate the results (gene ids) in the data frame*

---

### Description

generate the results (gene ids) in the data frame

### Usage

```
report.target.summary(pairwise.diff.gene.ids)
```

### Arguments

pairwise.diff.gene.ids  
a list of the the differentially expression genes (its index) for each pairwise fCI analysis.

### Details

TBD

### Value

NA                      No values will be returned

### Note

TBD

### Author(s)

Shaojun Tang

### References

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
print("See README")
```

---

setfCI*the generic function 'setfCI' for s4 class*

---

**Description**

the generic function 'setfCI' for s4 class

**Usage**

```
setfCI(.Object, wt.index, df.index, fold.cutoff.list,  
      center.distribution)
```

**Arguments**

|                                  |                                                                                  |
|----------------------------------|----------------------------------------------------------------------------------|
| <code>.Object</code>             | the fCI object                                                                   |
| <code>wt.index</code>            | the control sample column ids, such as c(1,2)                                    |
| <code>df.index</code>            | the case sample column ids, such as c(1,2)                                       |
| <code>fold.cutoff.list</code>    | the predefined fold change cut-off such as list(seq(from=1.1, to=3.0, by=0.1))   |
| <code>center.distribution</code> | a boolean value showing that if the users want to center the distribution or not |

**Details**

TBD

**Value**

NA No values will be returned

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**<http://software.steenlab.org/fCI/>

See Also

TBD

Examples

```
fci=new("NPCI")
fci=setfCI(fci, 7:8, 11:12, seq(from=1.1,to=3,by=0.1), TRUE)
```

---

|                |                                          |
|----------------|------------------------------------------|
| setfCI-methods | <i>~~ Methods for Function setfCI ~~</i> |
|----------------|------------------------------------------|

---

Description

~~ Methods for function setfCI ~~

Methods:

```
signature(.Object = "NPCI")
```

---

|              |                                                                                |
|--------------|--------------------------------------------------------------------------------|
| show.targets | <i>display the gene ids that are identified to be differentially regulated</i> |
|--------------|--------------------------------------------------------------------------------|

---

Description

display the gene ids that are identified to be differentially regulated

Usage

```
show.targets(.Object)
```

Arguments

.Object            the class object, for example, fCI=new("NPCI")

Details

TBD

Value

NA                No values will be returned

Note

TBD

**Author(s)**

Shaojun Tang

**References**<http://software.steenlab.org/fCI/>**See Also**

TBD

**Examples**

```
print("See README")
```

---

```
show.targets-methods    ~~ Methods for Function show.targets ~~
```

---

**Description**

~~ Methods for function show.targets ~~

**Methods:**

signature(.Object = "NPCI") the built-in method to show the fCI final DEGs.

---

```
summarize                result summerization
```

---

**Description**

summerize the result after fCI computation is done

**Usage**

```
summarize(.Object)
```

**Arguments**`.Object` the class object, for exaple, `fci = new("NPCI")`**Details**

TBD

**Value**

NA                      No values will be returned

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
data.file=data.frame(matrix(sample(3:100, 100*4, replace=TRUE), 100,4))
wt.index=c(1,2)
df.index=c(1,3)
npci=new("NPCI")
npci@wt.index=wt.index
npci@df.index=df.index
npci@sample.data.normalized=data.file
npci=initialize(npci)
npci=normalization(npci)
npci=populate(npci)
npci=summarize(npci)
```

---

summarize-methods

*result summerization*

---

**Description**

summerize the result after fCI computation is done

**Methods:**

signature(.Object = "NPCI")

---

```
total.library.size.normalization
```

*normalize the gene expression based on the library size (summation)  
of the first sample replicate*

---

**Description**

normalize the gene expression based on the library size (summation) of the first sample replicate

**Usage**

```
total.library.size.normalization(sample.data)
```

**Arguments**

|             |                                                                                                |
|-------------|------------------------------------------------------------------------------------------------|
| sample.data | a data frame of gene expression (noen-zero) with columns being the sample and rows being genes |
|-------------|------------------------------------------------------------------------------------------------|

**Details**

TBD

**Value**

|           |                                                                        |
|-----------|------------------------------------------------------------------------|
| dataframe | a data frame where column values were normalized by total library size |
|-----------|------------------------------------------------------------------------|

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
sample.data=data.frame(matrix(sample(3:100, 100*4, replace=TRUE), 100,4))  
total.library.size.normalization(sample.data)
```

---

`trim.size.normalization`*normalize gene expression by excluding genes on the top 5 and bottom 5 percentage*

---

**Description**

normalize gene expression by excluding genes on the top 5 and bottom 5 percentage

**Usage**

```
trim.size.normalization(sample.data)
```

**Arguments**

|                          |                                                                                                |
|--------------------------|------------------------------------------------------------------------------------------------|
| <code>sample.data</code> | a data frame of gene expression (noen-zero) with columns being the sample and rows being genes |
|--------------------------|------------------------------------------------------------------------------------------------|

**Details**

TBD

**Value**

|                        |                                                                                                                   |
|------------------------|-------------------------------------------------------------------------------------------------------------------|
| <code>dataframe</code> | a data frame where column values were normalized by all genes except the top 5 percent and bottom 5 percent genes |
|------------------------|-------------------------------------------------------------------------------------------------------------------|

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
sample.data=data.frame(matrix(sample(3:100, 100*4, replace=TRUE), 100,4))
trim.size.normalization(sample.data)
```

---

`two.sample.log.ratio`    *compute the log ratios of two vectors*

---

**Description**

compute the log ratios of two vectors

**Usage**

```
two.sample.log.ratio(a, b)
```

**Arguments**

|                |                                                           |
|----------------|-----------------------------------------------------------|
| <code>a</code> | a vector of numeric values (value must be greater than 0) |
| <code>b</code> | a vector of numeric values (value must be greater than 0) |

**Details**

TBD

**Value**

|                     |                               |
|---------------------|-------------------------------|
| <code>ratios</code> | the log ratios of two vectors |
|---------------------|-------------------------------|

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
a=10  
b=2  
two.sample.log.ratio(a, b)
```

---

```
two.sample.permutation.test
```

*perform permutation test on two vectors*

---

**Description**

perform permutation test on two vectors

**Usage**

```
two.sample.permutation.test(a, b)
```

**Arguments**

|   |                                                           |
|---|-----------------------------------------------------------|
| a | a vector of numeric values (value must be greater than 0) |
| b | a vector of numeric values (value must be greater than 0) |

**Details**

TBD

**Value**

|        |                                |
|--------|--------------------------------|
| pvalue | the pvalue of permutation test |
|--------|--------------------------------|

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
two.sample.permutation.test(sample(1:100, 20), sample(5:104, 20))
```

---

|             |                                                                                                              |
|-------------|--------------------------------------------------------------------------------------------------------------|
| venndiagram | <i>generate a venn diagram to show the differentially expression summaries accross pairwise fCI analysis</i> |
|-------------|--------------------------------------------------------------------------------------------------------------|

---

**Description**

generate a venn diagram to show the differentially expression summaries accross pairwise fCI analysis

**Usage**

```
venndiagram(.Object)
```

**Arguments**

|         |                                        |
|---------|----------------------------------------|
| .Object | the class object, i.e, fci=new("NPCl") |
|---------|----------------------------------------|

**Details**

TBD

**Value**

|    |                            |
|----|----------------------------|
| NA | No values will be returned |
|----|----------------------------|

**Note**

TBD

**Author(s)**

Shaojun Tang

**References**

<http://software.steenlab.org/fCI/>

**See Also**

TBD

**Examples**

```
print("See README")
```

---

venndiagram-methods    *~~ Methods for Function venndiagram ~~*

---

**Description**

~~ Methods for function venndiagram ~~

**Methods:**

signature(.Object = "NPCI") generate the venn diagram to show the targets that shared among different fCI analysis

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