

# Package ‘fCI’

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**Type** Package

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

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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

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---

call.npci                    *the s4 class function*

---

### **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      *~~ Methods for Function call.npci ~~*

---

### Description

~~ Methods for function call.npci ~~

### Methods:

signature(.Object = "NPCI")

---

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

---

### 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  
*find targets that have a consistent fold change in the same direction  
(either up- or down-regulation)*

---

**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, npcI,
use.normalization = FALSE, target.ratio = 0.5)
```

### Arguments

- `wt.index.in.list` a list of numeric values representing the column indexes for control samples
- `df.index.in.list` a list of numeric values representing the column indexes for experimental samples
- `npci` the object `npci`
- `use.normalization` a boolean value indicating if the normalization will be applied or not
- `target.ratio` 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(npci.data)
```

**Arguments**

`npci.data` a data frame containing non-zero numeric values (the data frame must contain more than one row and one column)

**Details**

TBD

**Value**

`data.frame` 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

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

---

### 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,  
npci=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.steen.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      *identify differentially expressed genes*

---

**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
```

```
~~ Methods for Function find.fci.targets ~~
```

---

**Description**

```
~~ Methods for function find.fci ~~
```

**Methods:**

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

---

```
find.mid.point
```

```
find the middle value of the density distribution
```

---

**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)
```

---

*get.fold.large.step*    *generate fold change cutoff values for fCI divergence computation*

---

**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.re
```

**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**

folders                    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)
```

---

```
get.rna.fold.step      generate fCI fold-change cutoff values for typical RNA-Seq data
```

---

**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()
```

---

```
initialize-methods     ~~ Methods for Function initialize ~~
```

---

**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`     *find the common values of all vectors of a list*

---

**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**

`mypkg` a R library name, such as FNN

**Details**

TBD

**Value**

`installation` 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  
*data frame of gene expression*

---

**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.steen.org

**References**

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

---

normalization      *generic function to normalize gene expression matrix*

---

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

ctr.indexes=1:2
trt.indexes=3:4
use.intersect=FALSE
symmetric.fold=TRUE
fold.cutoff.list=npcci@fold.cutoff.list
gene.indexes=npcci@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

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

---

`npci.venn.diagram`        *generate venn diagram for multiple fCI analysis*

---

**Description**

plot the overlap differentially expressed genes by pairwise fCI analysis

**Usage**

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

**Arguments**

<code>diff.gene.ids</code>	gene ids for genes that are differentially expressed
<code>i</code>	number of comparisons for fCI analysis, i.e 1 or 2
<code>k</code>	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	<i>the generic function 'setfCI' for s4 class</i>
--------	---

---

**Description**

the generic function 'setfCI' for s4 class

**Usage**

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

**Arguments**

.Object	the fCI object
wt.index	the control sample column ids, such as c(1,2)
df.index	the case sample column ids, such as c(1,2)
fold.cutoff.list	the predefined fold change cut-off such as list(seq(from=1.1, to=3.0, by=0.1))
center.distribution	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      *~~ Methods for Function setfCI ~~*

---

**Description**

~~ Methods for function setfCI ~~

**Methods:**

signature(.Object = "NPCI")

---

show.targets      *display the gene ids that are identified to be differentially regulated*

---

**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	<i>result summerization</i>
-----------	-----------------------------

---

**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

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 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**

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**

ratios              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("NPC1")

**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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