

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.

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

Suggests knitr, rmarkdown, BiocStyle

VignetteBuilder knitr

NeedsCompilation no

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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

foldes 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!")
```

`is.installed` *package*

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 boolean 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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