Package ‘MineICA’

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Type Package
Title Analysis of an ICA decomposition obtained on genomics data
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Author Anne Biton
Maintainer Anne Biton <anne.biton@gmail.com>
Description The goal of MineICA is to perform Independent Component Analysis (ICA) on multiple transcriptome datasets, integrating additional data (e.g molecular, clinical and pathological). This Integrative ICA helps the biological interpretation of the components by studying their association with variables (e.g sample annotations) and gene sets, and enables the comparison of components from different datasets using correlation-based graph.
License GPL-2
LazyLoad yes
Depends R (>= 2.10), methods, BiocGenerics (>= 0.13.8), Biobase, plyr, ggplot2, scales, foreach, xtable, biomaRt, gtools, GOstats, cluster, marray, mclust, RColorBrewer, colorspace, igraph, Rgraphviz, graph, annotate, Hmisc, fastICA, JADE
Imports AnnotationDbi, lumi, fpc, lumiHumanAll.db
Suggests biomaRt, GOstats, cluster, hgu133a.db, mclust, igraph, breastCancerMAINZ, breastCancerTRANSBIG, breastCancerUPP, breastCancerVDX, future, future.apply
Enhances doMC
Collate 'AllClasses.R' 'AllGeneric.R' 'methods-IcaSet.R'
    'methods-MineICAParams.R' 'compareAnalysis.R'
    'functions_comp2annot.R' 'functions_comp2annotests.R'
    'functions_enrich.R' 'functions.R' 'heatmap.plus.R'
    'heatmapsOnSel.R' 'runAn.R' 'compareGenes.R'
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R topics documented:

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```
Retrieve and set Source S and Mixing matrix A from IcaSet

These generic functions access and set the attributes S, SByGene and A stored in an object of class IcaSet.
**Usage**

```
S(object)
S(object) <- value
SByGene(object)
SByGene(object) <- value
A(object)
A(object) <- value
nbComp(object)
```

**Arguments**

- **object**: object of class `IcaSet`
- **value**: Data.frame with rows representing: features (for `S`), genes (for `SByGene`), or samples (for `A`) and columns representing components.

**Value**

`S` returns a data.frame containing feature projection values; `SByGene` returns a data.frame containing gene projection values; `A` returns a data.frame containing sample contribution values. `nbComp` returns the number of components, i.e. the number of columns of `A`.

**Author(s)**

Anne Biton

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### addGenesToGoReport

*Add Symbol IDs to hyperGTest results*

**Description**

Add gene Symbols contained in gene sets selected as significant by `hyperGTest` function

**Usage**

```
addGenesToGoReport(hgOver, universe, 
                   db = c("GO", "KEGG"), onto = c("CC", "MF", "BP"),
                   annotation = NULL, entrez2symbol = NULL)
```

**Arguments**

- **hgOver**: Output of function `hyperGTest`
- **universe**: A vector including all IDs on which enrichment analysis was applied
- **db**: The database to use, default is `c("GO","KEGG")`
- **onto**: A string specifying the GO ontology to use. Must be one of "BP", "CC", or "MF", see `GOHyperGParams`. Only used when argument `db` is "GO".
- **annotation**: An annotation package
- **entrez2symbol**: A vector indexed by Entrez Gene ID and filled with the corresponding Gene Symbols
Details

This function takes as inputs the outputs of `hyperGTest` which takes Entrez Gene IDs as inputs to perform the enrichment analysis. The goal of this function is to select the Entrez Gene IDs responsible for the significant enrichment of a given gene set and annotate them into gene Symbol IDs. When the annotation package `annotation` was used to map feature IDs to Entrez Gene ID, it can also be used here to map Entrez and Symbol IDs. If the annotation package was not used, but the Entrez Gene IDs were directly provided to the `hyperGtest` function, `annotation` is expected to be NULL and `entrez2symbol` must be specified.

This function returns the outputs of function `hyperGTest` which contain:

- **DB, ID, Term**: The database, the gene set ID, and the gene Set name,
- **P-value**: probability of observing the number of genes annotated for the gene set among the selected gene list, knowing the total number of annotated genes among the universe,
- **Expected counts**: expected number of genes in the selected gene list to be found at each tested category term/gene set,
- **Odds ratio**: odds ratio for each category term tested which is an indicator of the level of enrichment of genes within the list as against the universe,
- **Counts**: number of genes in the selected gene list which are annotated for the gene set,
- **Size**: number of genes from the universe annotated for the gene set.

Value

A data.frame containing the summary of the output of function `hyperGTest (summary(hgOver))` with an additional column providing the gene Symbols included in the significant gene sets.

Author(s)

Anne Biton

See Also

`hyperGTest`, `GOHyperGParams`
Arguments
object Object of class IcaSet.

Value
A list returns a list whose length equals the number of components contained in the IcaSet object. Each element of this list contains a vector of sample contributions indexed by the sample IDs.

Author(s)
Anne Biton

See Also
class-IcaSet

Description
Given a data.frame consisting of sample annotations, this function returns a vector which gives a colour per annotation level.

Usage
annot2Color(annot)

Arguments
annot a data.frame containing the sample annotations (of dimension ‘samples x annotations’).

Details
Arbitrary colours are attributed to some specific annotations met by the author, and for the remaining annotation levels, the colours are attributed using packages RColorBrewer and rcolorspace.

Value
A vector of colours indexed by the annotation levels.

Author(s)
Anne Biton
annotCarbayo

Carbayo annotation data

Description
Contains annotations for 93 samples of Carbayo data.

Author(s)
Anne Biton

References
http://jco.ascopubs.org/content/24/5/778/suppl/DC1

annotFeatures
Annotation of features using an annotation package

Description
This function annotates a set of features

Usage
annotFeatures(features, type, annotation)

Arguments

features Feature IDs to be annotated
type The object from the package used to annotate the features, must be available in
ls("package:package_name")
annotation An annotation package

Value
A vector of gene/object IDs indexed by the feature IDs.

Author(s)
Anne Biton

Examples
library(hgu133a.db)
annotFeatures(features = c("1007_s_at", "1053_at", "117_at", "121_at", "1255_g_at"),
type="SYMBOL", annotation="hgu133a.db")
This function annotates the features of an object of class IcaSet, and fills its attributes SByGene and datByGene.

**Usage**

```r
annotFeaturesComp(icaSet, params, 
    type = toupper(typeID(icaSet)["geneID_annotation"]),
    featureId = typeID(icaSet)["featureID_biomart"],
    geneId = typeID(icaSet)["geneID_biomart"])
```

**Arguments**

- `icaSet` An object of class IcaSet whose features have to be annotated. The attribute `annotation` of this object contains the annotation package to be used.
- `params` An object of class MineICAParams containing the parameters of the analysis.
- `type` The ID of the object of the annotation package to be used for the annotation, must be available in `ls("package:package_name")`.
- `featureId` The type of the feature IDs, in the biomaRt way (type `listFilters(mart)` to choose one). Used when `annotation(icaSet)` is of length 0.
- `geneId` The type of the gene IDs, in the biomaRt way (type `listAttributes(mart)` to choose one). Used when `annotation(icaSet)` is of length 0.

**Details**

This function is called by function `annotInGene` which will check the validity of the attributes `annotation`, `typeID`, `chipManu` and eventually `chipVersion` of icaSet. If available, the attribute `annotation` of argument icaSet must be an annotation package and will be used to annotate the `featureNames` of icaSet. If attribute `annotation` of argument icaSet is not available (of length 0), biomaRt is used to annotate the features.

This function fills the attributes SByGene and datByGene of the argument icaSet. When several feature IDs are available for a same gene ID, the median value of the corresponding features IDs is attributed to the gene (the median of projection values is used for attribute SByGene, and the median of expression values is used for attribute datByGene).

When attribute `chipManu` of the argument icaSet is "illumina", the features are first converted into nuID using the package `lumi*Mapping` and then annotated into genes. In that case, features can only be annotated in ENTREZID or SYMBOL. It means that `typeID(icaSet)["geneID_annotation"]` must be either 'ENTREZID' or 'SYMBOL'. You will need to annotate yourself the IcaSet object if you want to use different IDs.
**Value**

This function returns the argument icaSet with attributes SByGene and datByGene filled.

**Author(s)**

Anne Biton

**See Also**

annotFeatures, annotFeaturesWithBiomaRt, annotInGene

**Examples**

```r
## load an example of IcaSet
data(icaSetCarbayo)
params <- buildMineICAParams()
require(hgu133a.db)

####===================================================
## Use of annotation package contained in annotation(icaSet)
####====================================================
## annotation in SYMBOL
icaSetCarbayo_annot <- annotFeaturesComp(icaSet=icaSetCarbayo, params=params, type="SYMBOL")
# arg 'type' is optional since the function uses contents of typeID(icaSet) as the defaults,
# it is specified in these examples for pedagogy views

## annotation in Entrez Gene
icaSetCarbayo_annot <- annotFeaturesComp(icaSet=icaSetCarbayo, params=params, type="ENTREZID")

## Not run:
####===================================================
## Use of biomaRt, when annotation(icaSet) is of length 0
####====================================================
## empty attribute 'annotation' of the IcaSet object
# when this attribute is not specified, biomaRt is used for annotation
annotation(icaSetCarbayo) <- character()

# make sure the mart attribute is correctly defined
mart(icaSetCarbayo) <- useMart(biomart="ensembl", dataset="hsapiens_gene_ensembl")

## make sure elements "featureID_biomaRt" and "geneID_biomaRt" of typeID(icaSet) are correctly filled
# they will be used by function 'annotFeaturesComp' through biomaRt to query the database
typeID(icaSetCarbayo)

## run annotation of HG-U133A probe set IDs into Gene Symbols using biomaRt
icaSetCarbayo_annot <- annotFeaturesComp(icaSet=icaSetCarbayo, params=params)

## End(Not run)
```
annotFeaturesWithBiomaRt

Annotation of features using biomaRt

Description

This function annotates a set of features using biomaRt

Usage

annotFeaturesWithBiomaRt(features, featureId, geneId, mart = useMart(biomart = "ensembl", dataset = "hsapiens_gene_ensembl"))

Arguments

- **features**: Feature IDs to be annotated
- **featureId**: The type of the feature IDs, in the biomaRt way (type `listFilters(mart)` to choose one)
- **geneId**: The type of the gene IDs, in the biomaRt way (type `listAttributes(mart)` to choose one)
- **mart**: The mart object (database and dataset) used for annotation, see function `useMart` of package biomaRt

Value

A vector of gene IDs indexed by the feature IDs.

Author(s)

Anne Biton

Examples

```r
if (interactive()) {
  # define the database to be queried by biomaRt
  mart <- useMart(biomart = "ensembl", dataset = "hsapiens_gene_ensembl")

  # annotate a set of HG-U133a probe sets IDs into Gene Symbols
  annotFeaturesWithBiomaRt(features = c("1007_s_at", "1053_at", "117_at", "121_at", "1255_g_at"), featureId = "affy_hg_u133a", geneId = "hgnc_symbol", mart = mart)

  # annotate a set of Ensembl Gene IDs into Gene Symbols
  annotFeaturesWithBiomaRt(features = c("ENSG00000101412", "ENSG00000112242", "ENSG00000148773", "ENSG00000131747", "ENSG00000170312", "ENSG0000017399"), featureId = "ensembl_gene_id", geneId = "hgnc_symbol", mart = mart)
}
```
annotInGene

Features annotation of an object of class IcaSet.

Description
This function annotates the features of an IcaSet object and fills its attributes SByGene and datByGene.

Usage
annotInGene(icaSet, params, annot = TRUE)

Arguments
icaSet An object of class IcaSet to be annotated, must contain a valid annotation attribute.
params An object of class MineICAParams containing the parameters of the analysis.
annot TRUE (default) if the IcaSet object must indeed be annotated

Details
When attribute annotation of icaSet is not specified (of length 0), biomaRt is used to annotate the features through function annotFeaturesWithBiomaRt.
When specified, attribute annotation of argument icaSet must be an annotation package and will be used to annotate the featureNames of icaSet. In addition, the attribute typeID (a vector) of argument icaSet must contain a valid element geneID_annotation that determines the object of the package to be used for the annotation, see IcaSet.
When argument annot is TRUE, this function fills the attributes SByGene and datByGene of icaSet. When several feature IDs are available for a same gene ID, the median value of the corresponding features IDs is attributed to the gene (the median of the projection values is used for attribute SByGene, and the median of the expression values is used for attribute datByGene).
When attribute chipManu of the argument icaSet is "illumina", the features are first converted into nuID using the package 'lumi*Mapping' and then annotated into genes. In that case, features can only be annotated in ENTREZID or SYMBOL. It means that typeID(icaSet)["geneID_annotation"] must be either 'ENTREZID' or 'SYMBOL'. You will need to annotate yourself the IcaSet object if you want to use different IDs.

Value
The modified argument icaSet, with filled attributes SByGene and datByGene.

Author(s)
Anne Biton

See Also
annotFeaturesComp
Examples

```r
# load data
data(icaSetCarbayo)
require(hgu133a.db)

# run annotation of the features into gene Symbols as specified in 'typeID(icaSetCarbayo)["geneID_annotation"]', # using package hgu133a.db as defined in 'annotation(icaSetMainz)'
icaSetCarbayo <- annotInGene(icaSet=icaSetCarbayo, params=buildMineICAParams())

## Not run:
# load data
library(breastCancerMAINZ)
data(mainz)
# run ICA
resJade <- runICA(X=exprs(mainz), nbComp=5, method = "JADE", maxit=10000)

# build params
params <- buildMineICAParams(resPath="mainz/")

# build a new IcaSet object, omitting annotation of the features (runAnnot=FALSE) # but specifying the element "geneID_annotation" of argument 'typeID'
icaSetMainz <- buildIcaSet(params=params, A=data.frame(resJade$A), S=data.frame(resJade$S),
  dat=exprs(mainz), pData=pData(mainz),
  annotation="hgu133a.db", typeID= c(geneID_annotation = "SYMBOL",
  geneID_biomart = "hgnc_symbol", featureID_biomart = "affy_hg_u133a"),
  chipManu = "affymetrix", runAnnot=FALSE,
  mart=useMart(biomart="ensembl", dataset="hsapiens_gene_ensembl"))

# Attributes SByGene is empty and attribute datByGene refers to assayData
SByGene(icaSetMainz)
head(datByGene(icaSetMainz))

# run annotation of the features into gene Symbols as specified in 'typeID(icaSetMainz)["geneID_annotation"]', # using package hgu133a.db as defined in 'annotation(icaSetMainz)'
icaSetMainz <- annotInGene(icaSet=icaSetMainz, params=params)

## End(Not run)
```

annotReciprocal

Description

This function notes edges of a graph as reciprocal or not.

Usage

```r
annotReciprocal(dataGraph, file,
  keepOnlyReciprocal = FALSE)
```
**Arguments**

- **dataGraph**: data.frame which contains the graph description, must have two columns `n1` and `n2` filled with node IDs, each row denoting there is an edge from `n1` to `n2`.
- **file**: file where the graph description is written
- **keepOnlyReciprocal**: if TRUE, `dataGraph` is restricted to reciprocal edges, else all edges are kept (default).

**Value**

This function returns the argument `dataGraph` with an additional column named 'reciprocal' which contains TRUE if the edge described by the row is reciprocal, and FALSE if it is not reciprocal.

**Author(s)**

Anne Biton

**Examples**

annotReciprocal(dataGraph = dg)

---

**buildIcaSet**

This function builds an object of class `IcaSet`.

**Description**

This function builds an object of class `IcaSet`.

**Usage**

```r
buildIcaSet(params, A, S, dat, pData = new("data.frame"),
            fData = new("data.frame"), witGenes = new("character"),
            compNames = new("character"),
            refSamples = new("character"),
            annotation = new("character"),
            chipManu = new("character"),
            chipVersion = new("character"), alreadyAnnot = FALSE,
            typeID = c(geneID_annotation = "SYMBOL", geneID_biomart = "hgnc_symbol", featureID_biomart = ""),
            runAnnot = TRUE, organism = "Human",
            mart = new("Mart"))
```
Arguments

params
An object of class MineICAParams containing the parameters of the analysis

A
The mixing matrix of the ICA decomposition (of dimension samples x components).

S
The source matrix of the ICA decomposition (of dimension features x components).

dat
The data matrix the ICA was applied to (of dimension features x samples).

pData
Phenotype data, a data.frame which contains the sample informations of dimension samples x annotations.

fData
Feature data, a data.frame which contains the feature descriptions of dimensions features x annotations.

witGenes
A vector of witness genes. They are representative of the expression behavior of the contributing genes of each component. If missing or NULL, they will be automatically attributed using function selectWitnessGenes.

compNames
A vector of component labels.

refSamples
A vector of reference sample IDs (e.g. the "normal" samples).

annotation
An annotation package (e.g. a "db" package specific to the microarray used to generate dat).

chipManu
If microarray data, the manufacturer: either 'affymetrix' or 'illumina'.

chipVersion
For illumina microarrays: the version of the microarray.

alreadyAnnot
TRUE if the feature IDs contained in the row names of dat and S already correspond to the final level of annotation (e.g. if they are already gene IDs). In that case, no annotation is performed.

typeID
A character vector specifying the annotation IDs, it includes three elements:

  geneID_annotation the IDs from the package to be used to annotate the features into genes. It will be used to fill the attributes datByGene and SByGene of the IcaSet. It must match one of the objects the corresponding package supports (you can access the list of objects by typing ls("package:packagename")). If no annotation package is provided, this element is not useful.

  geneID_biomart the type of gene IDs, as available in listFilters(mart); where mart is specified as described in useMart. If you have directly built the IcaSet at the gene level (i.e. if no annotation package is used), featureID_biomart and geneID_biomart will be identical.

  featureID_biomart the type of feature IDs, as available in listFilters(mart); where mart is specified as described in function useMart. Not useful if you work at the gene level.

runAnnot
If TRUE, IcaSet is annotated with function annotInGene.

organism
The organism the data correspond to.

mart
The mart object (database and dataset) used for annotation, see function useMart of package biomaRt

Value

An object of class IcaSet
Author(s)
Anne Biton

See Also
selectWitnessGenes, annotInGene

Examples

dat <- data.frame(matrix(rnorm(10000), ncol=10, nrow=1000))
rownames(dat) <- paste("g", 1:1000, sep="")
colnames(dat) <- paste("s", 1:10, sep="")

## build a data.frame containing sample annotations
annot <- data.frame(type=c(rep("a",5), rep("b",5)))
rownames(annot) <- colnames(dat)

## run ICA
resJade <- runICA(X=dat, nbComp=3, method = "JADE")

## build params
params <- buildMineICAParams(resPath="toy/"

## build IcaSet object
icaSettoy <- buildIcaSet(params=params, A=data.frame(resJade$A), S=data.frame(resJade$S),
            dat=dat, pData=annot, alreadyAnnot=TRUE)
params <- icaSettoy$params
icaSettoy <- icaSettoy$icaSet

## Not run:
## load data
library(breastCancerMAINZ)
data(mainz)

## run ICA
resJade <- runICA(X=dataMainz, nbComp=10, method = "JADE", maxit=10000)

## build params
params <- buildMineICAParams(resPath="mainz/"

## build IcaSet object
# fill typeID, Mainz data originate from affymetrix HG-U133a microarray and are indexed by probe sets
# we want to annotate the probe sets into Gene Symbols
typeIDmainz <- c(geneID_annotation="SYMBOL", geneID_biomart="hgnc_symbol", featureID_biomart="affy_hg_u133a")
icaSetMainz <- buildIcaSet(params=params, A=data.frame(resJade$A), S=data.frame(resJade$S),
            dat=exprs(mainz), pData=pData(mainz),
            annotation="hgu133a.db", typeID= c(geneID_annotation = "SYMBOL", geneID_biomart = "hgnc_symbol", featureID_biomart = "affy_hg_u133a"),
            chipManu = "affymetrix", runAnnot=TRUE,
            mart=useMart(biomart="ensembl", dataset="hsapiens_gene_ensembl"))
buildMineICAParams

## End(Not run)

buildMineICAParams  *Creates an object of class MineICAParams*

### Description

This function builds an object of class *MineICAParams*. It contains the parameters that will be used by function *runAn* to analyze the ICA decomposition contained in an object of class *IcaSet*.

### Usage

```r
buildMineICAParams(Sfile = new("character"),
                    Afile = new("character"), datfile = new("character"),
                    annotfile = new("character"), resPath = ",
                    genesPath, annot2col = new("character"), pvalCutoff = 0.05,
                    selCutoff = 3)
```

### Arguments

- **Sfile**: A txt file containing the Source matrix S.
- **Afile**: A txt file containing the Mixing matrix A.
- **datfile**: A txt file containing the data (e.g expression data) on which the decomposition was calculated.
- **annotfile**: Either a "rda" or "txt" file containing the annotation data for the samples (must be of dimensions samples x annotations).
- **resPath**: The path where the outputs of the analysis will be written, default is the current directory.
- **genesPath**: The path _within_ the resPath where the gene projections will be written. If missing, will be automatically attributed as resPath/ProjByComp/.
- **annot2col**: A vector of colors indexed by annotation levels. If missing, will be automatically attributed using function annot2Color.
- **pvalCutoff**: The cutoff used to consider a p-value significant, default is 0.05.
- **selCutoff**: The cutoff applied to the absolute feature/gene projection values to consider them as contributors, default is 3. Must be either of length 1 and the same threshold is applied to all components, or of length equal to the number of components in order to a specific threshold is for each component.

### Value

An object of class *MineICAParams*

### Author(s)

Anne Biton
**build_sortHeatmap**

**Description**

This function returns the matrices that will be used to plot the heatmaps of each component. It restricts the data matrix of the `icaSet` object to the contributing genes/features, and order the features GENES and samples.

**Usage**

```r
build_sortHeatmap(icaSet, selCutoff, selectionByComp, level = c("features", "genes"), samplesOrder, featuresOrder)
```

**Arguments**

- `icaSet` The IcaSet object
- `selCutoff` The threshold used to select the contributing features/genes based on their projection values. Must be either of length 1 and the same threshold is applied to all components, or of length equal to the number of components and one specific threshold is used for each component.
- `selectionByComp` The list of gene projections per components already restricted to the contributing genes
- `level` A character indicating which data level is used to plot the heatmaps: 'features' to plot measured feature levels (e.g. probe sets expression values), 'genes' to plot measured gene values (e.g. gene expression values).
- `samplesOrder` A list providing the order of the samples, per component, to be used in the heatmaps. If NULL, the contribution values of the samples are used to rank the columns of the heatmaps.
- `featuresOrder` A list providing the features or genes order, per component, to be used in the heatmaps. If NULL, the projection values of the genes are used to rank the rows of the heatmaps.

**Examples**

```r
## define default parameters and fill resPath
params <- buildMineICAParams(resPath="resMineICACarbayo/"

## change the default cutoff for selection of contribugint genes/features
params <- buildMineICAParams(resPath="resMineICACarbayo/", selCutoff=4)
```
clusterFastICARuns

**Details**

This function is called by function `plot_heatmapsOnSel` and is not likely to be called alone.

**Value**

A list of matrices

**Author(s)**

Anne Biton

---

**clusterFastICARuns**  
*Run of fastICA and JADE algorithms*

**Description**

This function runs the fastICA algorithm several times with random initializations. The obtained components are clustered and the medoids of these clusters are used as the final estimates. The returned estimates are ordered by decreasing Iq values which measure the compactness of the clusters (see details).

**Usage**

```r
clusterFastICARuns(X, nbComp, nbIt = 100,
                    alg.type = c("deflation", "parallel"),
                    fun = c("logcosh", "exp"), maxit = 500, tol = 10^-6,
                    funClus = c("hclust", "agnes", "pam", "kmeans"),
                    row.norm = FALSE, bootstrap = FALSE, ...)
```

**Arguments**

- `X`  
  A data matrix with `n` rows representing observations (e.g genes) and `p` columns representing variables (e.g samples).
- `nbComp`  
  The number of components to be extracted.
- `nbIt`  
  The number of iterations of FastICA.
- `alg.type`  
  If `alg.type="parallel"` the components are extracted simultaneously (the default), if `alg.type="deflation"` the components are extracted one at a time, see `fastICA`.
- `fun`  
  The functional form of the G function used in the approximation to neg-entropy (see 'details' of the help of function `fastICA`).
- `row.norm`  
  a logical value indicating whether rows of the data matrix `X` should be standardized beforehand (see help of function `fastICA`)
- `maxit`  
  The maximum number of iterations to perform.
- `tol`  
  A positive scalar giving the tolerance at which the un-mixing matrix is considered to have converged.
funClus The clustering function to be used to cluster the estimates
bootstrap if TRUE the data is bootstraped before each fastICA iteration, else (default) only random initializations are done
... Additional parameters for codefunClus

Details

This function implements in R fastICA iterations followed by a clustering step, as defined in the matlab package ‘icasso’. Among the indices computed by icasso, only the Iq index is currently computed. As defined in 'icasso', the Iq index measures the difference between the intra-cluster similarity and the extra-cluster similarity. No visualization of the clusters is yet available.

If bootstrap=TRUE a bootstrap (applied to the observations) is used to perturb the data before each iteration, then function fastICA is applied with random initializations.

By default, in 'icasso', agglomerative hierarchical clustering with average linkage is performed. To use the same clustering, please use funClus="hclust" and method="average". But this function also allows you to apply the clustering of your choice among kmeans, pam, hclust, agnes by specifying funClus and adding the adequate additional parameters.

See details of the functions fastICA.

Value

A list consisting of:

A  the estimated mixing matrix
S  the estimated source matrix, itemWthe estimated unmixing matrix,
Iq  Iq indices.

Author(s)

Anne Biton

Examples

## generate a data
set.seed(2004);
M <- matrix(rnorm(5000*6,sd=0.3),ncol=10)
M[1:100,1:3] <- M[1:100,1:3] + 2

## Random initializations are used for each iteration of FastICA
## Estimates are clustered using hierarchical clustering with average linkage
res <- clusterFastICARuns(X=M, nbComp=2, alg.type="deflation",
                        nbIt=3, funClus="hclust", method="average")

## Data are boostraped before each iteration and random initializations
## are used for each iteration of FastICA
## Estimates are clustered using hierarchical clustering with ward
res <- clusterFastICARuns(X=M, nbComp=2, alg.type="deflation",
                        nbIt=3, funClus="hclust", method="ward")
clusterSamplesByComp  
Cluster samples from an IcaSet

Description
This function allows to cluster samples according to the results of an ICA decomposition. One clustering is run independently for each component.

Usage

clusterSamplesByComp(icaSet, params, 
  funClus = c("Mclust", "kmeans", "pam", "pamk", "hclust", "agnes"), 
  filename, clusterOn = c("A", "S"), 
  level = c("genes", "features"), nbClus, 
  metric = "euclidean", method = "ward", ...)

Arguments
icaSet   An IcaSet object
params   A MineICAParams object
funClus  The function to be used for clustering, must be one of c("Mclust", "kmeans", "pam", "pamk", "hclust", "agnes")
filename A file name to write the results of the clustering in
clusterOn Specifies the matrix used to apply clustering:
  "A": the clustering is performed in one dimension, on the vector of sample contributions,
  "S": the clustering is performed on the original data restricted to the contributing individuals.
level    The level of projections to be used when clusterOn="S", either "features" or "genes".
nbClus   The number of clusters to be computed, either a single number or a numeric vector whose length equals the number of components. If missing (only allowed if funClus is one of c("Mclust", "pamk"))
metric   Metric used in pam and hclust, default is "euclidean"
method   Method of hierarchical clustering, used in hclust and agnes
...      Additional parameters required by the clustering function funClus

Value
A list consisting of three elements
clus:  a list specifying the sample clustering for each component,
resClus: the complete output of the clustering function,
funClus: the function used to perform the clustering.

When clusterOn="S", if some components were not used because no contributing elements is selected using the cutoff, the icaSet with the corresponding component deleted is also returned.
Author(s)
Anne Biton

See Also
Mclust, kmeans, pam, pamk, hclust, agnes, cutree

Examples

data(icaSetCarbayo)
params <- buildMineICAParams(resPath="carbayo/", selCutoff=4)

## cluster samples according to their contributions
# using Mclust without a number of clusters
res <- clusterSamplesByComp(icaSet=icaSetCarbayo, params=params, funClus="Mclust",
clusterOn="A", filename="clusA")

# using kmeans
res <- clusterSamplesByComp(icaSet=icaSetCarbayo, params=params, funClus="kmeans",
clusterOn="A", nbClus=2, filename="clusA")

classicClusterSamplesByComp <- function(icaSet, params,...) {
  ...}

clusterSamplesByComp_multiple

Cluster samples from an IcaSet

Description
This function allows to cluster samples according to the results of an ICA decomposition. Several clustering functions and several levels of data for clustering can be performed by the function.

Usage
clusterSamplesByComp_multiple(icaSet, params,
funClus = c("Mclust", "kmeans", "pam", "pamk", "hclust", "agnes"),
filename, clusterOn = c("A", "S"),
level = c("genes", "features"), nbClus, metric = "euclidean", method = "ward", ...)

Arguments
icaSet An IcaSet object
params A MineICAParams object
funClus The function to be used for clustering, must be several of c("Mclust","kmeans","pam","pamk","hclust","agnes")
filename A file name to write the results of the clustering in
clusterOn Specifies the matrix used to apply clustering, can be several of:
"A": the clustering is performed in one dimension, on the vector of sample contributions,
"S": the clustering is performed on the original data restricted to the contributing individuals.

level The level of projections to be used when clusterOn="S", either "features" or "genes".

nbClus The number of clusters to be computed, either a single number or a numeric vector whose length equals the number of components. If missing (only allowed if funClus is one of c("Mclust", "pamk"))

metric Metric used in pam and hclust, default is "euclidean"

method Method of hierarchical clustering, used in hclust and agnes

... Additional parameters required by the clustering function funClus.

Details

One clustering is run independently for each component.

Value

A list consisting of three elements

clus: a data.frame specifying the sample clustering for each component using the different ways of clustering,
resClus: the complete output of the clustering function(s),
comparClus: the adjusted Rand indices, used to compare the clusterings obtained for a same component.

Author(s)

Anne

See Also

Mclust, adjustedRandIndex, kmeans, pam, pamk, hclust, agnes, cutree

Examples

data(icaSetCarbayo)
params <- buildMineICAParams(resPath="carbayo/", selCutoff=3)

## compare kmeans clustering applied to A and data restricted to the contributing genes
## on components 1 to 3
res <- clusterSamplesByComp_multiple(icaSet=icaSetCarbayo[,1:3], params=params, funClus="kmeans",
                                   nbClus=2, clusterOn=c("A","S"), level="features")
head(res$clus)
clusVarAnalysis

Tests association between clusters of samples and variables

Description

From a clustering of samples performed according to their contribution to each component, this function computes the chi-squared test of association between each variable level and the cluster, and summarizes the results in an HTML file.

Usage

clusVarAnalysis(icaSet, params, resClus, keepVar, keepComp, funClus = "", adjustBy = c("none", "component", "variable"), method = "BH", doPlot = FALSE, cutoff = params["pvalCutoff"], path = paste(resPath(params), "clus2var/", sep = ""), onlySign = TRUE, typeImage = "png", testBy = c("variable", "level"), filename)

Arguments

icaSet An object of class IcaSet
params An object of class MineICAParams providing the parameters of the analysis
resClus A list of numeric vectors indexed by sample IDs, which specifies the sample clusters. There must be one clustering by component of icaSet. The names of the list must correspond to the component indices.
keepVar The variable labels to be considered, i.e a subset of the variables of icaSet available in varLabels(icaSet).
keepComp A subset of components available in indComp(icaSet) to be considered, if missing all components are used.
funClus The name of the function used to perform the clustering (just for text in written files).
adjustBy The way the p-values of the Wilcoxon and Kruskal-Wallis tests should be corrected for multiple testing: "none" if no p-value correction has to be done, "component" if the p-values have to be corrected by component, "variable" if the p-values have to be corrected by variable.
testBy Chi-square tests of association can be performed either by "variable" (one test by variable, default) or by variable "level" (as many tests as there are annotation levels).
method The correction method, see p.adjust for details, default if "BH" for Benjamini & Hochberg.
doPlot If TRUE, the barplots showing the distribution of the annotation levels among the clusters are plotted and the results are provided in an HTML file 'cluster2annot.htm', else no plot is created.
clusVarAnalysis

cutoff
The threshold for statistical significance.
filename
File name for test results, if doPlot=TRUE will be an HTML file else will be a 'txt' file. If missing when doPlot=TRUE, will be "clusVar".
path
A directory within resPath(params) where the outputs are saved if doPlot=TRUE, default is 'cluster2annot/'.
onlySign
If TRUE (default), only the significant results are plotted.
typeImage
The type of image file where each plot is saved.

Details
When doPlot=TRUE, this function writes an HTML file containing the results of the tests as a table of dimension 'variable levels x components' which contains the p-values of the tests. When a p-value is considered as significant according to the threshold cutoff, it is written in bold and filled with a link pointing to the corresponding barplot displaying the distribution of the clusters across the levels of the variables.

One image is created by plot and located into the sub-directory "plots/" of path. Each image is named by index-of-component_var.png

Value
This function returns a list whose each element gives, for each component, the results of the association chi-squared tests between the clusters and the annotation levels.

Author(s)
Anne Biton

See Also
clusterSamplesByComp

Examples
```r
## load an example of IcaSet
data(icaSetCarbayo)
## build object of class MineICAParams
params <- buildMineICAParams(resPath="carbayo/")

## cluster samples according to the columns of the mixing matrix A with kmeans in 2 groups
resClus <- clusterSamplesByComp(icaSet=icaSetCarbayo, params=params, funClus="kmeans", clusterOn="A", nbClus=2)$clus

## specify directory for the function outputs (here same directory as the default one)
## this directory will be created by the function in resPath(params)
dir <- "clus2var/"

## compute chi-square tests of association, p-value are not adjusted (adjustBy="none"), # test results are written in txt format (doPlot=FALSE and filename not missing)
resChi <- clusVarAnalysis(icaSet=icaSetCarbayo, params=params, resClus=resClus, funClus="kmeans", dir=dir)
```
## Not run:
## compute chi-square tests of association, p-value are not adjusted (adjustBy="none"),
# write results and plots in HTML files (doPlot=TRUE)
resChi <- clusVarAnalysis(icaSet=icaSetCarbayo, params=params, resClus=resClus, funClus="kmeans",
        path=dir, adjustBy="none", doPlot=TRUE, filename="clusVarTests")

## compute chi-square tests of association by only considering a subset of components and variables,
# adjust p-values by component (adjustBy="component"),
# do not write results (doPlot=FALSE and filename is missing).
resChi <- clusVarAnalysis(icaSet=icaSetCarbayo, params=params, resClus=resClus, keepComp=1:10,
        keepVar=c("GENDER","STAGE"), funClus="kmeans", adjustBy="none",
        doPlot=FALSE)

## End(Not run)

**compareAn**

Comparison of IcaSet objects using correlation

### Description

Compare **IcaSet** objects by computing the correlation between either projection values of common features or genes, or contributions of common samples.

### Usage

```r
compareAn(icaSets, labAn,
    type.corr = c("pearson", "spearman"),
    cutoff_zval = 0,
    level = c("samples", "features", "genes"))
```

### Arguments

- **icaSets**: list of IcaSet objects, e.g. results of ICA decompositions obtained on several datasets.
- **labAn**: vector of names for each icaSet, e.g. the the names of the datasets on which were calculated the decompositions.
- **type.corr**: Type of correlation to compute, either 'pearson' or 'spearman'.
- **cutoff_zval**: either NULL or 0 (default) if all genes are used to compute the correlation between the components, or a threshold to compute the correlation on the genes that have at least a scaled projection higher than cutoff_zval. Will be used only when correlations are calculated on S or SByGene.
- **level**: Data level of the IcaSet objects on which is applied the correlation. It must correspond to a feature shared by the IcaSet objects: 'samples' if they were applied to common samples (correlations are computed between matrix X), 'features' if they were applied to common features (correlations are computed between matrix S), 'genes' if they share gene IDs after annotation into genes (correlations are computed between matrix SByGene).
The user must carefully choose the object on which the correlation will be computed. If `level='samples'`, the correlations are based on the mixing matrices of the ICA decompositions (of dimension samples x components). 'A' will be typically chosen when the ICA decompositions were computed on the same dataset, or on datasets that include the same samples. If `level='features'` is chosen, the correlation is calculated between the source matrices (of dimension features x components) of the ICA decompositions. 'S' will be typically used when the ICA decompositions share common features (e.g. same microarrays). If `level='genes'`, the correlations are calculated on the attributes 'SByGene' which store the projections of the annotated features. 'SByGene' will be typically chosen when ICA were computed on datasets from different technologies, for which comparison is possible only after annotation into a common ID, like genes.

cutoff_zval is only used when `level` is one of `c('genes','features')`, in order to restrict the correlation to the contributing features or genes.

When `cutoff_zval` is specified, for each pair of components, genes or features that are included in the circle of center 0 and radius `cutoff_zval` are excluded from the computation of the correlation.

It must be taken into account by the user that if `cutoff_zval` is different from NULL or 0, the computation will be much slower since each pair of component is treated individually.

Value

A list whose length equals the number of pairs of `IcaSet` and whose elements are outputs of function `cor2An`.

Author(s)

Anne Biton

See Also

cor2An

Examples

dat1 <- data.frame(matrix(rnorm(10000),ncol=10,nrow=1000))
rownames(dat1) <- paste("g", 1:1000, sep="")
colnames(dat1) <- paste("s", 1:10, sep="")
dat2 <- data.frame(matrix(rnorm(10000),ncol=10,nrow=1000))
rownames(dat2) <- paste("g", 1:1000, sep="")
colnames(dat2) <- paste("s", 1:10, sep="")

## run ICA
resJade1 <- runICA(X=dat1, nbComp=3, method = "JADE")
resJade2 <- runICA(X=dat2, nbComp=3, method = "JADE")

## build params
params <- buildMineICAParams(resPath="toy/"

## build IcaSet object
icaSettoy1 <- buildIcaSet(params=params, A=data.frame(resJade1$A), S=data.frame(resJade1$S),
This function builds a correlation graph from the outputs of function `compareAn`.
Usage

`compareAn2graphfile(listPairCor, useMax = TRUE, cutoff = NULL, useVal = c("cor", "pval"), file = NULL)`

Arguments

- `listPairCor`: The output of the function `compareAn`, containing the correlation between several pairs of objects of class `IcaSet`.
- `useMax`: If TRUE, the graph is restricted to edges that correspond to maximum score, see details.
- `cutoff`: Cutoff used to select pairs that will be included in the graph.
- `useVal`: The value on which is based the graph, either "cor" for correlation or "pval" for p-values of correlation tests.
- `file`: File name.

Details

When correlations are considered (useVal="cor"), absolute values are used since the components have no direction.

If `useMax` is TRUE each component is linked to the most correlated component of each different `IcaSet`.

If `cutoff` is specified, only correlations exceeding this value are taken into account during the graph construction. For example, if `cutoff` is 1, only relationships between components that correspond to a correlation value larger than 1 will be included.

When `useVal="pval"` and `useMax=TRUE`, the minimum value is taken instead of the maximum.

Value

A data.frame with the graph description, has two columns `n1` and `n2` filled with node IDs, each row denotes that there is an edge from `n1` to `n2`. Additional columns quantify the strength of association: correlation (`cor`), p-value (`pval`), \(1 - \text{abs}(\text{cor})\) (`distcor`), \log_{10}\text{pvalue (`logpval`).}

Author(s)

Anne Biton

See Also

`compareAn, cor2An`

Examples

dat1 <- data.frame(matrix(rnorm(10000), ncol=10, nrow=1000))
rownames(dat1) <- paste("g", 1:1000, sep="")
colnames(dat1) <- paste("s", 1:10, sep="")
dat2 <- data.frame(matrix(rnorm(10000), ncol=10, nrow=1000))
rownames(dat2) <- paste("g", 1:1000, sep="")
colnames(dat2) <- paste("s", 1:10, sep="")

# run ICA
resJade1 <- runICA(X=dat1, nbComp=3, method = "JADE")
resJade2 <- runICA(X=dat2, nbComp=3, method = "JADE")

# build params
params <- buildMineICAParams(resPath="toy/")

# build IcaSet object
icaSettoy1 <- buildIcaSet(params=params, A=data.frame(resJade1$A), S=data.frame(resJade1$S),
                        dat=dat1, alreadyAnnot=TRUE)$icaSet
icaSettoy2 <- buildIcaSet(params=params, A=data.frame(resJade2$A), S=data.frame(resJade2$S),
                        dat=dat2, alreadyAnnot=TRUE)$icaSet

resCompareAn <- compareAn(icaSets=list(icaSettoy1,icaSettoy2), labAn=c("toy1","toy2"),
                         type.corr="pearson", level="genes", cutoff_zval=0)

# Build a graph where edges correspond to maximal correlation value (useVal="cor"),
compareAn2graphfile(listPairCor=resCompareAn, useMax=TRUE, useVal="cor", file="myGraph.txt")

# Not run:
#### Comparison of 2 ICA decompositions obtained on 2 different gene expression datasets.
# load the two datasets
library(breastCancerMAINZ)
library(breastCancerVDX)
data(mainz)
data(vdx)

treat <- function(es, annot="hgu133a.db") {
  es <- selectFeatures_IQR(es,10000)
  exprs(es) <- t(apply(exprs(es),1,scale,scale=FALSE))
  colnames(exprs(es)) <- sampleNames(es)
  resJade <- runICA(X=exprs(es), nbComp=10, method = "JADE", maxit=10000)
  resBuild <- buildIcaSet(params=buildMineICAParams(), A=data.frame(resJade$A), S=data.frame(resJade$S),
                         dat=exprs(es), pData=pData(es), refSamples=character(0),
                         annotation=annot, typeID= typeIDmainz,
                         chipManu = "affymetrix", mart=mart)
  icaSet <- resBuild$icaSet
}
# Build the two IcaSet objects
icaSetMainz <- treat(mainz)
icaSetVdx <- treat(vdx)

# Compute correlation between every pair of IcaSet objects.
resCompareAn <- compareAn(icaSets=list(icaSetMainz,icaSetVdx),
                         labAn=c("Mainz","Vdx"), type.corr="pearson", level="genes", cutoff_zval=0)

# Same thing but adding a selection of genes on which the correlation between two components is computed:
# when considering pairs of components, only projections whose scaled values are not located within
# the circle of radius 1 are used to compute the correlation (cutoff_zval=1).
compareGenes <- compareAn(icaSets=list(icaSetMainz,icaSetVdx),
labAn=c("Mainz","Vdx"), type.corr="pearson", cutoff_zval=1, level="genes")

## Build a graph where edges correspond to maximal correlation value (useVal="cor"),
## i.e., component A of analysis i is linked to component B of analysis j,
## only if component B is the most correlated component to A amongst all component of analysis j.
compareAn2graphfile(listPairCor=resCompareAn, useMax=TRUE, useVal="cor", file="myGraph.txt")

## Restrict the graph to correlation values exceeding 0.4
compareAn2graphfile(listPairCor=resCompareAn, useMax=FALSE, cutoff=0.4, useVal="cor", file="myGraph.txt")

## End(Not run)

**compareGenes**

*Union and intersection of contributing genes*

**Description**

Compute and annotate the intersection or union between contributing genes of components originating from different IcaSet objects.

**Usage**

```r
compareGenes(keepCompByIcaSet, icaSets, lab, cutoff = 0,
            type = c("union", "intersection"), annotate = TRUE,
            file,
            mart = useMart("ensembl", "hsapiens_gene_ensembl"))
```

**Arguments**

- **icaSets**: List of IcaSet objects, the geneNames of the IcaSet objects must be from the same type (e.g. gene Symbols).
- **keepCompByIcaSet**: Indices of the components to be considered in each IcaSet.
- **lab**: The names of the icaSets (e.g the names of the datasets they originate from).
- **cutoff**: The cutoff (on the absolute centered and scaled projections) above which the genes have to be considered.
- **type**: “intersection” to restrict the list of genes to the ones that are common between all datasets, or “union” to consider all the union of genes available across the datasets.
- **annotate**: If TRUE (default) the genes are annotated using function writeGenes.
- **file**: The HTML file name where the genes and their annotations are written, default is typeGenes_lab1-i_lab2-j... where i and j are the component indices contained in keepCompByIcaSet.
- **mart**: The mart object (database and dataset) used for annotation, see function useMart of package biomaRt.
Value

A data.frame containing

typeID(icaSets[1])['geneID_biomart']: the gene IDs,
median_rank the median of the ranks of each gene across the IcaSet objects,
analyses the labels of the IcaSet objects in which each gene is above the given cutoff
min_rank the minimum of the ranks of each gene across the IcaSet objects,
ranks the ranks of each gene in each IcaSet where it is available,
scaled_proj the centered and reduced projection of each gene in each IcaSet where it is available.

Author(s)

Anne Biton

See Also

writeGenes

Examples

## Not run:
data(icaSetCarbayo)
mart <- useMart("ensembl", "hsapiens_gene_ensembl")

## comparison of two components
## here the components come from the same IcaSet for convenience
## but they must come from different IcaSet in practice.
compareGenes(keepCompByIcaSet = c(9,4), icaSets = list(icaSetCarbayo, icaSetCarbayo),
lab=c("Carbayo", "Carbayo2"), cutoff=3, type="union", mart=mart)

## End(Not run)
Arguments

mat1       matrix of dimension features/genes x number of components, e.g the results of an ICA decomposition
mat2       matrix of dimension features/genes x number of components, e.g the results of an ICA decomposition
lab         The vector of labels for mat1 and mat2, e.g the the names of the two datasets on which were calculated the two decompositions
type.corr   Type of correlation, either 'pearson' or 'spearman'
cutoff_zval  cutoff_zval: 0 (default) if all genes are used to compute the correlation between the components, or a threshold to compute the correlation on the genes that have at least a scaled projection higher than cutoff_zval.

Details

Before computing the correlations, the components are scaled and restricted to common row names.

It must be taken into account by the user that if cutoff_zval is different from NULL or zero, the computation will be slower since each pair of component is treated individually.

When cutoff_zval is specified, for each pair of components, genes that are included in the circle of center 0 and radius cutoff_zval are excluded from the computation of the correlation between the gene projection of the two components.

Value

This function returns a list consisting of:

cor        a matrix of dimensions '(nbcomp1+nbcomp2) x (nbcomp1*nbcomp2)', containing the correlation values between each pair of components,
pval       a matrix of dimension '(nbcomp1+nbcomp2) x (nbcomp1*nbcomp2)', containing the p-value of the correlation tests for each pair of components,
inter       the intersection between the features/genes of mat1 and mat2,
labAn       the labels of the compared matrices.

Author(s)

Anne Biton

See Also

rcorr, cor.test, compareAn

Examples

cor2An(mat1=matrix(rnorm(10000),nrow=1000,ncol=10), mat2=matrix(rnorm(10000),nrow=1000,ncol=10), lab=c("An1","An2"), type.corr="pearson")
**correl2Comp**

**Description**

This function computes the correlation between two components.

**Usage**

```r
correl2Comp(comp1, comp2, type.corr = "pearson", plot = FALSE, cutoff_zval = 0, test = FALSE, alreadyTreat = FALSE)
```

**Arguments**

- **comp1**
  - The first component, a vector of projections or contributions indexed by labels
- **comp2**
  - The second component, a vector of projections or contributions indexed by labels
- **type.corr**
  - Type of correlation to be computed, either 'pearson' or 'spearman'
- **plot**
  - if TRUE, plot comp1 vs comp2
- **cutoff_zval**
  - either NULL or 0 (default) if all genes are used to compute the correlation between the components, or a threshold to compute the correlation on the genes that have at least a scaled projection higher than cutoff_zval.
- **test**
  - if TRUE the correlation test p-value is returned instead of the correlation value
- **alreadyTreat**
  - if TRUE comp1 and comp2 are considered as being already treated (i.e scaled and restricted to common elements)

**Details**

Before computing the correlation, the components are scaled and restricted to common labels. When cutoff_zval is different from 0, the elements that are included in the circle of center 0 and radius cutoff_zval are not taken into account during the computation of the correlation.

**Value**

This function returns either the correlation value or the p-value of the correlation test.

**Author(s)**

Anne Biton
dataCarbayo

\begin{itemize}
\item \textbf{dat} \hspace{1cm} \textit{Retrieve and set data from IcaSet}
\end{itemize}

\textbf{Description}

These generic functions access and set the attributes \texttt{dat} stored in an object of class \texttt{IcaSet}.

\textbf{Usage}

\begin{verbatim}
dat(object)
dat(object) <- value
datByGene(object)
datByGene(object) <- value
geneNames(object)
\end{verbatim}

\textbf{Arguments}

\begin{description}
\item \texttt{object} \hspace{1cm} object of class \texttt{IcaSet}
\item \texttt{value} \hspace{1cm} Matrix with rows representing features or genes and columns samples.
\end{description}

\textbf{Value}

\texttt{dat} and \texttt{datByGene} return a matrix containing measured values (e.g. expression data) indexed by features and genes, respectively. \texttt{geneNames} returns the names of the genes, i.e. the row names of \texttt{datByGene}.

\textbf{Author(s)}

Anne

\textbf{dataCarbayo} \hspace{1cm} \textit{Carbayo expression data}

\textbf{Description}

Contains bladder cancer expression data based on HG-U133A Affymetrix microarrays. The data include 93 samples, were normalized with MAS5 by the authors of the paper using Quantile normalization and log2-transformation. They are restricted to the 10000 most variable probe sets.

\textbf{Author(s)}

Anne Biton

\textbf{References}

\url{http://jco.ascopubs.org/content/24/5/778/suppl/DC1}
doEnrichment

Runs enrichment analysis of contributing genes

Description

doEnrichment This internal function is called by hypergeoAn and runs hypergeometric tests through function hyperGTest to associate the contributing genes of a component to gene sets.

Usage

doEnrichment(compSel, chip, onto, hgCutoff, cond,
universe, path, db, pack.annot.EID, Slist, it, cutoff,
entrez2symbol)

Arguments

compSel A list containing three elements
  compSel the projection values of contributing genes that were selected based on their absolute projection
  compSel_neg the projection values of contributing genes that have negative projections
  compSel_pos the projection values of contributing genes that have positive projections
chip The annotation package
onto A string specifying the GO ontology to use. Must be one of 'BP', 'CC', or 'MF', see GOHyperGParams. Only used when argument db is 'GO'.
hgCutoff The p-value threshold
cond A logical indicating whether the calculation should conditioned on the GO structure, see GOHyperGParams.
universe The universe for the hypergeometric tests, see GOHyperGParams.
path The path where results will be saved
db The used database to use ('GO' or 'KEGG')
pack.annot.EID The name of the environment of the annotation package containing the annotation for Entrez Gene.
Slist The list of gene projections across all components
it The index of the component
cutoff The threshold applied on the gene projections, used to select the contributing genes
entrez2symbol A vector of all gene Symbols involved in the analysis indexed by their Entrez Gene IDs. It is only used when annotation(params) is empty, and allows to associate gene sets to Symbols.
**getComp**

**Value**

Object of class GOHyperGResult-class

**Author(s)**

Anne Biton

---

getComp

*Retrieve feature and sample values on a component stored in an IcaSet object.*

**Description**

This generic function retrieves, from an IcaSet object, the feature projections (contained in attribute $S$) and sample contributions (contained in attribute $A$) corresponding to a specific component.

**Usage**

getComp(object, level, ind)

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>Object of class IcaSet.</td>
</tr>
<tr>
<td>level</td>
<td>Either &quot;features&quot; to retrieve projections contained in $S$, or &quot;genes&quot; to retrieve projections contained in $SByGene$.</td>
</tr>
<tr>
<td>ind</td>
<td>The index of the component to be retrieved.</td>
</tr>
</tbody>
</table>

**Value**

getComp returns a list containing two elements:

- **proj**: the feature or gene projections on the given component,
- **contrib**: the sample contributions on the given component.

**Author(s)**

Anne Biton

**See Also**

class-IcaSet
getProj

Extract projection values

Description

Extract projection values of a given set of IDs on a subset of components.

Usage

getProj(icaSet, ids, keepComp,
       level = c("features", "genes"))

Arguments

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>icaSet</td>
<td>An object of class IcaSet</td>
</tr>
<tr>
<td>ids</td>
<td>feature or gene IDs</td>
</tr>
<tr>
<td>keepComp</td>
<td>Index of the components to be conserved, must be in indComp(icaSet)</td>
</tr>
<tr>
<td>level</td>
<td>The level of projections to be extracted, either &quot;features&quot; or &quot;genes&quot;</td>
</tr>
</tbody>
</table>

Value

A vector or a list of projection values

Author(s)

Anne Biton

Examples

## load an example of IcaSet
data(icaSetCarbayo)

##get the projection of your favorite proliferation genes
# on all components
getProj(icaSetCarbayo, ids=c("TOP2A","CDK1","CDC20"), level="genes")

# on some components
getProj(icaSetCarbayo, ids=c("TOP2A","CDK1","CDC20"),
        keepComp=c(1,6,9,12),level="genes")

##get the gene projection values on the sixth component
getProj(icaSetCarbayo, keepComp=6,level="genes")
**Description**

Compute standard deviation of the gene expression

**Usage**

```r
getSdExpr(features, dat)
```

**Arguments**

- `features` : IDs
- `dat` : Expression data indexed by IDs

**Value**

Returns a vector

**Author(s)**

Anne Biton

**Examples**

```r
dat <- matrix(rnorm(1000), ncol=10, nrow=100)
rownames(dat) <- 1:100
MineICA:::getSdExpr(features = 2:20, dat = dat)
```

---

**Description**

Example of output of function `hyperGtest`.

**Author(s)**

Anne Biton
Runs an enrichment analysis per component using package GOstats.

Description

Runs an enrichment analysis of the contributing genes associated with each component, using the function hyperGTest of package GOstats. The easiest way to run enrichment analysis is to use function runEnrich.

Usage

hypergeoAn(icaSet, params,
path = paste(resPath(params), "GOstatsEnrichAnalysis/", sep = "/"),
SlistSel, hgCutoff = 0.01, db = "go", onto = "BP",
cond = TRUE, universe, entrez2symbol)

Arguments

icaSet An object of class IcaSet
params An object of class MineICAParams containing the parameters of the analysis
path The path where results will be saved
SlistSel A list of contributing gene projection values per component. Each element of the list corresponds to a component and is restricted to the features or genes exceeding a given threshold. If missing, is computed by the function.
hgCutoff The p-value threshold
db The database to be used ("GO" or "KEGG")
onto A character specifying the GO ontology to use. Must be one of "BP", "CC", or "MF", see GOHyperGParams. Only used when argument db is "GO".
cond A logical indicating whether the calculation should conditioned on the GO structure, see GOHyperGParams.
universe The universe for the hypergeometric tests, see GOHyperGParams.
entrez2symbol A vector of all gene Symbols involved in the analysis indexed by their Entrez Gene IDs. It is only used when annotation(params) is empty, and allows to associate gene sets to Symbols.

Details

An annotation package must be available in annotation(icaSet) to provide the contents of the gene sets. If none corresponds to the technology you deal with, please choose the org.*.eg.db package according to the organism (for example org.Hs.eg.db for Homo sapiens). Save results of the enrichment tests in a `.rda` file located in path/db/onto/zvalCutoff(params).

Author(s)

Anne Biton
See Also

`runEnrich, xtable, useMart, hyperGTest, GOHyperGParams, mergeGostatsResults`

Examples

```r
## Not run:
## load an example of IcaSet
data(icaSetCarbayo)

## define params
# Use threshold 3 to select contributing genes.
# Results of enrichment analysis will be written in path 'resPath(params)/GOstatsEnrichAnalysis'
params <- buildMineICAParams(resPath = '~/resMineICAcarbayo/', selCutoff = 3)

## Annotation package for IcaSetCarbayo is hgu133a.db.
# check annotation package
annotation(icaSetCarbayo)

## Define universe, i.e the set of EntrezGene IDs mapping to the feature IDs of the IcaSet object.
universe <- as.character(na.omit(unique(unlist(AnnotationDbi::mget(featureNames(icaSetCarbayo), hgu133aENTREZID, ifnotfound = NA)))))

## Apply enrichment analysis (of the contributing genes) to the first components using gene sets from KEGG.
# Since an annotation package is available, we don't need to fill arg 'entrez2symbol'.
# run the actual enrichment analysis
hypergeoAn(icaSet = icaSetCarbayo[,,1], params = params, db = "GO", onto = "BP", universe = universe)

## End(Not run)
```

---

**IcaSet**

*Class to Contain and Describe an ICA decomposition of High-Throughput Data.*

**Description**

Container for high-throughput data and results of ICA decomposition obtained on these data. IcaSet class is derived from `eSet`, and requires a matrix named `dat` as assayData member.

**Extends**

Directly extends class `eSet`.

**Creating Objects**

```r
new("IcaSet")
new("IcaSet", annotation = character(0), experimentData = new("MIAME"), featureData = new("AnnotatedDataFrame"), phenoData = new("AnnotatedDataFrame"), protocolData = phenoData[,integer(0)], dat = new("matrix"), A = new("data.frame"), S = new("data.frame"), ...)```
This creates an IcaSet with assayData implicitly created to contain dat.

```r
new("IcaSet", annotation = character(0), assayData = assayDataNew(dat=new("matrix")),
     experimentData = new("MIAME"), featureData = new("AnnotatedDataFrame"), phenoData =
     new("AnnotatedDataFrame"), protocolData = phenoData[,integer(0)], A=new("data.frame"),
     S=new("data.frame"), ...)
```

This creates an IcaSet with assayData provided explicitly.

IcaSet instances are usually created through `new("IcaSet", ...)`. Usually the arguments to `new` include `dat` ('features x samples', e.g a matrix of expression data), `phenoData` ('samples x annotations', a matrix of sample annotations), `S` the Source matrix of the ICA decomposition ('features x comp'), `A` the Mixing matrix of the ICA decomposition ('samples x comp'), `annotation` the annotation package, `typeID` the description of the feature and gene IDs.

The other attributes can be missing, in which case they are assigned default values.

The function `buildIcaSet` is a more convenient way to create IcaSet instances, and allows to automatically annotate the features.

**Slots**

Inherited from eSet:

- **annotation**: See `eSet`
- **assayData**: Contains matrices with equal dimensions, and with column number equal to `nrow(phenoData)`. assayData must contain a matrix dat with rows representing features (e.g., reporters) and columns representing samples. Class: `AssayData-class`
- **experimentData**: See `eSet`
- **featureData**: See `eSet`
- **phenoData**: See `eSet`
- **protocolData**: See `eSet`
  - **organism**: Contains the name of the species. Currently only Human ("Human" or "Homo sapiens") and Mouse ("Mouse" or "Mus musculus") are supported. Only used when `chipManu="illumina"
  - **mart**: An output of `useMart` of package `biomaRt`. Only useful if no annotation package is available for argument `icaSet`.
- **datByGene**: Data.frame containing the data dat where features have been replaced by their annotations (e.g. gene IDs). Rows represent annotations of the features (e.g., gene IDs) and columns represent samples.
- **A**: The mixing matrix of the ICA decomposition, contained in a data.frame whose column number equals the number of components and row number equals `nrow(phenoData)` (dimension: 'samples x comp').
- **S**: The source matrix of the ICA decomposition, contained in a data.frame whose column number equals the number of components and row number equals `nrow(assayData)` (dimension: 'features x comp').
- **SByGene**: The matrix Source of the ICA decomposition, contained in a data.frame whose column number equals the number of components and row number equals `nrow(datByGene)` (dimension: 'annotatedFeatures x comp').
compNames: A vector of component labels with length equal to the number of component.

indComp: A vector of component indices with length equal to the number of component.

witGenes: A vector of gene IDs with length equal to the number of component.

chipManu: The manufacturer of the technology the data originates from. Useful for the annotation of the features when data originates from an _illumina_ microarray.

chipVersion: The version of the chip, only useful for when chipManu="illumina"

refSamples: A vector of sample IDs including the reference samples, e.g the "normal" samples. Must be included in sampleNames(object), i.e in colnames(dat).

typeID: A vector of characters providing the annotation IDs. It includes three elements:

  **geneID\_annotation** the IDs from the package to be used to annotate the features into genes.
  It will be used to fill the attributes datByGene and SByGene of the icaSet. It must match one of the objects the corresponding package supports (you can access the list of objects by typing lst("package:packagename")); If no annotation package is provided, this element is not useful.

  **geneID\_biomart** the type of gene IDs, as available in listFilters(mart); where mart is specified as described in useMart. If you have directly built the IcaSet at the gene level (i.e if no annotation package is used), featureID\_biomart and geneID\_biomart will be identical.

  **featureID\_biomart** the type of feature IDs, as available in listFilters(mart); where mart is specified as described in function useMart. Not useful if you work at the gene level.

Methods

Class-specific methods.

getComp(IcaSet, ind, level=c("features","genes")) Given a component index, extract the corresponding sample contribution values from A, and the feature (level="features") or gene (level="genes") projections from S. Returns a list with two elements: contrib the sample contributions and proj the feature or gene projections.

Access and set any slot specific to IcaSet:

slotName(IcaSet), and slotName(IcaSet)<-: Accessing and setting any slot of name slotName contained in an IcaSet object.

IcaSet["slotName"], and IcaSet["slotName"]<-: Accessing and setting any slot of name slotName contained in an IcaSet object.

Most used accessors and settors:

A(IcaSet), and A(IcaSet)<-: Accessing and setting Mixing matrix A.

S(IcaSet), and S(IcaSet)<-: Accessing and setting the data.frame Source S.

Slist(IcaSet): Accessing the data.frame Source as a list where names are preserved.

SByGene(IcaSet), and SByGene(IcaSet)<-: Accessing and setting the _annotated_ data.frame Source SByGene.

SlistByGene(IcaSet): Accessing the _annotated_ Source matrix as a list where names are preserved.

organism(IcaSet), organism(IcaSet, character)<- Access and set value in the organism slot.
dat(IcaSet), dat(IcaSet, matrix)<- Access and set elements named dat in the AssayData-class slot.

Derived from eSet:

pData(IcaSet), pData(IcaSet, value)<- See eSet
assayData(IcaSet): See eSet
sampleNames(IcaSet) and sampleNames(IcaSet)<- See eSet
featureNames(IcaSet), featureNames(IcaSet, value)<- See eSet
dims(IcaSet): See eSet
phenoData(IcaSet), phenoData(IcaSet, value)<- See eSet
varLabels(IcaSet), varLabels(IcaSet, value)<- See eSet
varMetadata(IcaSet), varMetadata(IcaSet, value)<- See eSet
experimentData(IcaSet), experimentData(IcaSet, value)<- See eSet
pubMedIds(IcaSet), pubMedIds(IcaSet, value) See eSet
abstract(IcaSet): See eSet
annotation(IcaSet), annotation(IcaSet, value)<- See eSet
protocolData(IcaSet), protocolData(IcaSet, value)<- See eSet
combine(IcaSet, IcaSet): See eSet
storageMode(IcaSet), storageMode(IcaSet, character)<- See eSet

Standard generic methods:

initialize(IcaSet): Object instantiation, used by new; not to be called directly by the user.
validObject(IcaSet): Validity-checking method, ensuring that dat is a member of assayData, and that the number of features, genes, samples, and components are consistent across all the attributes of the IcaSet object. checkValidity(IcaSet) imposes this validity check, and the validity checks of eSet.
IcaSet[slotName], IcaSet[slotName]<- Accessing and setting any slot of name slotName contained in an IcaSet object.
IcaSet[i, j, k]: Extract object of class "IcaSet" for features or genes with names i, samples with names or indices j, and components with names or indices k.

makeDataPackage(object, author, email, packageName, packageVersion, license, biocViews, filePath, description=paste(abstract(object), collapse="\n\n"), ...)
Create a data package based on an IcaSet object. See makeDataPackage.

show(IcaSet): See eSet
dim(IcaSet), ncol: See eSet
IcaSet[[index]]: See eSet
IcaSet$, IcaSet$<-: See eSet
IcaSet[[i]], IcaSet[[i]]<-: See eSet
See Also

eSet-class, buildIcaSet, class-IcaSet, class-MineICAParams.

Examples

# create an instance of IcaSet
new("IcaSet")
dat <- matrix(runif(100000), nrow=1000, ncol=100)
rownames(dat) <- 1:nrow(dat)
new("IcaSet",
  dat=dat,
  A=as.data.frame(matrix(runif(1000), nrow=100, ncol=10)),
  S=as.data.frame(matrix(runif(10000), nrow=1000, ncol=10), row.names = 1:nrow(dat)))
<table>
<thead>
<tr>
<th>icaSetKim</th>
<th><em>IcaSet</em>-object containing a FastICA decomposition of gene expression microarray-based data of bladder cancer samples.</th>
</tr>
</thead>
</table>

**Description**

Object of class *IcaSet* containing an ICA decomposition calculated by the FastICA algorithm (through matlab function "icasso") on bladder cancer expression data measured on illumina Human-6 BeadChip, version 2. It contains 20 independent components. The original expression data contain 165 tumor samples, were normalized by the authors of the paper with Illumina BeadStudio software using Quantile normalization and log2 transformation, and are restricted to the 10000 most variable probe sets.

**Author(s)**

Anne

**References**


<table>
<thead>
<tr>
<th>icaSetRiester</th>
<th><em>IcaSet</em>-object containing a FastICA decomposition of gene expression microarray-based data of bladder cancer samples.</th>
</tr>
</thead>
</table>

**Description**

Object of class *IcaSet* containing an ICA decomposition calculated by the FastICA algorithm (through matlab function "icasso") on gene expression data of urothelial tumors. measured on a HG-U133-plus2 Affymetrix microarrays. It contains 20 independent components. The original expression data contain 93 tumor samples, were normalized with GCRMA with log2-transformation, and are restricted to the 10000 most variable probe sets.

**Author(s)**

Anne Biton

**References**

icaSetStransky  

*IcaSet-object containing a FastICA decomposition of gene expression microarray-based data of bladder cancer samples.*

**Description**

Object of class *IcaSet* containing an ICA decomposition calculated by the FastICA algorithm (through matlab function "icasso") on bladder cancer expression data measured on HG-U133-95a and HG-U133-95av2 Affymetrix microarrays. It contains 20 independent components. The original expression data contain 63 tumor samples and were normalized by RMA with log2-transformation.

**Author(s)**

Anne Biton

**References**


---

**Description**

These generic functions access and set the attributes `compNames`, `indComp` and `witGenes` stored in an object of class *IcaSet*.

**Usage**

```r
indComp(object)  
indComp(object) <- value  
compNames(object)  
compNames(object) <- value  
witGenes(object)  
witGenes(object) <- value
```

**Arguments**

- `object`  
  object of class *IcaSet*

- `value`  
  Numeric vector for `indComp`, character vector for `compNames` and `witGenes`, with length equal to `nrow(A(object))` and containing: component indices (for `indComp`), labels (for `compNames`), or gene witness IDs (for `witGenes`).
mergeGostatsResults

Value

indComp returns a numeric vector containing component indices; compNames returns a character vector containing component labels; witGenes returns a character vector containing witness genes IDs.

Author(s)

Anne Biton

mergeGostatsResults  Merge enrichment results obtained for different databases into one file per component.

Description

This function is internal and called by function runEnrich. It merges enrichment results obtained with either KEGG, GO, or both databases into one file.

Usage

mergeGostatsResults(resPath, GOstatsPath, rdata = "hgres", cutoffs = NULL, hgCutoff = 0.01, cond = TRUE, pathGenes)

Arguments

resPath  The global path where results of ICA analysis are written
GOstatsPath  The path within argument resPath where files will be written
rdata  The name of the rdata file containing the enrichment analysis of all components
cutoffs  The threshold(s) used to select genes used in enrichment analysis
hgCutoff  The p-value threshold
cond  A logical indicating whether the calculation has been conditioned on the GO structure, see GOHyperGParams.
pathGenes  The path where HTML files containing gene projections for each component are located

Details

This function writes an HTML file per component, containing the outputs of the enrichment tests computed through the function hyperGTest. The results of the enrichment tests are loaded from .rda files located in resPath(icaSet)/GOstatsEnrichAnalysis/Db/db-name/ontology-name/. The results obtained for the different databases/ontologies are then merged into an array for each component, this array is written as an HTML file in the directory resPath(icaSet)/zvalCutoff(params). The arguments hgCutoff and cond have to be provided because they will be used in the file names of the resulting files.
This function makes several important assumptions: only databases GO and KEGG have been tested, p-values are not available for gene sets that have not been selected as significant.

The outputs of `hyperGTest` that are given in each table are:

- **DB, ID, Term**: The database, the gene set ID, and the gene set name,
- **P-value**: probability of observing the number of genes annotated for the gene set among the selected gene list, knowing the total number of annotated genes among the universe,
- **Expected counts**: expected number of genes in the selected gene list to be found at each tested category term/gene set,
- **Odds ratio**: odds ratio for each category term tested which is an indicator of the level of enrichment of genes within the list as against the universe,
- **Counts**: number of genes in the selected gene list which are annotated for the gene set,
- **Size**: number of genes from the universe annotated for the gene set.

### Value

NULL

### Author(s)

Anne Biton

### See Also

`xtable`, `useMart`, `hyperGTest`, `GOHyperGParams`, `hypergeoAn`, `mergeGostatsResults`

---

```
MineICAPrams Class to contain parameters for the analysis of an ICA decomposition.
```

### Description

Container for parameters used during the analysis of an ICA decomposition obtained on genomics data.

### Creating Objects

```r
new("MineICAPrams")
new("MineICAPrams", resPath="", genesPath="ProjByComp", pvalCutoff=0.05, selCutoff=3)
```
Slots

Sfile A txt file containing the Source matrix S.
Afile A txt file containing the Mixing matrix A.
datfile A txt file containing the data (typically expression data) on which the decomposition was calculated.
annotfile Either a RData or txt file containing the annotation data for the samples (must be of dimensions samples*annotations).
resPath The path where the outputs of the analysis will be written.
genesPath The path _within_ the resPath where the gene projections will be written. If missing, will be automatically attributed as resPath/gene2components/.
annot2col A vector of colors indexed by annotation levels. If missing, will be automatically attributed using function annot2Color.
pvalCutoff The cutoff used to consider a p-value significant, default is 0.05.
scCutoff The cutoff applied on the absolute feature/gene projection values to consider gene as contributing to a component, default is 3. Must be either of length 1 and the same threshold is applied to all components, or of length equal to the number of components in order to use a specific threshold for each component.

Methods

For any slot:

Accessing and setting any slot of name slotName contained in an MineICAParams object.

slotName(MineICAParams) and slotName(MineICAParams)<-

Author(s)

Anne Biton

See Also

class-MineICAParams, runAn.

Examples

# create an instance of LocSet
new("MineICAParams")
nbOccByGeneInComp

Description

For each feature/gene, this function returns the indices of the components they contribute to.

Usage

nbOccByGeneInComp(Slist, cutoff, sel)

Arguments

Slist A list whose each element contains projection values of features/genes on a component.
cutoff A threshold to be used to define a gene as contributor
sel A list whose each element contains projection values of contributing features/genes on a component (the difference with arg Slist is that sel is already restricted to the contributing genes).

Value

This function returns a list which gives for each feature/gene the indices of the components it contributes to.

Author(s)

Anne Biton

Examples

c1 <- rnorm(100); names(c1) <- paste("g",100:199,sep="")
c2 <- rnorm(100); names(c2) <- paste("g",1:99,sep="")
MineICA:::nbOccByGeneInComp(Slist=list(c1,c2), cutoff= 0.5)
Description

For each feature/gene, this function returns the components they contribute to and their projection values across all the components.

Usage

```
nbOccInComp(icaSet, params, selectionByComp = NULL, level = c("features", "genes"), file = NULL)
```

Arguments

- `icaSet`: An object of class `IcaSet`
- `params`: An object of class `MineICAParams` containing the parameters of the analysis, the attribute `cutoffSel` is used as a threshold on the absolute projections to determine which genes contribute to the components.
- `selectionByComp`: The list of components already restricted to the contributing genes
- `level`: The attribute of `icaSet` to be used, are reported the occurrences of either the "features" or the "genes".
- `file`: The file where the output data.frame and plots are written.

Details

A feature/gene is considered as a contributor when its scaled projection value exceeds the threshold `selCutoff(icaSet)`.

This function plots the number of times the feature/gene is a contributor as a function of the standard deviation of its expression profile.

The created files are located in `genePath(params)`. An extension '.htm' and '.pdf' is respectively added to the file name for the data.frame and the plot outputs.

Value

Returns a data.frame whose columns are: 'gene' the feature or gene ID, 'nbOcc' the number of components on which the gene contributes according to the threshold, 'components' the indices of these components, and then the component indices which contain its projection values.

Author(s)

Anne Biton
Examples

data(icaSetCarbayo)
params <- buildMineICAParams(resPath="carbayo/")
nbOc <- nbOccInComp(icaSet=icaSetCarbayo, params=params, level="genes", file="gene2MixingMatrix")

Description

For each feature/gene, this function returns the indices of the components they contribute to.

Usage

nbOccInComp_simple(icaSet, params, selectionByComp = NULL, level = c("features", "genes"))

Arguments

icaSet An object of class IcaSet.
params An object of class MineICAParams containing the parameters of the analysis. cutoffSel(params) is used as a threshold on the absolute projections to select the contributing features/genes.
selectionByComp The list of components already restricted to the contributing features/genes (each element is a vector of projection values indexed by features or genes).
level The attribute of icaSet to be used, the occurrences of either the "features" (using S(icaSet)) or the "genes" (using SByGene(icaSet)) will be reported.

Value

Returns a data.frame whose columns are: gene the feature or gene IDs, nbOc the number of components the gene contributes to, components the indices of those components.

Author(s)

Anne Biton

Examples

data(icaSetCarbayo)
params <- buildMineICAParams(resPath="carbayo/")
nbOc <- MineICA:::nbOccInComp_simple(icaSet=icaSetCarbayo, params=params, level="genes")
**nodeAttrs**

*Generate node attributes*

**Description**

This function builds a data.frame describing for each node of the graph its ID and which analysis/data it comes from.

**Usage**

```
nodeAttrs(nbAn, nbComp, labAn, labComp, file)
```

**Arguments**

- `nbAn`: Number of analyses being considered, i.e number of IcaSet objects
- `nbComp`: Number of components by analysis, if of length 1 then it is assumed that each analysis has the same number of components.
- `labAn`: Labels of the analysis, if missing it will be generated as an1, an2, ...
- `labComp`: List containing the component labels indexed by analysis, if missing will be generated as comp1, comp2, ...
- `file`: File where the description of the node attributes will be written

**Details**

The created file is used in Cytoscape.

**Value**

A data.frame describing each node/component

**Author(s)**

Anne Biton

**Examples**

```r
## 4 datasets, 20 components calculated in each dataset, labAn
nodeAttrs(nbAn=4, nbComp=20, labAn=c("tutu","titi","toto","tata"))
```
plotAllMix  

Plots the Gaussian fitted by Mclust on several numeric vectors

Description

Given a result of function Mclust applied on several numeric vectors, this function plots the fitted Gaussian on their histograms.

Usage

plotAllMix(mc, A, nbMix = NULL, pdf, nbBreaks = 20, xlim = NULL)

Arguments

mc  
A list consisting of outputs of function Mclust applied to each column of A, if this argument is missing Mclust is applied by the function.

A  
A data.frame of dimensions 'samples x components'.

nbMix  
The number of Gaussian to be fitted.

nbBreaks  
The number of breaks for the histogram.

xlim  
x-axis limits to be used in the plot.

pdf  
A pdf file.

Details

This function can only deal with at the most three Gaussian

Value

A list of Mclust results.

Author(s)

Anne Biton

See Also

plotMix, hist, Mclust

Examples

A <- matrix(c(c(rnorm(80, mean=-0.5, sd=1), rnorm(80, mean=1, sd=0.2)), rnorm(160, mean=0.5, sd=1), c(rnorm(80, mean=-1, sd=0.3), rnorm(80, mean=0, sd=0.2))), ncol=3)

## apply function Mclust to each column of A
mc <- apply(A, 2, Mclust)

## plot the corresponding Gaussians on the histogram of each column
plotAllMix(mc=mc, A=A)
plotCorGraph

## apply function Mclust to each column of A, and impose the fit of two Gaussian (G=2)
mc <- apply(A,2,Mclust,G=2)
## plot the corresponding Gaussians on the histogram of each column
plotAllMix(mc=mc,A=A)
## When arg 'mc' is missing, Mclust is applied by the function
plotAllMix(A=A)

---

**plotCorGraph**

*Plots graph using*

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### Description

This function plots the correlation graph in an interactive device using function `tkplot`.

### Usage

```r
plotCorGraph(dataGraph, edgeWeight = "cor", nodeAttrs,
             nodeShape, nodeCol = "labAn", nodeName = "indComp",
             col, shape, title = "", reciproCol = "reciprocal",
             tkplot = FALSE, ...)
```

### Arguments

- **dataGraph**
  A data.frame containing the graph description. It must have two columns `n1` and `n2`, each row denoting that there is an edge from `n1` to `n2`. Node labels in columns `n1` and `n2` of `dataGraph` must correspond to node IDs in column `id` of `nodeAttrs`.

- **edgeWeight**
  The column of `dataGraph` used to weight edges.

- **nodeAttrs**
  A data.frame with node description, see function `nodeAttrs`.

- **nodeShape**
  Denotes the column of `nodeAttrs` used to attribute the node shapes.

- **nodeCol**
  Denotes the column of `nodeAttrs` used to color the nodes in the graph.

- **nodeName**
  Denotes the column of `nodeAttrs` used as labels for the nodes in the graph.

- **col**
  A vector of colors, for the nodes, indexed by the unique elements of `nodeCol` column from `nodeAttrs`. If missing, colors will be automatically attributed.

- **shape**
  A vector of shapes indexed by the unique elements of column `nodeShape` from `nodeAttrs`. If missing, shapes will be automatically attributed.

- **title**
  Title for the plot.

- **reciproCol**
  Denotes the column of `dataGraph` containing TRUE if the row defines a reciprocal node, else FALSE. See `annotReciprocal`.

- **tkplot**
  If TRUE, performs interactive plot with function `tkplot`, else uses `plot.igraph`.

- **...**
  Additional parameters as required by `tkplot`.
Details

You have to slightly move the nodes to see cliques because strongly related nodes are often superimposed. The edgeWeight column is used to weight the edges within the fruchterman.reingold layout available in the package igraph.

The argument nodeCol typically denotes the column containing the names of the datasets. Colors are automatically attributed to the nodes using palette Set3 of package RColorBrewer. The corresponding colors can be directly specified in the ‘col’ argument. In that case, ‘col’ must be a vector of colors indexed by the unique elements contained in nodeCol column (e.g dataset ids).

As for colors, one can define the column of nodeAttrs that is used to define the node shapes. The corresponding shapes can be directly specified in the shape argument. In that case, shape must be one of c("circle", "square", "vcsquare", "rectangle", "crectangle", "vrectangle") and must be indexed by the unique elements of nodeShape column.

Unfortunately, shapes can’t be taken into account when tkplot is TRUE (interactive plot).

If reciproCol is not missing, it is used to color the edges, either in grey if the edge is not reciprocal or in black if the edge is reciprocal.

Value

A list consisting of

- dataGraph a data.frame defining the correlation graph
- nodeAttrs a data.frame describing the node of the graph
- graph the graph as an object of class igraph
- graphid the id of the graph plotted using tkplot

Author(s)

Anne Biton

See Also

compareAn, nodeAttrs, compareAn2graphfile, runCompareIcaSets

Examples

data1 <- data.frame(matrix(rnorm(10000), ncol=10, nrow=1000))
rownames(data1) <- paste("g", 1:1000, sep="")
colnames(data1) <- paste("s", 1:10, sep="")
data2 <- data.frame(matrix(rnorm(10000), ncol=10, nrow=1000))
rownames(data2) <- paste("g", 1:1000, sep="")
colnames(data2) <- paste("s", 1:10, sep="")

# run ICA
resJade1 <- runICA(X=data1, nbComp=3, method = "JADE")
resJade2 <- runICA(X=data2, nbComp=3, method = "JADE")

# build params
params <- buildMineICAParams(resPath="toy/"
## build IcaSet object
icaSettoy1 <- buildIcaSet(params=params, A=data.frame(resJade1$A), S=data.frame(resJade1$S),
                        dat=dat1, alreadyAnnot=TRUE)$icaSet
icaSettoy2 <- buildIcaSet(params=params, A=data.frame(resJade2$A), S=data.frame(resJade2$S),
                        dat=dat2, alreadyAnnot=TRUE)$icaSet
icaSets <- list(icaSettoy1, icaSettoy2)
resCompareAn <- compareAn(icaSets=list(icaSettoy1,icaSettoy2), labAn=c("toy1","toy2"),
                        type.corr="pearson", level="genes", cutoff_zval=0)

## Build a graph where edges correspond to maximal correlation value (useVal="cor"),
dataGraph <- compareAn2graphfile(listPairCor=resCompareAn, useMax=TRUE, useVal="cor", file="myGraph.txt")

## construction of the data.frame with the node description
nbComp <- rep(3,2) #each IcaSet contains 3 components
nbAn <- 2 # we are comparing 2 IcaSets
# labels of components created as comp*i*
labComp <- foreach(icaSet=icaSets, nb=nbComp, an=1:nbAn) %do% {
  paste(rep("comp",sum(nb)),1:nbComp(icaSet),sep = "")
}

## creation of the data.frame with the node description
nodeDescr <- nodeAttrs(nbAn = nbAn, nbComp = nbComp, labComp = labComp,
                        labAn = c("toy1","toy2"), file = "nodeInfo.txt")

## Plot correlation graph, slightly move the attached nodes to make the cliques visible
## use tkplot=TRUE to have an interactive graph
res <- plotCorGraph(title = "Compare toy 1 and 2", dataGraph = dataGraph, nodeName = "indComp", tkplot = FALSE,
                     nodeAttrs = nodeDescr, edgeWeight = "cor", nodeShape = "labAn", reciproCol = "reciprocal")

## Not run:
## load two microarray datasets
library(breastCancerMAINZ)
library(breastCancerVDX)
data(mainz)
data(vdx)

## Define a function used to build two examples of IcaSet objects
treat <- function(es, annot="hgu133a.db") {
  es <- selectFeatures_IQR(es,10000)
  exprs(es) <- t(apply(exprs(es),1,scale,scale=FALSE))
  colnames(exprs(es)) <- sampleNames(es)
  resJade <- runICA(X=exprs(es), nbComp=10, method = "JADE", maxit=10000)
  resBuild <- buildIcaSet(params=buildMineICAParams(), A=data.frame(resJade$A), S=data.frame(resJade$S),
                          dat=exprs(es), pData=pData(es), refSamples=character(0),
                          annotation=annot, typeID= typeIDmainz,
                          chipManu = "affymetrix", mart=mart)
  icaSet <- resBuild$icaSet
}

## Build the two IcaSet objects
icaSetMainz <- treat(mainz)
icaSetVdx <- treat(vdx)
icaSets <- list(icaSetMainz, icaSetVdx)
labAn <- c("Mainz", "Vdx")

## correlations between gene projections of each pair of IcaSet
resCompareAn <- compareAn(icaSets = icaSets, level = "genes", type.corr = "pearson",
labAn = labAn, cutoff_zval = 0)

## construction of the correlation graph using previous output
dataGraph <- compareAn2graphfile(listPairCor = resCompareAn, useMax = TRUE, file = "corGraph.txt")

## construction of the data.frame with the node description
nbComp <- rep(10, 2) # each IcaSet contains 10 components
nbAn <- 2 # we are comparing 2 IcaSets
labComp <- foreach(icaSet = icaSets, nb = nbComp, an = 1:nbAn) %do% {
  paste(rep("comp", sum(nb)), 1:nbComp(icaSet), sep = "")
}

## creation of the data.frame with the node description
nodeDescr <- nodeAttrs(nbAn = nbAn, nbComp = nbComp, labComp = labComp,
labAn = labAn, file = "nodeInfo.txt")

## Plot correlation graph, slightly move the attached nodes to make the cliques visible
res <- plotCorGraph(title = "Compare two ICA decompositions obtained on two microarray-based data of breast tumors", dataGraph = dataGraph, nodeName = "indComp",
nodeAttrs = nodeDescr, edgeWeight = "cor", nodeShape = "labAn", reciproCol = "reciprocal")

## End(Not run)

plotDens2classInComp_plotOnly

Plots the densities or boxplots of the component contributions using ggplot2.

Description

This internal function is called by plotDensOneAnnotInAllComp and qualVarAnalysis and is dedicated to the plot of the densities or boxplots using the package ggplot2.

Usage

plotDens2classInComp_plotOnly(annot, colAnnot, global, keepLev, comp.label = NULL, colours,
legend.title = NULL, pval, test, title.add = NULL,
data_ref = NULL, geneExpr = NULL, geneRef = NULL,
ylab = NULL, trace_globalExpression = FALSE,
trace_groupExpression = TRUE,
typePlot = c("density", "boxplot"), addPoints = FALSE)
Arguments

- **annot**: a data.frame of dimensions 'samples x annotations' with one column corresponding to the component to trait ('comp' column) and one column corresponding to the groups of interest ('interest' column).
- **colAnnot**: the name of a column of the argument annot with the groups of interest.
- **global**: a vector with the global distribution, e.g. the contribution values of all samples on the component.
- **keepLev**: the groups of interest, i.e. the levels of the annotation colAnnot to be considered.
- **comp.label**: the label of the component.
- **colours**: a vector of colours indexed by the names of the groups of interest.
- **legend.title**: the title of the legend, if NULL (default) colAnnot is used.
- **pval**: the p-value of the test, will be written in the title.
- **test**: name of test that gave the p-value.
- **title.add**: a title to add to the automatically generated title.
- **data_ref**: a data.frame similar to the argument annot but restricted to a set of reference samples.
- **geneExpr**: a vector of values representative of the component, e.g. the expression of the witness gene of the component.
- **geneRef**: the ID of the feature/gene geneExpr corresponds to, e.g. the name of the witness gene.
- **ylab**: A label for the y-axis (character).
- **trace_globalExpression**: if TRUE, geneExpr is plotted below the graph as a set of points whose colour is representative of the amount of expression, default is FALSE.
- **trace_groupExpression**: if TRUE (default), geneExpr is plotted below the graph, by group, as a set of points whose colour is representative of the amount of expression.
- **typePlot**: The type of plot, either "density" or "boxplot".
- **addPoints**: If TRUE, points are superimposed on the boxplots.

Value

- A

Author(s)

Anne Biton

See Also

- `geom_density`, `geom_boxplot`, `geom_point`
plotDensAllAnnotInAllComp

Tests if groups of samples are differently distributed on the components according and do the corresponding plots.

Description

This function tests if the groups of samples formed by the variables (i.e sample annotations) are differently distributed on the components, in terms of contribution value (i.e of values in matrix \( A(icaSet) \)). The distribution of the groups on the components are represented using density plots. It is possible to restrict the tests and the plots to a subset of samples and/or components.

Usage

\[
\text{plotDensAllAnnotInAllComp}(\text{icaSet, params, path, keepVar = NULL, keepComp, samples, legend.title_list = NULL, colours = params["annot2col"], doPlot = TRUE, pval.cutoff = params["pvalCutoff"], typeImage = "png", filename = NULL, onlySign = TRUE)}
\]

Arguments

- **icaSet**: an object of class `IcaSet`
- **params**: An object of the class `MineICAParams` containing the parameters of the analysis
- **path**: the directory where the plots will be located
- **keepVar**: The variable labels to be considered, i.e a subset of (\text{varLabels(icaSet)})
- **samples**: a subset of sample names available in \text{samplenames(icaSet)}, if NULL (default) all samples are used
- **keepComp**: a subset of components available in \text{indComp(icaSet)}, if NULL (default) all components are used
- **legend.title_list**: A list of titles for each component, indexed by elements of argument keepVar, default is NULL
- **colours**: A vector of colours indexed by the variable levels, if missing the colours are automatically generated using \text{annot2Color}
- **doPlot**: if TRUE (default), the plots are drawn, else if FALSE only the tests are performed
- **pval.cutoff**: The threshold p-value for statistical significance
- **typeImage**: The type of image file where each plot is saved
- **filename**: A file where the results will be displayed in format HTML, if NULL no file is created
- **onlySign**: if TRUE (default), only the significant results are plotted
plotDensOneAnnotInAllComp

Details

This function writes an HTML file containing the results of the tests and links to the corresponding density plots. One png image is created by plot and located in the sub-directory plots of path. Each image is named by index-of-component_var.png. Wilcoxon or Kruskal-Wallis tests are applied depending on the number of groups of interest from the considered annotation (argument keepLev).

Value

Returns a data.frame of dimensions 'components x variables’ containing the p-values of the non-parametric tests (Wilcoxon or Kruskal-Wallis tests) which test if the samples groups defined by each variable are differently distributed on the components.

Author(s)

Anne Biton

See Also

wilcoxOrKruskalOnA, writeHtmlResTestsByAnnot, plotDensOneAnnotInAllComp

Examples

```r
## Not run:
## load an example of IcaSet
data(icaSetCarbayo)
## have a look at the sample annotations which are available
varLabels(icaSetCarbayo)
## create parameters, specifying the result path
params <- buildMineICAParams(resPath="carbayo/"

## trace the contributions of the samples according to their cancer stages and gender on the components
restests <- plotDensAllAnnotInAllComp(icaSet=icaSetCarbayo, keepVar=c("stage","SEX"),
   params=params, path="testPlotDens")

## End(Not run)
```

plotDensOneAnnotInAllComp

Tests if groups of samples are differently distributed on the components and do the corresponding plots.

Description

Given a variable of the phenotype data (i.e vector of sample annotations), this function tests if the groups of samples formed by this variable are differently distributed on the components, in terms of contribution values. The distribution of the groups on the components are represented using density plots. It is possible to restrict the tests and the plots to a subset of samples and/or components.
plotDensOneAnnotInAllComp

Usage

plotDensOneAnnotInAllComp(icaSet, keepVar, path = NULL, samples, keepComp, keepLev = NULL, colours = NULL, legend.title = NULL, doPlot = TRUE, cutoff = 0.05, onlySign = TRUE, resTests)

Arguments

icaSet an object of class IcaSet
keepVar a variable label, i.e the label of a column of the pheno data of icaSet available in (varLabels(icaSet)) wich contains the groups of interest
path the directory where the plots will be located
samples a subset of sample names available in sampnames(icaSet), if NULL (default) all samples are used
keepComp a subset of components available in indComp(icaSet), if NULL (default) all components are used
keepLev the groups of interest, i.e the levels of the annotation keepVar to be considered
colours A vector of colours indexed by the elements of keepLev, if NULL the colours are generated automatically using annot2Color
legend.title title of the legend
cutoff The threshold p-value for statistical significance
doPlot if TRUE (default), the plots are drawn, else if FALSE only test results are returned
onlySign if TRUE (default), only the significant results are plotted
resTests a vector of p-values per component, if NULL (default) the p-values are calculated using Wilcoxon or Kruskal-Wallis test

Details

Wilcoxon or Kruskal-Wallis tests are applied depending on the number of groups of interest from the considered annotation (argument keepLev). The plots are saved in individual files (one file per component) in arg 'path' if specified or in the current directory if not specified. Each individual file is named 'index-of-component_colAnnot.png.' Recall that the sample-contribution values are contained in A(icaSet), and the sample annotations in pData(icaSet).

One png image is created by plot and located in path. Each image is named by 'index-of-component_keepVar.png'.

Value

Returns a data.frame of dimensions ‘components x 1’ containing the results of the non-parametric tests (Wilcoxon or Kruskal-Wallis tests) that test if the groups of interest are differently distributed on the components

Author(s)

Anne Biton
plotMclust

See Also

wilcoxOrKruskalOnA, codewriteHtmlResTestsByAnnot, codewilcox.test, codekruskal.test

Examples

## Not run:
## load an example of IcaSet
data(icaSetCarbayo)

## have a look at the sample annotations which are available
varLabels(icaSetCarbayo)

## with doPlot=TRUE trace the contributions of the samples according
## to their grade on the components
restests <- plotDensOneAnnotInAllComp(icaSet=icaSetCarbayo, keepVar="GRADE",
        doPlot=FALSE)

## End(Not run)

plotMclust

Plots the Gaussian fitted by Mclust

Description

Given a result of function Mclust applied on a numeric vector, this function add the fitted Gaussian
to a previous plot. This is an internal function called by plotPosSamplesInComp.

Usage

plotMclust(mc, data)

Arguments

mc The result of Mclust function applied to argument data
data The vector of numeric values on which was applied Mclust

Details

This function can only deal with at the most three Gaussian.

Value

NULL

Author(s)

Anne Biton
Examples

```r
## create a mix of two Gaussian
v <- c(rnorm(80, mean=-0.5, sd=1), rnorm(80, mean=1, sd=0.2))
## apply Mclust
mc <- Mclust(v)
## plot fitted Gaussian on histogram of v
hist(v, freq=FALSE)
MineICA:::plotMclust(mc=mc, data=v)
```

plotMix

Plots an histogram and Gaussian fitted by Mclust

Description

Given a result of function Mclust applied to a numeric vector, this function draws the fitted Gaussian on the histogram of the data values.

Usage

```r
plotMix(mc, data, nbBreaks, traceDensity = TRUE, title = "", xlim, ylim, ...)
```

Arguments

- `mc`: The result of Mclust function applied to argument `data`
- `data`: A vector of numeric values
- `nbBreaks`: The number of breaks for the histogram
- `traceDensity`: If TRUE (default) density are displayed on the y-axis, else if FALSE counts are displayed on the y-acis
- `title`: A title for the plot
- `xlim`: x-axis limits to be used in the plot
- `ylim`: y-axis limits to be used in the plot
- `...`: additional arguments for hist

Details

A shapiro test p-value is added to the plot title. This function can only deal with at the most three Gaussian.

Value

NULL

Author(s)

Anne Biton
plotPosAnnotInComp

See Also

hist, Mclust

Examples

```r
## create a mix of two Gaussian
v <- c(rnorm(80, mean=-0.5, sd=1), rnorm(80, mean=1, sd=0.2))
## apply Mclust
mc <- Mclust(v)
## plot fitted Gaussian on histogram of v
plotMix(mc=mc, data=v, nbBreaks=30)
```

plotPosAnnotInComp

Histograms of sample contributions for each annotation level

Description

This function plots the positions of groups of samples formed by the variables (i.e the sample annotations) across all the components of an object of class icaSet. For each variable level (e.g for each tumor stage) this function plots the positions of the corresponding samples (e.g the subset of samples having this tumor stage) within the histogram of the global sample contributions. The plots are saved in pdf file, one file is created per variable. The pdf files are names ‘variable.pdf’ and save either in pathPlot if specified or the current directory.

Usage

```r
plotPosAnnotInComp(icaSet, params,
keepVar = varLabels(icaSet),
keepComp = indComp(icaSet),
keepSamples = sampleNames(icaSet), pathPlot = NULL,
breaks = 20, colAll = "grey74", colSel, resClus,
funClus = c("Mclust", "kmeans"), nbClus = 2,
by = c("annot", "component"),
typeImage = c("pdf", "png", "none"), ...)
```

Arguments

- **icaSet**: An object of class IcaSet
- **params**: A MineICAParams object
- **keepVar**: The variable labels to be considered, i.e a subset of the column labels of the pheno data of icaSet available in (varLabels(icaSet))
- **keepComp**: A subset of components available in indComp(icaSet); by default, all components are used
- **keepSamples**: A subset of samples, must be available in sampleNames(icaSet); by default, all samples are used
- **pathPlot**: A character specifying the path where the plots will be saved
plotPosAnnotInComp

breaks The number of breaks to be used in the histograms

colSel The colour of the histogram of the group of interest, default is "red"

colAll The colour of the global histogram, default is "grey74"

resClus A list containing the outputs of function clusterSamplesByComp, which consists of sample clustering applied to matrix A of argument icaSet. If missing, the clustering is performed by the function.

funClus The clustering method to be used, either "Mclust" or "kmeans". If resClus is not missing, equals resClus$funClus.

nbClus If resClus is missing, it provides the number of clusters to be computed by funClus, default is 2

by Either "annot" to plot the histograms of each variable across all components, or "component" to plot the histograms for each component across variables. When by="annot" one pdf file is created by variable name, while when annot="component", one pdf file is created by component.

typeImage The type of image to be created, either "pdf" (default) or "png". "png" is not recommended, unless there are at the most 4 histograms to be plotted, because it does not allow to deal with multiple pages of plots.

... Additional parameters for function hist

Details

The plotted values are the sample contributions across the components, i.e across the columns of A(icaSet).

If argument resClus is missing, the function computes the clustering of the samples on each component (i.e on each column of A(icaSet)) using funClus and nbClus.

The association between the clusters and the considered sample group is tested using a chi-square test. The p-values of these tests are available in the title of each plot.

When by="annot" this function plots the histograms of each variable across all components, to plot the histograms for each component across variables, please use by="component".

Value

NULL

Author(s)

Anne Biton

See Also

plotPosSamplesInComp, chisq.test
Examples

## Not run:
## load an example of IcaSet
data(icaSetCarbayo)

## Use icaSetCarbayo, look at the available annotations
varLabels(icaSetCarbayo)

## Plot positions of samples in components according to annotations 'SEX' and 'STAGE'
# plots are saved in files SEX.pdf and STAGE.pdf created in the current directory
plotPosAnnotInComp(icaSet=icaSetCarbayo, keepVar=c("SEX","STAGE"), keepComp=1:2, funClus="Mclust")
# specify arg 'pathPlot' to save the pdf in another directory, but make sure it exists before
# specify arg 'by="comp"' to create one pdf file per component

## End(Not run)

---

plotPosOneAnnotInComp_ggplot

Tests if groups of samples are differently distributed on the components and do the corresponding plots.

Description

Given a variable of the phenoData, this function tests if the groups of samples formed by this variable are differently distributed, in terms of contribution value (i.e. values in matrix A(icaSet)), on the components. The distribution of the groups on the components are represented using density plots. It is possible to restrict the tests and the plots to a subset of samples and/or components.

Usage

plotPosOneAnnotInComp_ggplot(icaSet, params, colAnnot,
   keepLev = NULL, keepComp, samples, colAll = "grey74",
   binwidth = 0.1, addExpr = TRUE, file = NULL, ...)

Arguments

icaSet  An object of class IcaSet
params  An object of the class MineICAParams containing the parameters of the analysis
colAnnot  a variable label, i.e one of the variables available in varLabels(icaSet)) containing the groups of interest
samples  a subset of sample names available in sampleNames(icaSet), if NULL (default) all samples are used
keepComp  a subset of components available in indComp(icaSet), if NULL (default) all components are used
keepLev  the groups of interest, i.e the levels of the variable colAnnot to be considered
colAll  The colour of the global histogram, default is "grey74"
plotPosOneAnnotLevInComp_ggplot

file  the file where the histograms will be plotted
addExpr  if TRUE (default) the expression profiles of the witness genes of each component are added below the plot
binwidth  binwidth of the histogram (default is 0.1)
...  other parameters for geom_histogram function from ggplot2 package

Details

Wilcoxon or Kruskal-Wallis tests are applied depending on the number of groups of interest from the considered annotation (argument keepLev). One png image is created by plot and located in path. Each image is named by component-of-component_colAnnot.png.

Value

NULL

Author(s)

Anne Biton

See Also

plotPosOneAnnotLevInComp_ggplot, geom_histogram

plotPosOneAnnotLevInComp_ggplot

Plots the position of a subset of samples in the histogram of all samples using ggplot2.

Description

Given a sample annotation (e.g a tumor specific stage), this function plots the positions of the corresponding samples (e.g the subset of samples having this tumor stage) within the histogram of the global sample contributions. This function is called by plotPosOneAnnotInComp_ggplot and is only dedicated to the plot of the histogram using the package ggplot2.

Usage

plotPosOneAnnotLevInComp_ggplot(annot, colAnnot, selLev, comp, title = NULL, colSel = "red", colAll = "grey74", binwidth = 0.1, geneExpr = NULL, geneRef = NULL, ...)
Arguments

- **annot**: a data.frame of dimensions 'samples x annotations' with one column corresponding to the component to trait ("comp" column) and one column corresponding to the groups of interest ("interest" column)
- **colAnnot**: the name of a column of the argument annot with the groups of interest
- **selLev**: the name of the group of interest
- **comp**: a vector of sample contributions
- **colSel**: the colour of the histogram of the group of interest, default is "red"
- **colAll**: the colour of the global histogram
- **geneExpr**: a vector of values representative of the component, e.g. the expression of the witness gene of the component
- **geneRef**: the ID of the feature/gene geneExpr corresponds to, e.g. the name of the witness gene
- **title**: A title for the plot
- **binwidth**: set the width of the bins, see geom_histogram
- **...**: other parameters given to geom_histogram

Value

An object of class ggplot2 containing the histogram

Author(s)

Anne Biton

See Also

geom_histogram

---

plotPosSamplesInComp **Histograms of sample subsets**

Description

This function plots the positions of several groups of samples across all the components of an icaSet object.

Usage

plotPosSamplesInComp(samplesByGroup, labGroups = NULL, icaSet, keepComp = indComp(icaSet), file = NULL, breaks = 20, colAll = "grey74", colSel = "red", titlesup = ",", resClus, funClus = c("Mclust", "kmeans"), ...)
plotPosSamplesInComp

Arguments

- **samplesByGroup**: A list whose elements are vector of sample names, these sample names must be available in `sampleNames(icaSet)`. The list should be indexed by the name of the corresponding groups.
- **labGroups**: A vector of group names, will be used to add names to `sampleByGroup` if `names(samplesByGroup)` is NULL.
- **icaSet**: An object of class `IcaSet`
- **keepComp**: A subset of components available in `indComp(icaSet)`, if NULL (default) all components are used.
- **file**: A pdf file
- **breaks**: The number of breaks to be used in the histograms
- **colSel**: The colour of the histogram of the group of interest, default is "red"
- **colAll**: The colour of the global histogram, default is "grey74"
- **resClus**: A list containing the outputs of function `clusterSamplesByComp`, which consists of results of clustering applied to matrix A of argument icaSet.
- **funClus**: Specifies the clustering method used, either "Mclust" or "kmeans". If `resClus` is not missing, equals `resClus$funClus`.
- **titlesup**: Additional title for the histograms
- **...**: Additional parameters for function `hist`.

Details

For each subgroup of samples this function plots their positions within the histogram of the global sample contributions.

The values of interest are the sample contributions across the components, i.e across the columns `A(icaSet)`.

If argument `resClus` is not missing, the association between the clusters and the sub-groups of samples is tested using a chi-square test. The p-values of these tests are available in the title of each plot.

Value

- **NULL**

Author(s)

- Anne Biton

See Also

- `hist`, `IcaSet`
Examples

```r
## Not run:
## load an example of IcaSet
data(icaSetCarbayo)

## selection of sample groups according to annotations STAGE
samplesByGroup <- lapply(split(pData(icaSetCarbayo),pData(icaSetCarbayo)[c("STAGE")]), rownames)
# select groups including at least 2 samples
samplesByGroup <- samplesByGroup[which(unlist(lapply(samplesByGroup,length))>1)]

## clustering of samples according to A using Mclust imposing two Gaussian
resClus <- clusterSamplesByComp(icaSet=icaSetCarbayo,funClus="Mclust", nbClus=2, clusterOn="A")

## Plot positions of the groups in 5th component
pdf(file="stageOnIC5.pdf", height = 8.267717, width = 29.7/2.54, paper = 'a4r', title="stageOnIC5")
plotPosSamplesInComp(samplesByGroup=samplesByGroup, icaSet=icaSetCarbayo, funClus="Mclust", resClus = resClus, keepComp=5)
dev.off()

## End(Not run)
```

Description

This function plots the heatmaps representing the measured values of the contributing features/genes on each component. It also plots the sample annotations above each heatmap using colours.

Usage

```r
plot_heatmapsOnSel(icaSet, selCutoff = 4,
level = c("features", "genes"), samplesOrder,
featuresOrder, selectionByComp, keepVar,
keepComp = indComp(icaSet), doSamplesDendro = TRUE,
doGenesDendro = TRUE,
heatmapCol = maPalette(low = "blue", high = "red", mid = "yellow", k = 44),
file = "", path = "", annot2col, ...)
```

Arguments

- `icaSet` The IcaSet object
- `selCutoff` A numeric threshold used to select the contributing genes based on their projection values. Must be either of length 1 and the same threshold is applied to all components, or of length equal to the number of components and one specific threshold is used for each component.
samplesOrder  A list providing the order of the samples, per component, to be used in the heatmaps. If missing, the contribution values of the samples are used to rank the columns of the heatmaps.

featuresOrder  A list providing the order of the genes, per component, to be used in the heatmaps. If missing, the projection values of the genes are used to rank the rows of the heatmaps.

selectionByComp  A list of gene projections per component already restricted to the contributing genes, if missing is computed by the function.

level  A character indicating which data level is used to plot the heatmaps: either 'features' to represent the data at the feature levels (e.g expression profiles of probe sets), or 'genes' to represent the data at the annotated-features level (e.g gene expression profiles).

keepVar  The variable labels to be considered, i.e a subset of the column labels of the pheno data of icaSet available in (varLabels(icaSet))

keepComp  A subset of components, must be included in indComp(icaSet). By default, all components are used.

doSamplesDendro  A logical indicating whether a hierarchical clustering has to be performed on the data matrix restricted to the contributing features/genes, and whether the corresponding dendrogram has to be plotted, default is TRUE.

doGenesDendro  A logical indicating if the dendrogram of features/genes has to be plotted, default is FALSE.

heatmapCol  A list of colors used to for heatmap coloring (see argument col of the function image).

file  A character to add to each pdf file name. This function creates one file by component named "index-of-component_file.pdf".

path  A directory for the output pdf files, must end with "/". Default is current directory.

annot2col  A vector of colours indexed by the levels of the variables of icaSet (i.e all the annotation values available in pData(icaSet)). If missing the colours are generated automatically using the function annot2Color

Details

This function restricts the data matrix of an IcaSet object to the contributing genes/features, and order features/genes and samples either as asked by the user or according to their values in the ICA decomposition.

The heatmap is plotted using a slightly modified version of the function heatmap.plus from the package of the same name. By default in this function, the hierarchical clustering is calculated using the function agnes with euclidean metric and Ward’s method.
Value

A list with one element per component, each of them being a list consisting of three elements:

- **x** the matrix represented by the heatmap,
- **breaks** the breaks used for the colours of the heatmap,
- **dendro** the dendrogram.

Author(s)

Anne Biton

See Also

heatmap.plus, image, annot2Color, build_sortHeatmap

Examples

```r
## Not run:
## load an example of IcaSet object
data(icaSetCarbayo)

## check which variables you would like to use in the heatmap
varLabels(icaSetCarbayo)
keepVar <- c("STAGE","SEX")
## Use only component 1
keepComp <- 1

## For each component, select contributing *genes* using a threshold of 2 on the absolute projection values,
## and plot heatmaps of these contributing genes by ordering genes and samples according to their contribution values
plot_heatmapsOnSel(icaSet = icaSetCarbayo, selCutoff = 2, level = "genes", keepVar = keepVar,
                 keepComp=1, doSamplesDendro = TRUE, doGenesDendro = TRUE,
                 heatmapCol = maPalette(low = "blue",high = "red", mid = "yellow", k=44),
                 file = "heatmapWithoutDendro_zval3.pdf")

## For each considered component, select contributing *features* using a threshold of 2 on the absolute projection values,
## and plot heatmaps of these contributing genes with dendrograms
plot_heatmapsOnSel(icaSet = icaSetCarbayo, selCutoff = 2, level = "features", keepVar = keepVar,
                 keepComp=1, doSamplesDendro = TRUE, doGenesDendro = TRUE,
                 heatmapCol = maPalette(low = "blue",high = "red", mid = "yellow", k=44),
                 file = "heatmapWithDendro_zval3.pdf")

## End(Not run)
```
qualVarAnalysis  Tests association between qualitative variables and components.

Description

This function tests if the groups of samples formed by the variables are differently distributed on the components, in terms of contribution value (i.e. of values in matrix $A(icaSet)$). The distribution of the samples on the components are represented using either density plots or boxplots. It is possible to restrict the tests and the plots to a subset of samples and/or components.

Usage

```r
qualVarAnalysis(params, icaSet, keepVar,
    keepComp = indComp(icaSet),
    keepSamples = sampleNames(icaSet),
    adjustBy = c("none", "component", "variable"),
    method = "BH", doPlot = TRUE, typePlot = "density",
    addPoints = FALSE, onlySign = TRUE,
    cutoff = params["pvalCutoff"],
    colours = annot2col(params), path = "qualVarAnalysis/",
    filename = "qualVar", typeImage = "png")
```

Arguments

- `params` An object of class MineICAParams providing the parameters of the analysis.
- `icaSet` An object of class IcaSet.
- `keepVar` The variable labels to be considered, must be a subset of varLabels(icaSet).
- `keepComp` A subset of components, must be included in indComp(icaSet). By default, all components are used.
- `keepSamples` A subset of samples, must be included in sampleNames(icaSet). By default, all samples are used.
- `adjustBy` The way the p-values of the Wilcoxon and Kruskal-Wallis tests should be corrected for multiple testing: "none" if no p-value correction has to be done, "component" if the p-values have to be corrected by component, "variable" if the p-values have to be corrected by variable.
- `method` The correction method, see p.adjust for details, default is "BH" for Benjamini & Hochberg.
- `doPlot` If TRUE (default), the plots are done, else only tests are performed.
- `addPoints` If TRUE, points are superimposed on the boxplot.
- `typePlot` The type of plot, either "density" or "boxplot".
- `onlySign` If TRUE (default), only the significant results are plotted.
- `cutoff` A threshold p-value for statistical significance.
- `colours` A vector of colours indexed by the variable levels, if missing the colours are automatically generated using annot2Color.
**qualVarAnalysis**

- **path**
  A directory _within resPath(params)_ where the files containing the plots and the p-value results will be located. Default is "qualVarAnalysis/".

- **typeImage**
  The type of image file to be used.

- **filename**
  The name of the HTML file containing the p-values of the tests, if NULL no file is created.

**Details**

This function writes an HTML file containing the results of the tests as a an array of dimensions 'variables * components' containing the p-values of the tests. When a p-value is considered as significant according to the threshold cutoff, it is written in bold and filled with a link pointing to the corresponding plot. One image is created by plot and located into the sub-directory "plots/" of path. Each image is named by index-of-component_var.png. Wilcoxon or Kruskal-Wallis tests are performed depending on the number of groups of interest in the considered variable (argument keepLev).

**Value**

Returns A data.frame of dimensions 'components x variables' containing the p-values of the non-parametric tests (Wilcoxon or Kruskal-Wallis tests) wich test if the samples groups defined by each variable are differently distributed on the components.

**Author(s)**

Anne Biton

**See Also**

- [qualVarAnalysis](#), [p.adjust](#), [link{writeHtmlResTestsByAnnot}](#), [wilcox.test](#), [kruskal.test](#)

**Examples**

```r
### load an example of IcaSet
data(icaSetCarbayo)

### build MineICAParams object
params <- buildMineICAParams(resPath="carbayo/"

### Define the directory containing the results
dir <- paste(resPath(params), "comp2annot/", sep="")

### Run tests, make no adjustment of the p-values,
# for variable grade and components 1 and 2,
# and plot boxplots when 'doPlot=TRUE'.
qualVarAnalysis(params=params, icaSet=icaSetCarbayo, adjustBy="none", typePlot="boxplot",
keepVar="GRADE", keepComp=1:2, path=dir, doPlot=FALSE)
```
quantVarAnalysis  

Correlation between variables and components.

Description

This function tests if numeric variables are correlated with components.

Usage

quantVarAnalysis(params, icaSet, keepVar, 
keepComp = indComp(icaSet),
keepSamples = sampleNames(icaSet),
adjustBy = c("none", "component", "variable"),
method = "BH", typeCor = "pearson", doPlot = TRUE,
onlySign = TRUE, cutoff = 0.4,
cutoffOn = c("cor", "pval"), colours,
path = "quantVarAnalysis/", filename = "quantVar",
typeImage = "png")

Arguments

params  An object of class MineICAParams providing the parameters of the analysis.
icaSet  An object of class IcaSet.
keepVar The variable labels to be considered, must be a subset of varLabels(icaSet).
keepComp A subset of components, must be included in indComp(icaSet). By default, all components are used.
keepSamples A subset of samples, must be included in sampleNames(icaSet). By default, all samples are used.
adjustBy The way the p-values of the Wilcoxon and Kruskal-Wallis tests should be corrected for multiple testing: "none" if no p-value correction has to be done, "component" if the p-values have to be corrected by component, "variable" if the p-values have to be corrected by variable
method The correction method, see p.adjust for details, default is "BH" for Benjamini & Hochberg.
doPlot If TRUE (default), the plots are done, else only tests are performed.
onlySign If TRUE (default), only the significant results are plotted.
cutoff A threshold p-value for statistical significance.
cutoffOn The value the cutoff is applied to, either "cor" for correlation or "pval" for p-value
typeCor the type of correlation to be used, one of c("pearson", "spearman", "kendall").
colours A vector of colours indexed by the variable levels, if missing the colours are automatically generated using annot2Color.
path  A directory \_within resPath(params)\_ where the files containing the plots and
the p-value results will be located. Default is "quantVarAnalysis/".

typeImage  The type of image file to be used.

filename  The name of the HTML file containing the p-values of the tests, if NULL no file
is created.

Details

This function writes an HTML file containing the correlation values and test p-values as a an array
of dimensions 'variables * components' containing the p-values of the tests. When a p-value is
considered as significant according to the threshold cutoff, it is written in bold and filled with
a link pointing to the corresponding plot. One image is created by plot and located into the sub-
directory "plots/" of path. Each image is named by index-of-component\_var.png.

Value

Returns A data.frame of dimensions 'components x variables' containing the p-values of the non-
parametric tests (Wilcoxon or Kruskal-Wallis tests) wich test if the samples groups defined by each
variable are differently distributed on the components.

Author(s)

Anne Biton

See Also

qualVarAnalysis, p.adjust, link{writeHtmlResTestsByAnnot}, code

Examples

## load an example of IcaSet
data(icaSetCarbayo)

# build MineICAParams object
params <- buildMineICAParams(resPath="carbayo/")

# Define the directory containing the results
dir <- paste(resPath(params), "comp2annottest/", sep="")

# Check which variables are numeric looking at the pheno data, here only one  -> AGE
# pData(icaSetCarbayo)

## Perform pearson correlation tests and plots association corresponding
## to correlation values larger than 0.2
quantVarAnalysis(params=params, icaSet=icaSetCarbayo, keepVar="AGE", keepComp=1:2,
                adjustBy="none", path=dir, cutoff=0.2, cutoffOn="cor")

## Not run:
## Perform Spearman correlation tests and do scatter plots for all pairs
quantVarAnalysis(params=params, icaSet=icaSetCarbayo, keepVar="AGE", adjustBy="none", path=dir,
cutoff=0.1, cutoffOn="cor", typeCor="spearman", onlySign=FALSE)
## Perform pearson correlation tests and plots association corresponding to p-values lower than 0.05 when `doPlot=TRUE`
quantVarAnalysis(params=params, icaSet=icaSetCarbayo, keepVar="AGE", adjustBy="none", path=dir, cutoff=0.05, cutoffOn="pval", doPlot=FALSE)

## End(Not run)

---

**readA**

### Description
readA

### Usage

`readA(Afile, datfile, dat, annot = TRUE)`

### Arguments

- **Afile**: The file which contains the matrix of sample contributions. It must be a txt file where the separator is white space, that is one or more spaces, tabs, newlines or carriage returns
- **datfile**: The file which contains the matrix (of dimension features x samples) based on which the matrix A was calculated
- **dat**: The data based on which the matrix A was calculated (features x samples)
- **annot**: TRUE (default) if the Afile contains rownames of matrix A, FALSE if the rownames has to be extracted from dat

### Details

This function reads and annotates matrix A.

The matrix dat must be the one on which the matrix A was calculated. It is assumed that the number of components is lower than the number of samples, the matrix will be transposed to have dimension 'samples x components' according to this assumption. If annot is FALSE, colnames of dat are used to annotate rownames of A.

### Value

This function returns a matrix of dimension samples x components with rownames filled with sample IDs.

### Author(s)

Anne Biton
Description

This function reads and annotates matrix S.

Usage

\texttt{readS(Sfile, datfile, dat, annot = TRUE)}

Arguments

\begin{description}
\item[Sfile] The file which contains the matrix of feature projections. It must be a txt file where the separator is white space, that is one or more spaces, tabs, newlines or carriage returns.
\item[datfile] The file which contains the matrix (of dimension features x samples) based on which the matrix S was calculated. It must be a txt file where the separator is white space, that is one or more spaces, tabs, newlines or carriage returns.
\item[dat] The data based on which the matrix A was calculated (features x samples)
\item[annot] TRUE (default) if the Afile contains rownames of matrix A, FALSE if the rownames has to be extracted from dat
\end{description}

Details

The matrix dat must be the one on which the matrix S was calculated. It is assumed that the number of components is lower than the number of features, the matrix will be transposed to have dimension 'features x components' according to this assumption. If annot is FALSE, rownames of dat are used to annotate rownames of S.

Value

This function returns a matrix of dimension features x components with rownames filled with feature IDs.

Author(s)

Anne Biton
**relativePath**  
*Relative path*

**Description**
Computes the relative path between two imbricated paths

**Usage**
```r
relativePath(path1, path2)
```

**Arguments**
- `path1`: The first path
- `path2`: The second path

**Details**
- `path1` and `path2` must be imbricated.

**Value**
The relative path between `path1` and `path2`

**Author(s)**
Anne Biton

**Examples**
```r
path1 <- "home/lulu/res/gene2comp/
path2 <- "home/lulu/res/comp2annot/invasive/"
relativePath(path1,path2)
```

---

**runAn**  
*Run analysis of an IcaSet object*

**Description**
This function runs the analysis of an ICA decomposition contained in an IcaSet object, according to the parameters entered by the user and contained in a MineICAParams.
Usage

runAn(params, icaSet, keepVar,
     heatmapCutoff = params["selCutoff"],
     funClus = c("Mclust", "kmeans"), nbClus,
     clusterOn = "A", keepComp, keepSamples,
     adjustBy = c("none", "component", "variable"),
     typePlot = c("boxplot", "density"),
     mart = useMart(biomart = "ensembl", dataset = "hsapiens_gene_ensembl"),
     dbGOstats = c("KEGG", "GO"), ontoGOstats = "BP",
     condGOstats = TRUE,
     cutoffGOstats = params["pvalCutoff"],
     writeGenesByComp = TRUE, onlySign = T, runClustering = FALSE,
     plotHist = TRUE, plotHeatmap = TRUE)

Arguments

params An object of class MineICAParams containing the parameters of the analysis.
icaSet An object of class IcaSet.
keepVar The variable labels to be considered, i.e a subset of the annotation variables available in (varLabels(icaSet)).
keepSamples The samples to be considered, i.e a subset of (sampleNames(icaSet)).
heatmapCutoff The cutoff (applied to the scaled feature/gene projections contained in S/SByGene) used to select the contributing features/genes.
funClus The function to be used to cluster the samples, must be one of c("Mclust", "kmeans", "pam", "pamk", "hclust", "agnes"). Default is "Mclust".
bClus The number of clusters to be computed when applying funClus. Can be missing (default) if funClus="Mclust" or funClus="pamk".
keepComp The indices of the components to be analyzed, must be included in indComp(icaSet). If missing, all components are treated.
adjustBy The way the p-values of the Wilcoxon and Kruskal-Wallis tests should be corrected for multiple testing: "none" if no p-value correction has to be done, "component" if the p-values have to be corrected by component, "annotation" if the p-values have to be corrected by variable.
typePlot The type of plot used to show distribution of sample-groups contributions, either "density" or "boxplot"
mart A mart object used for annotation, see function useMart
dbGOstats The used database to use ("GO" and/or "KEGG"), default is both.
ontoGOstats A string specifying the GO ontology to use. Must be one of 'BP', 'CC', or 'MF', see GOHyperGParams. Only used when argument dbGOstats is 'GO'.
condGOstats A logical indicating whether the calculation should conditioned on the GO structure, see GOHyperGParams.
cutoffGOstats The p-value threshold used for selecting enriched gene sets, default is params["pvalCutoff"]
writeGenesByComp
If TRUE (default) the gene projections ($S_{\text{ByGene}}(\text{icaSet})$) are written in an html file and annotated using biomaRt for each component.

writeFeaturesByComp
If TRUE (default) the feature projections ($S(\text{icaSet})$) are written in an html file and annotated using biomaRt for each component.

runGOstats
If TRUE the enrichment analysis of the contributing genes is run for each component using package GOstats (default is TRUE).

plotHist
If TRUE the position of the sample annotations within the histograms of the sample contributions are plotted.

plotHeatmap
If TRUE the heatmap of the contributing features/genes are plotted for each component.

runClustering
If TRUE the potential associations between a clustering of the samples (performed according to the components), and the sample annotations, are tested using chi-squared tests.

runVarAnalysis
If TRUE the potential associations between sample contributions (contained in $A(\text{icaSet})$) are tested using Wilcoxon or Kruskal-Wallis tests.

onlySign
If TRUE (default), only the significant results are plotted in functions qualVarAnalysis, quantVarAnalysis, clusVarAnalysis, else all plots are done.

selCutoffWrite
The cutoff applied to the absolute feature/gene projection values to select the features/genes that will be annotated using package biomaRt, default is 2.5.

clusterOn
Specifies the matrix used to apply clustering if runClustering=TRUE:
"A": the clustering is performed in one dimension, on the vector of sample contributions,
"S": the clustering is performed on the original data restricted to the contributing individuals,
"AS": the clustering is performed on the matrix formed by the product of the column of A and the row of S.

Details
This function calls functions of the MineICA package depending on the arguments:

writeProjByComp (if writeGenesByComp=TRUE or writeFeaturesByComp) which writes in html files the description of the features/genes contributing to each component, and their projection values on all the components.

plot_heatmapsOnSel (if plotHeatmap=TRUE) which plots heatmaps of the data restricted to the contributing features/genes of each component.

plotPosAnnotInComp (if plotHist=TRUE) which plots, within the histogram of the sample contribution values of every component, the position of groups of samples formed according to the sample annotations contained in pData(icaSet).

clusterSamplesByComp (if runClustering=TRUE) which clusters the samples according to each component.

clusVarAnalysis (if runClustering=TRUE) which computes the chi-squared test of association between a given clustering of the samples and each annotation level contained in pData(icaSet), and summarizes the results in an HTML file.
runAn

runEnrich (if runGOstats=TRUE) which performs enrichment analysis of the contributing genes of the components using package GOstats.

qualVarAnalysis and quantVarAnalysis (if varAnalysis=TRUE) which tests if the groups of samples formed according to sample annotations contained in pData(icaSet) are differently distributed on the components, in terms of contribution value.

Several directories containing the results of each analysis are created by the function:

ProjByComp: contains the annotations of the features or genes, one file per component;
varAnalysisOnA: contains two directories: 'qual/' and 'quant/' which respectively contain the results of the association between components qualitative and quantitative variables;
Heatmaps: contains the heatmaps (one pdf file per component) of contributing genes by component;
varOnSampleHist: contains the histograms of sample contributions superimposed with the histograms of the samples grouped by variable;
cluster2var: contains the association between a clustering of the samples performed on the mixing matrix A and the variables.

Value

NULL

Author(s)

Anne Biton

See Also

writeProjByComp.

Examples

## Not run:

## load an example of IcaSet
data(icaSetCarbayo)
## make sure the 'mart' attribute is correctly defined
mart(icaSetCarbayo) <- useMart(biomart="ensembl", dataset="hsapiens_gene_ensembl")

## creation of an object of class MineICAParams
## here we use a low threshold because 'icaSetCarbayo' is already
# restricted to the contributing features/genes
params <- buildMineICAParams(resPath="~/resMineICA Carbayo test RunAn/", selCutoff=2, pvalCutoff=0.05)
require(hgu133a.db)

runAn(params=params, icaSet=icaSetCarbayo)

## End(Not run)
runCompareIcaSets

Description
This function encompasses the comparison of several IcaSet objects using correlations and the plot of the corresponding correlation graph. The IcaSet objects are compared by calculating the correlation between either projection values of common features or genes, or contributions of common samples.

Usage
runCompareIcaSets(icaSets, labAn,
  type.corr = c("pearson", "spearman"), cutoff_zval = 0,
  level = c("genes", "features", "samples"),
  fileNodeDescr = NULL, fileDataGraph = NULL,
  plot = TRUE, title = "", col, cutoff_graph = NULL,
  useMax = TRUE, tkplot = FALSE)

Arguments
icaSets List of IcaSet objects, e.g results of ICA decompositions obtained on several datasets.
labAn Vector of names for each icaSet, e.g the the names of the datasets on which were calculated the decompositions.
type.corr Type of correlation to compute, either 'pearson' or 'spearman'.
cutoff_zval Either NULL or 0 (default) if all genes are used to compute the correlation between the components, or a threshold to compute the correlation using the genes that have at least a scaled projection higher than cutoff_zval. Will be used only when level is one of c("features","genes").
level Data level of the IcaSet objects on which is applied the correlation. It must correspond to a data level shared by the IcaSet objects: 'samples' if they were applied to common samples (correlations are computed between matrix A), 'features' if they were applied to common features (correlations are computed between matrix S), 'genes' if they share gene IDs after annotation into genes (correlations are computed between matrix SBByGene).
fileNodeDescr File where node descriptions are saved (useful when the user wants to visualize the graph using Cytoscape).
fileDataGraph File where graph description is saved (useful when the user wants to visualize the graph using Cytoscape).
plot if TRUE (default) plot the correlation graph
title title of the graph
col vector of colors indexed by elements of labAn; if missing, colors will be automatically attributed
runCompareIcaSets

cutoff_graph the cutoff used to select pairs that will be included in the graph
useMax if TRUE, the graph is restricted to edges that correspond to maximum correlation between components, see details
tkplot If TRUE, performs interactive plot with function tkplot, else uses plot.igraph

Details

This function calls four functions: compareAn which computes the correlations, compareAn2graphfile which builds the graph, nodeAttrs which builds the node description data, and plotCorGraph which uses tkplot to plot the graph in an interactive device.

If the user wants to see the correlation graph in Cytoscape, he must fill the arguments fileDataGraph and fileNodeDescr, in order to import the graph and its node descriptions as a .txt file in Cytoscape.

When labAn is missing, each element i of icaSets is labeled as 'Ani'.

The user must carefully choose the data level used in the comparison: If level='samples', the correlations are based on the mixing matrices of the ICA decompositions (of dimension samples x components). 'A' will be typically chosen when the ICA decompositions were computed on the same dataset, or on datasets that include the same samples. If level='features' is chosen, the correlation is calculated between the source matrices (of dimension features x components) of the ICA decompositions. 'S' will be typically used when the ICA decompositions share common features (e.g same microarrays). If level='genes', the correlations are calculated on the attributes 'SByGene' which store the projections of the annotated features. 'SByGene' will be typically chosen when ICA were computed on datasets from different technologies, for which comparison is possible only after annotation into a common ID, like genes.

cutoff_zval is only used when level is one of c('features', 'genes'), in order to restrict the correlation to the contributing features or genes.

When cutoff_zval is specified, for each pair of components, genes or features that are included in the circle of center 0 and radius cutoff_zval are excluded from the computation of the correlation.

It must be taken into account by the user that if cutoff_zval is different from NULL or zero, the computation will be much slower since each pair of component is treated individually.

Edges of the graph are built based on the correlation values between the components. Absolute values of correlations are used since components have no direction.

If useMax is TRUE each component will be linked to only one component of each other IcaSet that corresponds to the most correlated component among all components of the same IcaSet. If cutoff_graph is specified, only correlations exceeding this value are taken into account to build the graph. For example, if cutoff is 1, only relationships between components that correspond to a correlation value higher than 1 will be included. Absolute correlation values are used since the components have no direction.

The contents of the returned list are

dataGraph: dataGraph data.frame that describes the correlation graph,
nodeAttrs: nodeAttrs data.frame that describes the node of the graph
graph graph the graph as an igraph-object,
graphid: graphid the id of the graph plotted using tkplot.
runCompareIcaSets

Value
A list consisting of

- **dataGraph**: a data.frame defining the correlation graph
- **nodeAttrs**: a data.frame describing the node of the graph,
- **graph**: the graph as an object of class *igraph*,
- **graphid** the id of the graph plotted with tkplot.

Author(s)
Anne Biton

See Also

`compareAn2graphfile`, `compareAn`, `cor2An`, `plotCorGraph`

Examples

dat1 <- data.frame(matrix(rnorm(10000),ncol=10,nrow=1000))
rownames(dat1) <- paste("g", 1:1000, sep="")
colnames(dat1) <- paste("s", 1:10, sep="")
dat2 <- data.frame(matrix(rnorm(10000),ncol=10,nrow=1000))
rownames(dat2) <- paste("g", 1:1000, sep="")
colnames(dat2) <- paste("s", 1:10, sep="")

## run ICA
resJade1 <- runICA(X=dat1, nbComp=3, method= "JADE")
resJade2 <- runICA(X=dat2, nbComp=3, method= "JADE")

## build params
params <- buildMineICAParams(resPath="toy/"

## build IcaSet objects
icaSettoy1 <- buildIcaSet(params=params, A=data.frame(resJade1$A), S=data.frame(resJade1$S),
dat=dat1, alreadyAnnot=TRUE)$icaSet
icaSettoy2 <- buildIcaSet(params=params, A=data.frame(resJade2$A), S=data.frame(resJade2$S),
dat=dat2, alreadyAnnot=TRUE)$icaSet

## compare IcaSet objects
## use tkplot=TRUE to get an interactive graph
rescomp <- runCompareIcaSets(icaSets=list(icaSettoy1, icaSettoy2), labAn=c("toy1","toy2"),
type.corr="pearson", level="genes", tkplot=FALSE)

## Not run:
## load the microarray-based gene expression datasets
## of breast tumors
library(breastCancerMAINZ)
library(breastCancerVDX)
data(mainz)
data(vdx)
## Define a function used to build two examples of IcaSet objects
## and annotate the probe sets into gene Symbols

treat <- function(es, annot="hgu133a.db") {
    es <- selectFeatures_IQR(es,10000)
    exprs(es) <- t(apply(exprs(es),1,scale,scale=FALSE))
    colnames(exprs(es)) <- sampleNames(es)
    resJade <- runICA(X=exprs(es), nbComp=10, method = "JADE", maxit=10000)
    resBuild <- buildIcaSet(params=buildMineICAParams(), A=data.frame(resJade$A), S=data.frame(resJade$S),
                           dat=exprs(es), pData=pData(es), refSamples=character(0),
                           annotation=annot, typeID= typeIDmainz,
                           chipManu = "affymetrix", mart=mart)

    icaSet <- resBuild$icaSet
}

## Build the two IcaSet objects
icaSetMainz <- treat(mainz)
icaSetVdx <- treat(vdx)

## compare the IcaSets
runCompareIcaSets(icaSets=list(icaSetMainz, icaSetVdx), labAn=c("Mainz","Vdx"), type.corr="pearson", level="genes")

## End(Not run)

---

### runEnrich

**Enrichment analysis through GOstats**

**Description**

This function tests the enrichment of the components of an IcaSet object using package GOstats through function hyperGTest.

**Usage**

```r
runEnrich(icaSet, params, dbs = c("KEGG", "GO"),
          ontos = c("BP", "CC", "MF"), cond = TRUE,
          hgCutoff = params["pvalCutoff"])
```

**Arguments**

- `icaSet` An object of class IcaSet
- `params` An object of class MineICAParams providing the parameters of the analysis
- `dbs` The database to use, default is c("GO","KEGG")
- `ontos` A string specifying the GO ontology to use. Must be one of "BP", "CC", or "MF", see GOHyperGParams-class. Only used when argument dbs includes "GO".
- `cond` A logical indicating whether the calculation should condition on the GO structure, see GOHyperGParams-class. Only used when argument dbs includes "GO".
- `hgCutoff` The threshold p-value for statistical significance, default is pvalCutoff(params)
Details

An annotation package should be available in `annotation(icaSet)` to provide the contents of the gene sets. If none corresponds to the technology you deal with, please choose the org.*.eg.db package according to the organism (for example org.Hs.eg.db for Homo sapiens). By default, if `annotation(icaSet)` is empty and organism is one of c("Human", "HomoSapiens", "Mouse", "Mus Musculus"), then either org.Hs.eg.db or org.Mm.eg.db is used.

Use of GOstats requires the input IDs to be Entrez Gene, this function will therefore annotate either the feature names or the gene names into Entrez Gene ID using either the annotation package (`annotation(icaSet)`) or biomaRt.

Three types of enrichment tests are computed for each component: the threshold is first used to select gene based on their absolute projections, then positive and negative projections are treated individually.

For each database `db` (each ontology if `db` is "GO"), this function writes an HTML file containing the outputs of the enrichment tests computed through the function `hyperGTest`. The corresponding files are located in `resPath(icaSet)/GOstatsEnrichAnalysis/byDb/`. The results obtained for each database/ontology are then merged into an array for each component, this array is written as an HTML file in the directory `resPath(icaSet)/GOstatsEnrichmentAnalysis/` (this directory is first deleted if it already exists). This file is the one the user should look at.

The outputs of `hyperGTest` that are given in each table are:

**DB, ID, Term:** the database, the gene set ID, and the gene Set name

**P-value:** probability of observing the number of genes annotated for the gene set among the selected gene list, knowing the total number of annotated genes among the universe,

**Expected counts:** expected number of genes in the selected gene list to be found at each tested category term/gene set,

**Odds ratio:** odds ratio for each category term tested which is an indicator of the level of enrichment of genes within the list as against the universe,

**Counts:** number of genes in the selected gene list that are annotated for the gene set,

**Size:** number of genes from the universe annotated for the gene set.

Value

NULL

Author(s)

Anne Biton

See Also

`buildIcaSet, useMart, hyperGTest, GOHyperGParams, hypergeoAn, mergeGostatsResults`
Examples

```r
## Not run:
# Load examples of IcaSet object
data(icaSetCarbayo)

## Define parameters
# Use threshold 3 to select contributing genes on which enrichment analysis will be applied
# Results of enrichment analysis will be written in path 'resPath(params)/GOstatsEnrichAnalysis'
params <- buildMineICAParams(resPath="carbayo/", selCutoff=3)

## Run enrichment analysis on the first two components contained in the icaSet object 'icaSetCarbayo'
runEnrich(params=params, icaSet=icaSetCarbayo[,,1:2], dbs="GO", ontos="BP")
```

## End(Not run)

---

**runICA**

*Run of fastICA and JADE algorithms*

**Description**

This function performs ICA decomposition of a matrix using functions *fastICA* and *JADE*.

**Usage**

```r
runICA(method = c("fastICA", "JADE"), X, nbComp, alg.type = c("deflation", "parallel"),
fun = c("logcosh", "exp"), maxit = 500, tol = 10^-6, ...
```

**Arguments**

- `method` The ICA method to use, either "JADE" (the default) or "fastICA".
- `X` A data matrix with n rows representing observations (e.g genes) and p columns representing variables (e.g samples).
- `nbComp` The number of components to be extracted.
- `alg.type` If alg.type="parallel" the components are extracted simultaneously (the default), if alg.type="deflation" the components are extracted one at a time, see *fastICA*.
- `fun` The functional form of the G function used in the approximation to neg-entropy (see 'details' of the help of function *fastICA*).
- `maxit` The maximum number of iterations to perform.
- `tol` A positive scalar giving the tolerance at which the un-mixing matrix is considered to have converged.
- `...` Additional parameters for *fastICA* and *JADE*.
Details

See details of the functions \texttt{fastICA} and \texttt{JADE}.

Value

A list, see outputs of \texttt{fastICA} and \texttt{JADE}. This list includes at least three elements:

- \(A\) the estimated mixing matrix
- \(S\) the estimated source matrix, \(W\) the estimated unmixing matrix

Author(s)

Anne Biton

Examples

```r
set.seed(2004);
M <- matrix(rnorm(5000*6, sd=0.3), ncol=10)
M[1:10,1:3] <- M[1:10,1:3] + 2
M[1:100,1:3] <- M[1:100,1:3] + 1
resJade <- runICA(X=M, nbComp=2, method = "JADE", maxit=10000)
```

---

**selectContrib**

*Select contributing features/genes*

**Description**

This function selects elements whose absolute scaled values exceed a given threshold.

**Usage**

```r
selectContrib(object, cutoff, level, ...)
```

**Arguments**

- **object**: Either an \texttt{IcaSet} object, or a list of projection vectors, e.g. the list of feature or gene projections on each component.
- **cutoff**: The threshold according to which the elements will be selected. Must be either of length 1 and the same threshold is applied to all components, or of length equal to the number of components in order to use a specific threshold for each component.
- **level**: The level of the selection: either "genes" to select contributing genes using \texttt{SByGene(icaSet)}, or "features" to select contributing features using \texttt{S(icaSet)}.
- **...**: Additional arguments.
Details

Each vector is first scaled and then only elements with an absolute scaled value higher than \texttt{cutoff} are kept.

Value

A list of projections restricted to the elements that are higher than \texttt{cutoff}.

Author(s)

Anne Biton

Examples

```r
## Not run:
## load an example of icaSet
data(icaSetCarbayo)

##### ========
##### When arg 'object' is an IcaSet object
##### ========

## select contributing genes
selectContrib(object=icaSetCarbayo, cutoff=3, level="genes")

## select contributing features
selectContrib(object=icaSetCarbayo, cutoff=3, level="features")

##### ========
##### When arg 'object' is a list
##### ========

c1 <- rnorm(100); names(c1) <- 100:199
c2 <- rnorm(100); names(c2) <- 1:99
selectContrib(object=list(c1, c2), cutoff= 0.5)

## select contributing features
contribFlist <- selectContrib(Slist(icaSetCarbayo), 3)

## select contributing genes
contribGlist <- selectContrib(SlistByGene(icaSetCarbayo), 3)

## End(Not run)
```
selectWitnessGenes

Description

This function selects the features having the largest Inter Quartile Range (IQR).

Usage

```r
selectFeatures_IQR(data, nb)
```

Arguments

- `data`: Measured data of dimension features x samples (e.g, gene expression data)
- `nb`: The number of features to be selected

Value

A subset of `data` restricted to the features having the `nb` highest IQR value

Author(s)

Pierre Gestraud

Examples

```r
dat <- matrix(rnorm(10000),ncol=10,nrow=1000)
rownames(dat) <- 1:1000
selectFeatures_IQR(data=dat, nb=500)
```

selectWitnessGenes

Description

This function selects a gene per component.

Usage

```r
selectWitnessGenes(icaSet, params,
    level = c("genes", "features"), maxNbOcc = 1,
    selectionByComp = NULL)
```

Arguments

- `icaSet`: An object of class `IcaSet`
- `params`: An object of class `MineICAParams` containing the parameters of the analysis, the attribute `cutoffSel` is used as the threshold.
- `level`: The attribute of `icaSet` to be used, the witness elements will be either selected within the "features" or the "genes"
maxNbOcc  The maximum number of components where the genes can have an absolute projection value higher than cutoffSel(params) in order to be selected.

selectionByComp  The list of components already restricted to the contributing genes.

Details

Selects as feature/gene witness, for each component, the first gene whose absolute projection is greater than a given threshold in at the most maxNbOcc components. These witnesses can then be used as representatives of the expression behavior of the contributing genes of the components.

When a feature/gene respecting the given constraints is not found, maxNbOcc is incremented of one until a gene is found.

Value

This function returns a vector of IDs.

Author(s)

Anne Biton

Examples

```
## load an example of IcaSet
data(icaSetCarbayo)

## define parameters: features or genes are considered to be contributor
# when their absolute projection value exceeds a threshold of 4.
params <- buildMineICAParams(resPath="carbayo/", selCutoff=4)

## selection, as gene witnesses, of the genes whose absolute projection is greater than 4 
# in at the most one component. I.e, a gene is selected as a gene witness of a component 
# if he has a large projection on this component only.
selectWitnessGenes(icaSet=icaSetCarbayo, params=params, level="genes", maxNbOcc=1)

## selection, as gene witnesses, of the genes whose absolute projection is greater than 4 
# in at the most two components.
# I.e, a gene is selected as a gene witness of a given component if he has a large projection 
# in this component and at the most another.
selectWitnessGenes(icaSet=icaSetCarbayo, params=params, level="genes", maxNbOcc=2)
```

Slist  

Retrieve feature/gene projections stored in an IcaSet object as a list.

Description

These generic functions retrieve, from an IcaSet object, the feature and gene projections contained in the attribute S and SByGene as a list where feature and gene IDs are preserved.
Usage

Slist(object)
SlistByGene(object)

Arguments

object Object of class IcaSet.

Value

Slist and SlistByGene return a list whose length equals the number of components contained in the IcaSet object. Each element of this list contains a vector of feature or gene projections indexed by the feature or gene IDs.

Author(s)

Anne Biton

See Also

class-IcaSet

wilcoxOrKruskalOnA Comparison of distributions of sample groups

Description

Compare the sample contributions according to their annotation level across the components.

Usage

wilcoxOrKruskalOnA(A, colAnnot, annot)

Arguments

A A matrix of dimensions ‘samples x components’ containing the sample contributions
annot A matrix of dimensions ‘samples x variables’ containing the sample annotations
colAnnot The name of the column of annot to be considered

Details

Wilcoxon or Kruskal-Wallis tests are performed depending on the number of levels in the considered annotation.

Value

A vector of p-values
writeGenes

Author(s)

Anne Biton

See Also

wilcox.test, kruskal.test

writeGenes

Description of features using package biomaRt.

Description

This function annotates IDs (typically gene IDs) provided by the user and returns an html file with their description.

Usage

```r
writeGenes(data, filename = NULL,
            mart = useMart(biomart = "ensembl", dataset = "hsapiens_gene_ensembl"),
            typeId = "hgnc_symbol", typeRetrieved = NULL,
            sortBy = NULL, sortAbs = TRUE, colAnnot = NULL,
            decreasing = TRUE, highlight = NULL, caption = "")
```

Arguments

data Either a data.frame whose rownames or one of its columns contain the IDs to be annotated, or a vector of IDs.
filename The name of the HTML file where gene annotations are written.
mart Output of function useMart from package biomaRt.
typeId The type of IDs available in data, in the biomaRt way (type listFilters(mart) to choose one).
typeRetrieved The descriptors used to annotate the features of data (type listAttributes(mart) to choose one).
sortBy Name of a column of data used to order the output.
sortAbs If TRUE absolute value of column sortBy is used to order the output.
colAnnot The column containing the IDs to be annotated, if NULL or missing and argument data is a data.frame, then rownames of data must contain the IDs.
decreasing If TRUE, the output is sorted by decreasing values of the sortBy column
highlight IDs to be displayed in colour red in the returned table
caption A title for the HTML table
Details

"hgnc_symbol", "ensembl_gene_id", "description", "chromosome_name", "start_position", "end_position", "band", and "strand", are automatically added to the list of fields available in argument typeRetrieved queried on biomaRt. The web-links to www.genecards.org and www.proteinatlas.org are automatically added in the columns of the output respectively corresponding to hgnc_symbol and ensembl_gene_id.

Value

This function returns a data.frame which contains annotations of the input data.

Author(s)

Anne Biton

See Also

getBM, listFilters, listAttributes, useMart

Examples

```r
if (interactive()) {
  ## define the database to be used
  mart <- useMart(biomart="ensembl", dataset="hsapiens_gene_ensembl")

  ### Describe:
  ## a set of hgnc symbols with default descriptions (typeRetrieved=NULL)
  genes <- c("TOP2A", "E2F3", "E2F1", "CDK1", "CDC20", "MKI67")
  writeGenes(data=genes, filename="foo", mart=mart, typeId = "hgnc_symbol")

  ## a data.frame indexed by hngc symbols, sort output according to column "values", add a title to the HTML output
  datagenes <- data.frame(values=rnorm(6), row.names = genes)
  writeGenes(data=datagenes, filename="foo", sortBy = "values", caption = "Description of some proliferation genes.

  ## a set of Entrez Gene IDs with default descriptions
  genes <- c("7153", "1871", "1869", "983", "991", "4288")
  writeGenes(data=genes, filename="foo", mart=mart, typeId = "entrezgene")
}
## Not run:
## add the GO category the genes belong to
## search in listAttributes(mart)[,1] which filter correspond to the Gene Ontology -> "go_id"
writeGenes(data=genes, filename="foo", mart=mart, typeId = "entrezgene", typeRetrieved = "go_id")
## End(Not run)
```
writeGostatsHtmltable  Writes enrichment results in a HTML file

Description

This function takes as input in argument d the output of function addGenesToGoReport whose goal is to add genes included in gene sets detected as significantly enriched by hyperGTest function. It writes the enrichment results in an HTML file which redirects each gene set ID to its web-description and each gene to its Gene Card web-page.

Usage

```r
writeGostatsHtmltable(d, label, side = "both", db, file, cutoff = 3)
```

Arguments

- `d`: A data.frame describing enrichment results, output of function hyperGTest
- `label`: The label of the data the results originate from
- `side`: The side of the component used for enrichment analysis
- `db`: The database used (“GO” or “KEGG”)
- `file`: File name for output
- `cutoff`: The threshold used to select the genes used to run the enrichment analysis

Value

NULL

Author(s)

Anne Biton

See Also

xtable, addGenesToGoReport, hyperGTest

Examples

```r
hgOver <- structure(list(GOBPID = c("GO:0003012", "GO:0030049"),
                           Pvalue = c(1.70848789161935e-10, 6.62508415367712e-05),
                           OddsRatio = c(22.1043956043956, 26.4190476190476),
                           ExpCount = c(1.19549929676512, 0.246132208157525),
                           Count = c(12L, 4L), Size = c(68L, 14L),
                           Term = c("muscle system process", "muscle filament sliding"),
                           In_geneSymbols = c("ACTA2,ACTC1,ACTG2,CASQ2,CNN1,DES,MYH3,MYLK,PTGS1,TPM2,MYL9,LMOD1","ACTC1,DES,MYH3,TPM2"),
                           class = "data.frame", row.names=1:2)
```
writeHtmlResTestsByAnnot

Tests if groups of samples are differently distributed on the components according and do the corresponding plots.

Description

This internal function creates an HTML file containing a table of dimensions 'variables x components' with p-values. When a p-value is considered as significant according to the threshold cutoff, it is written in bold and filled with a link pointing to the corresponding plot. These plots are contained in images located in the path pathplot. To be identified by the function, the file syntax of each image file must be "index-of-component_colAnnot.typeImage".

Usage

writeHtmlResTestsByAnnot(params, icaSet, res, res2, nameres = "p", nameres2 = "cor", onlySign = TRUE, cutoff = params["pvalCutoff"], cutoffDir = c("<=", "=>"), path, pathplot = "plots/", filename = NULL, typeImage = "png", caption = "", keepVar)

Arguments

params An object of class MineICAParams containing the parameters of the analysis
icaSet An object of class IcaSet
res A matrix or data.frame of dimension 'components x variables' containing numeric values that quantify the association of the components with sample variables (e.g p-values, FDR, correlation values). This is the matrix used to select the significant results according to cutoff and cutoffDir.
res2 A matrix or data.frame of dimension 'components x variables' containing numeric values that quantify the association of the components with sample annotations (e.g p-values, FDR, correlation values). It is only used as an additional result displayed in the output.
nameres Name of the values contained in res, default is "p"
nameres2 Name of the values contained in res2, default is "cor"
onlySign If TRUE (default), only the significant results are plotted
cutoff The threshold p-value for statistical significance
path A directory for the HTML file containing the p-value results
pathplot A directory for the plots
filename
The name of the file where the results will be displayed in format HTML, if NULL no file is created

typeImage
The type of image file where each plot is saved

caption
The title of the HTML table

cutoffDir
The direction to be used with the cutoff: "inf" for ",=" and "sup" for ",="

keepVar
The variable labels to be considered, i.e a subset of the variables of icaSet available in varLabels(icaSet).

Details
If argument onlySign is TRUE, then only links to plots that are significant according to the given threshold are provided.

When res2 is not missing, the values contained in res2 are pasted to the values contained in res in the output array. nameres and nameres2 are used such as every element in the output array contains two indexed values: nameres=x, nameres2=y.

Value
Returns a data.frame of dimensions 'components x variables' containing the p-values of the non-parametric tests (Wilcoxon or Kruskal-Wallis tests) which test if the samples groups defined by each variable are differently distributed on the components.

Author(s)
Anne Biton

See Also
p.adjust, qualVarAnalysis, quantVarAnalysis

Description
This function writes in an html file the description of the features, or genes, that contribute to each component. It also writes an html file containing, for each feature or gene, its projection value on every component.

Usage
writeProjByComp(icaSet, params, mart = useMart(biomart = "ensembl", dataset = "hsapiens_gene_ensembl"), typeRetrieved = NULL, addNbOcc = TRUE, selectionByComp = NULL, level = c("features", "genes"), typeId, selCutoffWrite=2.5)
writeProjByComp

Arguments

icaSet  
An object of class IcaSet

params  
An object of class MineICAParams containing the parameters of the analysis. The files are written in the path genesPath(params). selCutoff(params) is used to select the features or genes by component.

mart  
An output of function useMart containing the database used for annotation.

typeRetrieved  
The annotations biomaRt is queried about. They describe the feature or gene IDs of the argument icaSet, see listFilters.

addNbOcc  
If TRUE, the number of components the features/genes contribute to is added to the output. A gene/feature is considered as a contributor of a component if its absolute scaled projection value is higher than selCutoff(icaSet).

selectionByComp  
A list containing the feature/gene projections on each component, already restricted to the ones considered as contributors.

level  
The data level of icaSet that will be annotated: either the feature projections ("features"), or the gene projections ("genes").

typeId  
The type of ID the features or the genes of icaSet correspond to. By default typeId(icaSet) is used. It must be provided in the biomaRt way (type listFilters(mart) to choose the appropriate value).

selCutoffWrite  
The cutoff applied to the absolute projection values to select the features/genes that will be annotated using package biomaRt, default is 2.5.

Details

One file is created by component, each file is named by the index of the components (indComp(icaSet)) and located in the path genesPath(params).

In case you are interested in writing the description of features and their annotations, please remember to modify code genesPath(params), or the previous files will be overwritten.

The genes are ranked according to their absolute projection values.

This function also writes an html file named "genes2comp" providing, for each feature or gene, the number of components it contributes to (according to the threshold cutoffSel(params)), and its projection value on all the components. The projection values are scaled.

See function writeGenes for details.

Value

This function returns a list of two elements:

listAnnotComp:  
a list with the output of writeGenes for each component

nbOccInComp:  
a data.frame storing the projection values of each feature/gene (row) across all the components (columns).

Author(s)

Anne Biton
writeRnkFiles

Write rnk files containing gene projections

Description

Writes the gene projection values of each component in a '.rnk' file for GSEA.

Usage

writeRnkFiles(icaSet, abs = TRUE, path)
writeRnkFiles

Arguments

  icaSet    An object of class IcaSet
  abs       If TRUE (default) the absolute projection values are used.
  path      The path that will contain the rnk files.

Details

  The .rnk format requires two columns, the first containing the gene IDs, the second containing the
  projection values. The genes are ordered by projection values. The files are named "index-of-
  component_abs.rnk" if abs=TRUE, or "index-of-component.rnk" if abs=FALSE.

Value

  NULL

Author(s)

  Anne
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