Package 'consICA'

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Type Package

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Title consensus Independent Component Analysis

Version 2.10.0

Description consICA implements a data-driven deconvolution method – consensus independent component analysis (ICA) to decompose heterogeneous omics data and extract features suitable for patient diagnostics and prognostics.
The method separates biologically relevant transcriptional signals from technical effects and provides information about the cellular composition and biological processes.
The implementation of parallel computing in the package ensures efficient analysis of modern multicore systems.

BugReports https://github.com/biomod-lih/consICA/issues

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LazyData false

Imports fastICA (>= 1.2.1), sm, org.Hs.eg.db, GO.db, stats, SummarizedExperiment, BiocParallel, graph, ggplot2, methods, Rfast, pheatmap, survival, topGO, graphics, grDevices

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`anovaIC` *ANOVA test for independent component across factors*

Description

ANOVA (ANalysis Of VAriance) test produced for specific independent component across each (clinical) factor as 'aov(IC ~ factor)'. Plot distributions of samples' weight for top 9 significant factors.

Usage

```
anovaIC(
  cica,
  Var = NULL,
  icomp = 1,
  plot = TRUE,
  mode = "violin",
  color_by_pv = TRUE
)
```

Arguments

cica	list compliant to ‘consICA()‘ result
Var	matrix with samples’ metadata. Samples in rows and factors in columns
icomp	number of component to analyse
plot	if plot weights distributions for top factors
mode	type of plot. Can be ’violin’ or ’box’
color_by_pv	if TRUE plots will be colored by p-value ranges

Value

a data.frame with

factor	name of factor
p.value	p-value for ANOVA test for factor
p.value_disp	string for p-value printing

Examples

```
data("samples_data")
# Var <- data.frame(SummarizedExperiment::colData(samples_data))
# cica <-  consICA(samples_data, ncomp=10, ntry=1, ncores=1, show.every=0)
## Run ANOVA for 4th independent component
# anova <- anovaIC(cica, Var=Var, icomp = 4)
```

---

consICA *Calculate consensus Independent Component Analysis*

Description

calculate consensus independent component analysis (ICA) Implements efficient ICA calculations.

Usage

```
consICA(
  X,
  ncomp = 10,
  ntry = 1,
  show.every = 1,
  filter.thr = NULL,
  ncores = 1,
  bpparam = NULL,
  reduced = FALSE,
  fun = "logcosh",
  alg.typ = "deflation",
  verbose = FALSE,
  assay_string = NULL
)
```

Arguments

X	input data with features in rows and samples in columns. Could be a 'SummarizedExperiment' object, matrix or 'Seurat' object. For 'SummarizedExperiment' with multiple assays or 'Seurat' pass the name with 'assay_string' parameter, otherwise the first will be taken. See SummarizedExperiment-class
ncomp	number of components
ntry	number of consensus runs. Default value is 1
show.every	numeric logging period in iterations (disabled for 'ncore's > 1). Default value is 1
filter.thr	Filter out genes (rows) with max value lower than this value from 'X'
ncores	number of cores for parallel calculation. Default value is 4
bpparam	parameters from the 'BiocParallel'
reduced	If TRUE returns reduced result (no 'X', 'i.best', see 'return')
fun	the functional form of the G function used in the approximation to neg-entropy in fastICA. Default value is "logcosh"
alg.typ	parameter for fastICA(). If alg.typ == "deflation" the components are extracted one at a time. If alg.typ == "parallel" the components are extracted simultaneously. Default value is "deflation"
verbose	logic TRUE or FALSE. Use TRUE for print process steps. Default value is FALSE
assay_string	name of assay for 'SummarizedExperiment' or 'Seurat' input object 'X'. Default value is NULL

Value

a list with

X	input object

nsamples, nfeatures	dimension of X
S, M	consensus metagene and weight matrix
ncomp	number of components
X_num	input data in matrix format
mr2	mean R2 between rows of M
stab	stability, mean R2 between consistent columns of S in multiple tries. Applicable only for 'ntry' > 1
i.best	number of best iteration

Author(s)

Petr V. Nazarov

See Also

fastICA

Examples

```
data("samples_data")
# Deconvolve into independent components
cica <- consICA(samples_data, ncomp=15, ntry=10, ncores=1, show.every=0)
# X = S * M, where S - independent signals matrix, M - weights matrix
dim(samples_data)
dim(cica$S)
dim(cica$M)
```

---

coreICA *Fast Independent Component Analysis for multi-run mode*

Description

Adaptation of fastICA for quick multiple-run calculations for consensus Independent Component Analysis (ICA)

Usage

```
coreICA(
  X,
  n.comp,
  preICA = NULL,
  alg.typ = c("parallel", "deflation"),
  fun = c("logcosh", "exp"),
  w.init = NULL,
  alpha = 1,
```

```
  row.norm = FALSE,
  maxit = 200,
  tol = 1e-04,
  verbose = FALSE
)
```

Arguments

X	matrix with features in rows and samples in columns
n.comp	number of components.
preICA	output of ‘outICA()‘. Default is NULL
alg.typ	parameter for fastICA(). If alg.typ == "deflation" the components are extracted one at a time. If alg.typ == "parallel" the components are extracted simultaneously. Default value is "deflation"
fun	the functional form of the G function used in the approximation to neg-entropy in fastICA. Default value is "logcosh"
w.init	initial weights
alpha	default is 1
row.norm	set TRUE if the normalization by rows is needed. Default is FALSE
maxit	default is 200
tol	default is 1e-04
verbose	logic TRUE or FALSE. Use TRUE for print process steps. Default value is FALSE

Value

a list with (compliant to ‘fastICA()‘output)

X	pre-processed data matrix
K	pre-whitening matrix that projects data onto the first ‘n.comp‘ principal components
W	estimated un-mixing matrix
A	estimated mixing matrix
S	estimated source matrix

Author(s)

Maryna Chepeleva

enrichGO *Enrichment analysis of GO-terms based on Ensembl IDs*

Description

Enrichment analysis of GO-terms for independent components with Ensembl IDs based on topGO package

Usage

```
enrichGO(
  genes,
  fdr = NULL,
  fc = NULL,
  ntop = NA,
  thr.fdr = 0.05,
  thr.fc = NA,
  db = "BP",
  genome = "org.Hs.eg.db",
  id = c("entrez", "alias", "ensembl", "symbol", "genename"),
  algorithm = "weight",
  do.sort = TRUE,
  randomFraction = 0,
  return.genes = FALSE
)
```

Arguments

genes	character vector with list of ENSEBML IDs
fdr	numeric vector of FDR for each gene
fc	numeric vector of logFC for each gene
ntop	number of first taken genes
thr.fdr	significance threshold for FDR
thr.fc	significance threshold for absolute logFC
db	name of GO database: "BP","MF","CC"
genome	R-package for genome annotation used. For human - 'org.Hs.eg.db'
id	id
algorithm	algorithm for 'runTest()'
do.sort	if TRUE - resulted functions sorted by p-value
randomFraction	for testing only, the fraction of the genes to be randomized
return.genes	If TRUE include genes in output. Default value is FALSE

Value

list with terms and stats

Author(s)

Petr V. Nazarov

`estimateVarianceExplained` *Estimate the variance explained by the model*

Description

The method estimates the variance explained by the model and by each independent component. We used the coefficient of determination (R2) between the normalized input (X-mean(X)) and (S*M)

Usage

```
estimateVarianceExplained(cica, X = NULL)
```

Arguments

`cica`	list compliant to ‘consICA()‘ result
`X`	a ‘SummarizedExperiment‘ object. Assay used for the model. Will be used if consICA$X is NULL, ignore otherwise.

Value

a list of:

`R2`	total variance explained by the model
`R2_ics`	Amount of variance explained by the each independent component

Examples

```
data("samples_data")
# cica <- consICA(samples_data, ncomp=15, ntry=10, show.every=0)
# var_ic <- estimateVarianceExplained(cica)
```

getFeatures *Get features from consICA deconvolution result*

Description

Extract names of features (rows in ‘X‘ and ‘S‘ matrices) and their false discovery rates values

Usage

```
getFeatures(cica, alpha = 0.05, sort = FALSE)
```

Arguments

cica	list compliant to ‘consICA()‘ result
alpha	value in [0,1] interval. Used to filter features with FDR < ‘alpha‘. Default value is 0.05
sort	sort features decreasing FDR. Default is FALSE

Value

list of dataframes ‘pos‘ for positive and ‘neg‘ for negative affecting features with columns:

features	names of features
fdr	false discovery rate value

Author(s)

Petr V. Nazarov

Examples

```
data("samples_data")
# Get deconvolution of X matrix
cica <-  consICA(samples_data, ncomp=10, ntry=1, show.every=0)
# Get features names and FDR for each component
features <- getFeatures(cica)
# Positive affecting features for first components are
ic1_pos <- features$ic.1$pos
```

getGO *Assigns IC signatures to Gene Ontologies*

Description

Assigns extracted independent components to Gene Ontologies and rotate independent components (‘S‘ matrix) to set most significant Gene Ontologies as positive affecting features. Set ‘ncores‘ param for paralleled calculations.

Usage

```
getGO(
  cica,
  alpha = 0.05,
  genenames = NULL,
  genome = "org.Hs.eg.db",
  db = c("BP", "CC", "MF"),
  ncores = 4,
  rotate = TRUE
)
```

Arguments

cica	list compliant to ‘consICA()‘ result
alpha	value in [0,1] interval. Used to filter features with FDR < ‘alpha‘. Default value is 0.05
genenames	alternative names of genes. If NULL we use rownames of ‘S‘ matrix. We automatically identify type of gene identifier, you can use Ensembl, Symbol, Entrez, Alias, Genename IDs.
genome	R-package for genome annotation used. For human - ’org.Hs.eg.db’
db	name of GO database: "BP","MF","CC"
ncores	number of cores for parallel calculation. Default value is 4
rotate	rotate components in ‘S‘ and ‘M‘ matricies in ‘cica‘ object to set most significant Gene Ontologies as positive effective features. Default is TRUE

Value

rotated (if need) ‘cica‘ object with added ‘GO‘ - list for each db chosen (BP, CC, MM), with dataframes ‘pos‘ for positive and ‘neg‘ for negative affecting features for each component:

GO.ID	id of Gene Ontology term
Term	name of term
Annotated	number of annotated genes
Significant	number of significant genes

Expected	estimate of the number of annotated genes if the significant genes would be randomly selected from the gene universe classisFisher F-test
FDR	false discovery rate value
Score	genes score

Author(s)

Petr V. Nazarov

Examples

```
data("samples_data")
# Calculate ICA (run with ntry=1 for quick test, use more in real analysis)
#cica <- consICA(samples_data, ncomp=2, ntry=1, ncores=1, show.every=0)
# cica <- consICA(samples_data, ncomp=40, ntry=20, show.every=0)

# Annotate independent components with gene ontoligies
# cica <- getGO(cica, db = "BP", ncores=4)
## Positively affected GOs for 2nd independent component
#head(cica$GO$GOBP$ic02$pos)
```

---

get_score *Create score depending on threshold and paradigm*

Description

Create score depending on threshold and paradigm

Usage

```
get_score(genes, fc, thr.fc, fdr, thr.fdr, ntop)
```

Arguments

genes	character vector with list of ENSEBML IDs
fc	numeric vector of logFC for each gene
thr.fc	significance threshold for absolute logFC
fdr	numeric vector of FDR for each gene
thr.fdr	significance threshold for FDR
ntop	number of first taken genes

Value

numeric score vector

get_X_num *Convert input object as numeric matrix*

Description

Convert input object as numeric matrix

Usage

```
get_X_num(obj, assay_string = NULL)
```

Arguments

obj	input data with features in rows and samples in columns. Could be a 'SummarizedExperiment' object, matrix or 'Seurat' object. For 'SummarizedExperiment' with multiple assays or 'Seurat' pass the name with 'assay_string' parameter, otherwise the first will be taken. See SummarizedExperiment-class
assay_string	name of assay for 'SummarizedExperiment' or 'Seurat' input object 'obj'. Default value is NULL

Value

matrix

is.consICA *Is the object is consensus ICA compliant?*

Description

Check if the object is a list in the same format as the result of 'consICA()'

Usage

```
is.consICA(cica)
```

Arguments

cica	list

Value

TRUE or FALSE

Examples

```
# returns TRUE
is.consICA(list("ncomp" = 2, "nsples" = 2, "nfeatures" = 2,
                "S" = matrix(0,2,2),"M" = matrix(0,2,2)))
```

oneICA *Runs* fastICA

Description

Runs fastICA once and store in a consICA manner

Usage

```
oneICA(
  X,
  ncomp = 10,
  filter.thr = NULL,
  reduced = FALSE,
  fun = "logcosh",
  alg.typ = "deflation",
  assay_string = NULL
)
```

Arguments

X	input data with features in rows and samples in columns. Could be a 'SummarizedExperiment' object, matrix or 'Seurat' object. For 'SummarizedExperiment' with multiple assays or 'Seurat' pass the name with 'assay_string' parameter, otherwise the first will be taken. See SummarizedExperiment-class
ncomp	number of components. Default value is 10
filter.thr	filter rows in input matrix with max value > 'filter.thr'. Default value is NULL
reduced	If TRUE returns reduced result (no X, see 'return')
fun	the functional form of the G function used in the approximation to neg-entropy in fastICA. Default value is "logcosh"
alg.typ	parameter for fastICA(). if alg.typ == "deflation" the components are extracted one at a time. if alg.typ == "parallel" the components are extracted simultaneously. Default value is "deflation"
assay_string	name of assay for 'SummarizedExperiment' or 'Seurat' input object 'X'. Default value is NULL

Value

a list with

X	input 'SummarizedExperiment' object
nsamples, nfeatures	dimension of X assay
S, M	consensus metagene and weight matrix
ncomp	number of components

Author(s)

Petr V. Nazarov

See Also

fastICA

Examples

```
data("samples_data")
res <- oneICA(samples_data)
```

---

outICA *Outside part of multiple run Independent Component Analysis*

Description

Calculate a common part for consensus Independent Component Analysis (ICA)

Usage

```
outICA(X, n.comp, row.norm = FALSE, verbose = FALSE)
```

Arguments

X	matrix with features in rows and samples in columns
n.comp	number of components
row.norm	rows normalization flag. Default value is FALSE
verbose	logic TRUE or FALSE. Use TRUE for print process steps. Default value is FALSE

Value

a list with

X	input matrix
X1	interim calculated matrix
K	pre-whitening matrix that projects data onto the first ‘n.comp‘ principal components

Author(s)

Maryna Chepeleva

`overlapGO` *Similarity of two gene ontologies lists*

Description

Calculate similarity matrix of gene ontilogies (GOs) of independent components. The measure could be cosine similarity or Jaccard index (see details)

Usage

```
overlapGO(GO1, GO2, method = c("cosine", "jaccard"), fdr = 0.01)
```

Arguments

`GO1`	list of GOs for each independent component got from 'getGO()'
`GO2`	list of GOs for each independent component got from 'getGO()'
`method`	can be 'cosine' for non-parametric cosine similarity or 'jaccard' for Jaccadr index. See details
`fdr`	FDR threshold for GOs that would be used in measures. Default value is 0.01

Details

Jaccard index is a measure of the similarity between two sets of data. It calculated as intersection divided by union

$$J(A,B) = \frac{|A \cap B|}{|A \cup B|}.$$

Results are from 0 to 1.

Cosine similarity here is calculated in a non-parametric way: for two vectors of gene ontologies, the space is created as a union of GOs in both vectors. Then, two rank vectors in this space created, most enriched GOs get the biggest rank and GOs from space not included in the GO vector get 0. Cosine similarity is calculated between two scaled rank vectors. Such approach allows to take the order of enriched GO into account. Results are from -1 to 1. Zero means no similarity.

Value

a similarity matrix of cosine or Jaccard values, rows corresponds to independent components in 'GO1', columns to independent components in 'GO2'.

Author(s)

Maryna Chepeleva

Examples

```
## Not run:
data("samples_data")
# Calculate ICA (run with ntry=1 for quick test, use more in real analysis)
cica1 <- consICA(samples_data, ncomp=5, ntry=1, show.every=0)
# Search enriched gene ontologies
cica1 <- getGO(cica1, db = "BP", ncores = 1)
# Calculate ICA and GOs for another dataset
cica2 <- consICA(samples_data[,1:100], ncomp=4, ntry=1, show.every=0)
cica2 <- getGO(cica2, db = "BP", ncores = 1)
# Compare two lists of enriched GOs
# Jaccard index
jc <- overlapGO(GO1 = cica1$GO$GOBP, GO2 = cica2$GO$GOBP,
method = "jaccard", fdr = 0.01)
# Cosine similarity
cos_sim <- overlapGO(GO1 = cica1$GO$GOBP, GO2 = cica2$GO$GOBP,
method = "cosine", fdr = 0.01)

## End(Not run)
```

---

plotICVarianceExplained

Barplot variance explained by each IC

Description

Method to plot variance explained (R-squared) by the MOFA model for each view and latent factor. As a measure of variance explained for gaussian data we adopt the coefficient of determination (R2).
For details on the computation see the help of the `estimateVarianceExplained` function

Usage

```
plotICVarianceExplained(
  cica,
  sort = NULL,
  las = 2,
  title = "Variance explained per IC",
  x.cex = NULL,
  ...
)
```

Arguments

`cica`	consICA compliant list
`sort`	specify the arrangement as 'asc'/'desc'. No sorting if NULL
`las`	orientation value for the axis labels (0 - always parallel to the axis, 1 - always horizontal, 2 - always perpendicular to the axis, 3 - always vertical)

`title`	character string with title of the plot
`x.cex`	specify the size of the tick label numbers/text with a numeric value of length 1
`...`	extra arguments to be passed to `barplot`

Value

A numeric vector compliant to ‘barplot‘ output

Examples

```
data("samples_data")
# cica <- consICA(samples_data, ncomp=15, ntry=10, show.every=0)
# p <- plotICVarianceExplained(cica, sort = "asc")
```

---

samples_data *Samples of gene expression*

Description

A dataset containing the expression of 2454 genes for 472 samples from skin cutaneous melanoma (SKCM) TCGA cohort, their metadata such as age, gender, cancer type etc. and survival time-to-event data

Usage

```
data(samples_data)
```

Format

A SummarizedExperiment object:

assay expression matrix with genes by rows and samples by columns

colData data frame with sample metadata (clinical variables)

---

saveReport *Save PDF report with analysis of each independent component*

Description

Save PDF report with description of each independent component (IC) consists of most affected genes, significant Go terms, survival model for the component, ANOVA analysis for samples characteristics and stability

Usage

```
saveReport(
  cica,
  Genes = NULL,
  Var = NULL,
  surv = NULL,
  genenames = NULL,
  file = sprintf("report_ICA_%d.pdf", ncol(IC$S)),
  main = "Component # %d (stability = %.3f)",
  show.components = seq.int(1, ncol(cica$S))
)
```

Arguments

cica	list compliant to ‘consICA()‘ result. May include GO list with enrichment analysis appended with ‘getGO()‘ function
Genes	features list compilant to ‘getFeatures‘ output (list of dataframes ‘pos‘ for positive and ‘neg‘ for negative affecting features with names of features false discovery rates columns).If NULL will generated automatically
Var	matrix with samples metadata
surv	dataframe with time and event values for each sample
genenames	alternative gene names for printing in the report
file	report filename, ends with ".pdf"
main	title for each list discribes the component
show.components	which compont will be shown

Value

TRUE when successfully generate report

Author(s)

Petr V. Nazarov

Examples

```
if(FALSE){
  data("samples_data")
  cica <- consICA(samples_data, ncomp=15, ntry=10, ncores = 2, show.every=0)
  if(FALSE){
    cica <- getGO(cica, db = "BP")
  }
  saveReport(cica, Var=samples_data$Var, surv = samples_data$Sur)
}
```

setOrientation *Set orientation for independent components*

Description

Set orientation for independent components as positive in most enriched direction. Use first element of ‘GOs‘ for direction establishment.

Usage

```
setOrientation(cica, verbose = FALSE)
```

Arguments

cica	list compliant to ‘consICA()‘ result. Must contain GO, see ‘getGO()‘
verbose	logic TRUE or FALSE. Use TRUE for print process steps. Default is FALSE

Value

cica object after rotation, with rotated ‘S‘, ‘M‘ and added ‘compsign‘ which is vector defined rotation: ‘S_rot = S * compsign, M_rot = M * compsign, GO_rot = GO * compsign‘

Note

Implemented inside ‘getGO()‘ in version >= 1.1.1.

Author(s)

Petr V. Nazarov

Examples

```
## Not run:
data("samples_data")
# Get deconvolution of X matrix
#cica <-  consICA(samples_data, ncomp=10, ntry=1, show.every=0)
cica <- consICA(samples_data, ncomp=2, ntry=1, show.every=0) # timesaving
example
GOs <- getGO(cica, db = "BP")
# Get already rotated S matrix and Gene Ontologies
cica <- getGO(cica, db = "BP")

# Get Gene Ontologies without rotation (actually, you don't need to do this)
# This may used for GO generated with version < 1.1.1. Add GO to cica list.
cica <- getGO(cica, db = "BP", rotate = FALSE)
# Rotate components
cica <- setOrientation(cica, verbose = T)
# Which components was rotated
which(cica$compsign == -1)
```

```
## End(Not run)
```

`set_bpparam` *Set up for the parallel computing for biocParallel Adapt from 'FEAST' This function sets up the environment for parallel computing.*

Description

Set up for the parallel computing for biocParallel Adapt from 'FEAST' This function sets up the environment for parallel computing.

Usage

```
set_bpparam(ncores = 0, BPPARAM = NULL)
```

Arguments

`ncores`	number of processors
`BPPARAM`	bpparameter from bpparam

Value

BAPPARAM settings

`sortDataFrame` *Sort dataframe*

Description

Sort dataframe, adapted from http://snippets.dzone.com/user/r-fanatic

Usage

```
sortDataFrame(x,key, ...)
```

Arguments

`x`	a data.frame
`key`	sort by this column
`...`	other parameters for 'order' function (e. g. 'decreasing')

Value

sorted dataframe

Examples

```
df <- data.frame("features" = c("f1", "f2", "f3"), fdr = c(0.02, 0.002, 1))
sortDataFrame(df, "fdr")
```

---

sortFeatures *Sort Genes of consICA object*

Description

Sort Genes for independent components

Usage

```
sortFeatures(Genes)
```

Arguments

Genes	list compilant to ‘getFeatures‘output

Value

sorted list

Examples

```
#features <- list("ic1" = list(
#              "pos" = data.frame("features" = c("f1", "f2", "f3"),
#                                 "fdr" = c(0.0043, 0.4, 0.04)),
#              "neg" = data.frame("features" = c("f1", "f2", "f3"),
#                                 "fdr" = c(0, 0.1, 0.9))))
#sortFeatures(features)
```

---

survivalAnalysis *Survival analysis based on significant IC*

Description

Cox regression (based on R package ‘survival‘) on the weights of independent components with significant contribution in individual risk model. For more see Nazarov et al. 2019 In addition the function plot Kaplan-Meier diagram.

Usage

```
survivalAnalysis(cica, surv = NULL, time = NULL, event = NULL, fdr = 0.05)
```

Arguments

cica	list compliant to ‘consICA()‘ result
surv	dataframe with time and event values for each sample. Use this parameter or ‘time‘ and ‘event‘
time	survival time value for each sample
event	survival event factor for each sample (TRUE or FALSE)
fdr	false discovery rate threshold for significant components involved in final model. Default value is 0.05

Value

a list with

cox.model	an object of class ‘coxph‘ representing the fit. See ‘coxph.object‘ for details
hazard.score	hazard score for significant components (fdr < ‘fdr‘ in individual cox model)

Examples

```
data("samples_data")
# Get deconvolution of X matrix
cica <-  consICA(samples_data, ncomp=10, ntry=1, show.every=0)
surv <- survivalAnalysis(cica,
  surv = SummarizedExperiment::colData(samples_data)[,c("time", "event")])
```

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