Package ‘consICA’

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Type Package

biocViews Technology, StatisticalMethod, Sequencing, RNASEq, Transcriptomics, Classification, FeatureExtraction

Title consensus Independent Component Analysis

Version 2.0.0

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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Encoding UTF-8

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

Depends R (>= 4.2.0)

Suggests knitr, BiocStyle, rmarkdown, testthat, Seurat

VignetteBuilder knitr

RoxygenNote 7.2.3

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ANOVA test for independent component across factors

\textbf{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.

\textbf{Usage}

\begin{verbatim}
anovaIC(
  cica,
  Var = NULL,
  icomp = 1,
  plot = TRUE,
\end{verbatim}
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)

Description

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

Usage

c 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
coreICA

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)

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,
)
estimateVarianceExplained

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)
getFeatures

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
getGO

**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
icl_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**

getoGO(
  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’ matrices 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:

<table>
<thead>
<tr>
<th>GO.ID</th>
<th>id of Gene Ontology term</th>
</tr>
</thead>
<tbody>
<tr>
<td>Term</td>
<td>name of term</td>
</tr>
<tr>
<td>Annotated</td>
<td>number of annotated genes</td>
</tr>
<tr>
<td>Significant</td>
<td>number of significant genes</td>
</tr>
<tr>
<td>Expected</td>
<td>estimate of the number of annotated genes if the significant genes would be randomly selected from the gene universe classisFisher F-test</td>
</tr>
<tr>
<td>FDR</td>
<td>false discovery rate value</td>
</tr>
<tr>
<td>Score</td>
<td>genes score</td>
</tr>
</tbody>
</table>

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=4, ntry=1, ncores=1, show.every=0)
# cica <- consICA(samples_data, ncomp=40, ntry=20, show.every=0)

# Annotate independent components with gene ontologies
cica <- getGO(cica, db = "BP", ncores=1)
# 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)
get_X_num

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**

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

**Arguments**

- `cica` list

**Value**

TRUE or FALSE

**Examples**

```r
# 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**

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

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 ontologies (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)
```
overlapGO

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 Jaccard 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 is 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

```r
## 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)
```
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

plotICVariance Explained(
    cica,            # consICA compliant list
    sort = NULL,    # specify the arrangement as 'asc'/'desc'. No sorting if NULL
    las = 2,        # 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 = "Variance explained per IC", # character string with title of the plot
    x.cex = NULL,   # specify the size of the tick label numbers/text with a numeric value of length 1
    ...              # extra arguments to be passed to barplot
)

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
...

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))
)
setOrientation

Arguments

cica  
Genes  
Var  
surv  
genenames  
file  
main  
show.components

Value

TRUE when successfully generate report

Author(s)

Petr V. Nazarov

Examples

data("samples_data")
cica <- consICA(samples_data, ncomp=40, ntry=10, 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  
verbose

list compliant to ‘consICA()’ result. Must contain GO, see ‘getGO()’

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

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

ncores
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

**Description**

Sort Genes of consICA object

**Usage**

```r
sortFeatures(Genes)
```

**Arguments**

- **Genes**
  list compilant to 'getFeatures' output

**Value**

sorted list

**Examples**

```r
#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

**Description**

Survival analysis based on significant IC

**Usage**

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

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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