Package ‘STATegRa’
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Description Classes and tools for multi-omics data integration.
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R topics documented:

  bioDist ................................................................. 2
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Function to compute a bioDistClass object from profile data and a mapping. For details of the process see the user’s guide, but briefly the process involves using the mapping to identify reference features appropriate to each surrogate feature (if any), aggregating the surrogate data into pseudo-data for each reference feature, and then calculating the correlation distance between the reference features according to the surrogate data.

Usage

```r
bioDist(referenceFeatures=NULL, reference=NULL, mapping=NULL,
         referenceData=NULL, surrogateData=NULL, filtering=NULL,
         noMappingDist=NA, distance="spearman", aggregation="sum",
         maxitems=NULL, selectionRule="maxFC", expfac=NULL,
         name=NULL, ...)
```
bioDist

Arguments

referenceFeatures
subset of features to be considered for the computation of the distances. If NULL then the features are first gathered from the features in referenceData. If referenceData is not provided then the list of features are gathered from mapping (bioMap class) and using the reference.

reference
A character indicating the variable that is being used as features to compute distance between

mapping
The mapping between feature types

referenceData
ExpressionSet object with the data from the reference features.

surrogateData
ExpressionSet object with the data from the surrogate features.

filtering
A filtering for the bioMap class. To be implemented.

noMappingDist
Distance value to be used when a reference feature do not map to any surrogate feature. If "max", maximum indirect distance among the rest of reference features is taken. If NA, distance weights are re-scaled so this surrogate association is not considered. If a number then the missing values are replaces with that value.

distance
Distance between features to be computed. Possible values are "pearson", "kendall", "spearman", "euclidean", "maximum", "manhattan", "canberra", "binary" and "minkowski". Default is "spearman".

aggregation
Action to perform when a reference feature maps to more than one surrogate feature. Options are "max", "sum", "mean" or "median" and the the values are aggregated according to the chosen statistic.

maxitems
The maximum number of surrogate features per reference feature to be used, selected according to "selectionRule" parameter. Default is 2.

selectionRule
Rule to select the surrogate features to be used (the number is determined by "maxitems"). It can be one of the following: (1) "maxcor" those presenting maximum correlation with corresponding main feature; in this case "referenceData" must be provided and the columns must overlap in at least 3 samples; (2) "maxmean": average across samples is computed and those features with higher mean are selected; case (3) is similar to (2) but considering other statistics: "maxmedian", "maxdiff", "maxFC", "sd", "ee".

expfac
Not in use yet.

name
Character that describes the nature of the bioDist class computed

extra arguments passed to dist, eg "p=value" for the power used if calculating minkowski distance

Value
An object of class bioDist class containing distances between the features in surrogateData.

Author(s)
David Gomez-Cabrero
Examples

data(STATegRa_S1)
data(STATegRa_S2)
require(Biobase)

# Truncate data for brevity
Block1 <- Block1[1:100,]
Block2 <- Block2[1:100,]

## Create ExpressionSets
mRNA.ds <- createOmicsExpressionSet(Data=Block1,pData=ed,pDataDescr=c("classname"))
miRNA.ds <- createOmicsExpressionSet(Data=Block2,pData=ed,pDataDescr=c("classname"))

## Create the bioMap
map.gene.miRNA<-bioMap(name = "Symbol-miRNA",
                      metadata = list(type_v1="Gene",type_v2="miRNA",
                                      source_database="targetscan.Hs.eg.db",
                                      data_extraction="July2014"),
                      map=mapdata)

# Create Gene-gene distance computed through miRNA data
bioDistmiRNA<-bioDist(referenceFeatures = rownames(Block1),
                      reference = "Var1",
                      mapping = map.gene.miRNA,
                      surrogateData = miRNA.ds, ### miRNA data
                      referenceData = mRNA.ds, ### mRNA data
                      maxitems=2,
                      selectionRule="sd",
                      expfac=NULL,
                      aggregation = "sum",
                      distance = "spearman",
                      noMappingDist = 0,
                      filtering = NULL,
                      name = "mRNAbymiRNA")

# Create Gene-gene distance through mRNA data
bioDistmRNA<-new("bioDistclass",
                name = "mRNAbymRNA",
                distance = cor(t(exprs(mRNA.ds)),method="spearman"),
                map.name = "id",
                map.metadata = list(),
                params = list())

###### Generation of the list of Surrogated distances.
bioDistList<-list(bioDistmRNA,bioDistmiRNA)
sample.weights<-matrix(0,4,2)
sample.weights[,1]<-c(0,0.33,0.67,1)
sample.weights[,2]<-c(1,0.67,0.33,0)

###### Generation of the list of bioDistWclass objects.
bioDistWList<-bioDistW(referenceFeatures = rownames(Block1),
                        bioDistList = bioDistList,
                        weights=sample.weights)
### bioDistclass

#### Plot of distances.

```r
bioDistWPlot(referenceFeatures = rownames(Block1),
              listDistW = bioDistWList,
              method.cor = "spearman")
```

#### Computing the matrix of features/distances associated.

```r
fm <- bioDistFeature(Feature = rownames(Block1)[1],
                     listDistW = bioDistWList,
                     threshold.cor = 0.7)
bioDistFeaturePlot(data = fm)
```

---

#### bioDistclass

**Description**

Class to manage mappings between genomic features.

**Usage**

```r
bioDistclass(name, distance, map.name, map.metadata, params)
```

**Arguments**

- **name**: Name assigned to the object
- **distance**: Matrix giving the distance between features
- **map.name**: Charactering giving the name of the bioMap object used to compute the distance
- **map.metadata**: List of parameters used to generate the mapping
- **params**: List of parameters used to generate the distance

---

#### bioDistFeature

**Description**

Function that computes for a given selected feature the closest features given a selected set of weighted distances.

**Usage**

```r
bioDistFeature(Feature, listDistW, threshold.cor)
```

**Arguments**

- **Feature**: Feature A selected as a reference.
- **listDistW**: A list of bioDistWclass objects. All the objects must contain the Feature A selected and all of them must contain the same set of features.
- **threshold.cor**: A threshold to select the features associated to Feature A
Value

Matrix with the associated features given the different weighted distances considered

Author(s)

David Gomez-Cabrero

Examples

data(STATEGRa_S1)
data(STATEGRa_S2)
require(Biobase)

# Truncate data for brevity
Block1 <- Block1[1:100,]
Block2 <- Block2[1:100,]

## Create ExpressionSets
mRNA.ds <- createOmicsExpressionSet(Data=Block1,pData=ed,pDataDescr=c("classname"))
miRNA.ds <- createOmicsExpressionSet(Data=Block2,pData=ed,pDataDescr=c("classname"))

## Create the bioMap
map.gene.miRNA <- bioMap(name = "Symbol-miRNA",
metadata = list(type_v1="Gene",type_v2="miRNA",
source_database="targetscan.Hs.eg.db",
data_extraction="July2014"),
map=mapdata)

# Create Gene-gene distance computed through miRNA data
bioDistmiRNA <- bioDist(referenceFeatures = rownames(Block1),
reference = "Var1",
mapping = map.gene.miRNA,
surrogateData = miRNA.ds, ### miRNA data
referenceData = mRNA.ds, ### mRNA data
maxitems=2,
selectionRule="sd",
expfac=NULL,
aggregation = "sum",
distance = "spearman",
noMappingDist = 0,
filtering = NULL,
name = "mRNAbymiRNA")

# Create Gene-gene distance through mRNA data
bioDistmRNA <- new("bioDistclass",
name = "mRNAbymRNA",
distance = cor(t(exprs(mRNA.ds)),method="spearman"),
map.name = "id",
map.metadata = list(),
params = list())

# Generation of the list of Surrogated distances.

bioDistList <- list(bioDistmRNA, bioDistmiRNA)
sample.weights <- matrix(0,4,2)
sample.weights[,1] <- c(0,0.33,0.67,1)
```r
sample.weights[,2]<-c(1,0.67,0.33,0)

#### Generation of the list of bioDistWclass objects.
bioDistWList<-bioDistW(referenceFeatures = rownames(Block1),
                       bioDistList = bioDistList,
                       weights=sample.weights)

#### Plot of distances.
bioDistWPlot(referenceFeatures = rownames(Block1),
              listDistW = bioDistWList,
              method.cor="spearman")

#### Computing the matrix of features/distances associated.
fm<-bioDistFeature(Feature = rownames(Block1)[1],
                    listDistW = bioDistWList,
                    threshold.cor=0.7)
bioDistFeaturePlot(data=fm)
```

---

**bioDistFeaturePlot**

**bioDistFeaturePlot**

**Description**

Function that plots the results from a bioDistFeature analysis

**Usage**

```r
bioDistFeaturePlot(data)
```

**Arguments**

- **data** Matrix produced by `bioDistFeature`

**Value**

Generates a heatmap plot

**Author(s)**

David Gomez-Cabrero

**Examples**

```r
data(STATegRa_S1)
data(STATegRa_S2)
require(Biobase)

# Truncate data for brevity
Block1 <- Block1[1:100,]
Block2 <- Block2[1:100,]
```
## Create ExpressionSets

mRNA.ds <- createOmicsExpressionSet(Data=Block1,pData=ed,pDataDescr=c("classname"))

miRNA.ds <- createOmicsExpressionSet(Data=Block2,pData=ed,pDataDescr=c("classname"))

## Create the bioMap

map.gene.miRNA<-bioMap(name = "Symbol-miRNA",
metadata = list(type_v1="Gene",type_v2="miRNA",
source_database="targetscan.Hs.eg.db",
data_extraction="July2014"),
map=mapdata)

# Create Gene-gene distance computed through miRNA data

bioDistmiRNA<-bioDist(referenceFeatures = rownames(Block1),
reference = "Var1",
mapping = map.gene.miRNA,
surrogateData = miRNA.ds, ### miRNA data
referenceData = mRNA.ds, ### mRNA data
maxitems=2,
selectionRule="sd",
expfac=NULL,
aggregation = "sum",
distance = "spearman",
noMappingDist = 0,
filtering = NULL,
name = "mRNAbymiRNA")

# Create Gene-gene distance through mRNA data

bioDistmRNA<-new("bioDistclass",
name = "mRNAbymRNA",
distance = cor(t(exprs(mRNA.ds)),method="spearman"),
map.name = "id",
params = list())

###### Generation of the list of Surrogated distances.

bioDistList<-list(bioDistmRNA,bioDistmiRNA)

sample.weights<-matrix(0,4,2)
sample.weights[,1]<-c(0,0.33,0.67,1)
sample.weights[,2]<-c(1,0.67,0.33,0)

###### Generation of the list of bioDistWclass objects.

bioDistWList<-bioDistW(referenceFeatures = rownames(Block1),
bioDistList = bioDistList,
weights=sample.weights)

###### Plot of distances.

bioDistWPlot(referenceFeatures = rownames(Block1) ,
listDistW = bioDistWList,
method.cor="spearman")

###### Computing the matrix of features/distances associated.

fm<-bioDistFeature(Feature = rownames(Block1)[1],
listDistW = bioDistWList,
threshold.cor=0.7)
bioDistW

bioDistFeaturePlot(data=fm)

bioDistW  bioDistW

Description

Function that computes weighted distances between a list of bioDistclass objects.

Usage

bioDistW(referenceFeatures, bioDistList, weights)

Arguments

  referenceFeatures
    The set of features that weighted distance is computed between.

  bioDistList
    A list of bioDistclass objects. All the objects must contain the set of features
    selected.

  weights
    A matrix where the number of columns equals the number of elements included
    in the bioDistList list.

Value

Returns a list of bioDistWclass objects. Each element in the list returns the weighted distance
associated to each row in the "weights" matrix.

Author(s)

David Gomez-Cabrero

Examples

data(STATegRa_S1)
data(STATegRa_S2)
require(Biobase)

# Truncate data for brevity
Block1 <- Block1[1:100,]
Block2 <- Block2[1:100,]

## Create ExpressionSets
mRNA.ds <- createOmicsExpressionSet(Data=Block1,pData=ed,pDataDescr=c("classname"))
mirNA.ds <- createOmicsExpressionSet(Data=Block2,pData=ed,pDataDescr=c("classname"))

## Create the bioMap
map.gene.miRNA<-bioMap(name = "Symbol-miRNA",
        metadata = list(type_v1="Gene",type_v2="miRNA",
          source_database="targetscan.Hs.eg.db",
          data_extraction="July2014"),
        map=mapdata)
# Create Gene-gene distance computed through miRNA data
bioDistmiRNA<-bioDist(referenceFeatures = rownames(Block1),
reference = "Var1",
mapping = map.gene.miRNA,
surrogateData = miRNA.ds, ### miRNA data
referenceData = mRNA.ds, ### mRNA data
maxitems=2,  
selectionRule="sd",
expfac=NULL,
aggregation = "sum",
distance = "spearman",
noMappingDist = 0,
fILTERING = NULL,
name = "mRNAbymiRNA")

# Create Gene-gene distance through mRNA data
bioDistmRNA<-new("bioDistclass",
name = "mRNAbymRNA",
distance = cor(t(exprs(mRNA.ds)),method="spearman"),
map.name = "id",
map.metadata = list(),
params = list())

##### Generation of the list of Surrogated distances.
bioDistList<-list(bioDistmRNA,bioDistmiRNA)
sample.weights<-matrix(0,4,2)
sample.weights[,1]<-c(0,0.33,0.67,1)
sample.weights[,2]<-c(1,0.67,0.33,0)

##### Generation of the list of bioDistWclass objects.
bioDistWList<-bioDistW(referenceFeatures = rownames(Block1),
listDistW = bioDistList,
weights=sample.weights)

##### Plot of distances.
bioDistWPlot(referenceFeatures = rownames(Block1) ,
listDistW = bioDistWList,
method.cor="spearman")

##### Computing the matrix of features/distances associated.
fm<-bioDistFeature(Feature = rownames(Block1)[1] ,
listDistW = bioDistWList,
threshold.cor=0.7)
bioDistFeaturePlot(data=fm)

## Description

Function that plots the "distance relation" between features computed through different surrogate features.
bioDistWPlot

Usage

bioDistWPlot(referenceFeatures, listDistW, method.cor)

Arguments

referenceFeatures
The set of features to be used.

listDistW
A list of bioDistWclass objects.

method.cor
Method to compute distances between the elements in the listDistW. The default is spearman correlation.

Value

Makes a plot with the projected distance between the listDistW objects.

Author(s)

David Gomez-Cabrero

Examples

data(STATegRa_S1)
data(STATegRa_S2)
require(Biobase)

# Truncate data for brevity
Block1 <- Block1[1:100,]
Block2 <- Block2[1:100,]

## Create ExpressionSets
mRNA.ds <- createOmicsExpressionSet(Data=Block1,pData=ed,pDataDescr=c("classname"))
miRNA.ds <- createOmicsExpressionSet(Data=Block2,pData=ed,pDataDescr=c("classname"))

## Create the bioMap
map.gene.miRNA<-bioMap(name = "Symbol-miRNA",
metadata = list(type_v1="Gene",type_v2="miRNA",
source_database="targetscan.Hs.eg.db",
data_extraction="July2014"),
map=mapdata)

# Create Gene-gene distance computed through miRNA data
bioDistmiRNA<-bioDist(referenceFeatures = rownames(Block1),
reference = "Var1",
mapping = map.gene.miRNA,
surrogateData = miRNA.ds, ### miRNA data
referenceData = mRNA.ds, ### mRNA data
maxitems=2,
selectionRule="sd",
expfac=NULL,
aggregation = "sum",
distance = "spearman",
noMappingDist = 0,
filtering = NULL,
name = "mRNAbymiRNA")
# Create Gene-gene distance through mRNA data

```r
bioDistmRNA <- new("bioDistclass",
  name = "mRNAbymRNA",
  distance = cor(t(exprs(mRNA.ds)), method="spearman"),
  map.name = "id",
  map.metadata = list(),
  params = list())
```

##### Generation of the list of Surrogated distances.

```r
bioDistList <- list(bioDistmRNA, bioDistmiRNA)
```

```r
sample.weights <- matrix(0, 4, 2)
sample.weights[,1] <- c(0, 0.33, 0.67, 1)
sample.weights[,2] <- c(1, 0.67, 0.33, 0)
```

##### Generation of the list of bioDistWclass objects.

```r
bioDistWList <- bioDistW(referenceFeatures = rownames(Block1),
                        bioDistList = bioDistList,
                        weights = sample.weights)
```

##### Plot of distances.

```r
bioDistWPlot(referenceFeatures = rownames(Block1),
              listDistW = bioDistWList,
              method.cor = "spearman")
```

##### Computing the matrix of features/distances associated.

```r
fm <- bioDistFeature(Feature = rownames(Block1)[1],
                     listDistW = bioDistWList,
                     threshold.cor = 0.7)
```

```r
bioDistFeaturePlot(data = fm)
```

---

## bioMap

### Description

Function to generate a bioMap object.

### Usage

```r
bioMap(name, metadata, map)
```

### Arguments

- **name**: Name to assign the object
- **metadata**: A list with information of the mapping. Elements expected in the list are: (1) "type_v1" and "type_v2", refer to the nature of the features mapped; a vocabulary we recommend is "gene", "mRNA", "miRNA", "proteins", etc. (2) "source_database", provides information on the source of the mapping; from a specific data-base e.g. "targetscan.Hs.eg.db" to a genomic location mapping. (3) "data_extraction" stores information on the data the mapping was generated or downloaded.
biplotRes

**map**

A data.frame object storing the mapping. The data.frame may include an unlimited number of columns, however the first column must be named "Var1" and refer to the elements of "type_v1" and similarly for the second column ("Var2", "type_v2").

**Value**

An object of class bioMap

**Author(s)**

David Gomez-Cabrero

**Examples**

data(STATegRa_S2)
map.gene.miRNA <- bioMap(name = "Symbol-miRNA",
metadata = list(type_v1="Gene", type_v2="miRNA",
source_database="targetscan.Hs.eg.db",
data_extraction="July2014"),
map=mapdata)


---

**biplotRes**

**Biplot of component analysis**

**Description**

Generate a biplot of component analysis results

**Usage**

biplotRes(object, type, comps, block, title=NULL, colorCol=NULL, sizeValues=c(2, 4), shapeValues=c(17, 0), background=TRUE, pointSize=4, labelSize=NULL, axisSize=NULL, titleSize=NULL)

**Arguments**

- **object** caClass object containing component analysis results
- **type** Character specifying which components to plot; "common", "individual" or "both"
- **comps** Components to plot. If combined=FALSE, specifies the component indices to use as x and y for the plot. Otherwise, the component from the first block and the component from second block to plot together.
- **block** Which block to plot, either "1" or "2" or the name of the block.
- **title** Plot title
- **colorCol** Character specifying a pData column to use to colorise the plot points
- **sizeValues** Vector containing sizes for scores and loadings
- **shapeValues** Vector indicating the shapes for scores and loadings
- **background** Logical, whether to use a grey background
- **pointSize** Size of plot points
biplotRes

**labelSize**  Size of plot labels if not NULL
**axisSize**   Size of axis text
**titleSize**  Size of title text

**Value**
ggplot2 object

**Author(s)**
Patricia Sebastian-Leon

**Examples**

data("STATegRa_S3")
B1 <- createOmicsExpressionSet(Data=Block1.PCA,pData=ed.PCA, pDataDescr=c("classname"))
B2 <- createOmicsExpressionSet(Data=Block2.PCA, pData=ed.PCA,pDataDescr=c("classname"))

# Omics components analysis
discoRes <- omicsCompAnalysis(Input=list(B1,B2),Names=c("expr","mirna"),
method="DISCOSCA",Rcommon=2,Rspecific=c(2,2),
center=TRUE,scale=TRUE,weight=TRUE)
jiveRes <- omicsCompAnalysis(Input=list(B1,B2),Names=c("expr","mirna"),
method="JIVE",Rcommon=2,Rspecific=c(2,2),
center=TRUE,scale=TRUE,weight=TRUE)
o2plsRes <- omicsCompAnalysis(Input=list(B1,B2),Names=c("expr","mirna"),
method="O2PLS",Rcommon=2,Rspecific=c(2,2),
center=TRUE,scale=TRUE,weight=TRUE)

# Biplot common part. DISCO-SCA
biplotRes(object=discoRes,type="common",comps=c(1,2),block="",title=NULL,colorCol="classname",sizeValues=c(2,4),
shapeValues=c(17,0),background=TRUE,pointSize=4,labelSize=NULL,axisSize=NULL,titleSize=NULL)

# Biplot common part. O2PLS
p1 <- biplotRes(object=o2plsRes,type="common",comps=c(1,2),
block="expr",title=NULL,colorCol="classname",sizeValues=c(2,4),shapeValues=c(17,0),
background=TRUE,pointSize=4,labelSize=NULL,axisSize=NULL,titleSize=NULL)
p2 <- biplotRes(object=o2plsRes,type="common",comps=c(1,2),
block="mirna",title=NULL,colorCol="classname",sizeValues=c(2,4),shapeValues=c(17,0),
background=TRUE,pointSize=4,labelSize=NULL,axisSize=NULL,titleSize=NULL)

# Biplot distinctive part. O2PLS
p1 <- biplotRes(object=discoRes,type="individual",comps=c(1,2),
block="expr",title=NULL,colorCol="classname",sizeValues=c(2,4),shapeValues=c(17,0),
caClass-class

Stores the results of any of the omicsPCA analyses.

Slots

- **InitialData**: List of ExpressionSets, one for each set of omics data
- **Names**: Character vector giving names for the input data
- **preprocessing**: Character vector describing the preprocessing applied to the data
- **preproData**: List of matrices containing data after preprocessing
- **caMethod**: Character giving the component analysis method name
- **commonComps**: Numeric giving the number of common components
- **distComps**: Numeric vector giving the number of distinctive components for each block
- **scores**: List of matrices of common and distinctive scores
- **loadings**: List of matrices of common and distinctive loadings
- **VAF**: List of matrices indicating VAF (Variability Explained For) for each component in each block of data
- **others**: List containing other miscellaneous information specific to different SCA methods

Author(s)

Patricia Sebastian Leon

combiningMappings

*combiningMappings, combining several mappings for use in the omicsNPC function*

Description

This function combines several annotation so that measurements across different datasets are mapped to the same reference elements (e.g., genes). The annotations should all be either data frame / matrices, named vectors/lists, or bioMap objects. See the examples for further details.

Usage

`combiningMappings(mappings, reference = NULL, retainAll = FALSE)`
createOmicsExpressionSet

**Arguments**

- mappings: List of annotations.
- reference: If the annotations are data frame, matrices or bioMap objects, the name of the column containing the reference elements.
- retainAll: Logical, if set to TRUE measurements that have no counterparts in other datasets are retained.

**Value**

A data frame encoding the mapping across several dataset.

**Author(s)**

Vincenzo Lagani

**References**

Nestoras Karathanasis, Ioannis Tsamardinos and Vincenzo Lagani. omicsNPC: applying the Non-Parametric Combination methodology to the integrative analysis of heterogeneous omics data. Submitted to PlosONE.

**Examples**

### Example 1

# Mapping with data frames
mRNA <- data.frame(gene = rep(c('G1', 'G2', 'G3'), each = 2), probeset = paste('p', 1:6, sep = ''));
methylation <- data.frame(gene = c(rep('G1', 3), rep('G2', 4)),
                         methy = paste('methy', 1:7, sep = ''));
miRNA <- data.frame(gene = c(rep('G1', 2), rep('G2', 1), rep('G3', 2)),
                    miR = c('miR1', 'miR2', 'miR1', 'miR1', 'miR2'));
mappings <- list(mRNA = mRNA, methylation = methylation, miRNA = miRNA);
combiningMappings(mappings = mappings, retainAll = TRUE)

### Example 2

# Mapping with character vectors
mRNA <- rep(c('G1', 'G2', 'G3'), each = 2);
names(mRNA) = paste('p', 1:6, sep = '');
methylation <- c(rep('G1', 3), rep('G2', 4));
names(methylation) = paste('methy', 1:7, sep = '');
miRNA <- c(rep('G1', 2), rep('G2', 1), rep('G3', 2));
names(miRNA) = c('miR1', 'miR2', 'miR1', 'miR1', 'miR2');
mappings <- list(mRNA = mRNA, methylation = methylation, miRNA = miRNA);
combiningMappings(mappings = mappings, retainAll = TRUE)

---

createOmicsExpressionSet

**Description**

This function allows the user to create an ExpressionSet object from a matrix representing an omics dataset. It allows to include the experimental design and annotation in the ExpressionSet object.
getInitialData

Usage

createOmicsExpressionSet(Data, pData = NULL, pDataDescr = NULL, feaData = NULL, feaDataDescr = NULL)

Arguments

- **Data**: Omics data
- **pData**: Data associated with the samples/phenotype
- **pDataDescr**: Description of the phenotypic data
- **feaData**: Data associated with the variables/features annotation
- **feaDataDescr**: Description of the feature annotation

Details

In Data matrix, samples has to be in columns and variables has to be in rows

Value

ExpressionSet with the data provided

Author(s)

Patricia Sebastian-Leon

Examples

data(STATegRa_S3)
B1 <- createOmicsExpressionSet(Data=Block1.PCA, pData=ed.PCA, pDataDescr=c("classname"))
B2 <- createOmicsExpressionSet(Data=Block2.PCA, pData=ed.PCA, pDataDescr=c("classname"))

getInitialData

Retrieve initial data from caClass objects

Description

Generic function to retrieve the initial data used for by omicsCompAnalysis from a caClass-class object

Usage

getInitialData(x, block=NULL)

Arguments

- **x**: caClass-class object.
- **block**: Character indicating the block of data to be returned. It can be specified by the position of the block ("1" or "2") or the name assigned in the caClass-class object. If it is NULL both blocks are displayed.
getLoadings

Value
The requested data block or blocks

Author(s)
Patricia Sebastian-Leon

See Also
omicsCompAnalysis, caClass-class

Examples

data("STATegRa_S3")
B1 <- createOmicsExpressionSet(Data=Block1.PCA, pData=ed.PCA, pDataDescr=c("classname"))
B2 <- createOmicsExpressionSet(Data=Block2.PCA, pData=ed.PCA, pDataDescr=c("classname"))
# Omics components analysis
res <- omicsCompAnalysis(Input=list(B1, B2), Names=c("expr", "mirna"), method="DISCOSCA", Rcommon=2, Rspecific=c(2, 2), center=TRUE, scale=TRUE, weight=TRUE)
getInitialData(res)
getInitialData(res, block="expr")

getLoadings

Retrieve component analysis loadings

Description
Generic function to retrieve loadings (common and distinctive) found by omicsCompAnalysis on a caClass-class object.

Usage
getLoadings(x, part=NULL, block=NULL)

Arguments
x caClass-class object.
part Character indicating whether "common" or "distinctive" loadings should be displayed
block Character indicating the block of data for which the loadings will be given. It can be specified by the position of the block ("1" or "2") or the name assigned in the caClass-class object. If it is NULL both blocks are displayed.

Value
A list containing the requested information.

Author(s)
Patricia Sebastian-Leon
getMethodInfo

Retrieve information about component analysis method

Description

Generic function to retrieve information about the method used by omicsCompAnalysis on a caClass-class object.

Usage

getMethodInfo(x, method=FALSE, comps=NULL, block=NULL)

Arguments

x caClass-class object.
method Logical indicating whether to return the method name.
comps Character indicating which component number to return ("common", "distinctive" or "all")
block Character indicating the block of data for which the component count will be given. It can be specified by the position of the block ("1" or "2") or the name assigned in the caClass-class object. If it is NULL both blocks are displayed.

Value

A list containing the requested information.

Author(s)

Patricia Sebastian-Leon

See Also

omicsCompAnalysis, caClass-class
getPreprocessing

Retrieve information about preprocessing

Description

Generic function to retrieve information about the preprocessing done by `omicsCompAnalysis` on a `caClass-class` object.

Usage

getPreprocessing(x, process=FALSE, preproData=FALSE, block=NULL)

Arguments

- **x** `caClass-class` object.
- **process** Logical indicating whether to return information about the processing done.
- **preproData** Logical indicating whether to return the pre-processed data matrices.
- **block** Character indicating the block of data to be returned. It can be specified by the position of the block (“1” or “2”) or the name assigned in the `caClass-class` object. If it is NULL both blocks are displayed.

Value

If both `process` and `preproData` are specified, a list containing (otherwise the individual item):

- **process** Character indicating the processing done
- **preproData** Matrix (or list of matrices, depending on `block`) containing pre-processed data

Author(s)

Patricia Sebastian-Leon

See Also

`omicsCompAnalysis, caClass-class`
getScores

Examples

data("STATegRa_S3")
B1 <- createOmicsExpressionSet(Data=Block1.PCA, pData=ed.PCA,
PDataDescr=c("classname"))
B2 <- createOmicsExpressionSet(Data=Block2.PCA,
PData=ed.PCA, pDataDescr=c("classname"))
# Omics components analysis
res <- omicsCompAnalysis(Input=list(B1, B2), Names=c("expr", "mirna"),
method="DISCOSCA", Rcommon=2, Rspecific=c(2, 2),
center=TRUE, scale=TRUE, weight=TRUE)
getPreprocessing(res, process=TRUE)
getPreprocessing(res, preproData=TRUE, block="1")

gScores

Retrieve component analysis scores

Description

Generic function to retrieve scores (common and distinctive) found by omicsCompAnalysis on a caClass-class object.

Usage

gScores(x, part=NULL, block=NULL)

Arguments

x caClass-class object.

part Character indicating whether "common" or "distinctive" scores should be displayed.

block Character indicating the block of data for which the scores will be given. It can be specified by the position of the block ("1" or "2") or the name assigned in the caClass-class object. If it is NULL both blocks are displayed.

Value

A list containing the requested information.

Author(s)

Patricia Sebastian-Leon

See Also

omicsCompAnalysis, caClass-class
getVAF

Examples

data("STATegRa_S3")
B1 <- createOmicsExpressionSet(Data=Block1.PCA, pData=ed.PCA,
pDataDescr=c("classname"))
B2 <- createOmicsExpressionSet(Data=Block2.PCA,
pData=ed.PCA, pDataDescr=c("classname"))
# Omics components analysis
res <- omicsCompAnalysis(Input=list(B1, B2), Names=c("expr", "mirna"),
method="DISCOSCA", Rcommon=2, Rspecific=c(2, 2),
center=TRUE, scale=TRUE, weight=TRUE)
getScores(res)
getScores(res, part="common")
getScores(res, part="distinctive", block="expr")

getVAF Retrieve information about VAF

Description

Generic function to retrieve VAF found by omicsCompAnalysis on a caClass-class object.

Usage

getVAF(x, part=NULL, block=NULL)

Arguments

x caClass-class object.

part Character indicating whether "common" or "distinctive" VAF should be displayed

block Character indicating the block of data for which the VAF will be given. It can be specified by the position of the block ("1" or "2") or the name assigned in the caClass-class object. If it is NULL both blocks are displayed.

Value

A list containing the requested information.

Author(s)

Patricia Sebastian-Leon

See Also

omicsCompAnalysis, caClass-class
Examples

```r
data("STATegRa_S3")
B1 <- createOmicsExpressionSet(Data=Block1.PCA, pData=ed.PCA, pDataDescr=c("classname"))
B2 <- createOmicsExpressionSet(Data=Block2.PCA, pData=ed.PCA, pDataDescr=c("classname"))
# Omics components analysis
res <- omicsCompAnalysis(Input=list(B1, B2), Names=c("expr", "mirna"),
method="DISCOSCA", Rcommon=2, Rspecific=c(2, 2),
center=TRUE, scale=TRUE, weight=TRUE)
getVAF(res)
getVAF(res, part="common")
getVAF(res, part="distinctive", block="expr")
```

Description

This function is defunct. Use omicsNPC instead.

Usage

```
holistOmics(dataInput, dataTypes, comb.method = c("Fisher", "Liptak", "Tippett"),
numPerm = 1000, numCores = 1, verbose = FALSE)
```

Arguments

- `dataInput`: List of ExpressionSet objects, one for each data modality.
- `dataTypes`: Character vector with possible values: 'RNA-seq', 'microarray'
- `comb.method`: Character vector with possible values: 'Fisher', 'Liptak', 'Tippett', if more than one is specified, all will be used.
- `numPerm`: Number of permutations
- `numCores`: Number of CPU cores to use
- `verbose`: Logical, if set to TRUE holistOmics prints out the step that it performs

Value

A data.frame

Author(s)

Nestoras Karathanasis

References

Examples

```r
# Load the data
data("TCGA_BRCA_Batch_93")
# Setting dataTypes, the first two ExpressionSets include RNAseq data,
# the third ExpressionSet includes Microarray data.
dataTypes <- c("RNAseq", "RNAseq", "Microarray")
# Setting methods to combine pvalues
comb.method = c("Fisher", "Liptak", "Tippett")
# Setting number of permutations
numPerm = 1000
# Setting number of cores
numCores = 1
# Setting holistOmics to print out the steps that it performs.
verbose = TRUE
# Run holistOmics analysis.
# The output is a data.frame of p-values.
# Each row corresponds to a gene name. Each column corresponds to a method
# used in the analysis.
## Not run: out <- holistOmics(dataInput = TCGA_BRCA_Data, dataTypes = dataTypes,
##                             comb.method = comb.method, numPerm = numPerm,
##                             numCores = numCores, verbose = verbose)
## End(Not run)
```

**modelSelection**

*Find optimal common and distinctive components*

Description

Uses `selectCommonComps` and `PCA.selection` to estimate the optimal number of common and distinctive components according to given selection criteria.

Usage

```r
modelSelection(Input, Rmax, fac.sel, varthreshold=NULL, nvar=NULL, PCnum=NULL)
```

Arguments

- `Input`: List of two ExpressionSet objects
- `Rmax`: Maximum common components (see `selectCommonComps`)
- `fac.sel`: PCA criteria (see `PCA.selection`)
- `varthreshold`: Cumulative variance criteria (see `PCA.selection`)
- `nvar`: Relative variance criteria (see `PCA.selection`)
- `PCnum`: Fixed component number (see `PCA.selection`)

Value

- `common`: Number of common components
- `dist`: Number of distinct components per input block
omicsCompAnalysis

Author(s)
Patricia Sebastian-Leon

See Also
selectCommonComps, PCA.selection, omicsCompAnalysis

Examples

data(STATegRa.S3)
B1 <- createOmicsExpressionSet(Data=Block1.PCA, pData=ed.PCA, pDataDescr=c("classname"))
B2 <- createOmicsExpressionSet(Data=Block2.PCA, pData=ed.PCA, pDataDescr=c("classname"))
ms <- modelSelection(Input=list(B1, B2), Rmax=4, fac.sel="single\%", varthreshold=0.03)
ms

omicsCompAnalysis  Components analysis for multiple objects

Description
This function performs a components analysis of object wise omics data to understand the mech-
anisms that underlay all the data blocks under study (common mechanisms) and the mechanisms
underlying each of the data block independently (distinctive mechanisms). This analysis include
both, the preprocessing of data and the components analysis by using three different methodolo-
gies.

Usage

omicsCompAnalysis(Input, Names, method, Rcommon, Rspecific,
convThres=1e-10, maxIter=600, center=FALSE,
scale=FALSE, weight=FALSE)

Arguments

Input  List of ExpressionSet objects, one for each block of data.
Names  Character vector giving names for each Input object.
method  Method to use for analysis (either "DISCOSCA", "JIVE", or "O2PLS").
Rcommon Number of common components between all blocks
Rspecific Vector giving number of unique components for each input block
convThres Stop criteria for convergence
maxIter  Maximum number of iterations
center  Character (or FALSE) specifying which (if any) centering will be applied be-
        fore analysis. Choices are "PERBLOCKS" (each block separately) or "ALL-
        BLOCKS" (all data together).
scale  Character (or FALSE) specifying which (if any) scaling will be applied be-
        fore analysis. Choices are "PERBLOCKS" (each block separately) or "ALL-
        BLOCKS" (all data together).
weight  Logical indicating whether weighting is to be done.
Value

An object of class `caClass-class`.

Author(s)

Patricia Sebastian Leon

Examples

data("STATegRa_S3")
B1 <- createOmicsExpressionSet(Data=Block1.PCA,pData=ed.PCA,
pDataDescr=c("classname"))
B2 <- createOmicsExpressionSet(Data=Block2.PCA,
pData=ed.PCA,pDataDescr=c("classname"))
# Omics components analysis
discoRes <- omicsCompAnalysis(Input=list(B1,B2),Names=c("expr","mirna"),
method="DISCOSCA",Rcommon=2,Rspecific=c(2,2),
center=TRUE,scale=TRUE,weight=TRUE)
jiveRes <- omicsCompAnalysis(Input=list(B1,B2),Names=c("expr","mirna"),
method="JIVE",Rcommon=2,Rspecific=c(2,2),
center=TRUE,scale=TRUE,weight=TRUE)
o2plsRes <- omicsCompAnalysis(Input=list(B1,B2),Names=c("expr","mirna"),
method="O2PLS",Rcommon=2,Rspecific=c(2,2),
center=TRUE,scale=TRUE,weight=TRUE)

Description

This function applies the NonParametric Combination methodology on the integrative analysis of different omics data modalities. It retrieves genes associated to a given outcome, taking into account all omics data. First, each datatype is analyzed independently using the appropriate method. omicsNPC analyses continuous data (microarray) using limma, while count data (e.g., RNAseq) are first preprocessed with using the “voom” function. The user can also specify their own function for computing deregulation / association. The p-values from the single dataset analysis are then combined employing Fisher, Liptak and Tippett combining functions. The Tippett function returns findings which are supported by at least one omics modality. The Liptak function returns findings which are supported by most modalities. The Fisher function has an intermediate behavior between those of Tippett and Liptak.

Usage

omicsNPC(dataInput, dataMapping, dataTypes = rep('continuous', length(dataInput)),
combMethods = c("Fisher", "Liptak", "Tippett"), numPerms = 1000,
numCores = 1, verbose = FALSE, functionGeneratingIndex = NULL,
outcomeName = NULL, allCombinations = FALSE,
dataWeights = rep(1, length(dataInput))/length(dataInput),
returnPermPvalues = FALSE, ...)

omicsNPC

Arguments

dataInput List of ExpressionSet objects, one for each data modality.
dataMapping A data frame describing how to map measurements across datasets. See details for more information.
dataTypes Character vector with possible values: 'continuous', 'count'. Alternatively, a list of functions for assessing deregulation / association with an outcome
combMethods Character vector with possible values: 'Fisher', 'Liptak', 'Tippett'. If more than one is specified, all will be used.
numPerms Number of permutations
numCores Number of CPU cores to use
verbose Logical, if set to TRUE omicsNPC prints out the step that it performs
functionGeneratingIndex Function generating the indices for randomly permuting the samples
outcomeName Name of the outcome of interest / experimental factor, as reported in the design matrices. If NULL, the last column of the design matrices is assumed to be the outcome of interest.
allCombinations Logical, if TRUE all combinations of omics datasets are considered
dataWeights A vector specifying the weight to give to each dataset. Note that sum(dataWeights) should be 1.
returnPermPvalues Logical, should the p-values computed at each permutation being returned?
... Additional arguments to be passed to the user-defined functions

Value

A list containing: stats0 Partial deregulation / association statistics pvalues0 The partial p-values computed on each dataset pvaluesNPC The p-values computed through NPC. permPvalues The p-values computed at each permutation

Author(s)

Nestoras Karathanasis, Vincenzo Lagani

References


Examples

# Load the data
data("TCGA_BRCA_Batch_93")
# Setting dataTypes, the first two ExpressionSets include RNAseq data,
# the third ExpressionSet includes Microarray data.
dataTypes <- c("count", "count", "continuous")
# Setting methods to combine pvalues
combMethods = c("Fisher", "Liptak", "Tippett")
# Setting number of permutations
numPerms = 1000
# Setting number of cores
numCores = 1
# Setting omicsNPC to print out the steps that it performs.
verbose = TRUE
# Run omicsNPC analysis.
# The output contains a data.frame of p-values, where each row corresponds to a gene,
# and each column corresponds to a method used in the analysis.

## Not run: out <- omicsNPC(dataInput = TCGA_BRCA_Data, dataTypes = dataTypes,
combMethods = combMethods, numPerms = numPerms,
numCores = numCores, verbose = verbose)
## End(Not run)

### PCA.selection

Select an optimal number of components using PCA

**Description**

Selects the optimal number of components from data using PCA. There are four different criteria available: accumulated variance explained, individual explained variance of each component, absolute value of variability or fixed number of components.

**Usage**

PCA.selection(Data, fac.sel, varthreshold=NULL, nvar=NULL, PCnum=NULL)

**Arguments**

- **Data**: Data matrix (with samples in columns and features in rows)
- **fac.sel**: Selection criteria ("%accum", "single%", "rel.abs", "fixed.num")
- **varthreshold**: Threshold for "%accum" or "single%" criteria
- **nvar**: Threshold for "rel.abs"
- **PCnum**: Fixed number of components for "fixed.num"

**Value**

List containing:

- **PCAres**: List containing results of PCA, with fields "eigen", "var.exp", "scores" and "loadings"
- **numComps**: Number of components selected

**Examples**

data(STATegRa_S3)
pS <- PCA.selection(Data=Block2.PCA, fac.sel="singleX", varthreshold=0.03)
pS$numComps
plotRes

Plot component analysis results

Description
Plot scatterplots of scores or loadings, for common and distinctive parts as well as combined plots.

Usage
plotRes(object, comps=c(1, 2), what, type, combined, block, color=NULL, shape=NULL, labels=NULL, background=TRUE, palette=NULL, pointSize=4, labelSize=NULL, axisSize=NULL, titleSize=NULL)

Arguments

object caClass object containing component analysis results
comps If combined=FALSE, it indicates the x and y components of the type and block chosen. If combined=TRUE, it indicates the component to plot for the first block of information and the component for the second block of information to plot together. By default the components are set to c(1,2) if combined=FALSE and to c(1,1) if combined=TRUE.
what Either "scores" or "loadings"
type Either "common", "individual" or "both"
combined Logical indicating whether to make a simple plot of two components from one block, or components from different blocks
block Which block to plot, either "1" or "2" or the name of the block.
color Character specifying a pData column from the original data to use to color points
shape Character specifying a pData column to select point shape
labels Character specifying a pData column from which to take point labels
background Logical specifying whether to make a grey background
palette Vector giving the color palette for the plot
pointSize Size of plot points
labelSize Size of point labels if not NULL
axisSize Size of axis text
titleSize Size of title text

Value
ggplot object

Author(s)
Patricia Sebastian-Leon
Examples

data("STATegRa_S3")

B1 <- createOmicsExpressionSet(Data=Block1.PCA,pData=ed.PCA,
pDataDescr=c("classname"))
B2 <- createOmicsExpressionSet(Data=Block2.PCA,
pData=ed.PCA,pDataDescr=c("classname"))

# Omics components analysis
discoRes <- omicsCompAnalysis(Input=list(B1,B2),Names=c("expr","mirna"),
method="DISCOSCA",Rcommon=2,Rspecific=c(2,2),
center=TRUE,scale=TRUE,weight=TRUE)
jiveRes <- omicsCompAnalysis(Input=list(B1,B2),Names=c("expr","mirna"),
method="JIVE",Rcommon=2,Rspecific=c(2,2),
center=TRUE,scale=TRUE,weight=TRUE)
o2plsRes <- omicsCompAnalysis(Input=list(B1,B2),Names=c("expr","mirna"),
method="O2PLS",Rcommon=2,Rspecific=c(2,2),
center=TRUE,scale=TRUE,weight=TRUE)

# Scatterplot of scores variables associated to common components
# DISCO-SCA
plotRes(object=discoRes,comps=c(1,2),what="scores",type="common",
combined=FALSE,block="",color="classname",shape=NULL,labels=NULL,
background=TRUE,palette=NULL,pointSize=4,labelSize=NULL,
axisSize=NULL,titleSize=NULL)

# JIVE
plotRes(object=jiveRes,comps=c(1,2),what="scores",type="common",
combined=FALSE,block="",color="classname",shape=NULL,labels=NULL,
background=TRUE,palette=NULL,pointSize=4,labelSize=NULL,
axisSize=NULL,titleSize=NULL)

# O2PLS
# Scatterplot of scores variables associated to common components
# Associated to first block
p1 <- plotRes(object=o2plsRes,comps=c(1,2),what="scores",type="common",
combined=FALSE,block="expr",color="classname",shape=NULL,labels=NULL,
background=TRUE,palette=NULL,pointSize=4,labelSize=NULL,
axisSize=NULL,titleSize=NULL)

# Associated to second block
p2 <- plotRes(object=o2plsRes,comps=c(1,2),what="scores",type="common",
combined=FALSE,block="mirna",color="classname",shape=NULL,labels=NULL,
background=TRUE,palette=NULL,pointSize=4,labelSize=NULL,
axisSize=NULL,titleSize=NULL)

# Combined plot of scores variables associated to common components
plotRes(object=o2plsRes,comps=c(1,1),what="scores",type="common",
combined=TRUE,block="",color="classname",shape=NULL,labels=NULL,
background=TRUE,palette=NULL,pointSize=4,labelSize=NULL,
axisSize=NULL,titleSize=NULL)

# Loadings plot for individual components
# Separately for each block
p1 <- plotRes(object=discoRes,comps=c(1,2),what="loadings",type="individual",
combined=FALSE,block="expr",color="classname",shape=NULL,labels=NULL,
background=TRUE,palette=NULL,pointSize=4,labelSize=NULL,
axisSize=NULL,titleSize=NULL)
plotVAF

p2 <- plotRes(object=discoRes,comps=c(1,2),what="loadings",type="individual", combined=FALSE,block="mirna",color="classname",shape=NULL, labels=NULL,background=TRUE,palette=NULL,pointSize=4, labelSize=NULL,axisSize=NULL,titleSize=NULL)

# Combined plot
plotRes(object=discoRes,comps=c(1,1),what="loadings",type="individual", combined=TRUE,block="",color="classname",shape=NULL, labels=NULL,background=TRUE,palette=NULL,pointSize=4, labelSize=NULL,axisSize=NULL,titleSize=NULL)

plotVAF

Plot VAF (Variance Explained For) from Component Analysis

Description

This function visualises the VAF results from component analysis. The input is a caClass-class object from omicsCompAnalysis. VAF cannot be calculated if mode "O2PLS" was used. The plots for modes "DISCOSCA" and "JIVE" are different since DISCO-SCA distinctive components have some VAF in the other block. This VAF can be interpreted as an error in the rotation.

Usage

plotVAF(object, mainTitle="")

Arguments

object caClass-class object containing component analysis results
mainTitle Plot title

Value

ggplot object

Author(s)

Patricia Sebastian-Leon

Examples

data("STATegRa_S3")
require(ggplot2)
B1 <- createOmicsExpressionSet(Data=Block1.PCA,pData=ed.PCA,
pDataDescr=c("classname"))
B2 <- createOmicsExpressionSet(Data=Block2.PCA,
pData=ed.PCA,pDataDescr=c("classname"))

# Omics components analysis
discoRes <- omicsCompAnalysis(Input=list(B1,B2),Names=c("expr","mirna"), method="DISCOSCA",Rcommon=2,Rspecific=c(2,2), center=TRUE,scale=TRUE,weight=TRUE)
jiveRes <- omicsCompAnalysis(Input=list(B1,B2),Names=c("expr","mirna"), method="JIVE",Rcommon=2,Rspecific=c(2,2), center=TRUE,scale=TRUE,weight=TRUE)
selectCommonComps

# DISCO-SCA plotVAF
plotVAF(discoRes)

# JIVE plotVAF
plotVAF(jiveRes)

selectCommonComps  Select common components in two data blocks

Description

This function applies a Simultaneous Component Analysis (SCA). The idea is that the scores for both blocks should have a similar behaviour if the components are in the common mode. Evaluation is by the ratios between the explained variances (SSQ) of each block and the estimator. The highest component count with $0.8 < \text{ratio} < 1.5$ is selected.

Usage

selectCommonComps(X, Y, Rmax)

Arguments

X  Matrix of omics data
Y  Matrix of omics data
Rmax  Maximum number of common components to find

Value

A list with components:

common  Optimal number of common components
ssqs  Matrix of SSQ for each block and estimator
pssq  ggplot object showing SSQ for each block and estimator
pratios  ggplot object showing SSQ ratios between each block and estimator

Author(s)

Patricia Sebastian-Leon

Examples

data(STATegRa_S3)
cc <- selectCommonComps(X=Block1.PCA, Y=Block2.PCA, Rmax=3)
cc$common
cc$pssq
cc$pratios
STATegRa

Description

STATegRa is a package for the integrative analysis of multi-omic data-sets. For full information, see the user's guide.

See Also

STATegRaUsersGuide

Defunct functions in STATegRa

Description

These functions have are defunct and no longer available

Details

• holistOmics: replaced by omicsNPC

STATegRaUsersGuide

Description

Finds the location of the STATegRa User’s Guide and optionally opens it.

Usage

STATegRaUsersGuide(view = TRUE)

Arguments

view Whether to open a browser

Value

The path to the documentation

Author(s)

David Gomez-Cabrero

Examples

STATegRaUsersGuide(view=FALSE)
Description

mRNA data (Block1), miRNA data (Block2) and the design matrix (ed), from STATegRa_S1, provides selected data downloaded from https://tcga-data.nci.nih.gov/docs/publications/gbm_exp/. The mapping between miRNA and mRNA (mapdata, available in STATegRa_S2) contains, as a processed matrix, selected information available from TargetScan; we selected the set of miRNA target predictions for humans for those miRNA-mRNA pairs where both miRNA and mRNA were in Block1 and Block2 respectively.

The PCA version of the data (Block1.PCA, Block2.PCA, ed.PCA; available in STATegRa_S3), provides a similar data-set to Block1, Block2 and ed data; however in this case the data has been processed in order to provide a pedagogic example of OmicsPCA. Results obtained from OmicsPCA (omicsCompAnalysis) with the existing data should not be taken as clinically valid.

Format

Two matrices with mRNA and miRNA expression data, a design matrix that describes both and a mapping between miRNA and genes.

Author(s)

David Gomez-Cabrero, Patricia Sebastian-Leon, Gordon Ball

Source

(a) See https://tcga-data.nci.nih.gov/docs/publications/gbm_exp/. (b) Gabor Csardi, targetscan.Hs.eg.db: TargetScan miRNA target predictions for human. R package version 0.6.1

Examples

data(STATegRa_S1)
data(STATegRa_S2)
data(STATegRa_S3)

Description

Data were downloaded from TCGA data portal, https://tcga-data.nci.nih.gov/tcga/. We downloaded sixteen tumour samples and the sixteen matching normal, for Breast invasive carcinoma, BRCA, batch 93. Herein, three types of data modalities are included, RNAseq (TCGA_BRCA_Data$RNAseq), RNAseqV2 (TCGA_BRCA_Data$RNAseqV2) and Expression-Genes (TCGA_BRCA_Data$Microarray). The Data Level was set to Level 3. For each data type, we pooled all data to one matrix, where rows corresponded to genes and columns to samples. Only the first 100 genes are included.
Format

One list, which contains three ExpressionSet objects.

Author(s)

Nestoras Karathanasis, Vincenzo Lagani

Source

See https://tcga-data.nci.nih.gov/tcga/.

Examples

# load data
data(TCGA_BRCA_Batch_93)
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