

Package ‘projectR’

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Type Package

Title Functions for the projection of weights from PCA, CoGAPS, NMF, correlation, and clustering

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Description Functions for the projection of data into the spaces defined by PCA, CoGAPS, NMF, correlation, and clustering.

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alluvialMat

alluvialMat

Description

Function to provide alluvial matrix for generating alluvial plot

Usage

```
alluvialMat(
  projection,
  annotations,
  annotationName = "Cell type",
  annotationType = "Cell",
  plot = TRUE,
  minPropExplained = 0.75
)
```

Arguments

| | |
|------------------|--|
| projection | a projection generated from projectR, ensure that full = TRUE while generating projection |
| annotations | a character vector of annotations for the data |
| annotationName | a character for collective name of the annotations, default is "Cell type" |
| annotationType | a character indicating the type of data annotated, default is "Cell" |
| plot | logical indicating whether to return the alluvial plot, default is TRUE |
| minPropExplained | threshold for minimum proportion of samples that correspond to a pattern to be used for plotting |

Value

A matrix to generate alluvial plots

Examples

```
projection <- projectR(data=p.ESepiGen4c11$mRNA.Seq, loadings=AP.RNAseq613c3t$Amean,
  dataNames = map.ESepiGen4c11[["GeneSymbols"]], full = TRUE)
alluvialMat(projection, pd.ESepiGen4c11$Condition)
```

AP.RNAseq613c3t

CoGAPS patterns and genes weights for p.RNAseq613c3t

Description

AP.RNAseq613c3t contains the output of the gapsRun function in the CoGAPS package for data = p.RNAseq613c3t

Usage

```
AP.RNAseq613c3t
```

Format

A list of 12 items

| | |
|--------|---------------|
| aucMat | <i>aucMat</i> |
|--------|---------------|

Description

Calculates AUC values for each set of weights for each label and outputs the results as a matrix

Usage

```
aucMat(labels, weights)
```

Arguments

| | |
|---------|--|
| labels | a vector of labels whose length is equal to the number of columns in the weight matrix |
| weights | a matrix of weights from projection analysis |

Value

A matrix of AUC values for each set of weights classifying each label.

Examples

```
projectR(data=p.ESepiGen4c1l$mRNA.Seq,loadings=AP.RNaseq6l3c3t$Amean,
dataNames = map.ESepiGen4c1l[["GeneSymbols"]]) -> projection
aucMat(pd.ESepiGen4c1l$Condition,projection)
```

| | |
|-----------------|---|
| cluster2pattern | <i>Generic cluster2pattern function</i> |
|-----------------|---|

Description

Function to make patterns of continuous weights from clusters.

Usage

```
cluster2pattern(clusters, NP, Data, ...)

## S4 method for signature 'kmeans'
cluster2pattern(clusters, Data)

## S4 method for signature 'hclust'
cluster2pattern(clusters, NP, Data = NA)
```

Arguments

| | |
|----------|---|
| clusters | a cluster object which could be either an hclust or a kmeans object |
| NP | number of desired patterns |
| Data | data used to make clusters object |
| ... | Additional arguments to cluster2pattern |

Value

An object of class pclus containing pattern weights corresponding for each cluster.

Examples

```
k.RNAseq613c3t<-kmeans(p.RNAseq613c3t,22)
cluster2pattern(clusters=k.RNAseq613c3t,NP=22,Data=p.RNAseq613c3t)

distsp <- dist(p.RNAseq613c3t)
hc.RNAseq613c3t <- hclust(distsp)
cluster2pattern(clusters=hc.RNAseq613c3t,NP=22,Data=p.RNAseq613c3t)
```

clusterPlotR

Generic clusterPlotR function

Description

plotting function for clustering objects

Usage

```
clusterPlotR(cData, cls, x, NC, ...)

## S4 method for signature 'ANY,kmeans'
clusterPlotR(
  cData = NA,
  cls = NA,
  x = NA,
  NC = NA,
  annoIndx = NA,
  label = NULL,
  ...
)

## S4 method for signature 'ANY,hclust'
clusterPlotR(
  cData = NA,
  cls = NA,
  x = NA,
```

```

    NC = NA,
    annoIndx = NA,
    label = NULL,
    ...
)

```

Arguments

| | |
|----------|--|
| cData | data used to get clusters |
| cls | a cluster (kmeans or hclust) object |
| x | a vector of length equal to number of samples to use for plotting |
| NC | vector of integers indicating which clusters to use |
| ... | additional parameters for plotting. ex. pch,cex,col,labels, xlab, etc. |
| annoIndx | vector indexing into subsets for plotting |
| label | character vector to use for plotting text, defaults is NULL |

Value

A plot of the mean behavior for each cluster

Examples

```

## Not run:
k.RNAseq613c3t<-kmeans(p.RNAseq613c3t,22)
clusterPlotR(p.RNAseq613c3t, cls=k.RNAseq613c3t,NC=1,x=pd.RNAseq613c3t$days,
col=pd.RNAseq613c3t$color)

## End(Not run)

```

correlateR

correlateR

Description

Function to extract genes highly correlated with a gene or reference expression pattern.

Usage

```
correlateR(genes, dat, threshtype = "R", threshold = 0.7, absR = FALSE, ...)
```

Arguments

| | |
|------------|--|
| genes | gene or character vector of genes for reference expression pattern |
| dat | matrix or data frame with genes to be used for to calculate correlation |
| threshtype | Default "R" indicates thresholding by R value or equivalent. Alternatively, "N" indicates a numerical cut off. |
| threshold | numeric indicating value at which to make threshold. |
| absR | logical indicating where to include both positive and negatively correlated genes |
| ... | addition inputs to cor, such as method |

Details

If threshtype is "R" than threshold must be between -1 and 1. Otherwise if top N correlated genes are required, set threshtype as "N" and set threshold = N, i.e, the number of correlated genes required.

Value

A correlation matrix

Examples

```
cor2T<-correlateR(genes="T", dat=p.RNAseq6l3c3t, threshtype="N", threshold=10, absR=TRUE)
```

correlateR-class *correlateR*

Description

class of correlateR output.

Slots

corM correlation matrix obtained from correlateR

| | |
|------------|------------------------------------|
| geneMatchR | <i>Generic geneMatchR function</i> |
|------------|------------------------------------|

Description

Matches genes accross datasets

Usage

```
geneMatchR(  
  data1,  
  data2,  
  data1Names = NULL,  
  data2Names = NULL,  
  merge = FALSE,  
  ...  
)
```

Arguments

| | |
|------------|--|
| data1 | a data matrix, typically genes by samples |
| data2 | an amplitude matrix, typically genes by factors |
| data1Names | rownames of data matrix, for eg genenames |
| data2Names | rownames of amplitude matrix to be matched to rownames of datamatrix |
| merge | logical indicating wether or not to merged data sets |
| ... | Additional arguments to geneMatchR |

Value

A list of genes (intersection) in both datasets. (if merge = TRUE, Also returns merged data.)

Examples

```
geneMatchR(data1=p.ESepiGen4c11$mRNA.Seq,data2=p.RNAseq613c3t,  
data1Names=map.ESepiGen4c11[["GeneSymbols"]])
```

initialize,correlateR-method
Constructor for correlateR

Description

Constructor for correlateR

Usage

```
## S4 method for signature 'correlateR'  
initialize(.Object, corM, ...)
```

Arguments

| | |
|---------|---|
| .Object | correlateR object |
| corM | correlation matrix obtained from correlateR |
| ... | additional arguments to initialize correlateR |

Value

initialized correlateR object

initialize,rotatoR-method
Constructor for rotatoR

Description

Constructor for rotatoR

Usage

```
## S4 method for signature 'rotatoR'  
initialize(.Object, rotatedM, ...)
```

Arguments

| | |
|----------|--|
| .Object | rotatoR object |
| rotatedM | rotated matrix from rotatoR function |
| ... | additional arguments to initialize rotatoR |

Value

initialized rotatoR object

 intersectoR

Generic intersectoR function

Description

A function to find and test the intersecting values of two sets of objects, presumably the genes associated with patterns in two different datasets. Both the input objects need to be of the same type either kmeans or hclust.

Usage

```
intersectoR(pSet1, pSet2, pval, ...)

## S4 method for signature 'kmeans,kmeans'
intersectoR(pSet1 = NA, pSet2 = NA, pval = 0.05, full = FALSE)

## S4 method for signature 'hclust,hclust'
intersectoR(pSet1 = NA, pSet2 = NA, pval = 0.05, full = FALSE, k = NULL)
```

Arguments

| | |
|-------|--|
| pSet1 | an object for a set of patterns where each entry is a set of genes associated with a single pattern |
| pSet2 | an object for a second set of patterns where each entry is a set of genes associated with a single pattern |
| pval | the maximum p-value considered significant |
| ... | additional parameters depending on input object |
| full | logical indicating whether to return full data frame of significantly overlapping sets. Default is false will return summary matrix. |
| k | Numeric giving cut height for hclust objects, if a vector is given arguments will be applied to pSet1 and pSet2 in that order |

Value

A list containing: Overlap matrix, overlap index, and overlapping sets.

Examples

```
ESepiGen4c1lRNASeq <- p.ESepiGen4c1l$RNA.Seq
rownames(ESepiGen4c1lRNASeq) <- map.ESepiGen4c1l$GeneSymbols

k.RNAseq6l3c3t<-kmeans(p.RNAseq6l3c3t,22)
k.ESepiGen4c1l<-kmeans(ESepiGen4c1lRNASeq,10)
intersectoR(k.RNAseq6l3c3t, k.ESepiGen4c1l, pval=.05)

h.RNAseq6l3c3t<-hclust(as.dist(1-(cor(t(p.RNAseq6l3c3t))))))
```

```
h.ESepiGen4c1l<-hclust(as.dist(1-(cor(t(ESepiGen4c1lRNASeq))))))
intersectoR(pSet1=h.ESepiGen4c1l, pSet2=h.RNAseq6l3c3t, pval=.05, k=c(3,4))
```

| | |
|------------------|---|
| map.ESepiGen4c1l | <i>RNAseqing and ChIPSeq of matched genes in differentiated human iPS cells</i> |
|------------------|---|

Description

map.ESepiGen4c1l contains gene annotations

Usage

```
map.ESepiGen4c1l
```

Format

A data frames with 93 rows and 9 variables:

References

1. Gifford, C. A. et al. Transcriptional and epigenetic dynamics during specification of human embryonic stem cells. *Cell* 153, 1149-1163 (2013).

| | |
|------------------|--|
| map.RNAseq6l3c3t | <i>RNAseqing from human 3 iPS & 3 ES cell lines in 3 experimental condition at 3 time points</i> |
|------------------|--|

Description

map.RNAseq6l3c3 contains gene annotations for polyA bulk sequencing of 6 cell lines in 3 experimental condition at 3 time points.

Usage

```
map.RNAseq6l3c3t
```

Format

A data frames with 108 rows and 54 variables:

| | |
|----------------|---|
| p.ESepiGen4c11 | <i>RNAseqing and ChIPSeq of matched genes in differentiated human iPS cells</i> |
|----------------|---|

Description

p.ESepiGen4c11 contains $\log_2(\text{RPKM} + 1)$ values for polyA bulk sequencing and \log_2 counts of normalized ChIPSeq reads of 1 cell lines with 2 replicates in 4 experimental conditions at a single time point.

Usage

p.ESepiGen4c11

Format

p.ESepiGen4c11 is a list of 6 data frames each with with 93 rows and between 4 and 9 variables:

References

1. Gifford, C. A. et al. Transcriptional and epigenetic dynamics during specification of human embryonic stem cells. *Cell* 153, 1149-1163 (2013).

| | |
|----------------|--|
| p.RNAseq6l3c3t | <i>RNAseqing from human 3 iPS & 3 ES cell lines in 3 experimental condition at 3 time points</i> |
|----------------|--|

Description

p.RNAseq6l3c3 contains $\log_2(\text{RPKM} + 1)$ values for polyA bulk sequencing of 6 cell lines in 3 experimental condition at 3 time points.

Usage

p.RNAseq6l3c3t

Format

A data frames with 108 rows and 54 variables:

| | |
|-----------------|---|
| pd.ESepiGen4c11 | <i>RNAseqing and ChIPSeq of matched genes in differentiated human iPS cells</i> |
|-----------------|---|

Description

pd.ESepiGen4c11.4cond contains sample phenotype and experimental information

Usage

pd.ESepiGen4c11

Format

A data frames with 9 rows and 2 variables:

References

1. Gifford, C. A. et al. Transcriptional and epigenetic dynamics during specification of human embryonic stem cells. *Cell* 153, 1149-1163 (2013).

| | |
|-----------------|--|
| pd.RNAseq6l3c3t | <i>RNAseqing from human 3 iPS & 3 ES cell lines in 3 experimental condition at 3 time points</i> |
|-----------------|--|

Description

pd.RNAseq6l3c3t contains sample phenotype and experimental information for polyA bulk sequencing of 6 cell lines in 3 experimental condition at 3 time points.

Usage

pd.RNAseq6l3c3t

Format

A data frames with 54 rows and 38 variables:

`projectR`*Generic projectR function*

Description

A function for the projection of new data into a previously defined feature space.

Usage

```
projectR(data, loadings, dataNames = NULL, loadingsNames = NULL, ...)
```

```
## S4 method for signature 'matrix,matrix'
```

```
projectR(  
  data,  
  loadings,  
  dataNames = NULL,  
  loadingsNames = NULL,  
  NP = NA,  
  full = FALSE,  
  family = "gaussianff",  
  bootstrapPval = FALSE,  
  bootIter = 1000  
)
```

```
## S4 method for signature 'matrix,LinearEmbeddingMatrix'
```

```
projectR(  
  data,  
  loadings,  
  dataNames = NULL,  
  loadingsNames = NULL,  
  NP = NA,  
  full = FALSE,  
  model = NA,  
  family = "gaussianff",  
  bootstrapPval = FALSE,  
  bootIter = 1000  
)
```

```
## S4 method for signature 'matrix,prcomp'
```

```
projectR(  
  data,  
  loadings,  
  dataNames = NULL,  
  loadingsNames = NULL,  
  NP = NA,  
  full = FALSE  
)
```

```
## S4 method for signature 'matrix,rotator'  
projectR(  
  data,  
  loadings,  
  dataNames = NULL,  
  loadingsNames = NULL,  
  NP = NA,  
  full = FALSE  
)  
  
## S4 method for signature 'matrix,correlateR'  
projectR(  
  data,  
  loadings,  
  dataNames = NULL,  
  loadingsNames = NULL,  
  NP = NA,  
  full = FALSE,  
  bootstrapPval = FALSE,  
  bootIter = 1000  
)  
  
## S4 method for signature 'matrix,hclust'  
projectR(  
  data,  
  loadings,  
  dataNames = NULL,  
  loadingsNames = NULL,  
  full = FALSE,  
  targetNumPatterns,  
  sourceData,  
  bootstrapPval = FALSE,  
  bootIter = 1000  
)  
  
## S4 method for signature 'matrix,kmeans'  
projectR(  
  data,  
  loadings,  
  dataNames = NULL,  
  loadingsNames = NULL,  
  full = FALSE,  
  sourceData,  
  bootstrapPval = FALSE,  
  bootIter = 1000  
)
```

Arguments

| | |
|--------------------------------|---|
| <code>data</code> | Target dataset into which you will project. It must be of type matrix. |
| <code>loadings</code> | loadings learned from source dataset. |
| <code>dataNames</code> | a vector containing unique names, i.e. gene names, for the rows of the target dataset to be used to match features with the loadings, if not provided by <code>rownames(data)</code> . Order of names in vector must match order of rows in data. |
| <code>loadingsNames</code> | a vector containing unique names, i.e. gene names, for the rows of loadings to be used to match features with the data, if not provided by <code>rownames(loadings)</code> . Order of names in vector must match order of rows in loadings. |
| <code>...</code> | Additional arguments to <code>projectR</code> |
| <code>NP</code> | vector of integers indicating which columns of loadings object to use. The default of <code>NP=NA</code> will use entire matrix. |
| <code>full</code> | logical indicating whether to return the full model solution. By default only the new pattern object is returned. |
| <code>family</code> | VGAM family function for model fitting (default: "gaussianff") |
| <code>bootstrapPval</code> | logical to indicate whether to generate p-values using bootstrap, not available for <code>prcomp</code> and <code>rotatoR</code> objects |
| <code>bootIter</code> | number of bootstrap iterations, default = 1000 |
| <code>model</code> | Optional arguments to choose method for projection |
| <code>targetNumPatterns</code> | desired number of patterns with <code>hclust</code> |
| <code>sourceData</code> | data used to create cluster object |

Details

loadings can belong to one of several classes depending on upstream analysis. Currently permitted classes are `matrix`, `CogapsResult`, `CoGAPS`, `pclust`, `prcomp`, `rotatoR`, and `correlateR`.

Value

A matrix of sample weights for each input basis in the loadings matrix (if `full=TRUE`, full model solution is returned).

Examples

```
projectR(data=p.ESepiGen4c11$mRNA.Seq, loadings=AP.RNAseq613c3t$Amean,
dataNames = map.ESepiGen4c11[["GeneSymbols"]])

library("CoGAPS")
CR.RNAseq613c3t <- CoGAPS(p.RNAseq613c3t, params = new("CogapsParams",
nPatterns=5))
projectR(data=p.ESepiGen4c11$mRNA.Seq, loadings=CR.RNAseq613c3t,
dataNames = map.ESepiGen4c11[["GeneSymbols"]])

pca.RNAseq613c3t <- prcomp(t(p.RNAseq613c3t))
pca.ESepiGen4c11 <- projectR(data=p.ESepiGen4c11$mRNA.Seq,
```

```

loadings=pca.RNAseq6l3c3t, dataNames = map.ESepiGen4c1l[["GeneSymbols"]])

pca.RNAseq6l3c3t<-prcomp(t(p.RNAseq6l3c3t))
r.RNAseq6l3c3t<-rotatoR(1,1,-1,-1,pca.RNAseq6l3c3t$rotation[,1:2])
pca.ESepiGen4c1l<-projectR(data=p.ESepiGen4c1l$mRNA.Seq,
loadings=r.RNAseq6l3c3t, dataNames = map.ESepiGen4c1l[["GeneSymbols"]])

c.RNAseq6l3c3t<-correlateR(genes="T", dat=p.RNAseq6l3c3t, threshType="N",
threshold=10, absR=TRUE)
cor.ESepiGen4c1l<-projectR(data=p.ESepiGen4c1l$mRNA.Seq, loadings=c.RNAseq6l3c3t,
NP="PositiveCOR", dataNames = map.ESepiGen4c1l[["GeneSymbols"]])

```

rotatoR

rotatoR

Description

a function for rotating two basis about a point or line in that plane

Usage

```
rotatoR(x1, y1, x2, y2, basisSET)
```

Arguments

| | |
|----------|---|
| x1 | a value describing a the coordinate of a point in the first basis. If no values are provided for x2 |
| y1 | a value describing a the coordinate of a point in the second basis |
| x2 | a value describing a the coordinate of the second point in the second basis |
| y2 | a value describing a the coordinate of the second point in the second basis |
| basisSET | the basis to be rotated |

Value

An object of class rotatoR.

Examples

```

pca.RNAseq6l3c3t<-prcomp(t(p.RNAseq6l3c3t))
r.RNAseq6l3c3t<-rotatoR(1,1,-1,-1,pca.RNAseq6l3c3t$rotation[,1:2])

```

| | |
|---------------|----------------|
| rotatoR-class | <i>rotatoR</i> |
|---------------|----------------|

Description

class of rotatoR output.

Slots

rotatedM rotated basis set (matrix) that is output of rotatoR function

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