

# 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.

**License** GPL (==2)

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---

alluvialMat	<i>alluvialMat</i>
-------------	--------------------

---

### Description

Function to provide alluvial matrix for generating alluvial plot

### Usage

```
alluvialMat(
  projection,
  annotations,
  annotationName = "Cell type",
  annotationType = "Cell",
  plot = TRUE,
  minPropExplained = 0.75,
  pvalThreshold = 0.05,
  qualThreshold = 0.05
)
```

### 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
pvalThreshold	threshold level of significance for p-value
qualThreshold	threshold level of significance for Benjamini-Hochberg corrected p-value

### Value

A matrix to generate alluvial plots

### Examples

```
projection <- projectR(data=p.ESepiGen4c11$mRNA.Seq, loadings=AP.RNAseq6l3c3t$Amean,
  dataNames = map.ESepiGen4c11[["GeneSymbols"]], full = TRUE)
alluvialMat(projection, pd.ESepiGen4c11$Condition)
```

---

 AP.RNAseq6l3c3t

*CoGAPS patterns and genes weights for p.RNAseq6l3c3t*


---

### Description

AP.RNAseq6l3c3t contains the output of the gapsRun function in the CoGAPS package for data = p.RNAseq6l3c3t

### Usage

```
AP.RNAseq6l3c3t
```

### Format

A list of 12 items

---

aucMat

*aucMat*


---

### 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)
```

---

```
bonferroniCorrectedDifferences
      bonferroniCorrectedDifferences
```

---

**Description**

Calculate weighted/unweighted mean difference for each gene between 2 groups

**Usage**

```
bonferroniCorrectedDifferences(
  group1,
  group2,
  pvalue,
  diff_weights = NULL,
  mode = "CI"
)
```

**Arguments**

group1	count matrix 1
group2	count matrix 2
pvalue	significance value to threshold
diff_weights	loadings to weight the differential expression
mode	statistical approach, confidence intervals(CI) or pvalues(PV)

---

```
cluster2pattern      Generic cluster2pattern function
```

---

**Description**

Function to make patterns of continuous weights from clusters.

**Usage**

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

## S4 method for signature 'character'
cluster2pattern(clusters, data)

## S4 method for signature 'numeric'
cluster2pattern(clusters, 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(t(p.RNAseq613c3t),3)
cluster2pattern(clusters=k.RNAseq613c3t,data=p.RNAseq613c3t)

distsp <- dist(t(p.RNAseq613c3t))
hc.RNAseq613c3t <- hclust(distsp)
cluster2pattern(clusters=hc.RNAseq613c3t,NP=3,data=p.RNAseq613c3t)
```

---

cluster2pattern-class *cluster2pattern*

---

### Description

class of cluster2pattern output.

### Slots

clusterMatrix matrix of continuous values for projection that is output of cluster2pattern function

---

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.RNAseq613c3t, threshtype="N", threshold=10, absR=TRUE)
```

---

correlateR-class	<i>correlateR</i>
------------------	-------------------

---

**Description**

class of correlateR output.

**Slots**

corM correlation matrix obtained from correlateR

---

CR.RNAseq6l3c3t	<i>CogapsResult object for p.RNAseq6l3c3t</i>
-----------------	---

---

**Description**

CR.RNAseq6l3c3t contains the output of the CoGAPS function in the CoGAPS package for data = p.RNAseq6l3c3t

**Usage**

CR.RNAseq6l3c3t

**Format**

A CogapsResult object

---

cr_microglial	<i>CogapsResult object for microglial_counts</i>
---------------	--

---

**Description**

cr\_microglia contains the output of the CoGAPS function in the CoGAPS package for data = microglial\_counts

**Usage**

cr\_microglial

**Format**

A CogapsResult object

---

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"]])
```

---

getTSNE	<i>getTSNE</i>
---------	----------------

---

**Description**

Function to provide tSNE of projection

**Usage**

```
getTSNE(projection, axis = 2, ...)
```

**Arguments**

projection	matrix, a projection generated from projectR
axis	integer, either 1 umap of projection or 2 for umap of transpose of projection
...	additional arguments passed to tsne

**Examples**

```
projection <- projectR(data=p.ESepiGen4c1l$mRNA.Seq, loadings=AP.RNAseq6l3c3t$Amean,
  dataNames = map.ESepiGen4c1l[["GeneSymbols"]], full = TRUE)
projectionTSNE <- getTSNE(projection)
```

---

getUMAP	<i>getUMAP</i>
---------	----------------

---

**Description**

Function to provide umap of projection

**Usage**

```
getUMAP(projection, axis = 2, umapMethod = "naive", umapConfig = umap.defaults)
```

**Arguments**

projection	matrix, a projection generated from projectR
axis	integer, either 1 umap of projection or 2 for umap of transpose of projection
umapMethod	character, implementation. Available methods are 'naive' (an implementation written in pure R) and 'umap-learn' (requires python package 'umap-learn')
umapConfig	umap.config, a list of parameters to customize umap embedding

**Value**

A umap of projection

**Examples**

```
library(umap)
projection <- projectR(data=p.ESepiGen4c11$mRNA.Seq, loadings=AP.RNAseq6l3c3t$Amean,
  dataNames = map.ESepiGen4c11[["GeneSymbols"]], full = TRUE)
umapConfig = umap.defaults
umapConfig$n_neighbors = 3
projectionUMAP <- getUMAP(projection,umapConfig = umapConfig)
```

---

glial_counts	<i>log-normalized count data from astrocytes and oligodendrocytes in the p6 mouse cortex.</i>
--------------	---

---

**Description**

log-normalized count data from astrocytes and oligodendrocytes in the p6 mouse cortex.

**Usage**

```
glial_counts
```

**Format**

A gene (rows) by cell (column) matrix

---

initialize,cluster2pattern-method	<i>Constructor for cluster2pattern</i>
-----------------------------------	--

---

**Description**

Constructor for cluster2pattern

**Usage**

```
## S4 method for signature 'cluster2pattern'
initialize(.Object, clusterMatrix, ...)
```

**Arguments**

.Object	clusterMatrix object
clusterMatrix	matrix of continous values for projection that is output of cluster2pattern function
...	additional arguments to intialize cluster2pattern

**Value**

initialized cluster2pattern object

---

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 &amp; 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:

---

microglial_counts	<i>log-normalized count data from microglial cells in the p6 mouse cortex.</i>
-------------------	--

---

**Description**

log-normalized count data from microglial cells in the p6 mouse cortex.

**Usage**

```
microglial_counts
```

**Format**

A gene (rows) by cell (column) matrix

---

multivariateAnalysisR *Generic multivariateAnalysisR function*

---

**Description**

Performs multivariate analysis across specified clusters in datasets

**Usage**

```
multivariateAnalysisR(  
  significanceLevel = 0.05,  
  patternKeys,  
  seuratobj,  
  dictionaries,  
  customNames = NULL,  
  exclusive = TRUE,  
  exportFolder = "",  
  ANOVAwidth = 1000,  
  ANOVAheight = 1000,  
  CIwidth = 1000,  
  CIheight = 1000,  
  CIspaceing = 1  
)
```

**Arguments**

significanceLevel	double value for testing significance in ANOVA test
patternKeys	list of strings indicating pattern subsets from seuratobj to be analyzed
seuratobj	Seurat Object Data containing patternKeys in meta.data
dictionaries	list of dictionaries indicating clusters to be compared
customNames	list of custom names for clusters in corresponding order
exclusive	boolean value for determining interpolation between params in clusters
exportFolder	name of folder to store exported graphs and CSV files
ANOVAwidth	width of ANOVA png
ANOVAheight	height of ANOVA png
CIwidth	width of CI png
CIheight	height of CI png
CIspacing	spacing between each CI in CI graph

**Value**

a sorted list of ANOVA and CI results; ANOVA and Confidence Intervals are visualized and exported in both PNG and CSV

---

multivariateAnalysisR\_seurat\_test

*Truncated Seurat Object with latent space projection done to unspecified cells in different stages for multivariateAnalysisR analysis*

---

**Description**

Truncated Seurat Object with latent space projection done to unspecified cells in different stages for multivariateAnalysisR analysis

**Usage**

```
multivariateAnalysisR_seurat_test
```

**Format**

A Seurat Object with 31034 observations of 4 variables in meta.data:

---

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 &amp; 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 &amp; 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:

---

`pdVolcano`*pdVolcano*

---

**Description**

Generate volcano plot and gate genes based on fold change and pvalue, includes vectors that can be used with fast gene set enrichment (fgsea)

**Usage**

```
pdVolcano(
  result,
  FC = 0.2,
  pvalue = NULL,
  subset = NULL,
  filter.inf = FALSE,
  label.num = 5L,
  display = TRUE
)
```

**Arguments**

<code>result</code>	result output from projectionDriveR function in PV mode
<code>FC</code>	fold change threshold, default at 0.2
<code>pvalue</code>	significance threshold, default set stored pvalue
<code>subset</code>	vector of gene names to subset the plot by
<code>filter.inf</code>	remove genes that have pvalues below machine double minimum value
<code>label.num</code>	Number of genes to label on either side of the volcano plot, default 5
<code>display</code>	boolean. Whether or not to plot and display volcano plots

**Value**

A list with weighted and unweighted differential expression metrics

---

`plotConfidenceIntervals`*plotConfidenceIntervals*

---

**Description**

Generate point and line confidence intervals from provided estimates.

**Usage**

```
plotConfidenceIntervals(
  confidence_intervals,
  interval_name = c("low", "high"),
  pattern_name = NULL,
  sort = TRUE,
  genes = NULL,
  weights = NULL,
  weights_clip = 0.99,
  weights_vis_norm = "none",
  weighted = FALSE
)
```

**Arguments**

confidence_intervals	A dataframe of features x estimates.
interval_name	Estimate column names. Default: c("low","high")
pattern_name	string to use as the title for plots.
sort	Boolean. Sort genes by their estimates (default = TRUE)
genes	a vector with names of genes to include in plot. If sort=F, estimates will be plotted in this order.
weights	optional. weights of features to include as annotation.
weights_clip	optional. quantile of data to clip color scale for improved visualization. Default: 0.99
weights_vis_norm	Which version of weights to visualize as a heatmap. Options are "none" (uses provided weights) or "quantiles". Default: none
weighted	specifies whether the confidence intervals in use are weighted by the pattern and labels plots accordingly

**Value**

A list with pointrange estimates and a heatmap of pattern weights.

---

plotVolcano

*plotVolcano*

---

**Description**

Volcano plotting function

**Usage**

```
plotVolcano(stats, metadata, FC, pvalue, title)
```

**Arguments**

stats	data frame with differential expression statistics
metadata	#metadata from pdVolcano
FC	Fold change threshold
pvalue	p value threshold
title	plot title

---

projectionDriveR      *projectionDriveR*

---

**Description**

Calculate weighted expression difference between two groups (group1 - group2)

**Usage**

```
projectionDriveR(
  cellgroup1,
  cellgroup2,
  loadings,
  pattern_name,
  loadingsNames = NULL,
  pvalue = 1e-05,
  display = TRUE,
  normalize_pattern = TRUE,
  mode = "CI"
)
```

**Arguments**

cellgroup1	gene x cell count matrix for cell group 1
cellgroup2	gene x cell count matrix for cell group 2
loadings	A matrix of continuous values defining the features
pattern_name	column of loadings for which drivers will be calculated
loadingsNames	a vector with names of loading rows defaults to rownames
pvalue	confidence level. Default 1e-5
display	boolean. Whether or not to display confidence intervals
normalize_pattern	Boolean. Whether or not to normalize pattern weights
mode	statistical approach, confidence intervals or pvalues. default CI

**Value**

A list with unweighted/weighted mean differences and differential genes that meet the provided significance threshold.

---

projectR	<i>Generic projectR function</i>
----------	----------------------------------

---

**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,  
  bootstrapPval = FALSE,  
  bootIter = 1000  
)
```

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

```
projectR(  
  data,  
  loadings,  
  dataNames = NULL,  
  loadingsNames = NULL,  
  NP = NULL,  
  full = FALSE,  
  chopBy = 1000  
)
```

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

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

## S4 method for signature 'matrix,cluster2pattern'
projectR(
  data,
  loadings,
  dataNames = NULL,
  loadingsNames = NULL,
  full = FALSE,
  sourceData,
  bootstrapPval = FALSE,
  bootIter = 1000
)

```

### Arguments

data	Target dataset into which you will project. It must be of type matrix.
loadings	loadings learned from source dataset.
dataNames	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.
loadingsNames	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.
...	Additional arguments to <code>projectR</code>
NP	vector of integers indicating which columns of loadings object to use. The default of <code>NP=NA</code> will use entire matrix.
full	logical indicating whether to return the full model solution. By default only the new pattern object is returned.
bootstrapPval	logical to indicate whether to generate p-values using bootstrap, not available for <code>prcomp</code> and <code>rotatoR</code> objects
bootIter	number of bootstrap iterations, default = 1000
chopBy	number of columns to chop the data into (chopping helps running large datasets)
model	Optional arguments to choose method for projection
targetNumPatterns	desired number of patterns with <code>hclust</code>
sourceData	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. Please note that loadings should not contain NA.

**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$mRNA.Seq,loadings=AP.RNAseq6l3c3t$Amean,
dataNames = map.ESepiGen4c11[["GeneSymbols"]])

library("CoGAPS")
# CR.RNAseq6l3c3t <- CoGAPS(p.RNAseq6l3c3t, params = new("CogapsParams", nPatterns=5))
projectR(data=p.ESepiGen4c11$mRNA.Seq,loadings=CR.RNAseq6l3c3t,
dataNames = map.ESepiGen4c11[["GeneSymbols"]])

pca.RNAseq6l3c3t<-prcomp(t(p.RNAseq6l3c3t))
pca.ESepiGen4c11<-projectR(data=p.ESepiGen4c11$mRNA.Seq,
loadings=pca.RNAseq6l3c3t, dataNames = map.ESepiGen4c11[["GeneSymbols"]])

pca.RNAseq6l3c3t<-prcomp(t(p.RNAseq6l3c3t))
r.RNAseq6l3c3t<-rotatoR(1,1,-1,-1,pca.RNAseq6l3c3t$rotation[,1:2])
pca.ESepiGen4c11<-projectR(data=p.ESepiGen4c11$mRNA.Seq,
loadings=r.RNAseq6l3c3t, dataNames = map.ESepiGen4c11[["GeneSymbols"]])

c.RNAseq6l3c3t<-correlateR(genes="T", dat=p.RNAseq6l3c3t, threshtype="N",
threshold=10, absR=TRUE)
cor.ESepiGen4c11<-projectR(data=p.ESepiGen4c11$mRNA.Seq, loadings=c.RNAseq6l3c3t,
NP="PositiveCOR", dataNames = map.ESepiGen4c11[["GeneSymbols"]])

library("projectR")
data(p.RNAseq6l3c3t)
nP<-3
kClust<-kmeans(t(p.RNAseq6l3c3t),centers=nP)
kpattern<-cluster2pattern(clusters = kClust, NP = nP, data = p.RNAseq6l3c3t)
p<-as.matrix(p.RNAseq6l3c3t)
projectR(p,kpattern)
```

---

retinal\_patterns

*CoGAPS patterns learned from the developing mouse retina.*


---

**Description**

CoGAPS patterns learned from the developing mouse retina.

**Usage**

```
retinal_patterns
```

**Format**

A gene (rows) by pattern (column) matrix

**References**

1. Clark, B.S., & Stein-O'Brien G.L., et al. Single-Cell RNA-Seq Analysis of Development Identifies NFI Factors as Regulating Mitotic Exit and Late-Born Cell Specification. *Cell* 102, 1111-1126 (2019).

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rotatoR	<i>rotatoR</i>
---------	----------------

---

**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.RNAseq613c3t<-prcomp(t(p.RNAseq613c3t))
r.RNAseq613c3t<-rotatoR(1,1,-1,-1,pca.RNAseq613c3t$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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