Package 'CelliD'

October 14, 2021

Type Package

Title Unbiased Extraction of Single Cell gene signatures using Multiple Correspondence Analysis

Version 1.0.0

Description CelliD is a clustering-free multivariate statistical method for the robust extraction of per-cell gene signatures from single-cell RNA-seq.
CelliD allows unbiased cell identity recognition across different donors, tissues-of-origin, model organisms and single-cell omics protocols.
The package can also be used to explore functional pathways enrichment in single cell data.

Depends R (>= 4.1), Seurat (>= 4.0.1), SingleCellExperiment

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Author Akira Cortal [aut, cre], Antonio Rausell [aut, ctb]

Maintainer Akira Cortal <akira.cortal@institutimagine.org>

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`CelliD-package` *Multiple Correspondence Analysis on Single Cell for Joint Dimensionality Reduction of Gene and Cell, Cells Geneset Extraction and Geneset Enrichment Analysis*

Description

CelliD is a clustering-free multivariate statistical method for the robust extraction of per-cell gene signatures from single-cell RNA-seq. CelliD allows unbiased cell identity recognition across different donors, tissues-of-origin, model organisms and single-cell omics protocols. The package can also be used to explore functional pathways enrichment in single cell data.

Author(s)

Maintainer: Akira Cortal <akira.cortal@institutimagine.org>

Authors:

- Akira Cortal
- Antonio Rausell

References

- Rausell, A., Juan, D., Pazos, F., & Valencia, A. (2010). Protein interactions and ligand binding: from protein subfamilies to functional specificity. Proceedings of the National Academy of Sciences of the United States of America, 107(5), 1995–2000. https://doi.org/10.1073/pnas.0908044107
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- Aaron Lun and Davide Risso (2019). SingleCellExperiment: S4 Classes for Single Cell Data. R package version 1.4.1.

See Also

- McCarthy, D. J., Campbell, K. R., Lun, A. T. L., & Wills, Q. F. (2017). Scater: pre-processing, quality control, normalization and visualization of single-cell RNA-seq data in R. Bioinformatics, 33(8), btw777. https://doi.org/10.1093/bioinformatics/btw777
- Amezquita, R. A., Carey, V. J., Carpp, L. N., Geistlinger, L., Lun, A. T. L., Marini, F., … Hicks, S. C. (2019). Orchestrating Single-Cell Analysis with Bioconductor. BioRxiv, 590562. https://doi.org/10.1101/590562

`checkCelliDArg` *Check for CelliD arguments*

Description

Performs multiple check of consistency of the argument provided by the user for different CelliD functions. It notably check if the provided features or cells name ar e actually contained in the high level object.

Usage

```
checkCelliDArg(X, group.by, reduction, dims, features, cells)

## S3 method for class 'Seurat'
checkCelliDArg(
  X,
  group.by = NULL,
  reduction,
  dims,
  features = NULL,
  cells = NULL
)

## S3 method for class 'SingleCellExperiment'
checkCelliDArg(
  X,
  reduction,
  dims,
  features = NULL,
  cells = NULL,
  group.by = NULL
)
```

Arguments

X	Seurat or SingleCell Experiment Object
group.by	Name of meta.data or ColData column.
reduction	Which dimensionality reduction to use, must be based on MCA.
dims	A vector of integers indicating which dimensions to use of specified reduction embeddings and loadings.
features	Character vector of feature names to subset feature coordinates. If not specified will take all features available from specified reduction loadings.
cells	Character vector of cell names to subset cell coordinates. If not specified will take all features available from specified reduction Embeddigns.

Value

list of corrected arguments if no error is thrown.

DimPlotMC *Seurat DimPlot for MCA like Dimensionality Reduction*

Description

Small modification of the regular Seurat DimPlot function to enable plotting features for mca like dimensionality reduction. Allows to represent a set of genes of interest on top of the regular cell scatter plot. The label of the genes can be iverlayed also but it is recommended to plot less than 50 genes label as it can overcrowd the plot severely.

Usage

```
DimPlotMC(
  X,
  reduction = "mca",
  dims = c(1, 2),
  features = NULL,
  size.feature = 2,
  size.feature.text = 5,
  as.text = FALSE,
  ...
)
```

Arguments

X	a Seurat object
reduction	Which dimensionality reduction to use. If not specified, searches for mca.
dims	Dimensions to plot, must be a two-length numeric vector specifying x- and y-dimensions
features	character vector of features to plot, must be present in the specified dimension loadings
size.feature	integer indicating size of geom_point for features
size.feature.text	integer indicating size of geom_text for features
as.text	logical indicating as to include text label for feature plotting, will produce warning if TRUE and length(features) > 50
...	Other arguments passed to DimPlot

Value

A ggplot object

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
seuratPbmc <- DimPlotMC(seuratPbmc, features = Seurat::VariableFeatures(seuratPbmc))
```

DistSort *Sort Gene Cell Distance Matrix*

Description

Sort Gene Cell Distance Matrix

Usage

```
DistSort(distance)
```

Arguments

distance	distance matrix with features at rows and cell at columns

Value

list of ranking of genes by cells

fgseaCelliD *Slight change in fgsea for ram and speed efficiency in CelliD*

Description

Slight change in fgsea for ram and speed efficiency in CelliD

Usage

```
fgseaCelliD(
  pathways,
  stats,
  nperm = 1000,
  minSize = 10,
  maxSize = 500,
  gseaParam = 0
)
```

Arguments

pathways	List of gene sets to check
stats	Named vector of gene-level stats. Names should be the same as in 'pathways'
nperm	Number of permutations to do. Minimal possible nominal p-value is about 1/nperm
minSize	Minimal size of a gene set to test. All pathways below the threshold are excluded.

maxSize	Maximal size of a gene set to test. All pathways above the threshold are excluded.
gseaParam	GSEA parameter value, all gene-level stats are raised to the power of 'gseaParam' before calculation of GSEA enrichment scores

Value

A table with GSEA results. Each row corresponds to a tested pathway. The columns are the following:

- pathway – name of the pathway as in 'names(pathway)';
- pval – an enrichment p-value;
- padj – a BH-adjusted p-value;
- ES – enrichment score, same as in Broad GSEA implementation;
- NES – enrichment score normalized to mean enrichment of random samples of the same size;
- nMoreExtreme' – a number of times a random gene set had a more extreme enrichment score value;
- size – size of the pathway after removing genes not present in 'names(stats)'.
- leadingEdge – vector with indexes of leading edge genes that drive the enrichment, see http://software.broadinstitute.org/gsea/doc/GSEAUserGuideTEXT.htm#_Running_a_Leading.

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
ranking <- GetCellGeneRanking(seuratPbmc, reduction = "mca", dims = 1:5)
fgseaCelliD(pathways = Hallmark, stats = ranking[[1]])
```

GetCellGeneDistance *Distance Calculation*

Description

Small intermediate function for euclidean distance calculation between MCA feature coordinates and cell coordinates. Due to MCA pseudo barycentric relationship, the closer a gene g is to a cell c, the more specific to such a cell it can be considered.

Usage

```
GetCellGeneDistance(X, reduction, dims, features, cells)

## S3 method for class 'Seurat'
GetCellGeneDistance(X, reduction = "mca", dims, features = NULL, cells = NULL)

## S3 method for class 'SingleCellExperiment'
GetCellGeneDistance(X, reduction = "MCA", dims, features = NULL, cells = NULL)
```

Arguments

X	Seurat or SingleCell Experiment Object
reduction	Which dimensionality reduction to use, must be based on MCA.
dims	A vector of integers indicating which dimensions to use with reduction embedding and loading for distance calculation.
features	Character vector of feature names to subset feature coordinates. If not specified will take all features available from specified reduction Loading.
cells	Character vector of cell names to subset cell coordinates. If not specified will take all cells available from specified reduction Embedding.

Value

Distance Matrix with genes at row and cells at column

GetCellGeneRanking *Ranking Extraction*

Description

Intermediate function for ranking extraction from Cell Gene Distance Matrix. Genes are ordered from the most specific to the least specific to the cell according to their euclidean distances. Value indicates the euclidean distances between the cell and the genes in the MCA coordinates.

Usage

```
GetCellGeneRanking(X, reduction, dims, features, cells)

## S3 method for class 'Seurat'
GetCellGeneRanking(
  X,
  reduction = "mca",
  dims = seq(50),
  features = NULL,
  cells = NULL
)

## S3 method for class 'SingleCellExperiment'
GetCellGeneRanking(
  X,
  reduction = "MCA",
  dims = seq(50),
  features = NULL,
  cells = NULL
)
```

Arguments

X	Seurat or SingleCellExperiment Object
reduction	Which dimensionality reduction to use, must be based on MCA.
dims	A vector of integers indicating which dimensions to use with reduction embedding and loading for distance calculation.
features	Character vector of feature names to subset feature coordinates. If not specified will take all features available from specified reduction Loading
cells	Character vector of cell names to subset cell coordinates. If not specified will take all features available from specified reduction Embedding.

Value

A cell named list of gene rankings ordererd by distances from shortest (most specific) to farthest (less specific)

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
ranking <- GetCellGeneRanking(seuratPbmc, reduction = "mca", dims = 1:5)
```

GetCellGeneSet *Gene sets extraction from MCA*

Description

Calculate cells and genes distances, rank them per cell and extract top n features. The obtained top n features represents features thatare highly specific to that cell.

Usage

```
GetCellGeneSet(X, reduction = "mca", dims, features, cells, n.features)

## S3 method for class 'Seurat'
GetCellGeneSet(
  X,
  reduction = "mca",
  dims = seq(50),
  features = NULL,
  cells = NULL,
  n.features = 200
)

## S3 method for class 'SingleCellExperiment'
GetCellGeneSet(
  X,
  reduction = "MCA",
```

```
  dims = seq(50),
  features = NULL,
  cells = NULL,
  n.features = 200
)
```

Arguments

X	Seurat or SingleCell Experiment Object
reduction	Which dimensionality reduction to use, must be based on MCA.
dims	A vector of integers indicating which dimensions to use with reduction embeddings and loadings for distance calculation.
features	Character vector of feature names to subset feature coordinates. If not specified will take all features available from specified reduction Loadings
cells	Character vector of cell names to subset cell coordinates. If not specified will take all features available from specified reduction Embeddigns.
n.features	single integer specifying how many top features should be extracted from the ranking

Value

A cell named list of gene rankings ordererd by distances from shortest (most specfic) to farthest (less specific)

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
GroupGeneRanking <- GetGroupGeneRanking(seuratPbmc, group.by = "seurat_clusters", dims = 1:5)
```

GetGeneCellCoordinates

GeneCellCoordinates

Description

Get coordinates of both cells and features in a matrix

Usage

```
GetGeneCellCoordinates(X, reduction, dims, features)
```

Arguments

X	Seurat or SingleCellExperiment Object
reduction	Which dimensionality reduction to use, must be based on MCA.
dims	A vector of integers indicating which dimensions to use with reduction embeddings and loadings for distance calculation.
features	Character vector of feature names to subset feature coordinates. If not specified will take all features available from specified reduction Loadings.

Value

A matrix with gene and cell coordinates of MCA

GetGroupCoordinates *Centroids Coordinates*

Description

Centroids calculation for a given group of cells defined for instance by cell type/ condition.

Usage

```
GetGroupCoordinates(X, group.by, reduction, dims, ...)

## S3 method for class 'matrix'
GetGroupCoordinates(X, group.by, reduction = NULL, dims, ...)

## S3 method for class 'Seurat'
GetGroupCoordinates(X, group.by = NULL, reduction = "mca", dims = seq(50), ...)

## S3 method for class 'SingleCellExperiment'
GetGroupCoordinates(X, group.by = NULL, reduction = "MCA", dims, ...)
```

Arguments

X	Seurat or SingleCellExperiment object, alternatively a matrix.
group.by	column name of meta.data (Seurat) or ColData (SingleCellExperiment). For Seurat object if NULL active.ident slot will be taken.
reduction	Which dimensionality reduction to use, must be based on MCA.
dims	A vector of integers indicating which dimensions to use with reduction embeddings and loadings for distance calculation.
...	Other arguments passed to methods

Value

A data.table with coordinates of the group centroids for the specidied dims.

`GetGroupGeneDistance` *Centroids-Genes distances*

Description

Distance calculation between genes and group of cells centroids.

Usage

```
GetGroupGeneDistance(X, group.by, reduction, dims, features)

## S3 method for class 'Seurat'
GetGroupGeneDistance(
  X,
  group.by = NULL,
  reduction = "mca",
  dims = seq(50),
  features = NULL
)

## S3 method for class 'SingleCellExperiment'
GetGroupGeneDistance(
  X,
  group.by,
  reduction = "MCA",
  dims = seq(50),
  features = NULL
)
```

Arguments

`X`	Seurat or SingleCellExperiment object, alternatively a matrix.
`group.by`	column name of meta.data (Seurat) or ColData (SingleCellExperiment)
`reduction`	Which dimensionality reduction to use, must be based on MCA.
`dims`	A vector of integers indicating which dimensions to use with reduction embeddings and loadings for distance calculation.
`features`	A character vector of features name to subset feature coordinates for distance calculation.

Value

Distance Matrix between groups (column) and genes (row)

GetGroupGeneRanking *Gene Specificity Ranking Calculation*

Description

Gene Specificity Ranking Calculation

Usage

```
GetGroupGeneRanking(X, group.by, reduction, dims, features)

## S3 method for class 'Seurat'
GetGroupGeneRanking(
  X,
  group.by = NULL,
  reduction = "mca",
  dims = seq(50),
  features = NULL
)

## S3 method for class 'SingleCellExperiment'
GetGroupGeneRanking(
  X,
  group.by,
  reduction = "MCA",
  dims = seq(50),
  features = NULL
)
```

Arguments

X	Seurat or SingleCellExperiment object, alternatively a matrix.
group.by	column name of meta.data (Seurat) or ColData (SingleCellExperiment)
reduction	Which dimensionality reduction to use, must be based on MCA.
dims	A vector of integers indicating which dimensions to use with reduction embeddings and loadings for distance calculation.
features	A character vector of features name to subset feature coordinates for distance calculation.

Value

List of genes ranking for each groups

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
GroupGeneRanking <- GetGroupGeneRanking(seuratPbmc, group.by = "seurat_clusters", dims = 1:5)
```

GetGroupGeneSet *Extract cluster/group gene sets from MCA*

Description

Extract cluster/group gene sets from MCA

Usage

```
GetGroupGeneSet(X, group.by, reduction, dims, features, n.features)

## S3 method for class 'Seurat'
GetGroupGeneSet(
  X,
  group.by = NULL,
  reduction = "mca",
  dims = seq(50),
  features = NULL,
  n.features = 200
)

## S3 method for class 'SingleCellExperiment'
GetGroupGeneSet(
  X,
  group.by = NULL,
  reduction = "MCA",
  dims = seq(50),
  features = NULL,
  n.features = 200
)
```

Arguments

X	Seurat or SingleCellExperiment object, alternatively a matrix.
group.by	column name of meta.data (Seurat) or ColData (SingleCellExperiment).
reduction	Which dimensionality reduction to use, must be based on MCA.
dims	A vector of integers indicating which dimensions to use with reduction for distance calculation.
features	A character vector of features name to subset feature coordinates for distance calculation.
n.features	A single integer specifying how many top features will be extracted from ranking.

Value

Distance Matrix between groups (column) and genes (row)

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
GroupGeneSet <- GetGroupGeneSet(seuratPbmc, dims = 1:5, group.by = "seurat_clusters")
```

GetGSEAMatrix *Get Matrix from Enrichment Results*

Description

Extract enrcihment score Matrix from RunGSEA functions.

Usage

```
GetGSEAMatrix(X, metric = "ES")
```

Arguments

X	an enrichment results obtained by RunGroupGSEA or RunCellGSEA
metric	a character indicating which metric to use as value of matrix (ES, NES, padj, pval)

Value

A matrix of geneset enrichment metric with cell/group at columns and pathways/genesets at rows

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
GSEAResults <- RunGroupGSEA(seuratPbmc, Hallmark, group.by = "seurat_clusters", dims = 1:5)
GSEAMatrix <- GetGSEAMatrix(GSEAResults)
```

Hallmark *Hallmark Pathways from MSigDB*

Description

A dataset containing the Hallmark gene sets from MSigDB.

Usage

```
Hallmark
```

Format

A named list of length 50 containing Hallmark gene sets.

Source

http://software.broadinstitute.org/gsea/msigdb/download_file.jsp?filePath=/resources/msigdb/6.2/h.all.v6.2.symbols.gmt

References

Liberzon A, Birger C, Thorvaldsdóttir H, Ghandi M, Mesirov JP, Tamayo P. The Molecular Signatures Database (MSigDB) hallmark gene set collection. Cell Syst. 2015 Dec 23;1(6):417-425.

HgProteinCodingGenes *Homo Sapiens Protein Coding Genes*

Description

A gene list of human protein coding genes extracted from biomaRt.

Usage

```
HgProteinCodingGenes
```

Format

A list of 19308 gene onthology terms with the corresponding genes.

Source

http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C5

References

The Gene Ontology project in 2008, The Gene Ontology Consortium Nucleic Acids Research, Volume 36, Issue suppl_1, January 2008, Pages D440–D444,

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import *Import*

Description

Import

Usage

```
import()
```

Value

updates NAMESPACE import

MgProteinCodingGenes *Mus Musculus Protein Coding Genes*

Description

A gene list of mouse protein coding genes extracted from biomaRt.

Usage

```
MgProteinCodingGenes
```

Format

A list of 3857 gene onthology terms with the corresponding genes.

Source

http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C5

References

The Gene Ontology project in 2008, The Gene Ontology Consortium Nucleic Acids Research, Volume 36, Issue suppl_1, January 2008, Pages D440–D444,

pairDist *Distance Calculation*

Description

Small function to calculate quickly the distance between rows of two matrix.

Usage

```
pairDist(x, y)
```

Arguments

x	a matrix
y	a matrix

Value

A Distance Matrix

plotReducedDimMC *Scater plotReducedDim for MCA like dimensionality Reduction*

Description

Small modification of the Scater plotReducedDim function to enable plotting features for mca like dimensionality reduction. Allows to represent a set of genes of interest on top of the regular cell scatter plot. The label of the genes can be iverlayed also but it is recommended to plot less than 50 genes label as it can overcrowd the plot severely.

Usage

```
plotReducedDimMC(
  X,
  reduction = "MCA",
  dims = c(1, 2),
  features = NULL,
  size.feature = 3,
  size.feature.text = 5,
  as.text = FALSE,
  ...
)
```

Arguments

X	a Single Cell Experiment Object
reduction	Which dimensionality reduction to use. If not specified, searches for mca.
dims	Dimensions to plot, must be a two-length numeric vector specifying x- and y-dimensions
features	character vector of features to plot, must be present in the specified dimension loadings
size.feature	integer indicating size of geom_point for features
size.feature.text	integer indicating size of geom_text for features
as.text	logical indicating as to include text label for feature plotting, will produce warning if TRUE and length(features) > 50.
...	Other arguments passed to plotReducedDim

Value

A ggplot object

Examples

```
scePBMC <- as.SingleCellExperiment(seuratPbmc)
scePBMC <- RunMCA(scePBMC, nmcs = 5)
plotReducedDimMC(scePBMC)
```

RunCellGSEA *Run Gene Set Enrichment Analysis on cells*

Description

Calculate cells gene specificty ranking and then perform geneset enrichment analysis (fgsea) on it. However, due to the very long running time of gene set enrichment analysis, we recommend the usage of RunCellHGT.

Usage

```
RunCellGSEA(
  X,
  pathways,
  reduction,
  dims,
  features,
  cells,
  nperm,
  minSize,
  maxSize,
  gseaParam,
  n.core
)

## S3 method for class 'Seurat'
RunCellGSEA(
  X,
  pathways,
  reduction = "mca",
  dims = seq(50),
  features = NULL,
  cells = NULL,
  nperm = 1000,
  minSize = 10,
  maxSize = 500,
  gseaParam = 0,
  n.core = 1
)

## S3 method for class 'SingleCellExperiment'
RunCellGSEA(
  X,
  pathways,
  reduction = "mca",
  dims = seq(50),
  features = NULL,
```

```
  cells = NULL,
  nperm = 1000,
  minSize = 10,
  maxSize = 500,
  gseaParam = 0,
  n.core = 1
)
```

Arguments

X	Seurat or SingleCellExperiment object
pathways	List of gene sets to check
reduction	Which dimensionality reduction to use, must be based on MCA.
dims	A vector of integers indicating which dimensions to use with reduction embeddings and loadings for distance calculation.
features	Character vector of feature names to subset feature coordinates. If not specified will take all features available from specified reduction Loadings.
cells	Character vector of cell names to subset cell coordinates. If not specified will take all features available from specified reduction Embeddings
nperm	Number of permutations to do. Minimial possible nominal p-value is about 1/nperm
minSize	Minimal size of a gene set to test. All pathways below the threshold are excluded.
maxSize	Maximal size of a gene set to test. All pathways above the threshold are excluded.
gseaParam	GSEA parameter value, all gene-level statis are raised to the power of 'gseaParam' before calculation of GSEA enrichment scores
n.core	A single integer to specify the number of core for parallelisation.

Value

A data.table with geneset enrichment analysis statistics.

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
GSEAResults <- RunCellGSEA(seuratPbmc, Hallmark, dims = 1:5)
```

RunCellHGT *Run HyperGeometric Test on cells*

Description

RunCellHGT calculates the gene signatures for each cells and performs hypergeometric test against a user defined gene signatures/pathways (named list of genes). It returns a score of enrichment in the form of -log10 pvalue(see log.trans argument). The obtained matrix can then be integrated in Seurat or SingleCellExperiment object. It can notably be used with cell type signatures to predict cell types or with functionnal pathways

Usage

```
RunCellHGT(
  X,
  pathways,
  reduction,
  n.features,
  features,
  dims,
  minSize,
  log.trans,
  p.adjust
)

## S3 method for class 'SingleCellExperiment'
RunCellHGT(
  X,
  pathways,
  reduction = "MCA",
  n.features = 200,
  features = NULL,
  dims = seq(50),
  minSize = 10,
  log.trans = TRUE,
  p.adjust = TRUE
)

## S3 method for class 'Seurat'
RunCellHGT(
  X,
  pathways,
  reduction = "mca",
  n.features = 200,
  features = NULL,
  dims = seq(50),
  minSize = 10,
```

```
  log.trans = TRUE,
  p.adjust = TRUE
)
```

Arguments

X	Seurat or SingleCellExperiment object with mca performed
pathways	geneset to perform hypergeometric test on (named list of genes)
reduction	name of the MCA reduction
n.features	integer of top n features to consider for hypergeometric test
features	vector of features to calculate the gene ranking by default will take everything in the selected mca reduction.
dims	MCA dimensions to use to compute n.features top genes.
minSize	minimum number of overlapping genes in geneset and
log.trans	if TRUE tranform the pvalue matrix with -log10 and convert it to sparse matrix
p.adjust	if TRUE apply Benjamini Hochberg correction to p-value

Value

a matrix of benjamini hochberg adjusted pvalue pvalue or a sparse matrix of (-log10) benjamini hochberg adjusted pvalue

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
Enrichment <- RunCellHGT(X = seuratPbmc, pathways = Hallmark, dims = 1:5)
```

RunGroupGSEA *Run GSEA on cluster/groups*

Description

Calculate group gene specificty ranking and then perform geneset enrichment analysis on it.

Usage

```
RunGroupGSEA(
  X,
  pathways,
  group.by,
  reduction,
  dims,
  features,
  nperm,
  minSize,
```

```
  maxSize,
  gseaParam
)

## S3 method for class 'Seurat'
RunGroupGSEA(
  X,
  pathways,
  group.by = NULL,
  reduction = "mca",
  dims = seq(50),
  features = NULL,
  nperm = 1000,
  minSize = 10,
  maxSize = 500,
  gseaParam = 0
)

## S3 method for class 'SingleCellExperiment'
RunGroupGSEA(
  X,
  pathways,
  group.by,
  reduction = "MCA",
  dims = seq(50),
  features = NULL,
  nperm = 1000,
  minSize = 10,
  maxSize = 500,
  gseaParam = 0
)
```

Arguments

X	pathways List of gene sets to check
pathways	reduction Which dimensionality reduction to use, must be based on MCA.
group.by	dims A vector of integers indicating which dimensions to use with reduction embeddings and loadings for distance calculation.
reduction	features Character vector of feature names to subset feature coordinates. If not specified will take all features available from specified reduction Loadings.
dims	cells Character vector of cell names to subset cell coordinates. If not specified will take all features available from specified reduction Embeddings
features	cells Character vector of cell names to subset cell coordinates. If not specified will take all features available from specified reduction Embeddings
nperm	nperm Number of permutations to do. Minimial possible nominal p-value is about 1/nperm

minSize	minSize Minimal size of a gene set to test. All pathways below the threshold are excluded.
maxSize	maxSize Maximal size of a gene set to test. All pathways above the threshold are excluded.
gseaParam	gseaParam GSEA parameter value, all gene-level statis are raised to the power of 'gseaParam' before calculation of GSEA enrichment scores

Value

A data.table with geneset enrichment analysis statistics.

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
GSEAResults <- RunGroupGSEA(seuratPbmc, Hallmark, group.by = "seurat_clusters", dims = 1:5)
```

RunMCA *Run Multiple Correspondence Analysis*

Description

RunMCA allows to compute the Multiple Corespondence Analysis on the single cell data contained in Seurat or SingleCellExperiment. MCA is a statistical technique close to PCA that provides a simultaneous representation of observations (e.g. cells) and variables (e.g. genes) in low-dimensional space. The barycentric relation among cells and genes is a distinctive feature of MCA biplots and represents a major advantage as compared to other types of biplots such as those produced by Principal Component Analysis as well as over alternative low-dimensional transformations providing only cell projections. Thus, in the MCA biplot, analytical distances can be calculated not only between cells and between genes, but also between each cell and each gene in order to estimate its association. Thus, the closer a gene g is to a cell c, the more specific to such a cell it can be considered. Gene-to-cell distances can then be ranked for each individual cell, and the top-ranked genes may be regarded as a unique gene signature representing the identity card of the cell.

Usage

```
RunMCA(X, nmcs, features, reduction.name, slot, ...)

## S3 method for class 'matrix'
RunMCA(X, nmcs = 50, features = NULL, reduction.name = "MCA", ...)

## S3 method for class 'Seurat'
RunMCA(
  X,
  nmcs = 50,
  features = NULL,
  reduction.name = "mca",
  slot = "data",
```

```
  assay = DefaultAssay(X),
  ...
)

## S3 method for class 'SingleCellExperiment'
RunMCA(
  X,
  nmcs = 50,
  features = NULL,
  reduction.name = "MCA",
  slot = "logcounts",
  ...
)
```

Arguments

X	Seurat, SingleCellExperiment or matrix object
nmcs	number of components to compute and store, default set to 30
features	character vector of feature names. If not specified all features will be taken.
reduction.name	name of the reduction default set to 'MCA' for SingleCellExperiment and mca
slot	Which slot to pull expression data from? Default to logcounts for SingleCellExperiment and data for Seurat.
...	other aruments passed to methods
assay	Name of Assay MCA is being run on

Value

Seurat or SCE object with MCA calculation stored in the reductions slot.

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
```

RunMCDMAP *Diffusion Map on MCA coordinates*

Description

(!EXPERIMENTAL) Run DiffusionMap on MCA cell and feature coordinates. This will allow to draw the trajectory of both cells and the genes at the same time.

Usage

```
RunMCDMAP(X, reduction, features, dims, reduction.name, ...)

## S3 method for class 'Seurat'
RunMCDMAP(
  X,
  reduction = "mca",
  features = NULL,
  dims = seq(50),
  reduction.name = "mcdmap",
  assay = DefaultAssay(X),
  ...
)

## S3 method for class 'SingleCellExperiment'
RunMCDMAP(
  X,
  reduction = "MCA",
  features = NULL,
  dims = seq(50),
  reduction.name = "MCDMAP",
  ...
)
```

Arguments

X	Seurat or SingleCellExperiment object
reduction	Which dimensionality reduction to use, must be based on MCA.
features	Character vector of feature names to subset feature coordinates. If not specified will take all features available from specified reduction Loadings.
dims	A vector of integers indicating which dimensions to use with reduction embeddings and loadings for distance calculation.
reduction.name	name of the created dimensionlaity reduction, default set to "mca" for Seurat and "MCA" for SCE.
...	other arguments passed to methods or DiffusionMap
assay	Seurat Asssay slot name.

Value

Seurat or SingleCellExperiment object with MCDMAP stored in the reduction slot

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
seuratPbmc <- RunMCDMAP(seuratPbmc, dims = seq(5), k = 5)
```

RunMCTSNE *tSNE on MCA coordinates*

Description

(!EXPERIMENTAL) Run TSNE on MCA fetures and cells coordinates This will allow to embbed in 2D both cells and the genes at the same time.

Usage

```
RunMCTSNE(X, reduction, dims, features, reduction.name, ...)

## S3 method for class 'Seurat'
RunMCTSNE(
  X,
  reduction = "mca",
  dims = seq(50),
  features = NULL,
  reduction.name = "mctsne",
  assay = DefaultAssay(X),
  ...
)

## S3 method for class 'SingleCellExperiment'
RunMCTSNE(
  X,
  reduction = "MCA",
  dims = seq(50),
  features = NULL,
  reduction.name = "MCTSNE",
  ...
)
```

Arguments

X	Seurat or SingleCellExperiment object
reduction	Which dimensionality reduction to use, must be based on MCA.
dims	A vector of integers indicating which dimensions to use with reduction embeddings and loadings for distance calculation.
features	Character vector of feature names to subset feature coordinates. If not specified will take all features available from specified reduction Loadings.
reduction.name	name of the created dimensionlaity reduction, default set to "mca" for Seurat and "MCA" for SCE.
...	other arguments passed to methods or Rtsne::Rtsne
assay	Seurat assay slot. When not specified set with DefaultAssay(X)

Value

Seurat or SingleCellExperiment object with MCTSNE stored in the reduction slot

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
seuratPbmc <- RunMCTSNE(seuratPbmc, dims = seq(5))
```

RunMCUMAP *UMAP on MCA coordinates*

Description

(!EXPERIMENTAL) Run UMAP on MCA fetures and cells coordinates. This will allow to embbed in 2D both cells and the genes at the same time.

Usage

```
RunMCUMAP(X, reduction, dims, features, reduction.name, ...)

## S3 method for class 'Seurat'
RunMCUMAP(
  X,
  reduction = "mca",
  dims = seq(50),
  features = NULL,
  reduction.name = "mcumap",
  assay = DefaultAssay(X),
  ...
)

## S3 method for class 'SingleCellExperiment'
RunMCUMAP(
  X,
  reduction = "MCA",
  dims = seq(50),
  features = NULL,
  reduction.name = "MCUMAP",
  ...
)
```

Arguments

X	Seurat or SingleCellExperiment object
reduction	Which dimensionality reduction to use, must be based on MCA.
dims	A vector of integers indicating which dimensions to use with reduction embeddings and loadings for distance calculation.

features	Character vector of feature names to subset feature coordinates. If not specified will take all features available from specified reduction Loadings.
reduction.name	name of the created dimensionlaity reduction, default set to "mca" for Seurat and "MCA" for SCE.
...	other arguments passed to methods or Rtsne::Rtsne
assay	Seurat assay slot to assign MCUMAP. When not specified set to DefaultAssay(X)

Value

Seurat or SingleCellExperiment object with MCUMAP stored in the reduction slot

Examples

```
seuratPbmc <- RunMCA(seuratPbmc, nmcs = 5)
seuratPbmc <- RunMCUMAP(seuratPbmc, dims = seq(5))
```

---

setDimMCSlot *SetDimSlot*

Description

Integrate MCA in Seurat and SingleCellExperiment Dimensionlity reduction Slot. It will set also a small parameter inside the dimensionality reduction object to signal if it is a MCA or not.

Usage

```
setDimMCSlot(X, cellEmb, geneEmb, stdev, reduction.name, ...)

## S3 method for class 'Seurat'
setDimMCSlot(
  X,
  cellEmb,
  geneEmb,
  stdev = NULL,
  reduction.name = "mca",
  assay = DefaultAssay(X),
  ...
)

## S3 method for class 'SingleCellExperiment'
setDimMCSlot(X, cellEmb, geneEmb, stdev = NULL, reduction.name = "MCA", ...)
```

Arguments

X	Seurat or SingleCellExperiment object
cellEmb	cell coordinates returned by MCA
geneEmb	feature coordinates returned by MCA
stdev	eigen value returned by MCA
reduction.name	name of the created dimensionlaity reduction, default set to 'mca' for Seurat and 'MCA' for SCE.
...	other arguments passed to methods
assay	Seurat assay slot

Value

Seurat or SingleCellExperiment object with MC stored in the reduction slot

---

seuratPbmc *Seurat object of 400 PBMC cells*

Description

A subset of the PBMC3k data from Seurat vignette. Normalisation, VariableFeatures, ScaleData and PCA has alreay been computed with default Seurat parameter.

Usage

```
seuratPbmc
```

Format

A seurat object.

Source

https://s3-us-west-2.amazonaws.com/10x.files/samples/cell/pbmc3k/pbmc3k_filtered_gene_bc_matrices.tar.gz

References

Butler et al., Nature Biotechnology 2018.

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