

# Package ‘CelliD’

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**Type** Package

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

**Version** 1.16.0

**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

**License** GPL-3 + file LICENSE

**Encoding** UTF-8

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**Imports** Rcpp, RcppArmadillo, stats, utils, Matrix, tictoc, scater, stringr, irlba, data.table, glue, pbapply, umap, Rtsne, reticulate, fastmatch, matrixStats, ggplot2, BiocParallel, SummarizedExperiment, fgsea

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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.

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## 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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- Alexey Sergushichev. An algorithm for fast preranked gene set enrichment analysis using cumulative statistic calculation. *bioRxiv* (2016), <https://doi.org/10.1101/060012>
- Stuart and Butler et al. Comprehensive integration of single cell data. *bioRxiv* (2018). <https://doi.org/10.1101/460147>
- Aaron Lun and Davide Risso (2019). SingleCellExperiment: S4 Classes for Single Cell Data. R package version 1.4.1.

## See Also

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- 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 are 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 overlaid 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](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 ordered 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	<i>Gene sets extraction from MCA</i>
----------------	--------------------------------------

---

### Description

Calculate cells and genes distances, rank them per cell and extract top n features. The obtained top n features represents features that are 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 Embeddings.
n.features	single integer specifying how many top features should be extracted from the ranking

### Value

A cell named list of gene rankings ordered by distances from shortest (most specific) 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 specified 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	<i>Get Matrix from Enrichment Results</i>
---------------	---

---

**Description**

Extract enrichment 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	<i>Hallmark Pathways from MSigDB</i>
----------	--------------------------------------

---

**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](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 ontology 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,

---

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 ontology 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 specificity 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

<code>x</code>	Seurat or SingleCellExperiment object
<code>pathways</code>	List of gene sets to check
<code>reduction</code>	Which dimensionality reduction to use, must be based on MCA.
<code>dims</code>	A vector of integers indicating which dimensions to use with reduction embeddings and loadings for distance calculation.
<code>features</code>	Character vector of feature names to subset feature coordinates. If not specified will take all features available from specified reduction Loadings.
<code>cells</code>	Character vector of cell names to subset cell coordinates. If not specified will take all features available from specified reduction Embeddings
<code>nperm</code>	Number of permutations to do. Minimal possible nominal p-value is about 1/nperm
<code>minSize</code>	Minimal size of a gene set to test. All pathways below the threshold are excluded.
<code>maxSize</code>	Maximal size of a gene set to test. All pathways above the threshold are excluded.
<code>gseaParam</code>	GSEA parameter value, all gene-level statis are raised to the power of 'gseaParam' before calculation of GSEA enrichment scores
<code>n.core</code>	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  $-\log_{10}$  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 functional 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

<code>X</code>	Seurat or SingleCellExperiment object with mca performed
<code>pathways</code>	geneset to perform hypergeometric test on (named list of genes)
<code>reduction</code>	name of the MCA reduction
<code>n.features</code>	integer of top n features to consider for hypergeometric test
<code>features</code>	vector of features to calculate the gene ranking by default will take everything in the selected mca reduction.
<code>dims</code>	MCA dimensions to use to compute n.features top genes.
<code>minSize</code>	minimum number of overlapping genes in geneset and
<code>log.trans</code>	if TRUE transform the pvalue matrix with $-\log_{10}$ and convert it to sparse matrix
<code>p.adjust</code>	if TRUE apply Benjamini Hochberg correction to p-value

### Value

a matrix of benjamini hochberg adjusted pvalue pvalue or a sparse matrix of  $(-\log_{10})$  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 specificity 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. Minimal 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 Correspondence 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 arguments 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 dimensionality reduction, default set to "mca" for Seurat and "MCA" for SCE.
...	other arguments passed to methods or DiffusionMap
assay	Seurat Assay 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 embed 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

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

**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 embed 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 dimensionality 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 Dimensionality 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 dimensionality 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	<i>Seurat object of 400 PBMC cells</i>
------------	--

---

**Description**

A subset of the PBMC3k data from Seurat vignette. Normalisation, VariableFeatures, ScaleData and PCA has already 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](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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