Package 'hammers'

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Description hammers is a utilities suite for scRNA-seq data analysis compatible with both Seurat and SingleCellExperiment. It provides simple tools to address tasks such as retrieving aggregate gene statistics, finding and removing rare genes, performing representation analysis, computing the center of mass for the expression of a gene of interest in low-dimensional space, and calculating silhouette and cluster-normalized silhouette.

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`hammers-package` *hammers: Utilities for scRNA-seq data analysis*

Description

hammers is a utilities suite for scRNA-seq data analysis compatible with both Seurat and SingleCellExperiment. It provides simple tools to address tasks such as retrieving aggregate gene statistics, finding and removing rare genes, performing representation analysis, computing the center of mass for the expression of a gene of interest in low-dimensional space, and calculating silhouette and cluster-normalized silhouette.

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See Also

Useful links:

- https://github.com/andrei-stoica26/hammers
- Report bugs at https://github.com/andrei-stoica26/hammers/issues

`addCategory` *Add a categorical column to a data frame based on another column*

Description

This function adds a categorical column to a data frame based on another column.

Usage

```
addCategory(df, col, newCol, keys, values)
```

Arguments

`df`	A data frame.
`col`	Column whose values will be used for creating the new column.
`newCol`	Column to be added.
`keys`	A list of keys. If vectors are part of the keys, each of their elements will be assigned the corresponding value.
`values`	A vector of values. Must have the same length as `keys`.

Value

A data frame with a new categorical column.

Examples

```
df <- data.frame(fruit = c('apple', 'banana', 'cherry', 'grape'))
df <- addCategory(df,
                  'fruit',
                  'color',
                  list(c('apple', 'cherry'),
                  'banana',
                  'grape'),
                  c('red', 'yellow', 'purple'))
```

`addMetadataCategory` *Add a categorical column to a Seurat metadata or SingleCellExperiment coldata*

Description

Add a categorical column to a Seurat metadata or SingleCellExperiment coldata

Usage

```
addMetadataCategory(
  scObj,
  col,
  newCol,
  keys,
  values,
  newCol2 = NULL,
  values2 = NULL
)
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
col	Column whose values will be used for creating the new column.
newCol	Column to be added.
keys	A list of keys. If vectors are part of the keys, each of their elements will be assigned the corresponding value.
values	A vector of values. Must have the same length as keys.
newCol2	A second column to be added based on the same keys. Default is NULL (no second column will be added).
values2	A vector of values corresponding to the second column. Default is NULL (no second column will be added).

Value

A Seurat or SingleCellExpression object with one or two new categorical column(s) in the metadata/coldata.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
sceObj <- addMetadataCategory(sceObj, 'Cell_Cycle', 'Type',
list(c('G0', 'G1'), 'G2M', 'S'), c(2, 3, 1))
```

---

addNormSilhouette *Adds normalized silhouette column to a single-cell expression object*

Description

This function adds a normalized silhouette column to a single-cell expression object.

Usage

```
addNormSilhouette(scObj, normSilDF, normSilCol = "normSilhouette")
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
normSilDF	Normalized silhouette data frame.
normSilCol	The name of the normalized silhouette column to be added.

Value

The input object (Seurat or SingleCellExperiment) with an added metadata normalized silhouette column.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
df <- normalizeSilhouette(sceObj, 'Cluster')
sceObj <- addNormSilhouette(sceObj, df)
```

---

centerOfMass *Calculate the center of mass of columns*

Description

This function calculates the center of mass based on the columns of a data frame or matrix and a vector of weights.

Usage

```
centerOfMass(obj, weights)
```

Arguments

obj	A data frame or matrix.
weights	A vector of weights.

Value

A vector containing the center of mass.

Examples

```
obj <- matrix(data=c(2, 3, 1, 3, 6, 8), nrow=3, ncol=2)
weights <- c(0.8, 6, 16)
centerOfMass(obj, weights)
```

checkGenes *Check if all genes exist in the single-cell expression object*

Description

This function checks if all genes exist in the single-cell expression object.

Usage

```
checkGenes(scObj, genes)
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
genes	A character vector of genes.

Value

None. This function is called for its side effect.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
checkGenes(sceObj, c('Gene_0480', 'Gene_0481', 'Gene_0482'))
```

colCenters *Calculate the centers of mass of metadata/coldata columns*

Description

This function calculates the centers of mass of selected metadata/coldata columns from a Seurat or SingleCellExpression object.

Usage

```
colCenters(scObj, columns)
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
columns	Numeric columns.

Value

A data frame containing the coordinates of centers of mass.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
colCenters(sceObj, c('sizeFactor'))
```

---

colsDimPlot *Create a single-cell dimensionality reduction plot with added labeled points for numeric columns*

Description

This function creates a single-cell dimensionality reduction plot with added labeled points for metadata numeric columns.

Usage

```
colsDimPlot(scObj, cols, ...)
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
cols	Columns whose centers of mass will be plotted.
...	Additional parameters passed to pointsDimPlot.

Value

A ggplot object.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
colsDimPlot(sceObj, c('sizeFactor', 'silhouette'))
```

---

computeSilhouette *Compute cluster silhouette for single-cell expression object*

Description

This function computes the silhouette for each cell in the Seurat or SingleCellExperiment object.

Usage

```
computeSilhouette(scObj, idClass, silCol = "silhouette")
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
idClass	Identity class. Must be present among the metadata columns of the single-cell expression object.
silCol	The name of the silhouette column to be added.

Value

The input object (Seurat or SingleCellExperiment) with an added metadata silhouette column.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
sceObj <- computeSilhouette(sceObj, 'Cluster')
```

---

devPlot.default *Saves plot or list of plots*

Description

This function saves a plot or list of plots as a pdf. Can also take as input a function that returns a ggplot object together with its arguments.

Usage

```
## Default S3 method:
devPlot(plotObject, ...)

## S3 method for class '`function`'
devPlot(plotObject, ...)

## S3 method for class 'ggplot'
devPlot(plotObject, ...)

## S3 method for class 'list'
devPlot(plotObject, ...)

devPlot(plotObject, ...)
```

Arguments

plotObject	A function, ggplot object, or list of ggplot objects.
...	Additional arguments.

Value

No value. This function is called for its side effect.

Examples

```
library(ggplot2)
df <- data.frame(x = c(1, 2), y = c(3, 5))
p <- ggplot(df) + geom_point(aes(x, y))
devPlot(p)

simplePlot <- function(df, title)
    return(ggplot(df) + geom_point(aes(x, y)) + ggtitle(title))

devPlot(simplePlot, df, 'Plot title')

if (file.exists('Rplots.pdf'))
    file.remove('Rplots.pdf')
if (file.exists('Rplots1.pdf'))
    file.remove('Rplots1.pdf')
```

`distributionPlot` *Plot the distribution of cells across two columns*

Description

This function plots the distribution of cells across two columns.

Usage

```
distributionPlot(
  scObj,
  title = NULL,
  col1 = "seurat_clusters",
  col2 = "orig.ident",
  type = c("counts", "percs"),
  xLab = col1,
  yLab = if (type == "counts") "Count" else "Percentage",
  legendLab = col2,
  palette = "Spectral",
  legendPos = "right",
  legendTextSize = 10,
  legendTitleSize = 10,
  axisTextSize = 12,
  axisTitleSize = 12,
  sigDigits = 2
)
```

Arguments

`scObj`	A `Seurat`, `SingleCellExperiment`, `dgCMatrix` or `matrix` object.
`title`	Plot title.
`col1`	Column as string.
`col2`	Column as string.
`type`	Whether the plot should display counts ('counts', default) or percentages ('percs').

xLab	x axis label.
yLab	y axis label.
legendLab	Legend label.
palette	Color palette.
legendPos	Legend position.
legendTextSize	Legend text size.
legendTitleSize	Legend title size.
axisTextSize	Axis text size.
axisTitleSize	Axis title size.
sigDigits	Number of significant digits used by percentages displayed on the plot. Ignored if type is 'counts'.

Value

A ggplot object.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
p <- distributionPlot(sceObj, col1='Cluster', col2='Donor')
```

---

findRareGenes *Find rare genes in a Seurat or SingleCellExpression object*

Description

This function finds genes expressed in a low number of cells in a Seurat or SingleCellExpression object.

Usage

```
findRareGenes(scObj, nCells = 10)
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
nCells	Minimum number of cells in which a gene must be expressed to be regarded as non-rare.

Value

A data frame with the rare genes as rownames and a single column representing their frequencies.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
df <- findRareGenes(sceObj)
```

geneCellSets *Generates cell sets for each input gene*

Description

This function constructs, for each input gene, sets of cells expressing the gene

Usage

```
geneCellSets(scObj, genes = NULL)
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
genes	A character vector of genes.

Value

A named list of character vectors of cell names.

Examples

```
mat <- matrix(0, 1000, 500)
rownames(mat) <- paste0('G', seq(1000))
colnames(mat) <- paste0('C', seq(500))
mat[sample(length(mat), 70000)] <- sample(50, 70000, TRUE)
mat <- mat[paste0('G', sample(1000, 3)), ]
geneCellSets(mat)
```

geneCenters *Calculate the centers of mass of the expression of input genes*

Description

This function calculates the centers of mass of the expression of input genes.

Usage

```
geneCenters(scObj, genes)
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
genes	A character vector of genes.

Value

A data frame containing the centers of mass.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
geneCenters(sceObj, c('Gene_0480', 'Gene_0481', 'Gene_0482'))
```

`genePresence` *Extract gene presence from a Seurat or SingleCellExperiment object*

Description

This function extracts the number of cells in which a gene from a Seurat or SingleCellExperiment is expressed.

Usage

```
genePresence(scObj, genes = NULL, minCutoff = NULL, maxCutoff = NULL)
```

Arguments

`scObj`	A `Seurat`, `SingleCellExperiment`, `dgCMatrix` or `matrix` object.
`genes`	Genes for which the number of cells in which the gene is expressed will be computed. If `NULL` (as default), all genes will be included in the assessment.
`minCutoff`	Minimum cutoff for gene counts. Genes with counts below this value will be omitted.
`maxCutoff`	Maximum cutoff for gene counts. Genes with counts above this value will be omitted.

Value

A data frame with two columns. The first column lists the genes ordered decreasingly by the number of cells in which they appear, the second lists the corresponding numbers of cells.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
df <- genePresence(sceObj)
```

genesDimPlot — *Create a single-cell dimensionality reduction plot with added labeled points for genes*

Description

This function creates a single-cell dimensionality reduction plot with added labeled points for genes.

Usage

```
genesDimPlot(scObj, genes, ...)
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
genes	Genes whose centers of mass will be plotted.
...	Additional parameters passed to pointsDimPlot.

Value

A ggplot object.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
genesDimPlot(sceObj, c('Gene_0364', 'Gene_0388', 'Gene_0477'))
```

joinCharCombs — *Join all combinations of elements from character vectors*

Description

This function joins all combinations of elements from character vectors with a separating character.

Usage

```
joinCharCombs(..., joinChar = "_")
```

Arguments

...	Vectors passed to expandGrid.
joinChar	Character used to join combinations.

Value

A character vector.

Examples

```
joinCharCombs(c('a', 'b', 'c', 'd'), c('eee', 'ff'), c(1, 2, 3))
```

---

keyvalMap *Create a map from keys to values*

Description

This function creates a map from keys to values.

Usage

```
keyvalMap(keys, values)
```

Arguments

keys	A list of keys. If vectors are part of the keys, each of their elements will be assigned the corresponding value.
values	A vector of values. Must have the same length as keys.

Value

A named vector.

Examples

```
keyvalMap(list(2, c(3, 4, 5), 6, 8), c('a', 'b', 'c', 'd'))
```

---

normalizeSilhouette *Normalize silhouette by identity class for single-cell expression object*

Description

This function normalizes the already computed silhouette for each identity class in the single-cell expression object.

Usage

```
normalizeSilhouette(scObj, idClass, silCol = "silhouette")
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
idClass	Identity class. Must be present among the metadata columns of the single-cell expression object.
silCol	The name of the silhouette column.

Value

A data frame with normalized silhouettes for each unique element in the identity class.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
df <- normalizeSilhouette(sceObj, 'Cluster')
```

`pointsDimPlot` *Create a single-cell dimensionality reduction plot with added labeled points*

Description

This function creates a single-cell dimensionality reduction plot with added labeled points.

Usage

```
pointsDimPlot(
  scObj,
  title = NULL,
  pointsObj = NULL,
  alpha = 1,
  pointShape = 4,
  pointSize = 2,
  pointColor = "black",
  labelSize = 2.5,
  maxOverlaps = 30,
  ...
)
```

Arguments

`scObj`	A `Seurat`, `SingleCellExperiment`, `dgCMatrix` or `matrix` object.
`title`	Plot title.
`pointsObj`	A data frame or matrix of points with two columns representing x and y coordinates.
`alpha`	Opaqueness level.
`pointShape`	Point shape.
`pointSize`	Point size.
`pointColor`	Point color.
`labelSize`	Label size. If `NULL`, the points will not receive labels.
`maxOverlaps`	Maximum overlaps.
`...`	Additional parameters passed to `Seurat::DimPlot`.

Details

A wrapper around `scLang::dimPlot`.

Value

A ggplot object.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
pointsObj <- data.frame(x = c(2, 3),
y = c(1, 0),
row.names = c('P1', 'P2'))
pointsDimPlot(sceObj, pointsObj=pointsObj)
```

`prepAlluvial` *Prepare dataframe for alluvial plot*

Description

This function extracts the relevant information from a data frame and adjusts p-values to be used as weights for the alluvia.

Usage

```
prepAlluvial(
  df,
  pvalCol = "pvalAdj",
  colIndices = c(1, 2),
  weightExp = 1/2,
  pvalOffset = 1.00000023069254e-317
)
```

Arguments

`df`	A data frame.
`pvalCol`	Name of p-value column to be used by the alluvial plot.
`colIndices`	A vector respresenting the indices of the two categorical columns from the data frame that will be used.
`weightExp`	Exponent used in constructing weight from p-values.
`pvalOffset`	Offset used to avoid zeros inside the logarithm function.

Value

A data frame with weight scores in lieu of p-values.

Examples

```
df <- data.frame(A = c('a1', 'a2', 'a3', 'a4'),
B = c('b1', 'b2', 'b3', 'b4'),
pvalAdj = c(0.81, 1e-6, 1e-3, 0.022))
prepAlluvial(df)
```

`pvalRiverPlot` *Plot representation data frame*

Description

This function plots representation data frame as an alluvial plot.

Usage

```
pvalRiverPlot(
  df,
  pvalCol = "pvalAdj",
  colIndices = c(1, 2),
  weightExp = 1/2,
  pvalOffset = 1.00000023069254e-317,
  ...
)
```

Arguments

`df`	A data frame.
`pvalCol`	Name of p-value column to be used by the alluvial plot.
`colIndices`	A vector respresenting the indices of the two categorical columns from the data frame that will be used.
`weightExp`	Exponent used in constructing weight from p-values.
`pvalOffset`	Offset used to avoid zeros inside the logarithm function.
`...`	Additional parameters passed to `henna::riverPlot`

Value

A ggplot object

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
df <- repAnalysis(sceObj, 'Cluster', 'Donor')
pvalRiverPlot(df)
```

removeRareGenes — *Remove rare genes from a Seurat or SingleCellExpression object*

Description

This function removes genes expressed in a low number of cells in a Seurat or SingleCellExpression object.

Usage

```
removeRareGenes(scObj, nCells = 10, verbose = TRUE)
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
nCells	Minimum number of cells in which a gene must be expressed to be retained.
verbose	Logical; whether the output should be verbose.

Value

A Seurat or SingleCellExpression object with rare genes removed.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
sceObj <- removeRareGenes(sceObj, 30)
```

repAnalysis — *Find the differential representation of two Seurat or SingleCellExperiment columns*

Description

This function finds the differential representation of two Seurat or SingleCellExperiment columns.

Usage

```
repAnalysis(
  scObj,
  col1 = "seurat_clusters",
  col2 = "orig.ident",
  doOverrep = TRUE,
 mtMethod = c("BY", "holm", "hochberg", "hommel", "bonferroni", "BH", "fdr", "none"),
  ...
)
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
col1	Column as string.
col2	Column as string.
doOverrep	Whether to perform overrepresentation analysis (TRUE) or underrepresentation analysis (FALSE).
mtMethod	Multiple testing correction method. Choices are 'BY' (default), 'holm', hochberg', hommel', 'bonferroni', 'BH', 'fdr' and 'none'.
...	Additional parameters passed to LISTO::mtCorrectDF.

Value

An overrepresentation or underrepresentation data frame.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='hammers')
sceObj <- qs2::qs_read(scePath)
repAnalysis(sceObj, 'Cluster', 'Donor')
```

---

safeMessage *Message an input if verbose is set to TRUE*

Description

This function messages an input if verbose is set to TRUE.

Usage

```
safeMessage(msg, verbose = TRUE)
```

Arguments

msg	Message
verbose	Whether the message should be displayed.

Value

No return value. This function is called for its side effect (messaging the input if verbose is set to TRUE).

Examples

```
safeMessage('message')
```

`safeMinmax` *Perform min-max normalization when possible; otherwise return a single-value vector.*

Description

This function min-max-normalizes a vector when possible, and otherwise returns a single-value vector.

Usage

```
safeMinmax(scores, safeVal = 0)
```

Arguments

`scores`	Numeric vector.
`safeVal`	Value to replace all values with when all values in the vector are the same.

Value

Min-max-normalized scores or a single-value vector.

Examples

```
safeMinmax(c(0, 3, 2, 1, 4, 5.5, 6.32, 8, 1.1))
```

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