Package: scLang (via r-universe)

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Type Package

Title A unified language for interacting with Seurat and SingleCellExperiment

Version 1.1.3

Description scLang is a suite for package development for scRNA-seq analysis. It offers functions that can operate on both Seurat and SingleCellExperiment objects. These functions are primarily aimed to help developers build tools compatible with both types of input.

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`dimPlot` *Creates a dimensionality reduction plot*

Description

This function creates a dimensionality reduction plot

Usage

```
dimPlot(
  scObj,
  groupBy = NULL,
  title = NULL,
  dimred = "umap",
  dims = c(1, 2),
  legendTitle = "Group",
  noGroupsLegendLab = "Object",
  palette = "grDevices::rainbow",
  pointSize = 0.5,
  alpha = 0.7,
  legendPos = c("right", "top", "left", "bottom"),
  legendTextSize = 10,
  legendTitleSize = 10,
  axisTextSize = 12,
  axisTitleSize = 12,
  ...
)
```

Arguments

scObj	A Seurat or SingleCellExperiment object.
groupBy	Grouping variable. Must exist in the metadata/coldata of the single-cell expression object.
title	Plot title.
dimred	Dimensionality reduction.
dims	A numeric vector of size 2 representing the dimensions selected for the plot.
legendTitle	Legend title.
noGroupsLegendLab	Legend label to be used when no grouping is provided (groupBy is NULL)
palette	Color palette.
pointSize	Point size.
alpha	Opaqueness level.
legendPos	Legend position.
legendTextSize	Legend text size.
legendTitleSize	Legend title size.
axisTextSize	Axis text size.
axisTitleSize	Axis title size.
...	Additional arguments passed to henna::centerTitle.

Value

A dimensionality reduction plot.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='scLang')
sceObj <- qs2::qs_read(scePath)
dimPlot(sceObj, groupBy='Donor')
```

---

dimredNames.default *Extract the names of available dimensionality reductions from object*

Description

This function extracts the names of available dimensionality reductions from a Seurat or SingleCellExperiment object.

Usage

```
## Default S3 method:
dimredNames(scObj)

## S3 method for class 'Seurat'
dimredNames(scObj)

## S3 method for class 'SingleCellExperiment'
dimredNames(scObj)

dimredNames(scObj)
```

Arguments

scObj	A Seurat or SingleCellExperiment object.

Value

A character vector.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='scLang')
sceObj <- qs2::qs_read(scePath)
dimredNames(sceObj)
```

---

featurePlot *Create a dimensionality reduction plot to represent a feature*

Description

This function creates a dimensionality reduction plot to represent a feature (gene expression or numeric metadata column).

Usage

```
featurePlot(
  scObj,
  feature = rownames(scObj)[1],
  title = feature,
  dimred = "umap",
  dims = c(1, 2),
  legendTitle = NULL,
  palette = paletteer_d("wesanderson::Royal1")[c(3, 2)],
  pointSize = 0.5,
  alpha = 0.6,
```

```
  legendPos = c("right", "top", "left", "bottom"),
  legendTextSize = 10,
  legendTitleSize = 10,
  axisTextSize = 12,
  axisTitleSize = 12,
  ...
)
```

Arguments

scObj	A Seurat or SingleCellExperiment object.
feature	A gene name or metadata column name.
title	Plot title.
dimred	Dimensionality reduction.
dims	A numeric vector of size 2 representing the dimensions selected for the plot.
legendTitle	Legend title.
palette	Color palette.
pointSize	Point size.
alpha	Opaqueness level.
legendPos	Legend position.
legendTextSize	Legend text size.
legendTitleSize	Legend title size.
axisTextSize	Axis text size.
axisTitleSize	Axis title size.
...	Additional arguments passed to henna::centerTitle.

Value

A feature plot.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='scLang')
sceObj <- qs2::qs_read(scePath)
featurePlot(sceObj, 'Gene289')
```

metadataDF *Extract metadata from object as a data frame*

Description

This function extracts the metadata from a `Seurat` or `SingleCellExperiment` object as a data frame.

Usage

```
metadataDF(scObj)

## Default S3 method:
metadataDF(scObj)

## S3 method for class 'Seurat'
metadataDF(scObj)

## S3 method for class 'SingleCellExperiment'
metadataDF(scObj)
```

Arguments

`scObj`	A `Seurat` or `SingleCellExperiment` object.

Value

A metadata data frame.

Examples

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

metadataNames *Return metadata names*

Description

This function extracts metadata names from a Seurat or SingleCellExperiment object. It can also be used to modify metadata names.

Usage

```
metadataNames(scObj)
```

Arguments

scObj	A Seurat or SingleCellExperiment object.

Value

The names of the metadata columns.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='scLang')
sceObj <- qs2::qs_read(scePath)
colNames <- metadataNames(sceObj)
```

---

scCol *Extract a metadata/coldata column from object.*

Description

This function extracts a metadata/coldata column from a Seurat or SingleCellExperiment object.

Usage

```
scCol(scObj, col)

scCol(scObj, col) <- value

## Default S3 method:
scCol(scObj, col)

## Default S3 replacement method:
scCol(scObj, col) <- value

## S3 method for class 'Seurat'
scCol(scObj, col)

## S3 replacement method for class 'Seurat'
scCol(scObj, col) <- value

## S3 method for class 'SingleCellExperiment'
scCol(scObj, col)

## S3 replacement method for class 'SingleCellExperiment'
scCol(scObj, col) <- value
```

Arguments

scObj	A Seurat or SingleCellExperiment object.
col	Column name.
value	A vector to be added to the metadata/coldata of the single-cell expression object.

Value

A vector.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='scLang')
sceObj <- qs2::qs_read(scePath)
v <- scCol(sceObj, 'Cluster')
```

---

scColCounts *Extract per-group counts from the column of a single-cell expression object*

Description

This function extracts per-group counts from the column of single-cell expression object.

Usage

```
scColCounts(scObj, col)
```

Arguments

scObj	A Seurat or SingleCellExperiment object.
col	Column as string.

Value

A frequency vector with the unique column values as names.

Examples

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

scColPairCounts *Extract counts from two columns of a single-cell expression object*

Description

This function extracts count information from two columns of a single-cell expression object.

Usage

```
scColPairCounts(scObj, col1, col2)
```

Arguments

scObj	A Seurat or SingleCellExperiment object.
col1	Column as string.
col2	Column as string.

Value

A data frame listing the counts of all combinations of pairs from two categorical columns.

Examples

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

scColPairPercs *Extract percentages from two columns of a single-cell expression object*

Description

This function extracts percentage information from two columns of a single-cell expression object. For each i x j combination with i taken from column 1 and j taken from column 2, the function reports the percentage that j contributes to all combinations involving i.

Usage

```
scColPairPercs(scObj, col1, col2, sigDigits = 2)
```

Arguments

scObj	A Seurat or SingleCellExperiment object.
col1	Column as string.
col2	Column as string.
sigDigits	Number of significant digits.

Value

A data frame listing the percentages of all combinations of pairs from two categorical columns.

Examples

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

---

scColPairRatios *Extract observed-over-expected ratios from two columns of a single-cell expression object*

Description

This function extracts observed-over-expected ratios from two columns of a single-cell expression object.

Usage

```
scColPairRatios(scObj, col1, col2, sigDigits = 2)
```

Arguments

scObj	A Seurat or SingleCellExperiment object.
col1	Column as string.
col2	Column as string.
sigDigits	Number of significant digits.

Value

A data frame listing the observed-over-expected ratios of all combinations of pairs from two categorical columns.

Examples

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

scDimredMat.default *Extracts a dimensionality reduction matrix from object.*

Description

This function extracts a dimensionality reduction matrix from a `Seurat` or `SingleCellExperiment` object.

Usage

```
## Default S3 method:
scDimredMat(scObj, dimred)

## S3 method for class 'Seurat'
scDimredMat(scObj, dimred)

## S3 method for class 'SingleCellExperiment'
scDimredMat(scObj, dimred)

scDimredMat(scObj, dimred)
```

Arguments

`scObj`	A `Seurat` or `SingleCellExperiment` object.
`dimred`	Dimensionality reduction.

Value

A dimensionality reduction matrix.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='scLang')
sceObj <- qs2::qs_read(scePath)
pcaMat <- scDimredMat(sceObj, 'pca')
```

scExpMat.default *Extracts the expression matrix from object.*

Description

This function extracts an expression matrix from a `Seurat` or `SingleCellExperiment` object. For additional flexibility, the input can alternatively be provided as a `dgCMatrix` object (and an option to densify it is also available) or as a `matrix` object.

Usage

```
## Default S3 method:
scExpMat(scObj, slot = NULL, genes = NULL, densify = TRUE)

## S3 method for class 'Seurat'
scExpMat(scObj, slot = "data", genes = NULL, densify = TRUE)

## S3 method for class 'SingleCellExperiment'
scExpMat(scObj, slot = "logcounts", genes = NULL, densify = TRUE)

## S3 method for class 'dgCMatrix'
scExpMat(scObj, slot = NULL, genes = NULL, densify = TRUE)

## S3 method for class 'matrix'
scExpMat(scObj, slot = NULL, genes = NULL, densify = TRUE)

scExpMat(scObj, slot, genes = NULL, densify = TRUE)
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
slot	Gene expression slot. Ignored if scObj is of class dgCMatrix or matrix.
genes	Selected genes. If NULL, all genes will be retained.
densify	Whether to convert to dense matrix.

Value

An expression matrix.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='scLang')
sceObj <- qs2::qs_read(scePath)
mat <- scExpMat(sceObj, 'counts')
```

---

scGeneExp.default *Extracts the expression of a single gene*

Description

This function extracts the expression of a single gene from a Seurat, SingleCellExperiment, dgCMatrix or matrix object.

Usage

```
## Default S3 method:
scGeneExp(scObj, gene, slot = NULL)

## S3 method for class 'Seurat'
scGeneExp(scObj, gene, slot = "data")

## S3 method for class 'SingleCellExperiment'
scGeneExp(scObj, gene, slot = "logcounts")

## S3 method for class 'dgCMatrix'
scGeneExp(scObj, gene, slot = NULL)

## S3 method for class 'matrix'
scGeneExp(scObj, gene, slot = NULL)

scGeneExp(scObj, gene, slot)
```

Arguments

scObj	A Seurat, SingleCellExperiment, dgCMatrix or matrix object.
gene	Selected gene.
slot	Gene expression slot. Ignored if scObj is of class dgCMatrix or matrix.

Value

A gene expression vector.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='scLang')
sceObj <- qs2::qs_read(scePath)
v <- scGeneExp(sceObj, 'Gene291')
```

---

scPCAMat *Extracts the PCA matrix from object.*

Description

This function extracts the PCA matrix from a Seurat or SingleCellExperiment object.

Usage

```
scPCAMat(scObj)
```

Arguments

scObj	A Seurat or SingleCellExperiment object.

Value

A PCA matrix.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='scLang')
sceObj <- qs2::qs_read(scePath)
pcaMat <- scPCAMat(sceObj)
```

---

scUMAPMat *Extracts the UMAP matrix from object.*

Description

This function extracts the UMAP matrix from a Seurat or SingleCellExperiment object.

Usage

```
scUMAPMat(scObj)
```

Arguments

scObj	A Seurat or SingleCellExperiment object.

Value

A UMAP matrix.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='scLang')
sceObj <- qs2::qs_read(scePath)
umapMat <- scUMAPMat(sceObj)
```

violinPlot *Create a violin plot to represent a feature*

Description

This function creates a violin plot to represent a feature (gene expression or numeric metadata column).

Usage

```
violinPlot(
  scObj,
  feature = rownames(scObj)[1],
  groupBy = metadataNames(scObj)[1],
  title = feature,
  legendTitle = NULL,
  xLab = "Identity",
  yLab = "Expression level",
  palette = "grDevices::rainbow",
  pointSize = 0.5,
  alpha = 0.8,
  legendPos = c("right", "top", "left", "bottom"),
  legendTextSize = 10,
  legendTitleSize = 10,
  axisTextSize = 12,
  axisTitleSize = 12,
  xLabAngle = 45,
  xLabVjust = 0.5,
  ...
)
```

Arguments

scObj	A Seurat or SingleCellExperiment object.
feature	A gene name or metadata column name.
groupBy	Grouping variable. Must exist in the metadata/coldata of the single-cell expression object.
title	Plot title.
legendTitle	Legend title.
xLab	x axis label.
yLab	y axis label.
palette	Color palette.
pointSize	Point size.
alpha	Opaqueness level.

legendPos	Legend position.
legendTextSize	Legend text size.
legendTitleSize	Legend title size.
axisTextSize	Axis text size.
axisTitleSize	Axis title size.
xLabAngle	x axis label angle.
xLabVjust	x axis label vertical justification in [0, 1].
...	Additional arguments passed to henna::centerTitle.

Value

A violin plot.

Examples

```
scePath <- system.file('extdata', 'sceObj.qs2', package='scLang')
sceObj <- qs2::qs_read(scePath)
violinPlot(sceObj, 'Gene289')
```

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