# Package: scLang (via r-universe)

November 25, 2026

**Type** Package

**Title** A unified language for interacting with Seurat and SingleCellExperiment

**Version** 1.2.0

**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.

**License** MIT + file LICENSE

**Imports** dplyr, ggplot2, henna, methods, paletteer, rlang, S4Vectors, SeuratObject, SingleCellExperiment, stats, SummarizedExperiment

**Suggests** BiocStyle, knitr, qs2, rmarkdown, scater, scRNAseq, Seurat, testthat (>= 3.0.0)

**biocViews** Software, SingleCell, GeneExpression, Visualization

**Encoding** UTF-8

**URL** https://github.com/andrei-stoica26/scLang

**BugReports** https://github.com/andrei-stoica26/scLang/issues

**RoxygenNote** 7.3.3

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**Config/pak/sysreqs** libfontconfig1-dev libfreetype6-dev libglpk-dev libicu-dev libxml2-dev zlib1g-dev

**Repository** Bioconductor 3.24

**Date/Publication** 2026-11-23 22:55:40 UTC

**RemoteUrl** https://github.com/bioc/scLang

**RemoteRef** RELEASE_3_24

**RemoteSha** 5a33b367d40d1d323f03905945167f478b29f6c0

# Contents

dimPlot . . . 2
dimredNames.default . . . 3
featurePlot . . . 4
metadataDF . . . 6
metadataNames . . . 6
scCol . . . 7
scColCounts . . . 8
scColPairCounts . . . 9
scColPairPercs . . . 9
scColPairRatios . . . 10
scDimredMat.default . . . 11
scExpMat.default . . . 11
scGeneExp.default . . . 12
scPCAMat . . . 13
scUMAPMat . . . 14
violinPlot . . . 15

**Index** **17**

---

`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')
```

# Index

dimPlot, 2
dimredNames *(*dimredNames.default*)*, 3
dimredNames.default, 3

featurePlot, 4

metadataDF, 6
metadataNames, 6

scCol, 7
scCol<- *(*scCol*)*, 7
scColCounts, 8
scColPairCounts, 9
scColPairPercs, 9
scColPairRatios, 10
scDimredMat *(*scDimredMat.default*)*, 11
scDimredMat.default, 11
scExpMat *(*scExpMat.default*)*, 11
scExpMat.default, 11
scGeneExp *(*scGeneExp.default*)*, 12
scGeneExp.default, 12
scPCAMat, 13
scUMAPMat, 14

violinPlot, 15