

# Package ‘hammers’

May 8, 2026

**Type** Package

**Title** Utilities for scRNA-seq data analysis

**Version** 1.0.0

**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.

**License** MIT + file LICENSE

**Imports** cluster, dplyr, ggplot2, ggrepel, grDevices, henna, LISTO, liver, rlang, scLang, stats, text2vec,

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

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

**Encoding** UTF-8

**RoxygenNote** 7.3.3

**VignetteBuilder** knitr

**URL** <https://github.com/andrei-stoica26/hammers>

**BugReports** <https://github.com/andrei-stoica26/hammers/issues>

**Config/testthat/edition** 3

**git\_url** <https://git.bioconductor.org/packages/hammers>

**git\_branch** RELEASE\_3\_23

**git\_last\_commit** 26e166a

**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.23

**Date/Publication** 2026-05-07

**Author** Andrei-Florian Stoica [aut, cre] (ORCID:  
<https://orcid.org/0000-0002-5253-0826>)

**Maintainer** Andrei-Florian Stoica <andreistoica@foxmail.com>

## Contents

hammers-package . . . . .	2
addCategory . . . . .	3
addMetadataCategory . . . . .	4
addNormSilhouette . . . . .	5
centerOfMass . . . . .	5
checkGenes . . . . .	6
colCenters . . . . .	7
colsDimPlot . . . . .	7
computeSilhouette . . . . .	8
devPlot.default . . . . .	9
distributionPlot . . . . .	10
findRareGenes . . . . .	11
geneCellSets . . . . .	12
geneCenters . . . . .	12
genePresence . . . . .	13
genesDimPlot . . . . .	14
joinCharCombs . . . . .	14
keyvalMap . . . . .	15
normalizeSilhouette . . . . .	15
pointsDimPlot . . . . .	16
prepAlluvial . . . . .	17
pvalRiverPlot . . . . .	18
removeRareGenes . . . . .	19
repAnalysis . . . . .	20
safeMessage . . . . .	21
safeMinmax . . . . .	21

<b>Index</b>	<b>23</b>
--------------	-----------

---

hammers-package	<i>hammers: Utilities for scRNA-seq data analysis</i>
-----------------	---

---

## Description

hammers is a utilities suite for scRNA-seq data analysis compatible with both Seurat and SingleCell-Experiment. 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.

**Author(s)**

**Maintainer:** Andrei-Florian Stoica <andreistoica@foxmail.com> ([ORCID](#))

**See Also**

Useful links:

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

---

addCategory	<i>Add a categorical column to a data frame based on another column</i>
-------------	---

---

**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, dgCMatrx 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	<i>Adds normalized silhouette column to a single-cell expression object</i>
-------------------	---

---

**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, dgCMatix 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	<i>Calculate the center of mass of columns</i>
--------------	--

---

**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, dgMatrix 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	<i>Calculate the centers of mass of metadata/coldata columns</i>
------------	--

---

**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, dgCMatrx 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	<i>Create a single-cell dimensionality reduction plot with added labeled points for numeric columns</i>
-------------	---

---

**Description**

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

**Usage**

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

**Arguments**

scObj	A Seurat, SingleCellExperiment, dgCMatrx 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	<i>Compute cluster silhouette for single-cell expression object</i>
-------------------	---

---

**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, dgCMatix 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	<i>Saves plot or list of plots</i>
-----------------	------------------------------------

---

## 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, dgCMatix 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	<i>Find rare genes in a Seurat or SingleCellExpression object</i>
---------------	---

---

**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, dgMatrix 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	<i>Generates cell sets for each input gene</i>
--------------	--

---

**Description**

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

**Usage**

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

**Arguments**

scObj	A Seurat, SingleCellExperiment, dgCMatix 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	<i>Calculate the centers of mass of the expression of input genes</i>
-------------	---

---

**Description**

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

**Usage**

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

**Arguments**

scObj	A Seurat, SingleCellExperiment, dgCMatix 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	<i>Extract gene presence from a Seurat or SingleCellExperiment object</i>
--------------	---

---

**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, dgMatrix 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	<i>Create a single-cell dimensionality reduction plot with added labeled points for genes</i>
--------------	---

---

**Description**

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

**Usage**

```
genesDimPlot(sceObj, genes, ...)
```

**Arguments**

scObj	A Seurat, SingleCellExperiment, dgCMatix 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	<i>Join all combinations of elements from character vectors</i>
---------------	---

---

**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	<i>Create a map from keys to values</i>
-----------	---

---

**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	<i>Normalize silhouette by identity class for single-cell expression object</i>
---------------------	---

---

**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, dgCMatrx 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	<i>Create a single-cell dimensionality reduction plot with added labeled points</i>
---------------	---

---

**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, dgCMatrx 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 <code>Seurat::DimPlot</code> .

### 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 representing 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 representing 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 <code>henna::riverPlot</code>

**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	<i>Remove rare genes from a Seurat or SingleCellExpression object</i>
-----------------	---

---

**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, dgCMatix 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	<i>Find the differential representation of two Seurat or SingleCellExperiment columns</i>
-------------	---

---

## 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, dgCMatix 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	<i>Message an input if verbose is set to TRUE</i>
-------------	---

---

**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	<i>Perform min-max normalization when possible; otherwise return a single-value vector.</i>
------------	---

---

**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))
```

# Index

## \* **internal**

hammers-package, [2](#)

[addCategory, 3](#)

[addMetadataCategory, 4](#)

[addNormSilhouette, 5](#)

[centerOfMass, 5](#)

[checkGenes, 6](#)

[colCenters, 7](#)

[colsDimPlot, 7](#)

[computeSilhouette, 8](#)

[devPlot \(devPlot.default\), 9](#)

[devPlot.default, 9](#)

[distributionPlot, 10](#)

[findRareGenes, 11](#)

[geneCellSets, 12](#)

[geneCenters, 12](#)

[genePresence, 13](#)

[genesDimPlot, 14](#)

[hammers \(hammers-package\), 2](#)

[hammers-package, 2](#)

[joinCharCombs, 14](#)

[keyvalMap, 15](#)

[normalizeSilhouette, 15](#)

[pointsDimPlot, 16](#)

[prepAlluvial, 17](#)

[pvalRiverPlot, 18](#)

[removeRareGenes, 19](#)

[repAnalysis, 20](#)

[safeMessage, 21](#)

[safeMinmax, 21](#)