

# Package ‘scDotPlot’

September 15, 2025

**Title** Cluster a Single-cell RNA-seq Dot Plot

**Version** 1.2.1

**Description** Dot plots of single-cell RNA-seq data allow for an examination of the relationships between cell groupings (e.g. clusters) and marker gene expression. The scDotPlot package offers a unified approach to perform a hierarchical clustering analysis and add annotations to the columns and/or rows of a scRNA-seq dot plot. It works with SingleCellExperiment and Seurat objects as well as data frames.

**License** Artistic-2.0

**URL** <https://github.com/ben-laufer/scDotPlot>

**BugReports** <https://github.com/ben-laufer/scDotPlot/issues>

**biocViews** Software, Visualization, DifferentialExpression,  
GeneExpression, Transcription, RNASeq, SingleCell, Sequencing,  
Clustering

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**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**Depends** R (>= 4.4.0)

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grDevices, magrittr, purrr, rlang, scales, scater, Seurat,  
SingleCellExperiment, stats, stringr, tibble, tidyr

**Suggests** AnnotationDbi, BiocStyle, knitr, rmarkdown, scran, scRNAseq,  
scuttle, SeuratObject, testthat, vdiff

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Contents

|                             |           |
|-----------------------------|-----------|
| scDotPlot-package . . . . . | 2         |
| .annotateDotPlot . . . . .  | 3         |
| .baseDotPlot . . . . .      | 4         |
| .createAnno . . . . .       | 5         |
| scDotPlot . . . . .         | 6         |
| <b>Index</b>                | <b>10</b> |

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|                   |                                                          |
|-------------------|----------------------------------------------------------|
| scDotPlot-package | <i>scDotPlot: Cluster a Single-cell RNA-seq Dot Plot</i> |
|-------------------|----------------------------------------------------------|

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Description

Dot plots of single-cell RNA-seq data allow for an examination of the relationships between cell groupings (e.g. clusters) and marker gene expression. The scDotPlot package offers a unified approach to perform a hierarchical clustering analysis and add annotations to the columns and/or rows of a scRNA-seq dot plot. It works with SingleCellExperiment and Seurat objects as well as data frames.

Author(s)

**Maintainer:** Benjamin I Laufer <blaufer@gmail.com>  
Authors:  
• Brad A Friedman

See Also

- Useful links:
- <https://github.com/ben-laufer/scDotPlot>
  - Report bugs at <https://github.com/ben-laufer/scDotPlot/issues>

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*.annotateDotPlot*      *Cluster Dot Plot*

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**Description**

Cluster Dot Plot

**Usage**

```
.annotateDotPlot(  
  dotPlot,  
  clusterRows = TRUE,  
  clusterColumns = TRUE,  
  groupAnno = FALSE,  
  featureAnno = FALSE,  
  treeWidth = 0.1,  
  treeHeight = 0.1,  
  annoWidth = 0.05,  
  annoHeight = 0.02,  
  annoColors = NULL,  
  groupLegends = TRUE,  
  featureLegends = TRUE,  
  fontSize = 11,  
  fontFamily = "",  
  flipPlot = FALSE  
)
```

**Arguments**

|                             |                                                                                                                                  |
|-----------------------------|----------------------------------------------------------------------------------------------------------------------------------|
| <code>clusterRows</code>    | Logical specifying whether to perform hierarchical clustering analysis on the rows                                               |
| <code>clusterColumns</code> | Logical specifying whether to perform hierarchical clustering analysis on the columns                                            |
| <code>groupAnno</code>      | Cell annotations that are stored as names of columns in <code>colData</code> of <code>sce</code> with annotations                |
| <code>featureAnno</code>    | Feature annotations that are stored as names of rows in <code>rowData</code> of <code>sce</code> with annotations                |
| <code>treeWidth</code>      | Numeric specifying width of the row tree relative to the <code>dotPlot</code>                                                    |
| <code>treeHeight</code>     | Numeric specifying height of the column tree relative to the <code>dotPlot</code>                                                |
| <code>annoWidth</code>      | Numeric specifying the width of the row annotation relative to the <code>dotPlot</code>                                          |
| <code>annoHeight</code>     | Numeric specifying height of the column annotation relative to the <code>dotPlot</code>                                          |
| <code>annoColors</code>     | A list with a name for each annotation that contains a named vector of colors, where the name is the pairing of values to colors |
| <code>groupLegends</code>   | Logical indicating whether to show legends for group annotations                                                                 |

|                |                                                                    |
|----------------|--------------------------------------------------------------------|
| featureLegends | Logical indicating whether to show legends for feature annotations |
| fontSize       | Numeric specifying the base font size in pts                       |
| fontFamily     | Character specifying the base font family                          |
| flipPlot       | Logical indicating whether to flip the x and y coordinates         |

Value

A aplot

---

|              |                      |
|--------------|----------------------|
| .baseDotPlot | <i>Dot Plot Base</i> |
|--------------|----------------------|

---

Description

Dot Plot Base

Usage

```
.baseDotPlot(  
  plotData,  
  group = NULL,  
  scale = NULL,  
  AverageThreshold = NULL,  
  NumDetectedThreshold = NULL,  
  dotColors = NULL,  
  fontSize = 11,  
  fontFamily = "",  
  flipPlot = FALSE  
)
```

Arguments

|                      |                                                                                                                                                                                                       |
|----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| group                | Column name from colData/metadata of the object to group cells by                                                                                                                                     |
| scale                | Logical indicating whether the data should be scaled and centered                                                                                                                                     |
| AverageThreshold     | Numeric specifying threshold for average expression, where values below AverageThreshold and NumDetectedThreshold are transparent                                                                     |
| NumDetectedThreshold | Numeric specifying threshold for fraction of cells, where values below AverageThreshold and NumDetectedThreshold are transparent                                                                      |
| dotColors            | A character vector specifying the colors to be used in the gradient for the dots. If scale is set to TRUE, the first 3 colors will be used for the negative, zero, and positive values, respectively. |
| fontSize             | Numeric specifying the base font size in pts                                                                                                                                                          |
| fontFamily           | Character specifying the base font family                                                                                                                                                             |
| flipPlot             | Logical indicating whether to flip the x and y coordinates                                                                                                                                            |

**Value**

A `ggplot2`

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`.createAnno`*Create column annotations*

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**Description**

Create column annotations

**Usage**

```
.createAnno(  
  annoLabel,  
  annoType = c("column", "row"),  
  dotPlot = dotPlot,  
  annoColors = NULL,  
  groupLegends = TRUE,  
  featureLegends = TRUE,  
  fontSize = 11,  
  fontFamily = "",  
  flipPlot = FALSE  
)
```

**Arguments**

|                             |                                                                                                                                  |
|-----------------------------|----------------------------------------------------------------------------------------------------------------------------------|
| <code>annoColors</code>     | A list with a name for each annotation that contains a named vector of colors, where the name is the pairing of values to colors |
| <code>groupLegends</code>   | Logical indicating whether to show legends for group annotations                                                                 |
| <code>featureLegends</code> | Logical indicating whether to show legends for feature annotations                                                               |
| <code>fontSize</code>       | Numeric specifying the base font size in pts                                                                                     |
| <code>fontFamily</code>     | Character specifying the base font family                                                                                        |
| <code>flipPlot</code>       | Logical indicating whether to flip the x and y coordinates                                                                       |

**Value**

A `ggplot2`

---

`scDotPlot`*scDotPlot*

---

## Description

Create dot plot of gene expression profiles that can be annotated with hierarchical clustering from [ggtree](#) using [aplot](#)

## Usage

```
## S3 method for class 'SingleCellExperiment'
scDotPlot(
  object,
  features = features,
  group = NULL,
  block = NULL,
  swap_rownames = NULL,
  scale = FALSE,
  cluster = TRUE,
  clusterRows = cluster,
  clusterColumns = cluster,
  AverageThreshold = ifelse(scale == FALSE, 0, -Inf),
  NumDetectedThreshold = 0.01,
  groupAnno = FALSE,
  featureAnno = FALSE,
  treeWidth = 0.1,
  treeHeight = 0.1,
  annoWidth = 0.05,
  annoHeight = 0.02,
  annoColors = NULL,
  dotColors = NULL,
  groupLegends = TRUE,
  featureLegends = TRUE,
  fontSize = 11,
  fontFamily = "",
  flipPlot = FALSE,
  ...
)

## S3 method for class 'Seurat'
scDotPlot(
  object,
  features = features,
  group = NULL,
  block = NULL,
  swap_rownames = NULL,
  scale = FALSE,
```

```

    cluster = TRUE,
    clusterRows = cluster,
    clusterColumns = cluster,
    AverageThreshold = ifelse(scale == FALSE, 0, -Inf),
    NumDetectedThreshold = 0.01,
    groupAnno = FALSE,
    featureAnno = FALSE,
    treeWidth = 0.1,
    treeHeight = 0.1,
    annoWidth = 0.05,
    annoHeight = 0.02,
    annoColors = NULL,
    dotColors = NULL,
    groupLegends = TRUE,
    featureLegends = TRUE,
    fontSize = 11,
    fontFamily = "",
    flipPlot = FALSE,
    ...
)

```

## Default S3 method:

```

scDotPlot(
  object,
  features = NULL,
  group = NULL,
  block = NULL,
  swap_rownames = NULL,
  scale = FALSE,
  cluster = TRUE,
  clusterRows = cluster,
  clusterColumns = cluster,
  AverageThreshold = ifelse(scale == FALSE, 0, -Inf),
  NumDetectedThreshold = 0.01,
  groupAnno = FALSE,
  featureAnno = FALSE,
  treeWidth = 0.1,
  treeHeight = 0.1,
  annoWidth = 0.05,
  annoHeight = 0.02,
  annoColors = NULL,
  dotColors = NULL,
  groupLegends = TRUE,
  featureLegends = TRUE,
  fontSize = 11,
  fontFamily = "",
  flipPlot = FALSE,
  ...
)

```

)

scDotPlot(object, ...)

**Arguments**

|                      |                                                                                                                                                                                                                                                            |
|----------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| object               | An object with normalized data <ul style="list-style-type: none"> <li>• <a href="#">SingleCellExperiment</a></li> <li>• <a href="#">Seurat</a></li> <li>• A data.frame with the following columns: "NumDetected", "Feature", "Group", "Average"</li> </ul> |
| features             | Character vector with genes of interest                                                                                                                                                                                                                    |
| group                | Column name from colData/metadata of the object to group cells by                                                                                                                                                                                          |
| block                | Column name from colData of a SingleCellExperiment object to use as a blocking factor (e.g. batch or sample)                                                                                                                                               |
| swap_rownames        | Column name from rowData of a SingleCellExperiment object to match to features                                                                                                                                                                             |
| scale                | Logical indicating whether the data should be scaled and centered                                                                                                                                                                                          |
| cluster              | Logical specifying whether to perform hierarchical clustering analysis on both the rows and columns                                                                                                                                                        |
| clusterRows          | Logical specifying whether to perform hierarchical clustering analysis on the rows                                                                                                                                                                         |
| clusterColumns       | Logical specifying whether to perform hierarchical clustering analysis on the columns                                                                                                                                                                      |
| AverageThreshold     | Numeric specifying threshold for average expression, where values below AverageThreshold and NumDetectedThreshold are transparent                                                                                                                          |
| NumDetectedThreshold | Numeric specifying threshold for fraction of cells, where values below AverageThreshold and NumDetectedThreshold are transparent                                                                                                                           |
| groupAnno            | Cell annotations that are stored as names of columns in colData of sce with annotations                                                                                                                                                                    |
| featureAnno          | Feature annotations that are stored as names of rows in rowData of sce with annotations                                                                                                                                                                    |
| treeWidth            | Numeric specifying width of the row tree relative to the dotPlot                                                                                                                                                                                           |
| treeHeight           | Numeric specifying height of the column tree relative to the dotPlot                                                                                                                                                                                       |
| annoWidth            | Numeric specifying the width of the row annotation relative to the dotPlot                                                                                                                                                                                 |
| annoHeight           | Numeric specifying height of the column annotation relative to the dotPlot                                                                                                                                                                                 |
| annoColors           | A list with a name for each annotation that contains a named vector of colors, where the name is the pairing of values to colors                                                                                                                           |
| dotColors            | A character vector specifying the colors to be used in the gradient for the dots. If scale is set to TRUE, the first 3 colors will be used for the negative, zero, and positive values, respectively.                                                      |



|                |                                                                    |
|----------------|--------------------------------------------------------------------|
| groupLegends   | Logical indicating whether to show legends for group annotations   |
| featureLegends | Logical indicating whether to show legends for feature annotations |
| fontSize       | Numeric specifying the base font size in pts                       |
| fontFamily     | Character specifying the base font family                          |
| flipPlot       | Logical indicating whether to flip the x and y coordinates         |
| ...            | Additional unused arguments                                        |

### Details

The data for the dot plot is generated from different sources depending on the object:

- SingleCellExperiment: [plotDots](#)
- Seurat: [DotPlot](#)

### Value

- When cluster = TRUE, a aplot object
- When cluster = FALSE, a ggplot2 object

### References

<https://yulab-smu.top/pkgdocs/aplot.html#a-single-cell-example>

### Examples

```
data("pbmc_small", package = "SeuratObject")
pbmc_small |>
  scDotPlot(features = Seurat::VariableFeatures(pbmc_small),
            group = "RNA_snn_res.1")
```

# Index

## \* **internal**

- .annotateDotPlot, [3](#)
- .baseDotPlot, [4](#)
- .createAnno, [5](#)
- scDotPlot-package, [2](#)

- .annotateDotPlot, [3](#)

- .baseDotPlot, [4](#)

- .createAnno, [5](#)

aplot, [6](#)

DotPlot, [9](#)

ggtree, [6](#)

plotDots, [9](#)

scDotPlot, [6](#)

scDotPlot-package, [2](#)

Seurat, [8](#)

SingleCellExperiment, [8](#)