

# Package ‘scDotPlot’

September 3, 2025

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

**Version** 1.3.1

**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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**RoxygenNote** 7.3.2

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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 | <i>Cluster Dot Plot</i> |
|------------------|-------------------------|

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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**

|                |                                                                                                                                  |
|----------------|----------------------------------------------------------------------------------------------------------------------------------|
| clusterRows    | Logical specifying whether to perform hierarchical clustering analysis on the rows                                               |
| clusterColumns | Logical specifying whether to perform hierarchical clustering analysis on the columns                                            |
| 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 |
| 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                                                                       |

**Value**

A aplot

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`.baseDotPlot`*Dot Plot Base*

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**Description**

Dot Plot Base

**Usage**

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

**Arguments**

|                                   |                                                                                                                                                                                                                                  |
|-----------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>group</code>                | Column name from <code>colData</code> /metadata of the object to group cells by                                                                                                                                                  |
| <code>scale</code>                | Logical indicating whether the data should be scaled and centered                                                                                                                                                                |
| <code>AverageThreshold</code>     | Numeric specifying threshold for average expression, where values below <code>AverageThreshold</code> and <code>NumDetectedThreshold</code> are transparent                                                                      |
| <code>NumDetectedThreshold</code> | Numeric specifying threshold for fraction of cells, where values below <code>AverageThreshold</code> and <code>NumDetectedThreshold</code> are transparent                                                                       |
| <code>dotColors</code>            | A character vector specifying the colors to be used in the gradient for the dots. If <code>scale</code> is set to <code>TRUE</code> , the first 3 colors will be used for the negative, zero, and positive values, respectively. |
| <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`

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|                          |                                  |
|--------------------------|----------------------------------|
| <code>.createAnno</code> | <i>Create column annotations</i> |
|--------------------------|----------------------------------|

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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`

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|                        |                  |
|------------------------|------------------|
| <code>scDotPlot</code> | <i>scDotPlot</i> |
|------------------------|------------------|

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### 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")
```

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