

Package ‘scDotPlot’

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Title Cluster a Single-cell RNA-seq Dot Plot

Version 1.1.0

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.

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

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

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Author Benjamin I Laufer [aut, cre],

Brad A Friedman [aut]

Maintainer Benjamin I Laufer <blaufer@gmail.com>

Contents

| | |
|-----------------------------|---|
| scDotPlot-package | 2 |
| .annotateDotPlot | 3 |
| .baseDotPlot | 4 |
| .createAnno | 5 |
| scDotPlot | 6 |

Index **10**

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

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>

.annotateDotPlot *Cluster Dot Plot*

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

| | |
|---------------------|----------------------|
| <i>.baseDotPlot</i> | <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`

`.createAnno`*Create column annotations*

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"> • SingleCellExperiment • Seurat • A data.frame with the following columns: "NumDetected", "Feature", "Group", "Average" |
| 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