Package ‘scDotPlot’

July 10, 2025

Title Cluster a Single-cell RNA-seq Dot Plot

Version 1.2.0

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`>

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`scDotPlot-package` *scDotPlot: Cluster a Single-cell RNA-seq Dot Plot*

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

`.baseDotPlot` *Dot Plot Base*

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

`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 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 • 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")
```

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