Package 'scDotPlot'

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Title Cluster a Single-cell RNA-seq Dot Plot

Version 1.6.0

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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`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)

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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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