Package: scDotPlot (via r-universe)

July 4, 2024

Title Cluster a Single-cell RNA-seq Dot Plot

Version 0.99.3

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

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

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Depends R (>= 4.3.0)

Imports aplot, BiocGenerics, cli, dplyr, ggplot2, ggsci, ggtree,
grDevices, magrittr, purrr, rlang, scales, scater, Seurat,
SingleCellExperiment, stats, stringr, tibble, tidyr

Suggests AnnotationDbi, BiocStyle, knitr, rmarkdown, scran, scRNAseq,
scuttle, SeuratObject, testthat, vdiffr

VignetteBuilder knitr

Config/testthat/edition 3

LazyData false

Repository https://bioc.r-universe.dev

RemoteUrl https://github.com/bioc/scDotPlot

RemoteRef HEAD

RemoteSha b8606e8e265b3fed7a0f62831880a559c5c6184b

Contents

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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,
  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,
    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,
    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
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