Package 'schex'

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Type Package

Title Hexbin plots for single cell omics data

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Description Builds hexbin plots for variables and dimension reduction stored
in single cell omics data such as SingleCellExperiment and SeuratObject. The
ideas used in this package are based on the excellent work of Dan Carr,
Nicholas Lewin-Koh, Martin Maechler and Thomas Lumley.

Depends SingleCellExperiment (>= 1.7.4), Seurat, ggplot2

Imports hexbin, stats, methods, cluster, dplyr, entropy

Suggests ggrepel, knitr, rmarkdown, testthat (>= 2.1.0), covr,
TENxPBMCData, scater, shinydashboard, iSEE, igraph, scran

URL https://github.com/SaskiaFreytag/schex

BugReports https://github.com/SaskiaFreytag/schex/issues

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biocViews Software, Sequencing, SingleCell, DimensionReduction,
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VignetteBuilder knitr

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R topics documented:

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make_hexbin   *Bivariate binning of single cell data into hexagon cells.*

Description

make_hexbin returns a `SingleCellExperiment` or `Seurat-class` object of binned hexagon cells.

Usage

```
make_hexbin(sce, nbins = 80, dimension_reduction = "UMAP", use_dims = c(1, 2))

## S4 method for signature 'SingleCellExperiment'
make_hexbin(sce, nbins = 80, dimension_reduction = "UMAP", use_dims = c(1, 2))

## S4 method for signature 'Seurat'
make_hexbin(sce, nbins = 80, dimension_reduction = "UMAP", use_dims = c(1, 2))
```

Arguments

sce	A `SingleCellExperiment` or `Seurat-class` object.
nbins	The number of bins partitioning the range of the first component of the chosen dimension reduction.
dimension_reduction	
	A string indicating the reduced dimension result to calculate hexagon cell representation of.
use_dims	A vector of two integers specifying the dimensions used.

Details

This function bins observations with computed reduced dimension results into hexagon cells. For a `Seurat-class` object the results from this function are stored in @misc. For a `SingleCellExperiment` as a list in the @metadata. The list contains two items. The first item stores a vector specifying the hexagon ID for each observation. The second item stores a matrix with the x and y positions of the hexagon cells and the number of observations in each of them.

Value

A `SingleCellExperiment` or `Seurat-class` object.

Methods (by class)

- `SingleCellExperiment`: Bivariate binning of SingleCellExperiment into hexagon cells.

- `Seurat`: Bivariate binning of Seurat into hexagon cells.

Examples

```
# For Seurat object
library(Seurat)
data("pbmc_small")
pbmc_small <- make_hexbin(pbmc_small, 10, dimension_reduction = "PCA")
# For SingleCellExperiment object
## Not run:
library(TENxPBMCData)
library(scater)
tenx_pbmc3k <- TENxPBMCData(dataset = "pbmc3k")
rm_ind <- calculateAverage(tenx_pbmc3k)<0.1
tenx_pbmc3k <- tenx_pbmc3k[!rm_ind,]
tenx_pbmc3k <- normalize(tenx_pbmc3k)
tenx_pbmc3k <- runPCA(tenx_pbmc3k)
tenx_pbmc3k <- make_hexbin( tenx_pbmc3k, 80, dimension_reduction = "PCA")

## End(Not run)
```

---

make_hexbin_label *Group label plot position.*

Description

Group label plot position.

Usage

```
make_hexbin_label(sce, col)

## S4 method for signature 'Seurat'
make_hexbin_label(sce, col)

## S4 method for signature 'SingleCellExperiment'
make_hexbin_label(sce, col)
```

Arguments

sce	A [SingleCellExperiment](#) or [Seurat-class](#) object.
col	The name referring to one column in meta data for which the label position on the plot is calculated for every level. The chosen column needs to be a factor.

Value

A dataframe.

Methods (by class)

- Seurat: Group label position for Seurat object.

- SingleCellExperiment: Group label position for SingleCellExperiment object.

Examples

```
#' # For Seurat object
library(Seurat)
data("pbmc_small")
pbmc_small <- make_hexbin(pbmc_small, 10, dimension_reduction = "PCA")
make_hexbin_label(pbmc_small, col="RNA_snn_res.1")
```

---

plot_hexbin_density	*Plot of density of observations from single cell data in bivariate hexagon cells.*

Description

Plot of density of observations from single cell data in bivariate hexagon cells.

Usage

```
plot_hexbin_density(sce, title = NULL, xlab = NULL, ylab = NULL)

## S4 method for signature 'SingleCellExperiment'
plot_hexbin_density(sce, title = NULL, xlab = NULL, ylab = NULL)

## S4 method for signature 'Seurat'
plot_hexbin_density(sce, title = NULL, xlab = NULL, ylab = NULL)
```

Arguments

sce	A SingleCellExperiment or Seurat-class object.
title	A string containing the title of the plot.
xlab	A string containing the title of the x axis.
ylab	A string containing the title of the y axis.

Value

A ggplot2{ggplot} object.

Methods (by class)

- SingleCellExperiment: Plot of cell density in hexagon cell for SingleCellExperiment object.
- Seurat: Plot of cell density in hexagon cell for Seurat object.

Examples

```
#' # For Seurat object
library(Seurat)
data("pbmc_small")
pbmc_small <- make_hexbin(pbmc_small, 10, dimension_reduction = "PCA")
plot_hexbin_density(pbmc_small)
## Not run:
library(TENxPBMCData)
```

```
library(scater)
tenx_pbmc3k <- TENxPBMCData(dataset = "pbmc3k")
rm_ind <- calcAverage(tenx_pbmc3k)<0.1
tenx_pbmc3k <- tenx_pbmc3k[!rm_ind,]
tenx_pbmc3k <- calculateQCMetrics(tenx_pbmc3k)
tenx_pbmc3k <- normalize(tenx_pbmc3k)
tenx_pbmc3k <- runPCA(tenx_pbmc3k)
tenx_pbmc3k <- make_hexbin( tenx_pbmc3k, 20, dimension_reduction = "PCA")
plot_hexbin_density(tenx_pbmc3k)

## End(Not run)
```

---

plot_hexbin_feature	*Plot of external feature expression of single cells in bivariate hexagon cells.*

Description

Plot of external feature expression of single cells in bivariate hexagon cells.

Usage

```
plot_hexbin_feature(
  sce,
  mod,
  type,
  feature,
  action,
  title = NULL,
  xlab = NULL,
  ylab = NULL
)

## S4 method for signature 'SingleCellExperiment'
plot_hexbin_feature(
  sce,
  mod,
  type,
  feature,
  action,
  title = NULL,
  xlab = NULL,
  ylab = NULL
)

## S4 method for signature 'Seurat'
plot_hexbin_feature(
  sce,
  mod,
  type,
  feature,
  action,
```

```
    title = NULL,
    xlab = NULL,
    ylab = NULL
)
```

Arguments

sce	A [SingleCellExperiment](#) or [Seurat-class](#) object.
mod	A string referring to the name of the alternative object in a [SingleCellExperiment](#) or the assay in a [Seurat-class](#) object that stores the protein information.
type	A string referring to the type of assay in the [SingleCellExperiment](#) object or the data transformation in the [Seurat-class](#) object.
feature	A string referring to the name of one external feature.
action	A strings pecifying how meta data of observations in binned hexagon cells are to be summarized. Possible actions are prop_0, mode, mean and median (see details).
title	A string containing the title of the plot.
xlab	A string containing the title of the x axis.
ylab	A string containing the title of the y axis.

Details

This function plots the expression of any feature in the hexagon cell representation calculated with [make_hexbin](#). The chosen gene expression is summarized by one of four actions prop_0, mode, mean and median:

prop_0 Returns the proportion of observations in the bin greater than 0. The associated meta data column needs to be numeric.

mode Returns the mode of the observations in the bin. The associated meta data column needs to be numeric.

mean Returns the mean of the observations in the bin. The associated meta data column needs to be numeric.

median Returns the median of the observations in the bin. The associated meta data column needs to be numeric.

Value

A [ggplot2](#){ggplot} object.

Methods (by class)

- SingleCellExperiment: Plot of gene expression into hexagon cell for SingleCellExperiment object.

- Seurat: Plot of gene expression into hexagon cell for Seurat object.

Examples

```
# For Seurat object
library(Seurat)
data("pbmc_small")
pbmc_small <- make_hexbin(pbmc_small, 10, dimension_reduction = "PCA")
protein <- matrix(rnorm(10* ncol(pbmc_small)), ncol=ncol(pbmc_small))
rownames(protein) <- paste0("A", seq(1,10,1))
colnames(protein) <- colnames(pbmc_small)
pbmc_small[["ADT"]] <- CreateAssayObject(counts = protein)
pbmc_small <- make_hexbin(pbmc_small, 10, dimension_reduction = "PCA")
plot_hexbin_feature(pbmc_small, type="counts", mod="ADT",
    feature="A1", action="prop_0")
```

---

plot_hexbin_gene	*Plot of gene expression of single cells in bivariate hexagon cells.*

Description

Plot of gene expression of single cells in bivariate hexagon cells.

Usage

```
plot_hexbin_gene(
  sce,
  type,
  gene,
  action,
  title = NULL,
  xlab = NULL,
  ylab = NULL
)

## S4 method for signature 'SingleCellExperiment'
plot_hexbin_gene(
  sce,
  type,
  gene,
  action,
  title = NULL,
  xlab = NULL,
  ylab = NULL
)

## S4 method for signature 'Seurat'
plot_hexbin_gene(
  sce,
  type,
  gene,
  action,
  title = NULL,
  xlab = NULL,
  ylab = NULL
)
```

Arguments

sce	A [SingleCellExperiment](#) or [Seurat-class](#) object.
type	A string referring to the type of assay in the [SingleCellExperiment](#) object or the data transformation in the [Seurat-class](#) object.
gene	A string referring to the name of one gene.
action	A strings pecifying how gene expression of observations in binned hexagon cells are to be summarized. Possible actions are prop_0, mode, mean and median (see details).
title	A string containing the title of the plot.
xlab	A string containing the title of the x axis.
ylab	A string containing the title of the y axis.

Details

This function plots the expression of any gene in the hexagon cell representation calculated with [make_hexbin](#). The chosen gene expression is summarized by one of four actions prop_0, mode, mean and median:

prop_0 Returns the proportion of observations in the bin greater than 0. The associated meta data column needs to be numeric.

mode Returns the mode of the observations in the bin. The associated meta data column needs to be numeric.

mean Returns the mean of the observations in the bin. The associated meta data column needs to be numeric.

median Returns the median of the observations in the bin. The associated meta data column needs to be numeric.

Value

A [ggplot2](#){ggplot} object.

Methods (by class)

- SingleCellExperiment: Plot of gene expression into hexagon cell for SingleCellExperiment object.
- Seurat: Plot of gene expression into hexagon cell for Seurat object.

Examples

```
# For Seurat object
library(Seurat)
data("pbmc_small")
pbmc_small <- make_hexbin(pbmc_small, 10, dimension_reduction = "PCA")
plot_hexbin_gene(pbmc_small, type="counts", gene="TALDO1", action="prop_0")
# For SingleCellExperiment object
## Not run:
library(TENxPBMCData)
library(scater)
tenx_pbmc3k <- TENxPBMCData(dataset = "pbmc3k")
rm_ind <- calcAverage(tenx_pbmc3k)<0.1
tenx_pbmc3k <- tenx_pbmc3k[!rm_ind,]
```

```
colData(tenx_pbmc3k) <- cbind(colData(tenx_pbmc3k),
    perCellQCMetrics(tenx_pbmc3k))
tenx_pbmc3k <- normalize(tenx_pbmc3k)
tenx_pbmc3k <- runPCA(tenx_pbmc3k)
tenx_pbmc3k <- make_hexbin( tenx_pbmc3k, 20, dimension_reduction = "PCA")
plot_hexbin_gene(tenx_pbmc3k, type="logcounts",
    gene="ENSG00000135250", action="mean")
plot_hexbin_gene(tenx_pbmc3k, type="logcounts",
    gene="ENSG00000135250", action="mode")

## End(Not run)
```

---

plot_hexbin_interact	*Plot of interaction of expression of single cells in bivariate hexagon cells.*

Description

Plot of interaction of expression of single cells in bivariate hexagon cells.

Usage

```
plot_hexbin_interact(
  sce,
  mod,
  type,
  feature,
  interact,
  title = NULL,
  xlab = NULL,
  ylab = NULL
)

## S4 method for signature 'SingleCellExperiment'
plot_hexbin_interact(
  sce,
  mod,
  type,
  feature,
  interact,
  title = NULL,
  xlab = NULL,
  ylab = NULL
)

## S4 method for signature 'Seurat'
plot_hexbin_interact(
  sce,
  mod,
  type,
  feature,
  interact,
```

```
    title = NULL,
    xlab = NULL,
    ylab = NULL
)
```

Arguments

sce	A [SingleCellExperiment](#) or [Seurat-class](#) object.
mod	A vector of strings referring to the names of the modularities. For [SingleCellExperiment](#) use "RNA" to access the RNA expression data stored as the main experiment type.
type	A vector of strings referring to the types of assays in the [SingleCellExperiment](#) or the types of transformation in [Seurat-class](#) object.
feature	A vector of strings referring to the names of one features in the same order as the vector of modularities.
interact	A string specifying how interaction between features is calculated. Possible interaction measures are corr_spearman and mi (see details).
title	A string containing the title of the plot.
xlab	A string containing the title of the x axis.
ylab	A string containing the title of the y axis.

Details

This function plots the interaction between any features in the hexagon cell representation calculated with [make_hexbin](#). The interaction between the chosen features is calculated by one of two measurers corr_spearman, and mi:

mi Returns the mutual information coefficient.

corr_spearman Returns the Spearman correlation.

Value

A [ggplot2](#){ggplot} object.

Methods (by class)

- SingleCellExperiment: Plot of gene expression into hexagon cell for SingleCellExperiment object.
- Seurat: Plot of gene expression into hexagon cell for Seurat object.

Examples

```
# For Seurat object
library(Seurat)
data("pbmc_small")
pbmc_small <- make_hexbin(pbmc_small, 10, dimension_reduction = "PCA")
protein <- matrix(rnorm(10* ncol(pbmc_small)), ncol=ncol(pbmc_small))
rownames(protein) <- paste0("A", seq(1,10,1))
colnames(protein) <- colnames(pbmc_small)
pbmc_small[["ADT"]] <- CreateAssayObject(counts = protein)
plot_hexbin_interact(pbmc_small, type=c("counts", "counts"),
    mod=c("RNA", "ADT" ), feature=c("CD7", "A1"), interact="mi")
```

---

plot_hexbin_meta   *Plot of meta data of single cell data in bivariate hexagon cells.*

Description

Plot of meta data of single cell data in bivariate hexagon cells.

Usage

```
plot_hexbin_meta(
  sce,
  col,
  action,
  no = 1,
  colors = NULL,
  title = NULL,
  xlab = NULL,
  ylab = NULL
)

## S4 method for signature 'SingleCellExperiment'
plot_hexbin_meta(
  sce,
  col,
  action,
  no = 1,
  colors = NULL,
  title = NULL,
  xlab = NULL,
  ylab = NULL
)

## S4 method for signature 'Seurat'
plot_hexbin_meta(
  sce,
  col,
  action,
  no = 1,
  colors = NULL,
  title = NULL,
  xlab = NULL,
  ylab = NULL
)
```

Arguments

sce	A [SingleCellExperiment](#) or [Seurat-class](#) object.
col	A string referring to the name of one column in the meta data of sce by which to colour the hexagons.

action	A string specifying how meta data of observations in binned hexagon cells are to be summarized. Possible actions are `majority`, `prop`, `prop_0`, `mode`, `mean` and `median` (see details).
no	An integer specifying which level to plot of the column. Only in effect when `action=prop`.
colors	A vector of strings specifying which colors to use for plotting the different levels in the selected column of the meta data. Only in effect when the selected `action="majority"`.
title	A string containing the title of the plot.
xlab	A string containing the title of the x axis.
ylab	A string containing the title of the y axis.

Details

This function plots any column of the meta data in the hexagon cell representation calculated with [make_hexbin](#). The chosen meta data column is summarized by one of six actions `majority`, `prop`, `prop_0`, `mode`, `mean` and `median`:

majority Returns the value of the majority of observations in the bin. The associated meta data column needs to be a factor or character.

prop Returns the proportion of each level or unique character in the bin. The associated meta data column needs to be a factor or character.

prop_0 Returns the proportion of observations in the bin greater than 0. The associated meta data column needs to be numeric.

mode Returns the mode of the observations in the bin. The associated meta data column needs to be numeric.

mean Returns the mean of the observations in the bin. The associated meta data column needs to be numeric.

median Returns the median of the observations in the bin. The associated meta data column needs to be numeric.

Value

A [ggplot2](#){ggplot} object.

Methods (by class)

- `SingleCellExperiment`: Plot of meta data into hexagon cell for SingleCellExperiment object.
- `Seurat`: Plot of meta data into hexagon cell for Seurat object.

Examples

```
#' # For Seurat object
library(Seurat)
data("pbmc_small")
pbmc_small <- make_hexbin(pbmc_small, 10, dimension_reduction = "PCA")
plot_hexbin_meta(pbmc_small, col="RNA_snn_res.1", action="prop", no=1)
plot_hexbin_meta(pbmc_small, col="RNA_snn_res.1", action="prop", no=2)
# For SingleCellExperiment object
## Not run:
```

```
library(TENxPBMCData)
library(scater)
tenx_pbmc3k <- TENxPBMCData(dataset = "pbmc3k")
rm_ind <- calculateAverage(tenx_pbmc3k)<0.1
tenx_pbmc3k <- tenx_pbmc3k[-rm_ind,]
colData(tenx_pbmc3k) <- cbind(colData(tenx_pbmc3k),
    perCellQCMetrics(tenx_pbmc3k))
tenx_pbmc3k <- normalize(tenx_pbmc3k)
tenx_pbmc3k <- runPCA(tenx_pbmc3k)
tenx_pbmc3k <- make_hexbin( tenx_pbmc3k, 20, dimension_reduction = "PCA")
plot_hexbin_meta(tenx_pbmc3k, col="total", action="median")

## End(Not run)
```

---

schex   *schex: A package for plotting hexbin plots for single cell omics data.*

Description

Builds hexbin plots for variables and dimension reduction stored single cell omics data such as SingleCellExperiment and SeuratObject. The ideas used in this package are based on the excellent work of Dan Carr, Nicholas Lewin-Koh, Martin Maechler and Thomas Lumley.

Details

Please see the help pages listed below:

- make_hexbin
- plot_hexbin_gene
- plot_hexbin_meta

Also see the vignettes for more usage examples.

Please report issues and suggest improvements at Github:

https://github.com/SaskiaFreytag/schex

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