Package ‘Nebulosa’

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Type Package

Title Single-Cell Data Visualisation Using Kernel Gene-Weighted Density Estimation

Version 1.12.0

Description This package provides an enhanced visualization of single-cell data based on gene-weighted density estimation. Nebulosa recovers the signal from dropped-out features and allows the inspection of the joint expression from multiple features (e.g. genes). Seurat and SingleCellExperiment objects can be used within Nebulosa.

URL https://github.com/powellgenomicslab/Nebulosa

BugReports https://github.com/powellgenomicslab/Nebulosa/issues

License GPL-3

Encoding UTF-8

LazyData true

Depends R (>= 4.0), ggplot2, patchwork

Imports Seurat, SingleCellExperiment, SummarizedExperiment, ks, Matrix, stats, methods

RoxygenNote 7.1.1

VignetteBuilder knitr

Suggests testthat, BiocStyle, knitr, rmarkdown, covr, scater, scran, DropletUtils, igraph, BiocFileCache, SeuratObject

biocViews Software, GeneExpression, SingleCell, Visualization, DimensionReduction

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calculate_density

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**calculate_density**  
*Estimate weighted kernel density*

**Description**

Estimate weighted kernel density

**Usage**

calculate_density(w, x, method, adjust = 1, map = TRUE)

**Arguments**

- `w`  Vector with weights for each observation
- `x`  Matrix with dimensions where to calculate the density from. Only the first two dimensions will be used
- `method`  Kernel density estimation method:
  - `ks`: Computes density using the kde function from the ks package.
  - `wkde`: Computes density using a modified version of the kde2d function from the MASS package to allow weights. Bandwidth selection from the ks package is used instead.
- `adjust`  Numeric value to adjust to bandwidth. Default: 1. Not available for ks method
- `map`  Whether to map densities to individual observations

**Value**

If map is TRUE, a vector with corresponding densities for each observation is returned. Otherwise, a list with the density estimates from the selected method is returned.

**Author(s)**

Jose Alquicira-Hernandez
Examples

dens <- Nebulosa:::calculate_density(iris[, 3], iris[, 1:2], method = "wkde")

plot_density(object, features, slot = NULL, joint = FALSE, reduction = NULL, dims = c(1, 2), method = c("ks", "wkde"), adjust = 1, size = 1, shape = 16, combine = TRUE, pal = "viridis", ...)

`plot_density` function to plot gene-weighted 2D kernel density.

Description

Plot gene-weighted 2D kernel density.

Usage

```r
plot_density(object, features, slot = NULL, joint = FALSE, reduction = NULL, dims = c(1, 2), method = c("ks", "wkde"), adjust = 1, size = 1, shape = 16, combine = TRUE, pal = "viridis", ...)  
```

## S4 method for signature 'Seurat'

```r
plot_density(object, features, slot = NULL, joint = FALSE, reduction = NULL, dims = c(1, 2), method = c("ks", "wkde"), adjust = 1, size = 1, shape = 16, combine = TRUE, pal = "viridis", ...)  
```

## S4 method for signature 'SingleCellExperiment'

```r
plot_density(object, features, slot = NULL, joint = FALSE, reduction = NULL, dims = c(1, 2), method = c("ks", "wkde"), adjust = 1, size = 1, shape = 16, combine = TRUE, pal = "viridis", ...)  
```
plot_density(
  object, 
  features, 
  slot = NULL, 
  joint = FALSE, 
  reduction = NULL, 
  dims = c(1, 2), 
  method = c("ks", "wkde"), 
  adjust = 1, 
  size = 1, 
  shape = 16, 
  combine = TRUE, 
  pal = "viridis", 
  ...
)

Arguments

- **object**: Seurat or SingleCellExperiment object
- **features**: Features (e.g. genes) to visualize
- **slot**: Type of data: `counts` or `data` for Seurat objects and `counts`, `logcounts`, or `normcounts` for SingleCellExperiment objects
- **joint**: Return joint density plot? By default `FALSE`
- **reduction**: Name of the reduction to visualize. If not provided, last computed reduction is visualized
- **dims**: Vector of length 2 specifying the dimensions to be plotted. By default, the first two dimensions are considered.
- **method**: Kernel density estimation method:
  - `ks`: Computes density using the `kde` function from the `ks` package.
  - `wkde`: Computes density using a modified version of the `kde2d` function from the `MASS` package to allow weights. Bandwidth selection from the `ks` package is used instead.
- **adjust**: Numeric value to adjust to bandwidth. Default: 1. Not available for `ks` method
- **size**: Size of the geom to be plotted (e.g. point size)
- **shape**: Shape of the geom to be plotted
- **combine**: Create a single plot? If `FALSE`, a list with ggplot objects is returned
- **pal**: String specifying the viridis color palette to use.
- **...**: Further scale arguments passed to `scale_color_viridis_c` Options:
  - `viridis`
  - `magma`
  - `cividis`
  - `inferno`
  - `plasma`
**Value**

A scatterplot from a given reduction showing the gene-weighted density

**Methods (by class)**

- **Seurat**: Plot gene-weighted 2D kernel density
- **SingleCellExperiment**: Plot gene-weighted 2D kernel density

**Author(s)**

Jose Alquicira-Hernandez

**Examples**

```r
data <- SeuratObject::pbmc_small
plot_density(data, "CD3E")
```

---

**Description**

Plot density estimates

**Usage**

```r
plot_density_(
  z,
  feature,
  cell_embeddings,
  dim_names,
  shape,
  size,
  legend_title,
  pal = c("viridis", "magma", "cividis", "inferno", "plasma"),
  ...
)
```

**Arguments**

- `z` Vector with density values for each cell
- `feature` Name of the feature being plotted
- `cell_embeddings` Matrix with cell embeddings
- `dim_names` Names of the dimensions from the cell embeddings
- `shape` Geom shape
size          Geom size
legend_title  String used as legend title
pal           String specifying the viridis color palette to use
               Further scale arguments passed to scale_color_viridis_c

Value
A ggplot object

Author(s)
Jose Alquicira-Hernandez

wkde2d Weighted 2D kernel density estimation

Description
Weighted 2D kernel density estimation

Usage
wkde2d(x, y, w, h, adjust = 1, n = 100, lims = c(range(x), range(y)))

Arguments
x            Dimension 1
y            Dimension 2
w            Weight variable
h            vector of bandwidths for x and y directions. Defaults to normal reference bandwidth (ks::hpi). A scalar value will be taken to apply to both directions.
adjust       Bandwidth adjustment
n            Number of grid points in each direction. Can be scalar or a length-2 integer vector.
lims         The limits of the rectangle covered by the grid as c(xl, xu, yl, yu).

Value
A list of three components.

- x, y The x and y coordinates of the grid points, vectors of length n.
Author(s)
Jose Alquicira-Hernandez

Examples

```r
set.seed(1)
x <- rnorm(100)

set.seed(2)
y <- rnorm(100)

set.seed(3)
w <- sample(c(0, 1), 100, replace = TRUE)

dens <- Nebulosa:::wkde2d(x, y, w)
```
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