Package ‘Nebulosa’

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Type Package

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

Version 1.17.0

Description This package provides a 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

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Encoding UTF-8

Depends R (>= 4.0), ggplot2, patchwork

Imports SingleCellExperiment, SummarizedExperiment, SeuratObject, ks, Matrix, stats, methods, ggrastr

RoxygenNote 7.2.3

VignetteBuilder knitr

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

biocViews Software, GeneExpression, SingleCell, Visualization, DimensionReduction

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Contents

`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` *Plot gene-weighted 2D kernel density*

Description

Plot gene-weighted 2D kernel density

Usage

```
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",
  raster = TRUE,
  ...
)

## S4 method for signature 'Seurat'
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",
  raster = TRUE,
  ...
)

## S4 method for signature 'SingleCellExperiment'
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",
  raster = TRUE,
  ...
)
```

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.
`raster`	Rasterise plot
`...`	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)

- `plot_density(Seurat)`: Plot gene-weighted 2D kernel density
- `plot_density(SingleCellExperiment)`: Plot gene-weighted 2D kernel density

Author(s)

Jose Alquicira-Hernandez

Examples

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

`plot_density_` *Plot density estimates*

Description

Plot density estimates

Usage

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

Arguments

`z`	Vector with density values for each cells
`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
`raster`	Rasterise plot
`...`	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.
- `z` An n[1] by n[2] matrix of the weighted estimated density: rows correspond to the value of x, columns to the value of y.

Author(s)

Jose Alquicira-Hernandez

Examples

```
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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