Package ‘Nebulosa’
April 2, 2024

Type Package
Title Single-Cell Data Visualisation Using Kernel Gene-Weighted Density Estimation
Version 1.12.1
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
License GPL-3
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
git_url https://git.bioconductor.org/packages/Nebulosa
git_branch RELEASE_3_18
git_last_commit a0f8110
git_last_commit_date 2024-03-01
Repository Bioconductor 3.18
Date/Publication 2024-04-01

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**Description**

Estimate weighted kernel density

**Usage**

```r
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**

```r
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**

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

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

## 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", raster = TRUE, 

Arguments
---

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>Seurat or SingleCellExperiment object</td>
</tr>
<tr>
<td>features</td>
<td>Features (e.g. genes) to visualize</td>
</tr>
<tr>
<td>slot</td>
<td>Type of data: counts or data for Seurat objects and counts, logcounts, or normcounts for SingleCellExperiment objects</td>
</tr>
<tr>
<td>joint</td>
<td>Return joint density plot? By default FALSE</td>
</tr>
<tr>
<td>reduction</td>
<td>Name of the reduction to visualize. If not provided, last computed reduction is visualized</td>
</tr>
<tr>
<td>dims</td>
<td>Vector of length 2 specifying the dimensions to be plotted. By default, the first two dimensions are considered.</td>
</tr>
<tr>
<td>method</td>
<td>Kernel density estimation method:</td>
</tr>
<tr>
<td></td>
<td>• ks: Computes density using the kde function from the ks package.</td>
</tr>
<tr>
<td></td>
<td>• 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.</td>
</tr>
<tr>
<td>adjust</td>
<td>Numeric value to adjust to bandwidth. Default: 1. Not available for ks method</td>
</tr>
<tr>
<td>size</td>
<td>Size of the geom to be plotted (e.g. point size)</td>
</tr>
<tr>
<td>shape</td>
<td>Shape of the geom to be plotted</td>
</tr>
<tr>
<td>combine</td>
<td>Create a single plot? If FALSE, a list with ggplot objects is returned</td>
</tr>
<tr>
<td>pal</td>
<td>String specifying the viridis color palette to use.</td>
</tr>
<tr>
<td>raster</td>
<td>Rasterise plot</td>
</tr>
<tr>
<td>...</td>
<td>Further scale arguments passed to scale_color_viridis_c Options:</td>
</tr>
<tr>
<td></td>
<td>• viridis</td>
</tr>
<tr>
<td></td>
<td>• magma</td>
</tr>
<tr>
<td></td>
<td>• cividis</td>
</tr>
<tr>
<td></td>
<td>• inferno</td>
</tr>
<tr>
<td></td>
<td>• plasma</td>
</tr>
</tbody>
</table>
**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**

```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"),  
  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
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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