

# Package ‘Nebulosa’

October 17, 2024

**Type** Package

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

**Version** 1.14.0

**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

**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, scan,  
DropletUtils, igraph, BiocFileCache, Seurat

**biocViews** Software, GeneExpression, SingleCell, Visualization,  
DimensionReduction

**git\_url** <https://git.bioconductor.org/packages/Nebulosa>

**git\_branch** RELEASE\_3\_19

**git\_last\_commit** 9d3aebf

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-10-16

**Author** Jose Alquicira-Hernandez [aut, cre]  
(<https://orcid.org/0000-0002-9049-7780>)

**Maintainer** Jose Alquicira-Hernandez <[alquicirajose@gmail.com](mailto:alquicirajose@gmail.com)>

## Contents

|                             |   |
|-----------------------------|---|
| calculate_density . . . . . | 2 |
| plot_density . . . . .      | 3 |
| plot_density_ . . . . .     | 5 |
| wkde2d . . . . .            | 6 |

|              |          |
|--------------|----------|
| <b>Index</b> | <b>8</b> |
|--------------|----------|

---

|                   |   |
|-------------------|---|
| calculate_density | <i>Estimate weighted kernel density</i> |
|-------------------|---|

---

### 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: <ul style="list-style-type: none"> <li>ks: Computes density using the kde function from the ks package.</li> <li>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.</li> </ul> |
| 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 | <i>Plot gene-weighted 2D kernel density</i> |
|--------------|---|

---

**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: <ul style="list-style-type: none"> <li>ks: Computes density using the kde function from the ks package.</li> <li>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.</li> </ul> |
| 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: <ul style="list-style-type: none"> <li>viridis</li> <li>magma</li> <li>cividis</li> <li>inferno</li> <li>plasma</li> </ul>  |

**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_ | <i>Plot density estimates</i> |
|---------------|-------------------------------|

---

**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**

|                              |  |
|------------------------------|--|
| <code>z</code>               | Vector with density values for each cells        |
| <code>feature</code>         | Name of the feature being plotted                |
| <code>cell_embeddings</code> | Matrix with cell embeddings                      |
| <code>dim_names</code>       | 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)
```

# Index

`calculate_density`, [2](#)

`plot_density`, [3](#)

`plot_density`, Seurat-method

(`plot_density`), [3](#)

`plot_density`, SingleCellExperiment-method

(`plot_density`), [3](#)

`plot_density_`, [5](#)

`wkde2d`, [6](#)