

# Package ‘Nebulosa’

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**Type** Package

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

**Version** 1.15.0

**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

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

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### 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")
```

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|              |                                             |
|--------------|---------------------------------------------|
| 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                     |
| <code>shape</code>           | Geom shape                                                           |
| <code>size</code>            | Geom size                                                            |
| <code>legend_title</code>    | String used as legend title                                          |
| <code>pal</code>             | String specifying the viridis color palette to use                   |
| <code>raster</code>          | Rasterise plot                                                       |
| <code>...</code>             | Further scale arguments passed to <code>scale_color_viridis_c</code> |

**Value**

A ggplot object

**Author(s)**

Jose Alquicira-Hernandez

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`wkde2d`*Weighted 2D kernel density estimation*

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**Description**

Weighted 2D kernel density estimation

**Usage**

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

**Arguments**

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

**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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