

# Package ‘Nebulosa’

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**Type** Package

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

**Version** 1.19.0

**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>
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## 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")
```

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plot_density_	<i>Plot density estimates</i>
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**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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