

# Package ‘Nebulosa’

October 15, 2023

**Type** Package

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

**Version** 1.10.0

**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

**LazyData** true

**Depends** R (>= 4.0), ggplot2, patchwork

**Imports** Seurat, SingleCellExperiment, SummarizedExperiment, ks,  
Matrix, stats, methods

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

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

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

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

**git\_branch** RELEASE\_3\_17

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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",  
  ...  
)
```

```
## 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",  
  ...  
)
```

```
## 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",
...
)

```

### Arguments

<code>object</code>	Seurat or SingleCellExperiment object
<code>features</code>	Features (e.g. genes) to visualize
<code>slot</code>	Type of data: counts or data for Seurat objects and counts, logcounts, or normcounts for SingleCellExperiment objects
<code>joint</code>	Return joint density plot? By default FALSE
<code>reduction</code>	Name of the reduction to visualize. If not provided, last computed reduction is visualized
<code>dims</code>	Vector of length 2 specifying the dimensions to be plotted. By default, the first two dimensions are considered.
<code>method</code>	Kernel density estimation method: <ul style="list-style-type: none"> <li>• <code>ks</code>: Computes density using the <code>kde</code> function from the <code>ks</code> package.</li> <li>• <code>wkde</code>: Computes density using a modified version of the <code>kde2d</code> function from the <code>MASS</code> package to allow weights. Bandwidth selection from the <code>ks</code> package is used instead.</li> </ul>
<code>adjust</code>	Numeric value to adjust to bandwidth. Default: 1. Not available for <code>ks</code> method
<code>size</code>	Size of the geom to be plotted (e.g. point size)
<code>shape</code>	Shape of the geom to be plotted
<code>combine</code>	Create a single plot? If FALSE, a list with ggplot objects is returned
<code>pal</code>	String specifying the viridis color palette to use.
<code>...</code>	Further scale arguments passed to <code>scale_color_viridis_c</code> Options: <ul style="list-style-type: none"> <li>• <code>viridis</code></li> <li>• <code>magma</code></li> <li>• <code>cividis</code></li> <li>• <code>inferno</code></li> <li>• <code>plasma</code></li> </ul>

### Value

A scatterplot from a given reduction showing the gene-weighted density

**Methods (by class)**

- Seurat: Plot gene-weighted 2D kernel 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"),
  ...
)
```

**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
...	Further scale arguments passed to scale_color_viridis_c

**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**

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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