calculate_density

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

Maintainer Jose Alquicira-Hernandez <alquicirajose@gmail.com>

R topics documented:

- calculate_density
- plot_density
- plot_density_<
- wkde2d

Index

calculate_density

---

### 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

dens <- Nebulosa::calculate_density(iris[, 3], iris[, 1:2], method = "wkde")

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

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:
  • 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
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.
  ... Further scale arguments passed to scale_color_viridis_c Options:
    • viridis
    • magma
    • cividis
    • inferno
    • plasma
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
```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"),
  ...
)
```

Arguments
- `z`: Vector with density values for each cell
- `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
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.
**wkde2d**

**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)
```
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